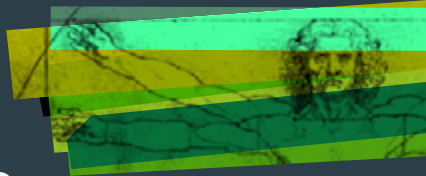


LE STUDIUM

# CONFERENCES

ORLÉANS | 2023



25-29 September 2023

# Conservation, Ecology and Systematics of Lepidoptera in a changing world

## The 23rd European Congress of Lepidopterology & 11th Forum Herbulot



### LOCATION

Hôtel Dupanloup  
1, rue Dupanloup  
45000 Tours - FR

### CONVENORS

**Dr Carlos Lopez-  
Vaamonde**

Forest Zoology Research Unit (URZF) /  
Centre INRAE Val de Loire - FR

& Insect Biology Research Institute (IRBI),  
University of Tours / CNRS - FR

.....

This conference is organised in the framework of the regional thematic research network "Entomocentre"

Picture by Antoine Guiguet

# LE STUDIUM CONFERENCES

ORLÉANS | 2023

## ABSTRACTS

## Conservation, Ecology and Systematics of Lepidoptera in a changing world

The 23rd European Congress of  
Lepidopterology & 11th Forum  
Herbulot

### CONVENOR

**Dr Carlos Lopez Vaamonde,**

Forest Zoology Research Unit (URZF) / Centre INRAe Val de Loire - FR  
& Insect Biology Research Institute (IRBI), University of Tours / CNRS - FR

### ORGANIZING COMMITTEE

**Sophie Gabillet, General Secretary**

**Dr Aurélien Montagu, Scientific Manager**

**Maurine Villiers, Communication and Events Manager**

LE STUDIUM Loire Valley Institute for Advanced Studies • Région Centre-Val de Loire • FR

# EDITO

Created in 1996 on the CNRS campus in Orleans La Source, LE STUDIUM has evolved to become the multidisciplinary Loire Valley Institute for Advanced Studies (IAS), operating in the Centre-Val de Loire region of France. LE STUDIUM has its headquarters in the city centre of Orleans in a newly renovated 17th century building. The amazing facilities are shared with the University of Orleans. In 2014 new developments and programmes linked to the smart specialisation of the Centre-Val de Loire region came to strengthen existing IAS collaborative relationships with the local and the international community of researchers, developers and innovators.

LE STUDIUM IAS offers to internationally competitive senior research scientists the opportunity to discover and work in one of the IAS's affiliate laboratories from the University of Tours, the University of Orleans, National Institute of Applied Sciences (INSA) Centre Val de Loire and ESAD Orléans, as well as of nationally accredited research institutions located in the region Centre-Val de Loire (BRGM, CEA, CNRS, INSERM, INRAE). Our goal is to develop and nurture trans-disciplinary approaches as innovative tools for addressing some of the key scientific, socio-economic and cultural questions of the 21st century. We also encourage researchers' interactions with industry via the IAS's links with Poles of Competitiveness, Clusters, Technopoles, and Chambers of Commerce etc.

LE STUDIUM has attracted more than two hundred and seventy experienced researchers coming from 48 countries for long-term residencies. In addition to their contribution in their host laboratories, researchers participate in the scientific life of the IAS through attendance at monthly interdisciplinary meetings called LE STUDIUM THURSDAYS. Their presentations and debates enrich the regional scientific community at large (researchers of public and private laboratories, PhD students, research stakeholders' representatives, etc...)

For the period 2015-2021, LE STUDIUM has operated with an award from the European Commission, a programme supporting the mobility of international researchers, the Marie Skłodowska-Curie Actions (MSCA) COFUND

programme. For the period 2022-2025, LE STUDIUM has joined the FIAS Programme (French Institute for Advanced Study) along side six other institutes in France, also supported by the MSCA Actions. Since 2013, LE STUDIUM is also an official partner of the Ambition Research and Development programmes initiated by the Centre-Val de Loire Regional Council to support the smart specialisation strategy (S3) around priority domains: biopharmaceuticals, renewable energies, cosmetics, environmental metrology, digital twins, materials, forestry and natural and cultural heritage. Furthermore our current collaboration with the ATHENA European University Consortium allows us to welcome fellows from ten European partners universities. New programmes are currently designed to include all major societal challenges.

Researchers are invited and supported by the IAS to organise, during their residency and in collaboration with their host laboratory, a two-day LE STUDIUM CONFERENCE. It provides them with the opportunity to invite internationally renowned researchers to a cross-disciplinary conference, on a topical issue, to examine progress, discuss future studies and strategies to stimulate advances and practical applications in the chosen field. The invited participants are expected to attend for the duration of the conference and contribute to the intellectual exchange. Past experience has shown that these conditions facilitate the development or extension of existing collaborations and enable the creation of productive new research networks.

The present LE STUDIUM CONFERENCE named «*Conservation, Ecology and Systematics of Lepidoptera in a changing world*» is the 135th in a series started at the end of 2010 listed at the end of this booklet.

We thank you for your participation and wish you an interesting and intellectually stimulating conference. Also, we hope that scientific exchanges and interactions taking place during this conference will bring opportunities to start a productive professional relationship with presenting research laboratories and LE STUDIUM Loire Valley Institute for Advanced Studies.

**Yves-Michel GINOT**

Chairman  
LE STUDIUM

# INTRODUCTION

Insect declines are a major cause of public concern. One of the most affected, and sensitive groups for monitoring is Lepidoptera (moths and butterflies), which play a major role in the functioning of our ecosystems. They are one of the most important groups of herbivores and pollinators, as well as comprising a vast prey biomass and hosting an extensive specialized web of parasitic Hymenoptera. Being mostly readily visible and intricately patterned, they include the most iconic, charismatic and popular of all invertebrates. Many are model organisms for evolutionary and genetic studies, a few are significant economic pests, and some are vital sources of protein or silk. Understanding their ecology, genetics and systematics is crucial for efficient conservation management to understand and even reverse their decline.

The conference will bring together world experts to discuss the conservation, ecology and systematics of Lepidoptera. It will be a joint event organized by the Society for European Lepidopterology (SEL) (<http://www.soceurlep.eu/>) and the International Forum Herbulot (FH) (<http://www.herbulot.de/>), which organizes a regular conference for the study of looper moths (Geometridae). It is the first time that SEL & FH have organized their biennial conferences together (<http://www.soceurlep.eu/congresses/>).

SEL is a society with 514 members founded in 1976, which promotes the study and conservation of Lepidoptera and publishes the journal *Nota Lepidopterologica* (<https://nl.pensoft.net/>). FH is an international research initiative focused on the second largest family, Geometridae or looper moths, a society with approx. 150 members from 42 countries.

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EntomoCentre



EntomoCentre

EntomoCentre is a network of 28 members, including universities, research laboratories, private companies, naturalist associations and amateur entomological societies working on insects at the Centre-Val de Loire Region in France.

Funded in 2019, EntomoCentre's main aim is to support entomological research, training, innovation and decision-making activities in Region Centre. Our main actions are:

- To promote the interactions between academic and non-academic members to support the setting up of national and international research projects. To organize international conferences on insects (such as SEL & Forum Herbulot conference).
- To create new training courses on Entomology such as a new Master course Erasmus Mundus at the universities of Tours & Orléans.
- To provide support to the development and establishment of companies working on industrial production of insects (ie. insects as food and feed).
- To foster exchanges between scientists, stakeholders and policy-makers.



**Directors:** Carlos Lopez-Vaamonde & David Giron

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## Forum Herbulot



Forum Herbulot was founded in the year 2000 and it currently includes over 160 members (Herbulotians) from 42 countries. This network promotes and coordinates diverse research lines on geometroid moths globally.

Forum Herbulot is an informal community, it has free membership and it avoids formal association structures. Strategic activities are steered by a scientific board, but Forum Herbulot invites bottom-up ideas from its members, particularly such that benefit from collaborations. Among key activities are biennial meetings, coordination and fostering of the research activities, and information exchange (including newsletters). Recent milestones include publication of “an online taxonomic facility of Geometridae” and several collaborative projects, which have made Geometroidea one of the most-used model groups of Lepidoptera.

The initiative is named after French lepidopterist Claude Herbulot (1908–2006), who assembled the world’s largest collection of geometrid moths. His collection is deposited at the Bavarian State Collection of Zoology in Munich, Germany.

You will find more information about our community, contact details to join, as well as the updated Catalogue of the geometrid moths of the world, in our website: <https://geometroidea.smns-bw.org/>

All presentations on Geometridae in the SEL congress have been put together and will be presented in Forum Herbulot session on Wednesday afternoon. Looking forward to see you in this session.

**Website:** <https://geometroidea.smns-bw.org/>

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## Societas Europaea Lepidopterologica



Societas Europaea Lepidopterologica

The SEL was founded as Societas Europaea Lepidopterologica in 1976 and has always been a society for both the professional Lepidopterists and the advanced amateurs. Currently there are slightly more than 400 members, representing not only most European countries, but also other parts of the world.

The biennial congresses are the glue of the society: Since 1978 23 Congresses were organised in 19 countries throughout Europe. Here the latest scientific news is presented, and members meet and discuss their common interest and start new joint projects. There is often time for informal fieldwork during or after the congress, sometimes leading to interesting discoveries. We also have had two field congresses: one in Italy (Sesvenna) and another in Northern Macedonia (Shar Planina). Since 2012, three annual meetings of the Lepidopterist’s Society in North America were organised in collaboration with SEL.

The society publishes the journal *Nota Lepidopterologica*, now in its 46th volume. Since 2014 the journal is published open access in collaboration with Pensoft publishers (<https://nl.pensoft.net/>). Old volumes of *Nota* are now also online as Open access through the Biodiversity Heritage Library and ZOBODAT. Members can receive a printed volume at a reduced price and can freely publish up to 25 pages per year. SEL also publishes a newsletter online, now with the name SELepidoptera News.

Currently SEL is going through a modernisation stage and the General Meeting during this congress. will decide on the change of its name into “Society for European Lepidopterology”.

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Head of Research Unit INRAE Forest Ecosystems. My research aims at identifying forest practices and landscape features beneficial to biodiversity including butterflies. I also contributed to atlas and inventories of moth at the county and regional scale.



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Laurence Després is Professor at University Grenoble Alpes (France), where she teaches evolutionary ecology and phylogenetics. Her main research interests are in the evolutionary processes leading to population diversification and speciation. Most projects combine population genetics and phylogenomic analyses together with ecological, biochemical and behavioral studies to test hypotheses about evolutionary processes or adaptation to multiple constraints mainly in the Alps.



**Marianne Elias**

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Marianne Elias is an evolutionary biologist and a team leader with a strong interest in the ecology and evolution of butterflies. Her team has contributed major advances in systematics, community ecology and history of diversification of the neotropical butterfly tribe Ithomiini, comprising nearly 400 species and engaging in Müllerian mimetic interactions with other Lepidoptera. Marianne also has interest in understanding how butterfly populations and community respond to variable environments across elevation gradients in temperate and tropical regions.



**David Lees**

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David Lees is a Senior Curator at the Natural History Museum in London, where he curates the traditional 'Microlepidoptera' and is an Editor-in-Chief of *Nota Lepidopterologica*. His research interests are molecular and morphological systematics, taxonomy and biogeography of butterflies and moths worldwide, with a long-term interest in the fauna of Madagascar.



### Carlos Lopez-Vaamonde

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Carlos Lopez-Vaamonde is a research scientist at the Forest Zoology Unit of INRAE Orléans and research associate at the Institute of Research on Insect Biology (IRBI) at Tours. He currently studies the responses of moths to environmental disturbances, biosurveillance of invasive species and systematics of Gracillariidae leaf-mining micromoths. He was general secretary of the Society for European Lepidopterology from 2015 till 2019 and is currently ordinary member of the council. He served as chief editor of *Nota Lepidopterologica* in 2015 and is now subject editor.



### Rodolphe Rougerie

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Rodolphe Rougerie is a researcher and curator for Lepidoptera at the Muséum national d'Histoire Naturelle (MNHN) in Paris. His research focuses on the evolutionary dynamics and macroecological patterns of species diversity in wild silkmoths (Saturniidae) and hawkmoths (Sphingidae), building on the use of phylogenomics and large-scale databases of species diversity, distribution and traits. He is also involved in the development of DNA-based species identification (DNA barcoding) and its applications (e. g. metabarcoding for biosurveillance) in Lepidoptera and other organisms.



### Jadranka Rota

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Jadranka Rota received her PhD in Entomology from the University of Connecticut, USA. She has worked as curator at Biological Museum, Lund University, Lund, Sweden since 2018. Her research interest is broadly in evolutionary history of Lepidoptera, including taxonomy, molecular phylogenetics and phylogenomics, as well as historical biogeography. Jadranka taxonomically specializes in the family Choreutidae, but has published on a number of different groups of Lepidoptera, including micros and macros. She is currently in the council of the Society for European Lepidopterology and she serves as a subject editor for *Nota Lepidopterologica*.



### Nils Ryrholm

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Nils Ryrholm received his PhD in Entomology at Uppsala University, Sweden. His thesis was about the influence of local- and microclimate on the distribution of Lepidopteran species. He is presently working as professor at the University of Gävle in Sweden. He has continued to study climatic impact on insects, in recent years mainly changes due to global warming. He is also working with the development of sexual pheromones as a tool in insect conservation. Nils is also strongly involved in several conservation projects like enhancing biodiversity in infra-structural habitats, the red-listing of butterflies and moths – on both national and European level.



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Pasi Sihvonen is Director of zoology unit at the Finnish Museum of Natural History, University of Helsinki. His research focuses on systematics and biodiversity of geometrid moths globally, a megadiverse insect radiation of 24 000 species. Sihvonen has worked in several director, manager and expert positions at the University of Helsinki, Academy of Finland and the European Commission in research funding, research infrastructures, service development and research administration. Sihvonen promotes Diversity, Equity and Inclusion <https://orcid.org/0000-0003-2237-9325>

## KEYNOTE SPEAKER



### Marc Holderied

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**ECOLOGY**

As sensory ecologist and bio-acoustician with strong links to bio-inspired engineering professor Holderied's international research excellence is in the emerging fields of acoustic camouflage and biosonar navigation, with a continued passion for acoustic arms races and wildlife acoustics. He develops lepidoptera-inspired noise control solutions and as international consultant for the automotive industry helps establish Ultrasonic Vision technology. He studied Biology at the University of Erlangen, Germany (1997 Diploma, 2001 PhD) and since 2005 leads the BASElab at the University of Bristol, UK.

### Wingtip decoys and Stealth cloaks - Acoustic Defences of Moths against detection by echolocating Bats

Invisibility cloaks are fantastic devices in popular culture from Harry Potter to Star Trek. But even in the real world so-called metamaterials (synthetic composite materials with emergent new properties) can act as (partial) cloaks both against light (vision) and sound (acoustics). We recently discovered that the 65MY old arms race with their echolocating bat predators has equipped silkmoths (Saturniidae) with remarkable acoustic metamaterials on their wings and bodies. These ultrathin sound absorbers offer protection because the strength of the echo bouncing off the moth's body determines the distance over which bats can detect it. In the talk we will use innovative acoustic tomographies to visualise how fur on bodies and scales on wings of moths provide acoustic cloaking. Turning the moth wing into bio-inspired thinner and better sound absorbers ('sonic wallpaper') can help us in the struggle to maintain healthy living and working environments in our ever noisier world.

**Keywords:** Echolocation, Lepidopteran wings, scales, metamaterial sound absorber

# KEYNOTE SPEAKER



**Joana Meier**

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## SYSTEMATICS

Joana Meier is an evolutionary biologist working on speciation in cichlid fishes, butterflies and peacock spiders. During her PhD and postdoc with Ole Seehausen at the University of Bern, Joana worked on the rapid adaptive radiation of Lake Victoria cichlid fishes. She found an important role of admixture facilitating their rapid diversification. In 2018 to 2022, Joana held a Bateson Research Fellowship at the University of Cambridge and later also a Branco Weiss Fellowship. Here, she started to work on South American butterflies. In collaboration with Chris Jiggins, she worked on parallel hybrid zones in *Heliconius* butterflies. Since July 2022, she leads a research group at the Wellcome Sanger Institute in the Tree of Life Programme. In addition, she was awarded a Royal Society University Research Fellowship in October 2022. Her team works on speciation in *ithomiini* and *Heliconius* butterflies. Combining comparative methods and population genomics approaches, she studies how speciation rates are affected by structural variants, admixture and the genetic architecture of traits involved in speciation.

### The role of hybridisation and chromosomal rearrangements in rapid speciation

Speciation rates vary massively across the tree of life. Some lineages diversify rapidly into many species, whereas their close relatives speciate at a much slower pace in the same environment. The factors influencing such lineage-specific speciation rates are poorly understood. Hybridisation and chromosomal rearrangements are two of the factors that may contribute. Both of these factors can both increase or reduce the likelihood of speciation. Hybridisation can homogenise genomic regions under divergent selection or even lead to the merging of species. However, it can also enrich the genetic variation fuelling adaptation and speciation. Large-scale chromosomal rearrangements can facilitate speciation by reducing hybrid fitness or decreasing recombination in the vicinity of the rearrangement and thus locking co-adapted genes together. However, chromosomal rearrangements can also facilitate the evolution of polymorphisms, e.g. via supergenes, allowing a species to utilise multiple niches without speciating.

Together with a network of collaborators in the Americas and Europe, my team compares rapidly and slowly speciating lineages of *ithomiini* and *Heliconius* butterflies. These South- and Central American butterflies are well-known for their Müllerian mimicry rings and high species richness. The large variation in speciation rates across different lineages, particularly within the *ithomiini* tribe, make them an ideal system to study factors affecting speciation rates. *Ithomiini* and one lineage of *Heliconius* butterflies also show high rates of chromosomal evolution with karyotypes ranging from five to 120 chromosomes (Brown et al. 2004). We reconstruct chromosome-level reference genomes and combine micro- and macro-evolutionary approaches to elucidate the roles of hybridisation and large-scale chromosomal rearrangements in speciation and species persistence.

**Keywords:** Speciation, chromosomal rearrangements, hybridisation, *ithomiini*, *Heliconius*

# SPEAKERS

## SYSTEMATICS



**Issei Ohshima**

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Issei Ohshima is an associate professor at the Kyoto Prefectural University (KPU) and a vice-director of Center for Frontier Natural History at KPU. My research interests span evolution, ecology and systematics of Lepidoptera, and my lab especially focuses on the process and mechanism of speciation and the genetic background of host-plant adaptation using the leaf-mining moth family Gracillariidae. We are also interested in the evolution of gall-inducing leaf miners and the biological interactions between leaf miners and their parasitoids.

**Co-authors:** Koyo Tanaka<sup>1</sup>, Kei Katsube<sup>1</sup>

**Affiliation:** <sup>1</sup>Kyoto Prefectural University - JP

### More than 5% COI divergence without morphological differentiation: Four host-associated cryptic populations in *Psydrocercops wisteriae* (Gracillariidae)

In insect taxonomy, differences of morphology especially in mating organs have been used traditionally as a criterion for species delimitation. In recent years, DNA barcoding, which uses specific gene sequences to identify species, has become more common. However, speciation is a continuous process, beginning from the same species to different species via accumulation of various divergence, thus the species delimitation depends on which species criteria are used. Nevertheless, we know very little about the relative evolutionary trends of frequently used species criteria, such as the monophyly of the DNA barcoding region, that of genome-wide markers, ecological and behavioral traits, and morphology used in the classical taxonomy. Here, we assessed the degree of differentiation of species criteria among host-associated populations in *Psydrocercops wisteriae* (Gracillariidae), which uses either Fabaceae, Malvaceae or Cannabaceae/Ulmaceae. Both phylogenetic and population genetic analyses using COI and RAD-seq dataset indicated that each host-associated population has already diverged into the level of different species. Larval transplantation experiments also showed clear differences in host adaptation between Fabaceae-associated and Cannabaceae/Ulmaceae-associated populations. In contrast, mating experiments revealed that the pre-mating isolation between the two host-associated populations was still incomplete. Moreover, the four host-associated populations show no morphological differences even in male and female genitalia in terms of classic taxonomical observation, and morphological divergences were detected only when morphometric measurements were incorporated. These results suggest that qualitative morphological differences that is used in the traditional insect taxonomy tend to be established at a (very) later-stage of speciation even those are slight morphological divergences.

**Keywords:** genitalia, host adaptation, mating compatibility, RAD-seq, speciation



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### SYSTEMATICS

Originally from Tennessee, USA, I received a B.S. in Biology from Davidson College (North Carolina, USA) in 2018 and a M.Sc. in Entomology from Cornell University (New York, USA) in 2020 where my thesis focused on the systematics of Caribbean Tortricidae. I am now a 4th year Ph.D. student in Entomology at the University of Hawai'i at Mānoa in the lab of Dr. Dan Rubinoff where I am studying the ecology, conservation, and systematics of Hawaiian Lepidoptera, with a focus on Tortricidae.

**Co-author:** Dan Rubinoff<sup>1</sup>

**Affiliation:** <sup>1</sup>University of Hawai'i at Mānoa - USA

### Tortricidae: the most successful family of terrestrial animal life in Hawai'i?

Hawai'i is world-renowned for the astounding number and diversity of unusual life history strategies that have evolved on its islands, whether it be waterfall-climbing fish, terrestrial damselflies, or carnivorous caterpillars. Part of the reason such bizarre behaviors have arisen in Hawaii is because of the islands' isolation from continental land masses and the difficulty of initial colonization. Countless globally diverse and otherwise ubiquitous families of insects never made it to Hawai'i. Why is it then that tortricids have been able to colonize the Hawaiian Islands not just once, but more than a dozen independent times? What makes them especially well-suited for long-distance dispersal and establishment? By using ecological, morphological, and molecular data, I seek to demonstrate that in terms of the number of independent colonization events, the Tortricidae are the most successful family of animal life in Hawai'i and explain why that may be the case.

**Keywords:** Island biogeography, colonization, microlepidoptera, host plant specialization, phylogenetics



### Alena Sucháčková

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### SYSTEMATICS

I am a postdoc at the Laboratory of Temperate Biodiversity, Institute of Entomology, Biology Centre CAS, Czech Republic. My research focus is the biogeography of butterflies in the context of Cenozoic climatic oscillations, the impact of extinct megafauna on the Quaternary ecosystems and the practical implications of this history for butterfly (and habitat) conservation.

**Co-authors:** Zdeněk Faltýnek Fric<sup>1</sup>, Kristián Grell<sup>1,2</sup>, Julia Canitz<sup>3</sup>, Martin Wiemers<sup>3</sup>, Thomas Schmitt<sup>3,4</sup>

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### Biogeography of Palearctic woodland butterflies through their entire ranges

The temperate deciduous woodlands represent a legacy of Tertiary forests once covering the entire globe. This habitat became largely restricted to the eastern and western Eurasia during the Pleistocene. Species of woodland butterflies of the genera *Apatura*, *Neptis* and *Limenitis*, well known to public for their outstanding beauty, differ in their range sizes and locations. Some have small ranges, restricted to either East Asia or Europe. Other species achieved continuous distribution across the entire Palearctic. Very intriguing are the species that have disjunctive ranges comprising of populations on both sides of the continent, but not in its central parts. In this first analysis, we started with two species – *Neptis rivularis* with wide continuous range across the Eurasian continent, and *Limenitis camilla* with disjunctive distribution. We sampled the populations across their ranges and used double digest restriction-site associated DNA (ddRAD) sequencing together with species distribution models, to uncover the species' phylogeographic patterns. The main questions are: How were the different ranges shaped – what was the species' ancestral area and biogeographic scenario? What was the range dynamics of these species during Pleistocene? Does the range dynamics differ between East Asia and Europe, and across the different range types? When was the last time the disjunctive populations were connected?

**Keywords:** ddRAD; disjunctive range; distribution models; phylogeography



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Professor of Zoology at the University of Valencia. Most of my research devoted to Lepidoptera, especially Tortricidae. I have also worked on dragonflies and cockroaches. Also interested in environmental problems concerning insect conservation as the case of the Apollo butterfly and the effect of Light Pollution on insect populations. I like interdisciplinary approaches from molecular to the population and ecosystem level, including morphology. Specially interested in the reproductive biology of the Lepidoptera through the functional morphology of genital characters and scent organs.

**Co-authors:** Saul Bernat-Ponce<sup>1</sup>, José Vicente Pérez Santa-Rita<sup>1</sup>, Carlos Cordero<sup>2</sup>, Joaquín Baixeras<sup>1</sup>

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#### Form and function of deciduous cornuti: the case of the cornuti caltrop in *Peridea anceps* (Goeze, 1781) (Lepidoptera: Notodontidae)

The endophallus or vesica of many Lepidoptera is known to bear some taxon dependent sclerotized, frequently spine like, structures known as cornuti. In some cases, the cornuti may become deciduous, detached from the membrane of the vesica. Deciduous cornuti are not recovered by the male and are frequently detected in the female bursa copulatrix even after digestion of the spermatophore. Among the various forms that the deciduous cornuti can take, the cornuti caltrop (CC) are the most intriguing. CC have been reported from Sphingidae, Nolidae and Geometridae, but are common in Notodontidae. In this work, we have explored the characteristics of these structures in *Peridea anceps* (Goeze, 1781) in a comparative basis. We have examined the structure and mechanism of attachment of the CC as well as the general variation in spine shape, number, and distribution. Once the vesica is everted the male is unable to recover the CC, that are shed as a whole and only once. On the other hand, the female cannot remove the CC from inside the bursa copulatrix. A mechanism for vesica eversion and expulsion of the CC is proposed. Some possible functional -non necessarily alternative- hypotheses for the CC in *Peridea anceps* and other notodontids are discussed, including female genital tract blocking, female bursa copulatrix piercing and male spermatophore breaking. All of them suggest a sexual selection scenario, leading to the reduction of the sperm competition.

**Keywords:** Cornuti caltrop, Notodontidae, sexual selection, functional morphology, lepidoptera genitalia



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I was born on 17 May 1982 in Sofia, Bulgaria. My research is focused primarily on taxonomy of Tortricidae. I work also on functional morphology of genitalia of Lepidoptera. To date I am assistant professor at the Institute of Biodiversity and Ecosystem Research in Sofia, Bulgaria.

**Co-authors:** Vladislav Vergilov<sup>1</sup>, José Vicente Pérez Santa-Rita<sup>2</sup>, Joaquín Baixeras<sup>2</sup>

**Affiliations:** <sup>1</sup>National Museum of Natural History at the Bulgarian Academy of Sciences, Sofia - BG, <sup>2</sup>Cavanilles Institute of Biodiversity and Evolutionary Biology, University of Valencia - ES

#### First 3D reconstruction of copulation in Lepidoptera: interaction of genitalia in *Tortrix viridana* (Tortricidae)

The mechanism of copulation of *Tortrix viridana* L. was studied via serial morphology. Three-dimensional models based on micro-CT scanned copulating pairs were generated allowing visualisation of the position of the male and female counterparts, spatial changes during copulation, and the skeleto-muscular apparatus involved in the process. The male genitalia and their musculature are simplified in comparison with other lineages of the family, but the opposite is true for the female genitalia. The attachment of the couple is achieved only through flexion of the valvae, clasping the large and sclerotised sternite 7 of the female. The anal cone and socii of the male are in contact with certain parts of the anal papillae and the sterigma of the female. The long tubular vesica is inserted into the narrow posterior part of the ductus bursae. Its eversion is achieved by an increase in haemolymph pressure. A possible mechanism of stimulation of the female via pulsations of the diverticulum of the vesica was discovered. A compressed sclerotised area of the ductus bursae putatively serves as a valve controlling the transfer of ejaculated materials. Copulation progresses through two phases: in the first the vesica and its diverticulum are inflated by haemolymph, and in the second the diverticulum is not inflated, and the vesica is occupied by viscous ejaculated material. The formation of the spermatophore was observed, and we discovered that sperm is transferred very late in the copulation process.

**Keywords:** genitalia, functional morphology, micro-CT, CLSM, SEM



## Mikael Englund

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Mikael is a PhD researcher in Finnish Museum of Natural History of University of Helsinki and a seasoned lepidopterologist focusing on geometrid moth systematics and ecology.

**Co-authors:** Mikael Englund<sup>1</sup>, Pritha Dey<sup>2</sup>, Simeão Souza Moraes<sup>3</sup>, Max Söderholm<sup>1</sup> and Pasi Sihvonen<sup>1</sup>

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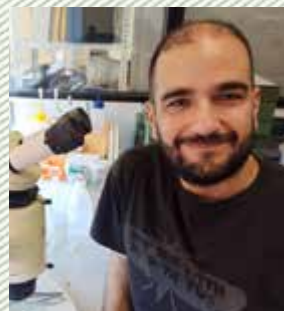
### You can now both have your specimen and dissect it – micro-CT scanning revisited as a non-destructive imaging method for precious dried and pinned insects

Imaging techniques are powerful tools in integrative insect taxonomy, providing unambiguous images of diagnostic structures, often being more informative than written descriptions. In scale-covered Lepidoptera, the morphology of numerous structures and internal organs cannot be exposed for photographic imaging using traditional dissection methods without strongly manipulating or destroying the target specimen. Micro-CT x-ray scanning combined with modern post-image processing and rendering protocols provide a non-destructive means to produce high-quality images from relevant inner structures portrayed at any desired point of view. This technique has been rather sparsely used in Lepidoptera (e.g. Robinson et al., 2018; Simonsen & Kitching, 2014) to yield images especially from dried and pinned museum specimens.

We present several unpublished 2D images of lepidopteran wing venation, tympanal organs and genitalia based on micro-CT scans on dried and pinned museum specimens. We demonstrate how we use these images in our forthcoming papers to describe new lepidopteran taxa, and present protocols including artificial intelligence used to yield the images. Images of the same structures produced through traditional dissection and slide mounting protocols are presented for comparison. We also demonstrate how rotating 3D footage can be used to reveal details only visible from certain view angles.

The possibility to scrutinise inner structures of unique museum artifacts, such as type specimens, without breaking them might open new avenues for research design while preserving the rare specimens for future research using techniques yet to be discovered. New material acquisition costs could be avoided to counterbalance the still relatively costly and laborious process of producing micro-CT images of arthropod organs. We consider micro-CT imaging of dried and pinned museum specimens to be an important complimentary or even sole means of producing diagnostic images of internal organs to be used in integrative insect taxonomy.

**Keywords:** Non-destructive imaging, micro-CT, artificial intelligence, integrative taxonomy, Geometridae



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I have a degree in Biology from the University of Valencia (Spain) in 2013 with an Award in the Master's Degree in Biodiversity: Conservation and Evolution from the same University. During my undergraduate studies I began to collaborate in the Entomology Laboratory of the Cavanilles Institute of Biodiversity and Evolutionary Biology. Currently, I am a PhD student at the same institute, under the supervision of Joaquín Baixeras. My project deals with the Tortricidae family and the evolution of the male scent organs in a phylogenetic context. I am familiar with molecular and morphological techniques, including electron and confocal microscopy.

**Co-authors:** John W. Brown<sup>1</sup>, Joaquín Baixeras<sup>2</sup>

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### Towards a better understanding of male scent organs in Tortricidae: morphological and evolutionary perspectives of the hindwing anal roll in Olethreutini (Lepidoptera: Tortricidae: Olethreutinae)

The female-pheromone system is a plesiomorphic trait among Lepidoptera, with evidence of similar glandular systems in the sister group Trichoptera. Nevertheless, the male-pheromone system is evolutionarily more labile and prone to homoplasy. A detailed examination of the scent organs in male wings reveals sophisticated structures that are widespread throughout Lepidoptera phylogeny. However, the access to their structure has not received adequate attention by taxonomists due to the technical difficulties. The family Tortricidae is rich in male scent organs. In previous research, we explored the costal roll in male hindwing of Cochylini tribe, including the ecological and evolutionary scenario. Other tribes of Tortricidae have developed similar structures but in alternative morphological position.

The presence of hindwing anal roll is a common feature in the tribe Olethreutini, previously identified in the literature, in which its morphology has been superficially examined and its phylogenetic utility has been questioned. The anal roll is a complex structure; the membrane of the anal margin is highly modified appearing variably convoluted. It includes a set of microscales inside the roll that project towards an area of folded integument. It seems to work in combination with hairpencils of the legs and/or thorax. In this research, both optical and scanning electron microscopy are used to investigate this structure in a set of representative specimens. Although a phylogeny of the Olethreutini is not available, a close examination of the genera bearing the organ allows us to conjecture about the phylogenetic and evolutionary scenario in which these structures have been developed.

**Keywords:** Secondary sexual characters, scent organs, pheromones, insect host plant relationships, phylogenetic traits

# KEYNOTE SPEAKER



**Marko Mutanen**

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SYSTEMATICS

Marko Mutanen has specialized on North European Lepidoptera and sawfly diversity. He is particularly interested in finding better solutions to understand the bewildering biological diversity surrounding us. He is a proponent of both DNA barcoding and DNA taxonomy and he believes that achieving global bio-literacy will require wide-scale adoption of genomics approaches. Mutanen leads the Finnish Barcode of Life (FinBOL) initiative. He also is leading several research projects that focus on finding solutions to taxonomic impediment. Furthermore, he directs the multidisciplinary Biodiverse Anthropocenes (2021-2026) programme. Mutanen has published ca 120 scientific articles.

## What do unexpected patterns in DNA barcodes indicate? Insights from genomics

Many nations are building a DNA barcode reference library for their biome. Lepidoptera researchers across the world have been particularly active on this front. Presently, DNA barcodes are available for over 100,000 species of Lepidoptera. In addition to species identification, DNA barcoding is helpful in revealing cryptic diversity and speeding up taxonomic workflows. Consequently, new species have been revealed even in well-investigated regions. Several cases from North Europe provide an example.

Ideally, the DNA barcode shows little variability within species and much more between them, but two main phenomena may compromise their efficacy. First, DNA barcodes may differ only little, or not at all, between species. Second, they may show extraordinary variability within species that may even exceed variation typically observed between species. It is not unusual to find two or more highly distinct clusters of barcodes in a single species.

Unexpected patterns in DNA barcodes may be due to either 'operational' or biological causes. A deviant barcode instantly raises questions e.g. over the correctness of identification, contamination or amplification of a pseudogene. Barcode sharing, in turn, can result from taxonomic over-splitting. Ruling out such operational causes often requires re-examinations and re-analyses of specimens. Mitonuclear discordance may also result from several biological causes. Two species may share the same barcode because their recent speciation. Although deep intraspecific split may reveal a cryptic species, it can also result from other biological processes, such as retained genetic polymorphism or introgression.

To understand the numerous observed cases of unexpected patterns observed in DNA barcodes of European Lepidoptera, our team has studied several cases using genomic approaches, including ddRAD sequencing and Target Capture, under various settings, including sympatry, parapatry and allopatry. These studies have revealed a variety of patterns and provided likely explanations for them, suggesting that mitochondrial genome is shaped by biological processes which understanding requires insights from the nuclear genome. Our studies have also revealed evident cases of cryptic diversity and taxonomic over-splitting.



**Matthew Greenwood**

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SYSTEMATICS

I am a PhD candidate at the Laboratoire d'Écologie Alpine (LECA), Université Grenoble Alpes supervised by Prof. Laurence Després and Dr. Thibaut Capblancq. As part of my thesis, I am aiming to resolve and contextualize the diversification of *Coenonympha* (Nymphalidae) butterflies. My current research combines aspects of wetland work, molecular systematics, and comparative phylogenetics. I am, nevertheless, more broadly interested in the genomic mechanisms that promote speciation and trait evolution across the mega-diverse Arthropoda.

**Co-authors:** Laurence Després<sup>1</sup>, Tibaut Capblancq<sup>1</sup>, Niklas Wahlberg<sup>2</sup>

**Affiliations:** <sup>1</sup>Alpine Ecology Laboratory (LECA), Grenoble Alpes University – FR, <sup>2</sup>Systematic Biology Group, Lund University – SE

## Resolving the radiation of *Coenonympha* butterflies in the phylogenomic era

Levels of aridity, cooling, geological activity, and land connectivity have changed drastically in the Palearctic region over the past 40 million years. The Satyrinae (Nymphalidae) butterfly group has undergone rapid bouts of diversification in this region over the same timeframe, leading to the emergence of several large, diverse lineages. One particularly intriguing lineage is the *Coenonympha* genus, which contains approximately 40 species distributed predominantly throughout Eurasia. Across this distribution, *Coenonympha* species are strictly adapted to montane grasslands, lowland meadows, or peatland habitats, all of which differ to a large extent with respect to temperature, wetness, and vegetation structure. The *Coenonympha* genus may, therefore, constitute a rich model for understanding butterfly diversification and adaptation processes.

This study aims to characterise *Coenonympha* evolution using a large phylogenomic dataset produced with genome-skimming methods from field-caught and museum specimens. Different inference methods recover robust, congruent phylogenetic hypotheses for the lineage. Nevertheless, gene concordance analyses, as well as comparisons between mitochondrial and nuclear trees, identify several nodes of high marker discordance along the *Coenonympha* backbone. Analysis of diversification rates and introgression tests suggest that this discordance is likely driven by past instances of burst radiation and hybridisation, respectively. These findings serve to clarify and contextualise uncertainty in prior phylogenetic hypotheses for *Coenonympha* and highlight the genus as an interesting model for understanding butterfly diversification in the Palearctic.

**Keywords:** Phylogeny, evolution, discordance, palearctic, diversity



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Jadranka Rota received her PhD in Entomology from the University of Connecticut, USA. She works as curator at Biological Museum, Lund University, Lund, Sweden. Her research interest is broadly in evolutionary history of Lepidoptera, including taxonomy, molecular phylogenetics and phylogenomics, as well as historical biogeography. Jadranka taxonomically specializes in the family Choreutidae, but has published on various groups of Lepidoptera, including micros and macros. She is currently in the council of the Society for European Lepidopterology and serves as a subject editor for *Nota Lepidopterologica*.

**Co-authors:** Niklas Wahlberg<sup>1</sup>, Robert Hoare<sup>2</sup>, Victoria Twort<sup>3</sup>, Maria Heikkilä<sup>3</sup>, Lauri Kaila<sup>3</sup>

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### Evolutionary history of Tineoidea

Tineoidea, with about 4 000 described species are a relatively small superfamily species wise, but because of their phylogenetic position are important for our understanding of the lepidopteran evolutionary history. They are the oldest superfamily belonging to Ditrysia – the most diverse lepidopteran clade including more than 150 000 described species, and as such are relevant for our understanding of the immense diversification that occurred within this large group that consists of 98% of all currently known Lepidoptera. However, the exact phylogenetic position of Tineoidea is unclear. The question is whether Tineoidea are a natural group and as a whole form the sister lineage to the rest of Ditrysia, as has been hypothesised based on the examination of their morphology as well as a combined analysis of morphological characters and several nuclear genes. Another possibility, strongly suggested by several but not all large molecular datasets, is that Tineoidea actually consist of several different lineages, only one of which is the sister to the rest of the Ditrysia. Establishing which group is the sister to Ditrysia has implications for our understanding of the evolution of larval diet in Ditrysia. Typical ditrysians are herbivores, unlike many Tineoidea, whose larvae tend to be detritivores and fungivores. We set to try to answer this question with a phylogenomic dataset consisting of 330 single-copy orthologous genes sequenced from 111 tineoid taxa, representing all five tineoid families: Dryadulidae, Eriocottidae, Meessiidae, Psychidae, and Tineidae.

**Keywords:** Ditrysia, phylogenomics



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Vineesh Nedumpally is a second year PhD student at the University of Tartu, Estonia. He is working on reconstructing the phylogenetic tree of North European moths, especially Geometridae and Noctuidae. He is the first author or a co-author in 16 papers in peer reviewed international journals in the field of molecular biology and taxonomy. Having worked previously on fishes, he has recently switched to Lepidoptera.

**Co-authors:** Erki Õunap<sup>1,2</sup>, Toomas Tammaru<sup>1</sup>, Etkä Yapar<sup>3</sup>, and Alan Lemmon<sup>4</sup>

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### Phylogenomics of North European Noctuidae based on anchored hybrid enrichment technology

Noctuids are one of the largest families of Lepidoptera, comprising more than 12,000 species. Numerous efforts have been made to recover the phylogeny of Noctuidae, but there are still many genera which have received very little to no attention in the molecular phylogenetic framework. In the present study, we aimed to construct a phylogenetic tree for Noctuidae occurring in Northern Europe, utilizing the anchored hybrid enrichment (AHE) technology. We used molecular data from nearly 800 nuclear protein-coding loci, totalling almost 250,000 bp, to build the phylogenetic tree comprising 271 species covering all genera represented in the region, and 37 outgroup taxa. Raw data obtained using AHE method were processed using different bioinformatic tools like FastQC (for checking raw reads quality), Cutadapt (removing adapter content from the raw reads), HybPiper (assembling the sequence), Diamond (aligning DNA sequences against a protein reference database), a python script for trimming and translation, MAFFT (aligning amino acids) etc. A phylogenetic tree has been constructed using IQ-TREE 2.1.2 in the CIPRES portal. Phylogeny recovered in our analysis is largely consistent with the current (but not traditional) classification of Noctuidae, but also points at the need for taxonomic rearrangements in some groups. In addition to just shedding light on the phylogenetic relationships within Noctuidae, the derived phylogeny will serve as a much-awaited tool for comparative evolutionary ecological studies using the species-rich family as the target group.

**Keywords:** Noctuidae, Northern Europe, Phylogenomics, Anchored hybrid enrichment



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Rodolphe Rougerie is a researcher and curator for Lepidoptera at the Muséum national d'Histoire Naturelle (MNHN) in Paris. His research focuses on the evolutionary dynamics and macroecological patterns of species diversity in wild silkmoths (Saturniidae) and hawkmoths (Sphingidae), building on the use of phylogenomics and large-scale databases of species diversity, distribution and traits. He is also involved in the development of DNA-based species identification (DNA barcoding) and its applications (e. g. metabarcoding for biosurveillance) in Lepidoptera and other organisms.

**Co-authors:** Astrid Cruaud<sup>2</sup>, Pierre Arnal<sup>1,2</sup>, Liliana Ballesteros-Mejia<sup>1,3</sup>, Fabien L. Condamine<sup>4</sup>, Thibaud Decaëns<sup>5</sup>, Marianne Elias<sup>1</sup>, Delphine Gey<sup>6,7</sup>, Paul D. N. Hebert<sup>8</sup>, Ian J. Kitching<sup>9</sup>, Sébastien Lavergne<sup>10</sup>, Carlos Lopez-Vaamonde<sup>11,12</sup>, Jérôme Murienne<sup>13</sup>, Yves Cuenot<sup>13</sup>, Sabine Nidelet<sup>2</sup>, Jean-Yves Rasplus<sup>2</sup>

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### The evolutionary history of capital-breeding moths through the lens of wild silkmoths (Saturniidae) phylogenomics

Wild silkmoths (Saturniidae) are large capital-breeding insects with non-feeding adults that have short lifespan entirely devoted to reproduction. They exhibit a dazzling diversity of sizes, forms, and life-histories inviting questions about the role that key traits may have played in spurring out species diversification and biogeographical movements in organisms with such extreme reproductive strategy. Yet, the absence of a robust phylogenetic framework based on comprehensive taxonomic sampling impedes our understanding of their evolutionary history.

We analyzed 1,024 ultraconserved elements (UCEs) and their flanking regions to infer the relationships among 338 species of Saturniidae representing all subfamilies, tribes, and genera. We performed dating and historical biogeographic analyses to reconstruct their evolutionary history in space and time.

Rather unexpectedly for a taxonomically well-known family such as Saturniidae, the alignment of taxonomic divisions and ranks with our phylogenetic results led us to propose substantial rearrangements of the family classification.

Saturniids most likely originated in the Neotropics, shortly after the Cretaceous-Paleogene extinction event (ca 64.0-52.0 Ma). Old World lineages stemmed from two independent colonization events during the Eocene, presumably through the Bering-Land-Bridge. Extant subfamilies showed limited mobility across biogeographical regions, except for Saturniinae, a subfamily now present on all continents but Antarctica.

These results provide a framework for the integration of saturniid evolutionary history into further global studies of biodiversity and conservation, as well as for in-depth investigations of the spatial and temporal dynamics in all lineages and of the role that key innovations played in driving species diversification of these capital-breeding moths.



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I am a PhD student currently working on phylogenomics of Lepidoptera in Lund University.

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### Phylogenomic Tree of Gelechioidea

Gelechioidea is a highly diverse superfamily of moths including more than 18,000 described species with diverse diets and life history traits among which, some are pests of agriculturally significant plants. Despite the group's significance, it is perhaps the least studied group within lepidoptera partly due to scarcity of genomic-scale molecular data in the age of phylogenomics. Utilizing published genomes and raw transcriptomic data, we analyze using maximum likelihood methods more than a thousand nuclear protein coding genes from 55 ingroup taxa, making up 15 of 16 currently accepted families. Here, for the first time, we present a well-supported molecular phylogeny of Gelechioidea which provides new insights into interfamilial relationships within the superfamily.

**Keywords:** Systematics, Phylogenomics, Gelechioidea



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#### The first molecular phylogeny of Chalcosiinae (Zygaenidae) and the its influences on the revised classification and inference of character evolution

Amongst the zygaenid subfamilies, the Chalcosiinae are a diverse group, and they probably exhibit the highest diversity in both morphology and ecology within the Zygaenoidea and within the non-obtectomeran apoditrysiian Lepidoptera. Owing to their often brilliant coloration, high level of sexual dimorphism, complicated mimetic patterns, little-known biology and rarity in museum collections, they have received the attention of many researchers and insect collectors. The group's taxonomy has remained confusing since its initial documentation in the 18th century. Although Yen et al. (2004) reconstructed a huge phylogeny by using 414 morphological characters obtained from 411 species representing 73 genera, some internal relationships of the subfamily remain unclear. In the present study, we used 4 markers, viz. COI (mtDNA 1470 b.p.) + 28S (nuDNA 749 b.p.) + ef1a (nuDNA 1202 b.p.) + RpS5 (nuDNA 600 b.p.) to reconstruct the first molecular phylogeny of this group and Himantopteridae, Anomeotidae, Limacodidae, Lacturidae and Phaudidae were selected as the outgroups. The phylogenetic analysis shows that the Chalcosiinae with the current contents is not monophyletic. The genus Chalcosiopsis should be placed in its own family, and Inouelinae, which was placed in Chalcosiinae, is found nested within Procridinae to in some analyses. All the tribes of Chalcosiinae are not monophyletic due to convergence and mimicry so that many new tribes are supposed to be erected to stabilize the classification. The new phylogeny also reveals that the evolutionary trends of complexity of androconial system, reduction of genitalia and specialization of the male 8th tergite and sternite.

**Keywords:** chemical defence, mimicry, aposematism, convergence, character evolutions



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Dr. Adamski has been an entomologist with the Systematic Entomology Laboratory, USDA, at the Smithsonian in Washington DC and Beltsville, Md for 28 years. Now retired he is a Research Associate with the Smithsonian Institution where he maintains and conducts a research program on the Blastobasidae, a taxon that he has been studying for over 40 years. His expertise involves studying night-flying moths, so you won't see him in the summer months unless you're in the middle for a forest around the "witching hour."

**Co-author:** Paul Frandsen<sup>1</sup>

**Affiliations:** <sup>1</sup>Genetics, Genomics of Biotechnology, Department of Plant and Wildlife Sciences, Brigham Young University, Provo - USA

#### Morphological Phylogenetics of World Blastobasidae (Lepidoptera: Gelechioidea): A Comparative Approach Using Exemplar and Super-Dense Taxon Sampling

Multistate morphological character matrices were generated with super-dense taxon sampling and analysed using cladistics for the world Blastobasidae (Lepidoptera: Gelechioidea). Although phylogenies generated from an exemplar data matrix using maximum parsimony resulted in resolved trees, limited monophyly was evident due to small sample sizes. Bayesian and maximum likelihood analyses also resulted in polytomies. Only with a super-saturated taxon sampling of taxa using maximum parsimony with bootstrapping, most clades were recovered. Moreover, this highly resolved tree simulation, based on dense taxon sampling, shows significant advantages in recovering monophyly at various categorical levels resulting in many nomenclatural changes at the species and generic levels, and ultimately, a more «natural» phylogenetic-classification compared to those previously published.

**Keywords:** Comparative Sampling, Morphology Phylogenetic Systematics



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**SYSTEMATICS**

My focus lies on the systematics and evolution of snouth moths (Lepidoptera: Pyraloidea). I have also strong interest in developing new ways to accelerate species description in untapped, species-rich groups. I am presently the scientific head of the Lepidoptera collection at the Museum für Naturkunde in Berlin. Beside my research duties, I am in charge of the curation and planning of the future digitization of our collections.

**Co-authors:** Margot Belot<sup>1</sup>, Leonardo Preuss<sup>1</sup>, Joël Tuberosa<sup>1</sup>, Magdalena Claessen<sup>1</sup>, Olha Svezhentseva<sup>1</sup>, Franziska Schuster<sup>1</sup>, Christian Bölling<sup>1</sup>

**Affiliations:** <sup>1</sup>Museum für Naturkunde, Leibniz Institute for Evolutionary and Biodiversity Research - DE

### A pipeline to extract and process digitized insect label information

Natural history collections are home to millions of insect specimens worldwide. To ensure their sustainability and facilitate knowledge transfer, large-scale digitization initiatives are being undertaken in several museums around the world. This process involves the acquisition of specimen photographs along with their associated labels. Insect labels contain essential data such as the collecting locality and date, specimen identification, associated vouchers and type status. While image datasets are piling up, a time-effective and automated way to extract label information from pictures and integrate it into a common database is currently missing. Here, we present scalable solutions to extract and classify information from insect label images using deep learning and unsupervised clustering. The resulting pipeline includes the following steps: 1) label detection and characterization with a region-based convolutional neural network; 2) text extraction via optical character recognition; 3) text clustering for redundancy detection and differential processing. The performance of these tools was assessed on samples of digitized collections from different museums. We discuss the potential of this approach to support the global efforts to make natural history collections more easily accessible, as well as further developments such as label class identification and metadata parsing.

**Keywords:** collections; Deep Learning; digitization; museum; pipeline



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**SYSTEMATICS**

My research mainly focuses on lepidoptera taxonomy especially agricultural pests, and invasive insect pest detection and management. My group published more than 55 publications in reputed journals. We have described more than 14 new species and two new genera, many new records to India, new host records, and 5 checklists. My expertise in DNA barcoding of insect generated more than 700 DNA-Barcodes which aid in authentic identification of domestic and invasive insect pests.

**Co-authors:** Pathour R. Shashank<sup>1,2</sup>, Brandon M. Parker<sup>2,8,9</sup>, Santosh R. Rananaware<sup>3</sup>, David Plotkin<sup>2</sup>, Christian Couch<sup>2</sup>, Lilia G. Yang<sup>3</sup>, Long T. Nguyen<sup>3</sup>, N. R. Prasannakumar<sup>5</sup>, W. Evan Braswell<sup>4</sup>, Piyush K. Jain<sup>3,6,7</sup>, Akito Y. Kawahara<sup>2</sup>

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### CRISPR-based diagnostics successfully detects invasive insect pests

Invasive insect pests are a significant threat to agriculture, forestry, and natural ecosystem processes. Rapid detection of insect pests is necessary for quick management response, but this can be challenging especially for species that are difficult to identify. CRISPR-based diagnostics offers a novel and rapid alternative to other identification methods and can revolutionize our ability to detect pests with high accuracy. Here we describe a CRISPR-based diagnostic, which we test on three difficult-to-identify invasive moth pest species (*Phthorimaea absoluta*, *Keiferia lycopersicella*, and *Scrobipalpa atriplicella*) that are major agricultural pests globally. We designed and optimized a recombinase polymerase amplification (RPA) assay (a fast isothermal alternative to PCR) followed by a CRISPR assay through fluorescent and lateral flow strip readout in a two-pot assay system. Using the mitochondrial cytochrome oxidase I (mtCOI) gene as a target, we achieved 100% accuracy for identification of all the three species, with a detection limit of up to 120 fM for *P. absoluta* and 400 fM for *K. lycopersicella* and *S. atriplicella*. We optimized this approach into an even more efficient, one-pot assay, which reduces the risk of cross-contamination, and can be accomplished at one temperature (37 °C) and completed in 60 min (excluding extraction). The sensitivity of our approach is much higher than recently developed, published RT-PCR assays. This work serves as proof of concept which can be expanded to any organism and has the potential to revolutionize insect detection and monitoring.

**Keywords:** CRISPR; Cas12a; RPA; Diagnostics; Invasive pests



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**SYSTEMATICS**

At NHMUK I am a Senior Curator responsible for the traditional 'Microlepidoptera'. I am involved in both molecular and morphological works on butterflies and moths worldwide, with a long-term interest in their taxonomy, evolution, biogeography and faunistics, especially in Madagascar. I am an Editor-in-Chief of *Nota Lepidopterologica*.

**Co-authors:** Joël MINET<sup>1</sup>, Carlos Lopez-Vaamonde<sup>2,3</sup>

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### Diversity and endemism of the Lepidoptera of Madagascar

At the most recent census of described lepidopteran taxa in 2021, 1,418 genera and 5,016 species were recognised for the island of Madagascar. However, the species endemism rate, although clearly exceptional for such a large landmass (ca. 600,000 km<sup>2</sup>), has remained poorly known. That figure is now estimated to exceed 80% in this highly isolated island. Some 28 superfamilies and 83 families of moths and butterflies are known to occur there. Whereas the five superfamilies within Macroheterocera, comprising around 681 genera and at least 2,989 species, are relatively well known, extrapolations of the total fauna suggest well in excess of 10,000 species are present. On BOLD 2,903 COI-5P species clusters (BINs) are publicly available, 2,400 of which are unnamed to species. Malaise trapping is rapidly adding to the number of unidentified BINs; a recent Malaise sample from Andasibe in two seasons containing 1,527 BINs found that less than 20% were Macroheterocera whilst >98% of 510 non-macroheteroceran BINs were novel to BOLD.

# KEYNOTE SPEAKER



**Andrea Battisti**

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**EVOLUTION**

Professor of entomology at the University of Padova, Department DAFNAE. His research activity addresses topics of forest entomology and insect ecology, with special emphasis on the effect of climate change on the insect populations. He's also developing innovative techniques for the study and the control of insect pests. He coordinates a research group involved in several national and international research projects. Processionary moths are the most studied group of insects and several aspects of the ecology and evolution of the group were addressed in more than 40 years of studies in Europe, Africa, Asia and Australia.

### Ecology and evolution of processionary moths

Processionary moths belong to a group of insect herbivores well known since the ancient Greek and Roman times for their association with the host plants, their particular behaviour, and their urticating and envenomation ability. A few species of processionary moths are plant pests in Africa, Asia, Australia and Europe. All species are protected against vertebrate predators by urticating setae either as larvae or adults and these setae may threaten animal and human health. Three major clades can be identified: i. Australian, with 29 species; ii. African, with 39 species; and iii. Eurasian-African, with 26 species. A molecular phylogeny of the European species supports the hypothesis that they should be treated as members of a single genus, *Thaumetopoea*. The ancestor originated in the eastern Mediterranean area and used broadleaved host plants. Subsequently, a switch to conifers occurred, just once, in a large subclade. The ancestor pupated in the soil, like several current species, but in a few taxa this trait was lost, together with the related morphological adaptations. The pine processionary moth, *Thaumetopoea pityocampa* (Denis and Schiffermüller), is an iconic insect in the Mediterranean culture because of its economic and medical importance and the unique traits of the life history, namely the winter feeding and the construction of conspicuous silk tents by the larvae. Its taxonomic status, however, is unclear because the type material is not available and several species and subspecies have been described in the last centuries. molecular information is reliable to separate species in most cases whereas morphology is not. In addition, hybridization among taxa makes it difficult to delimit species in contact zones when mating barriers are not present.

**Keywords:** Notodontidae, *Thaumetopoea*, sociality, urtication, delimitation



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**EVOLUTION**

I am a PhD scholar at the department of Ecology and Genetics at the University of Oulu, Finland. I have a Biotechnology degree from the University of Karachi, Pakistan, and extensive experience in laboratory techniques such as DNA extraction, purification, PCR, and other molecular biology techniques. During my Masters in Ecology and Population Genetics at the University of Oulu, I developed Bioinformatic and Ecological method skills and became proficient in using R studio, Python, Unix/Linux, and Puhti supercomputers. My master's thesis focused on Species Delimitation of a moth species pair using genomic methods and mitochondrial DNA sequencing, demonstrating the benefits of DNA-based approaches in biodiversity research. I also worked as a research assistant with the Insect Genomic Systematics Group at the University of Oulu, where I learned about the importance of DNA barcoding in species recognition and discovery. I am passionate about research and dedicated to contributing to efforts to mitigate biodiversity loss.

**Co-authors:** <sup>1</sup>Mukta Joshi, <sup>2</sup>Marianne Espeland, <sup>3</sup>Peter Huemer, <sup>4,5</sup>Carlos Lopez Vaamonde, <sup>1</sup>Marko Mutanen

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### Patterns of Speciation in a parapatric pair of *Saturnia* moths as revealed by Target Capture

The focus of this study was to understand the evolutionary relationships and taxonomy of widely distributed parapatric pair of *Saturnia pavonia* and *Saturnia pavoniella* (Lepidoptera: Saturniidae) in Europe. To address species delimitation challenges associated with many parapatric taxa, target enrichment and mtDNA sequencing was employed alongside analyses of admixture, gene flow, hybridization, and introgression. The dataset included individuals from both species as well as two hybrids from and broadly outside the contact zone. Nuclear markers strongly supported both *S. pavonia* and *S. pavoniella* as two distinct species, with the hybrids grouping together as intermediate and separate from both species. However, the maximum likelihood (ML) tree generated from mtDNA sequencing data presented a different picture, showing both taxa to be phylogenetically intermixed. This inconsistency may be attributed to mitonuclear discordance, which can arise from biological factors (e.g., introgressive hybridization or incomplete lineage sorting) or operational factors (e.g., misidentification or incorrect species delimitation). We further discuss our results from evolutionary point of view taking into consideration the past climatic oscillations that has likely shaped the present dynamics between the species. Overall, this study demonstrated the effectiveness of the target enrichment approach in resolving the phylogenetic relationships and providing insights into the taxonomic and phylogenetic relationships between these species.

**Keywords:** Target capture, parapatry, speciation, genomics, taxonomic delimitation



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**EVOLUTION**

I am working at the University of Grenoble, as a postdoc, on a project that explores adaptation and speciation at the genomic level in alpine butterflies. In general, I am particularly interested in using genomic data to investigate the history of populations divergence and adaptation.

**Co-authors:** Thibaut Capblancq<sup>1</sup>, Fabrice Legeai<sup>2</sup>, Frédéric Boyer<sup>1</sup>, Mathieu Joron<sup>3</sup>, Laurence Després<sup>1</sup>

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### The genomics of speciation with secondary contact: a case study in *Coenonympha* butterflies

In this study we took advantage of a newly produced *Coenonympha* reference genome and whole genome re-sequencing data to explore the genomic landscape of speciation between the two butterfly species *C. arcania* and *C. gardetta*. Knowing that these two species diverged relatively recently, still hybridized occasionally in the wild and occupied two very different ecological niches, we wanted to understand if their isolation relied on a genome-wide resistance to gene flow or was dependent on a few highly divergent genomic regions that particularly drove reproductive isolation. We started our investigations by re-inferring the demographic history of speciation between the two sister species and formally tested if gene flow accompanied their divergence. We inferred multiple population genetics statistics to look for genomic regions of high differentiation, low diversity and/or high linkage among loci. In parallel, we screened the genomes of the species in search for genomic regions of reduced gene flow using coalescent inferences and model comparison. Interestingly, the two lineages show high overall differentiation with many regions of high genomic divergence and low diversity. The process-based models were able to identify several autosomal regions acting as barrier to reproduction between the two species and suggest an important role of the Z chromosome in their divergence. With these results, our study provides new insights on the genomics processes associated with speciation with gene flow and sheds light on the diversification of these butterfly species.

**Keywords:** Islands of differentiation - Speciation genomics - Whole genome sequencing - Z chromosome



## Antoine Guiguet

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EVOLUTION

I am an entomologist specializing in plant-insect interactions. I completed my PhD at the University of Tours and the Prefectural University of Kyoto (2015-2019), directed by David Giron, Carlos Lopez-Vaamonde, and Issei Ohshima. My research focused on investigating the evolution and molecular mechanisms underlying gall induction in Gracillariidae. I pursued a postdoctoral position at Penn State (2020-2022). I explored the role of female venom in gall induction in Cynipidae gall wasps. Currently, I am based in the Netherlands, continuing my research in this field.

**Co-authors:** Antoine Guiguet<sup>1, 2</sup>, Seisuke Kimura<sup>3, 4</sup>, Tomoaki Sakamoto<sup>5</sup>, Carlos Lopez-Vaamonde<sup>1, 4</sup>, David Giron<sup>1</sup>, Issei Ohshima<sup>2</sup>

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### Intra- and inter-specific comparative transcriptomic approaches to reveal candidate effectors of gall induction in the micromoth *Caloptilia cecidophora* (Gracillariidae, Lepidoptera)

While gall-inducing insects exert a high level of control over their host development and physiology, the molecular mechanisms underlying these manipulation processes are still poorly understood. One way to address this question is to focus on effectors produced by insects and susceptible to undermine the plant immune system and modulate the cellular processes. To find candidate effectors involved in gall induction, we compared the gene expression in the larvae of the micromoth *Caloptilia cecidophora* (Lepidoptera, Gracillariidae) that induces galls on *Glochidion obovatum* (Phyllanthaceae) to the larval transcriptome *C. ryukyuensis*, a closely related non-gall-inducing species both sympatric and growing of host plant of the same genus. Three independent methods were used to analyze the transcriptomic data. First, we isolated genes showing a peak of expression at the initiation of the gall induction (third instar), and 505 genes were significantly upregulated in third instar compared to the second and the fourth instars. Among them 22 were specific in *C. cecidophora* transcripts and successfully annotated. Secondly, we selected genes with expression patterns matching gall-induction using a principal component analysis and a self-organizing map. Ortholog comparisons revealed 36 genes showing an opposite expression pattern between the two species. Finally, we looked for candidate genes based on literature and compared their expression patterns between the two species and among instars. All together, we obtained a list of 58 genes coding for possible effectors. Preliminary results point toward the production of anti-oxidant enzymes and chitinases and suggest the implication of secreted auxin in gall formation.



## Jean-Michel Drezen

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EVOLUTION

Jean-Michel Drezen is senior researcher at the Research Institute on Insect Biology in Tours. His research focuses on the study of endogenous viruses of parasitoid wasps and their impact on lepidopteran genomes via horizontal gene transfer events. Following such events immune genes of wasp origin are currently used by some species of Lepidoptera. He is involved in comparative genomics and published in 2021 the first genome of a parasitoid wasp obtained at chromosomal scale, which was analysed by the "Cotesia consortium" involving 51 collaborators.

**Co-authors:** Marion Scheidegger<sup>1</sup>, Karine Musset<sup>1</sup>, Camille Heisserer<sup>1</sup>, Thibaut Josse<sup>1</sup>, Carlos Lopez-Vaamonde<sup>1,2</sup>, Elisabeth Huguet<sup>1</sup>, Jean-Michel Drezen<sup>1</sup>

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### Recent and potentially ongoing invasion of lepidopteran genomes by a helitron

A large part of eukaryotic genomes is composed of inactivated mobile elements (TEs for Transposable Elements), corresponding to remnants of ancient waves of TE invasions. TEs also play a very important role in adaptation to new ecological conditions. The most famous example is the industrial melanism of the peppered moth: the black color has been shown to result from the insertion of a transposon within a gene. Considerable progress in sequencing approaches now makes it possible to assemble TE-rich regions within genomes. We found that a TE of the helitron type secreted in the genital fluid of a parasitoid wasp is present as identical copies in the genome of 5 Lepidopteran species sequenced by the Darwinian tree of life project from specimens collected in UK, suggesting a recent wave of introduction of this TE in Lepidoptera. We hypothesize that increase of parasitoid introductions worldwide could, as for viral infections, increase the rate of TE invasions, and play a role in populations decline. We recently amplified the helitron from specimens collected in France indicating that the spread of this TE is not limited to UK. We will map the extent of the invasion in the geographical range of the species *Pararge aegeria* and *Polyommatus icarus*, in particular in areas where these species have been recently introduced such as Madeira island (*P. aegeria*) and Québec (*P. icarus*) since founders of the current populations could have been introduced before helitron spread, thus allowing an approximate dating of the epidemic.

**Keywords:** transposable elements, helitron, parasitoid wasp, lepidopteran genomes, global changes



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## EVOLUTION

I am an evolutionary ecologist with a deep interest in understanding patterns, processes and drivers of phenotypic evolution. I mainly used butterflies as models and employ a range of methods including ecological experiments, field work, morphometrics and phylogenetic comparative analyses to unravel patterns at both micro and macroevolutionary scales.

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### Strong phylogenetic inertia drives the evolution of eye size in temperate butterflies

Quantifying the mode, tempo and drivers of trait evolution is a central tenet in evolutionary biology. Sensory organs offer a unique opportunity to address these key questions as these traits, especially eyes, can play a crucial role in shaping animal lifestyles.

Mounting evidence suggests that diel activity is a major driver of eye design in animals, but other factors are seldom explored. Furthermore, diurnal versus nocturnal animals experience dramatically different light conditions and can mask differences in eye design within diurnal lineages, for example, those occupying different habitats. To address this gap, for the first time, we quantify mode and tempo and drivers of eye size evolution in butterflies in a macroevolutionary framework.

We generated 3D micro-CT scans of 460 individuals across 59 species of European butterflies for measuring eye surface area. Firstly, after accounting for phylogeny, there was strong allometric scaling between eye surface area and body size (forewing length) and males generally had larger eyes than females. Phylogenetic comparative analyses further suggested that size-corrected eye surface area had a strong phylogenetic signal and followed a Brownian motion process. Furthermore, homogenous rate Brownian motion models had a better fit than variable-rate models and predictors (habitat, male mating strategy, sexual dichromatism, hostplant quality) did not affect eye size evolution.

Overall, phylogenetic inertia, not ecology and behaviour, is a major driver of eye size evolution in temperate butterflies which is in stark contrast to the widely held belief. The consequences this has on community assembly remain an exciting arena.

**Keywords:** allometry, comparative analysis, macroevolution, microCT, vision



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## EVOLUTION

My work focuses on macroevolution and biogeography of tropical insects. I received my MSc degree in Finland, where I worked on molecular systematics and diversification of neotropical butterflies. My PhD studies were in the Czech Republic, where I worked on biogeography and molecular ecology of Indo-Pacific ants. My post-doctoral research in Sweden was on phylogenomics and biogeography of neotropical butterflies, and in the Czech Republic, we are revisiting the origin and mechanisms maintaining biodiversity (species and genetic diversity) in selected groups of Neotropical butterflies.

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### Bridging macro- and microevolutionary studies in Neotropical butterflies

Multidisciplinary efforts are needed to uncover the evolutionary and ecological processes generating biodiversity patterns. I will show our latest findings on the mechanisms that might have generated one of the largest radiations of neotropical butterflies, the Skipper subfamily Eudaminae (Hesperiidae). We couple genomic data to understand macro- and microevolutionary processes, together with ecological experiments in the lab and in the field. We provide evidence that the apparent phenotypic convergences in wing shape (hindwing tails) along the phylogeny of the tribe Eudamini might be the result of predation pressure and avian selection. We showed that hindwing tails and certain colour patterns found in Eudamini might advertise prey escape ability. We tested such predictions in a rainforest locality in Peru, where we found evidence that multiple defences, including evasive ability and unpalatability, might explain their strong unprofitability to local insectivorous birds. Finally, we revealed species diversification patterns, including lineages that have radiated rapidly and recently, and others that have gradually accumulated over millions of years. The differential diversification rates may be explained by strong intrinsic barriers to gene flow. For example, the recently diverged and syntopic *Spicauda* species in localities in Peru and Panama have their genomes strongly differentiated. Altogether, we are starting to reveal the evolutionary and ecological mechanisms that have promoted the extant diversity and distribution of neotropical butterflies.

**Keywords:** prey unprofitability, phenotypic convergence, rapid diversification



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I am Professor at the University Grenoble Alpes (France), teaching evolutionary ecology and phylogenetics. I got a PhD from the University of Montpellier, France. My main research interests are in the evolutionary processes leading to population diversification and speciation. Most projects combine population genetics and phylogenomic analyses together with ecological, biochemical and behavioral studies to test hypotheses about evolutionary processes or adaptation to multiple constraints, mainly in the Alps.

**Co-authors:** Caroline Kebaili<sup>1</sup>, Stéphanie Sherpa<sup>2</sup>, Thomas Francisco<sup>1</sup>, Thibaut Capblancq<sup>1</sup>

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### Demographic and adaptive responses to climate change in *Parnassius apollo*

Cold-adapted species can respond to current climate warming by tracking their optimal climatic conditions along the altitudinal/latitudinal gradient (range shift) or by adapting to new environmental conditions (genomic shift). We tested for demographic changes in response to climate changes and searched for evidence for climate-driven adaptation in the Apollo butterfly *Parnassius apollo*. We studied the genetic structure and demographic history of Apollo populations in France using single nucleotide polymorphisms (SNPs) and revealed seven main genetic groups: two in Massif Central (Auvergne, Ardeche/Cevennes), one in the Pyrenees, and four in the Alps (Jura, North Alps, Chartreuse, South-Alps). Paleogeographic distribution based on species distribution models (SDMs) and effective population size, show that the cooling period between the LIG and LGM was a favorable period of population expansion throughout the large climatically suitable Rhône valley between glaciated summits. The Massif Central, Pyrenees, Jura and Alps populations started diverging before the LGM but remained largely connected until the mid-Holocene. Since then, global warming and glaciers retreat drove population fragmentation and range shifts along elevational gradients, with strong population decline in the ancestral core population (Massif Central) that still retains the largest diversity in ancestry coefficients. We then showed that current climate was a best predictor of genetic variation than geography or population history, suggesting that populations are adapted to their local climatic conditions, and identified several SNPs associated to warm and dry low-elevation conditions. Finally, using a space-for-time approach, we identified the populations the most vulnerable to genetic maladaptation under future climate scenarios.

**Keywords:** Population genomics, climate change, range shift, adaptation



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My background is in Evolutionary ecology, ranging from field and experimental ecology to genetics and genomics. I got a PhD from the University of Montpellier, and worked in Leiden (NL), London, Edinburgh (UK), and the Natural History Museum in Paris. My main research interests are in the evolutionary and ecological processes underlying adaptive evolution of complex traits. My main models have been butterfly colour patterns and their roles in mimicry, the importance of chromosomal inversions in the evolution of supergenes, and altitudinal adaptation in temperate butterflies and moths.

**Co-authors:** Yann Le Poul<sup>1</sup>, Mathieu Joron<sup>1</sup>

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### Understanding phenological changes along altitudinal gradients in butterflies and moths

Local adaptation involves a diversity of traits changing among different ecological conditions, such as different climate or habitat dimensions. In temperate regions, Lepidopteran phenologies are known to be diverse, varying in the wintering stage, voltinism, timing of generation(s), and environmental clues. Latitudinal changes in phenology are well understood, but altitudinal variations tend to be more difficult to predict as they vary on short spatial scales with fast-changing environmental factors, such as temperature, exposure, orientation, vegetation cover, land use. The way phenology is influenced by these environmental factors may have an important impact on local adaptation, gene flow, and speciation. There are to our knowledge no generalized analysis of species phenology variation and their drivers. Here, we explore the diversity of phenologies in relation to altitude. Using participatory data from French repositories, we analyzed and modelled the variation in phenology for more than 150 species of moths and butterflies with large altitudinal ranges. Results show unexpected, non-linear patterns of phenological shifts across altitudes, and strong differences among generations. This analysis provides insight into the main drivers of phenological adaptation along the altitudinal gradients, and allows formulating testable hypotheses regarding the evolutionary responses to similar cues at different altitudes. We will discuss implications on patterns of gene flow and speciation among populations and community assembly at different altitudes.

**Keywords:** Adaptive evolution, citizen science, climate change, thermal tolerance, phenotypic plasticity

# KEYNOTE SPEAKER



**Jérôme Casas**

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## ECOLOGY

Trained as a population ecologist, his interests span organismal biology and ecology; behavior and population dynamics of consumer-resource interactions; the sensory ecology of mimetism; flow sensing in biotic interactions; locomotion in granular materials and at the air-water interface, physicochemical transport in olfaction and biologically inspired microtechnology. His group is composed of engineers, theoretical and soft-matter physicists, biologists and applied mathematicians working in the field of physical ecology. A notable feature of his approach is the blending of natural history with both state-of-the-art technology and modeling. He was the director of the Institut de Recherche sur la Biologie de l'Insecte (UMR CNRS) for 7 years. He contributes or did so to many scientific boards, the most notable being BLOKON-The International Biomimetics Association (Berlin) as well as the interdisciplinary committee of the Canada Research Chairs program (Ottawa). He was awarded the ETH medal for a thesis in the University's top 10%, was nominated junior and later senior member of the IUF (Institut Universitaire Français) and was the Distinguished Invited Professor of the Center for Insect Science at the University of Arizona in Tucson. He did hold the excellency Chair for bio-inspired technologies at the LETI CEA, a research powerhouse on micro-technologies in Grenoble. He was awarded a Humboldt research prize for lifetime achievement and is a corresponding fellow Royal Society of Edinburgh. Prof. Casas also served on the editorial board of a number of ecological, physiological and interdisciplinary journals and is currently co-editor in chief of Current Opinion in Insect Sciences.

### Transport and capture of pheromones: a mesoscale approach

Moths are models of chemical communication, performing highly specific, long-range communication via minute amounts of pheromones through a cascade of highly improbable events occurring in succession — transport in the air, capture by an antenna and entry into a sensory pore — this mystery remains intact since Fabre. Critical gaps remain in our knowledge, concerning physicochemical aspects in particular: how can such tiny amounts of pheromones be released and efficiently transported over large distances? When molecules are captured on the antenna, how do they reach the nanometer-wide olfactory pore on the cuticle? What fluid dynamics govern the large diversity of insect antennal forms? How does the environment modify signals? The sensory ecology program I develop with my colleagues, Ph.D. students and post-docs aims to quantify the mechanisms underlying this efficiency, using silkmoths and their feathery antennae as a model. I will focus on two processes — transport and capture — at the meso-scale, between molecules and organisms. Cutting-edge techniques from fluid dynamics (PIV), atmospheric chemistry (FIGAERO-ToF-CIMS) and materials science (AFM) will be used. I will first quantify the partitioning of pheromone transport between the gas and aerosol phases, making use of the finding that pheromones can be efficiently transported not only as single molecules, but also bound to aerosols. I will determine the roles of antennal surface patterning and architecture in capture efficiency, by studying the viscous boundary layers of antennae. If time permits, I will decipher the interfacial processes transporting the molecules to the sensory pores and present our first attempts to integrate our knowledge into an integrated microfluidic biochip performing the first two processes with an unprecedented degree of control.



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## FORUM HERBULOT

Hossein Rajaei is the curator of Lepidoptera collection at State Museum of Natural History, Stuttgart. His research is mainly focused on Geometrid Moths of West Palearctic.

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### Forum Herbulot: a successful collaborative network coordinating research on geometrid moths

We present an overview of Forum Herbulot network, which coordinates research on geometrid moths globally. The idea was laid in 2000, when the famous geometrid collection of Claude Herbulot (Paris) was purchased by the ZSM Munich. Manfred Sommerer and few key people started to organize and manage the global research initiative «Forum Herbulot» with the aim to coordinate the research on Geometridae and to facilitate friendships and networking among the global community of geometridologists. The background philosophy was simple: “come together and have fun...” Free membership and avoiding formal association structures helped to make many things easy and flexible. Since the beginning, key activities have been biennial meetings, often in interesting, remote sites, where the main focus is laid on friendship, collecting, and project planning (e.g. at the campfire), with scientific talks just as an additional business. During the recent years, Forum Herbulot has also been used as a platform for project planning, writing grant proposals, writing joint statements, and to run large-scale projects in a synergetic way. Among those are an initiative to build global molecular phylogeny for Geometroidea (ongoing, planned publication in 2024) and Forum Herbulot website <https://geometroidea.smns-bw.org/> with global database of geometrid moths (2022 published version has about 35 000 names). The future plans include to update the database regularly, and to expand the database to cover entire Geometroidea and to include photographs.

**Keywords:** Forum Herbulot, Geometridae, collaboration, global



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Axel Hausmann has been studying Geometridae for over 30 years and has authored approx 500 scientific articles on Lepidoptera. He recently completed the book series Geometrid Moths of Europe and initiated major projects on DNA barcoding.

### We want them all ! - Completing the DNA-library for European Lepidoptera in the BGE project

20 years after its first proposal, DNA Barcoding has become an important part in the integrative taxonomic research on Lepidoptera. Out of the 10,000+ European Lepidoptera species, currently 58% have DNA barcodes in the Barcode of Life data systems (BOLD). The pattern is somewhat biased, 72% of the European macrolepidopteran species being represented by at least 3 barcodes in the reference library, while the so-called Microlepidoptera show a much lower coverage. Among the hyperdiverse lepidopteran families, Geometridae are best represented in the DNA library (83% coverage with at least three DNA barcodes >600bp; 95% with at least one).

In 2022, an EU grant (HORIZON-CL6-2021-BIODIV) allowed us to start the project "Biodiversity Genomics Europe (BGE)" aiming at filling the remaining gaps. The Bavarian State Collection Munich (SNSB-ZSM) is responsible for the "Gap Analysis" and for the "Reference Library Curation" for addressing and correcting misidentifications, misspellings, outdated taxonomy, lab errors, pseudogenes a.s.o.. Moreover, this 3-years-project will allow for a genomic skimming of 33,000 identified, old museum specimens focused on the gaps and including type specimens. In the case of Geometridae, the collection of the SNSB-ZSM in Munich allows to raise the barcode coverage to >99%. A remaining gap list for European Geometridae is presented to the participants of Forum Herbulot. We present details on the workflow and progress of the BGE project, as well as on potential benefits for accelerated species detection, e.g. in understudied groups of 'dark taxa'.

**Keywords:** DNA barcoding, Europe, gap analysis, Geometridae, integrative taxonomy



**Flavia Rossina Joele  
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My name is Flavia Rossina Joele Alves de Moraes, I'm a 25 years old female graduate student from Brazil. I am passionate about biology and my academic interests are focused on insect systematics and taxonomy. During my undergraduate career I worked with a phytophagous group of parasitoid wasps in the family Braconidae, the genus *Allorhogas*. I just finished my masters program at UNAM, where I conducted a phylogenomic analysis of the geometrid tribe Palyadini to study the evolution of wing color characters.

**Co-authors:** Manoel M. Dias Filho<sup>2</sup>, Jovana M. Jasso-Martinez<sup>3</sup>, Ivonne J. Garzón-Orduña<sup>1</sup>

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### Phylogenomics of a neotropical geometrid tribe reveal contrasting patterns of phylogenetic signal in wing color characters

Next generation sequencing techniques currently represent a practical and efficient way to infer robust evolutionary hypotheses. Palyadini is a small neotropical tribe of geometrid moths composed of six genera that feature strikingly colorful wings. Here, we investigated patterns of evolution and amount of phylogenetic signal contained in various color characters featured in the wings of members of this tribe by (1) inferring a robust phylogenetic hypothesis using Ultraconserved Elements (UCEs), and afterwards, (2) mapping the morphological characters onto the molecular topology under a parsimonious ancestral character optimization. Our matrix, obtained with 60% completeness, includes 754 UCE loci and 73 taxa (64 ingroup, 9 outgroup). Maximum likelihood and Parsimony generated largely identical topologies with strongly supported nodes, except for one node inside the genus *Opisthoxia*. According to our preferred topology, most wing color characters are reconstructed as homoplastic, particularly at the tribe level, but five of the seven provide evidence supporting common ancestry at the genus level. Our results emphasize, once again, that no character system is infallible, and that more research is necessary to take our understanding of the evolution of wing color in moths to a level comparable to the knowledge we have of butterflies'.

**Keywords:** Lepidoptera, moths, Geometridae, UCEs, eyespots, homoplasy



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**FORUM HERBULOT**

Dr. Leidys Murillo-Ramos is associate lecturer at Universidad de Sucre, Colombia. Leidys studies systematics, patterns of diversification and biogeography of geometrid moths using molecular data in combination with different phylogenetic inference approaches.

**Co-author:** Leidys Murillo-Ramos<sup>1,3</sup>, Hamid Ghanavi<sup>2</sup>, Kyung Min<sup>3</sup>, Elina Laiho<sup>3</sup>, Axel Hausmann<sup>4</sup>, Herman Staude<sup>5</sup>, Egbert Friedrich<sup>6</sup>, Gunnar Brehm<sup>7</sup>, Pasi Sihvonen<sup>3</sup>

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### Emptying the taxonomic trash bin: molecular phylogenies resolve the polyphylies of Oenochrominae and Desmobathrinae

Systematics of the small geometrid subfamilies Oenochrominae (mostly Austral-Asian) and Desmobathrinae (pantropical) have been the focus of recent morphological and molecular studies. These studies have made visible the taxonomic impediment and the polyphyletic nature of in the mentioned lineages. Molecular phylogenetic hypotheses have suggested that some taxa need to be transferred to other Geometridae subfamilies, while genera require deep taxonomic revisions. Here, we expand the taxon sampling to cover these lineages globally and retrieving data from Murillo-Ramos et al., we built a dataset of 1396 taxa from all geometrid subfamilies with up to eleven gene markers. We analyzed 47 taxa from Oenochrominae, 29 of Desmobathrinae and 14 from the recently described subfamily Epidesmiinae. The phylogenetic trees were inferred under a Maximum Likelihood approach in IQTREE2. The preliminary results support previous hypotheses, highlighting that Oenochrominae and Desmobathrinae are polyphyletic and reclassifications are needed to delimit the monophyly of those subfamilies.

**Keywords:** Geometridae, moths, taxonomy



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**FORUM HERBULOT**

Ms Shabnam Kumari is a PhD student and a CSIR fellow at the Wildlife Institute of India. With her keen interest in the systematics and ecology of moths in the Geometridae family, she is exploring the elevational diversity patterns and potential indicator species (altitude and forest types) of the family for the long-term monitoring of environmental changes in the North-western and Trans-Himalayan biogeographic provinces of the Indian Himalayan region (IHR). Her particular interest is resolving the Indian Himalayan Sterrhinae by using the integrative taxonomic approach.

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### What underlies the unimodal elevational species richness pattern of Geometridae moths (Lepidoptera: Heterocera) in the protected area of the North-western Himalayan Biogeographic province, Himachal Pradesh, India?

Elevational gradients are considered an important natural experimental setup for studying the factors and processes underlying the distribution of species in space and time. To understand the generality of the factors and processes different elevational gradients all over the world have been evaluated using different model taxon. Among the insect herbivorous taxa, the family Geometridae of moths in the Order Lepidoptera is among the most well-established in the world. An elevational gradient of Dhauladhar Wildlife Sanctuary (DWLS) protected area constituting north-western Himalayan (2A) biogeographic province of the Indian Himalayan region (IHR) has been explored for the family Geometridae over the period of two years (from September 2020 to June 2022). The elevational gradient of 1500–3200 m has been sampled at every 300 m stratum in different vegetation types following a stratified random sampling study design. A total of 12 sites (two sites in every 300 m elevational zone) were sampled using a LepiLED light trap in two different seasons: pre-monsoon (April to Mid-June) and post-monsoon (Mid-August to October). The species richness and diversity for the family and of different subfamilies were estimated using different statistical estimates and indices. Overall, the species richness and diversity in the family have revealed a unimodal peak along the gradient. The role of different environmental factors has been evaluated using CCA analysis, where the first two axes have explained 62.63% of the cumulative variation and altitude, slope, temperature and NDVI have been found to demonstrate a significant role in shaping the overall diversity pattern.

**Keywords:** Diversity and distribution, assemblage pattern, biodiversity monitoring, macroecology



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Being interested in insects and particularly in Lepidopterans since childhood, I started studying biology in University of Tartu, Estonia in 1995. After graduating in 2000 with ecology-oriented thesis, my interests strongly shifted towards systematics and faunistics. Since my Master study, completed in 2002, I have adored using molecular phylogenetics for updating and correcting the system of Lepidopterans in the modern integrative framework, with family Geometridae being the main focus group.

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### **Molecular phylogeny of North European Geometridae (Lepidoptera, Geometroidea)**

Phylogenetic relationships between Geometridae of Northern Europe were studied using two-step approach. First, a phylogenomic backbone was created for the subset of local fauna, using more than 600 loci from nuclear protein-coding genes for 117 species of Geometridae and 35 species of outgroup taxa from different families, totalling more than 200,000 bp. Second, up to 11 'traditional' markers totalling more than 7,800 bp were sequenced for all 376 species of North European geometrids, complemented by nearly 100 taxa belonging to taxonomic key groups of Geometridae from other parts of the world in order to put the results into a global context. Phylogenomic backbone created in the first analysis was used as a topological constraint in the second step of the study. Results are compared to earlier phylogenetic studies and current classification of Geometridae. Taxonomically important findings including new tribe descriptions, new tribe associations, revised statuses of tribes and genera, and new synonyms are discussed.

**Keywords:** phylogenomics, hybrid enrichment, taxonomy, systematics



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Kadri Ude is a first year PhD student at the University of Tartu, Estonia. She is studying the evolution of phenological adaptations in moths, focusing on the "winter moth syndrome", as well as comparative wing morphology in Lepidoptera.

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### **A phylogenetic-comparative study on wing shape in Geometridae**

Success in moving around in space is an important determinant of fitness in most animals, flying insects included. Strong selective pressures on wing morphology are therefore expected. Previous studies on wing shape in Lepidoptera have found some support for hypotheses relating wing shape to environment-specific optimisation of aerodynamic performance. Here we present a phylogenetic-comparative study on wing shape in the lepidopteran family Geometridae, covering all 374 species of the North-European fauna. We focused on 10 forewing traits such as aspect ratio, wing roundness and the pointedness of the apex, as well as the ratio the areas of the forewing and the hindwing. All measures were taken from images available on the internet, using a combination of tools available in Fiji and original scripts in R. We found that wing shape is an evolutionarily conservative trait in Geometridae, showing equal or higher lambda values than many of its potential predictors. Several parameters of wing shape showed statistically significant associations with predictors such as body size, phenology and preference of forest habitats. Overall, however, all these associations remained notably weak so that any wing shapes can occur under the entire range of the values of the predictors, including body size. We conclude that wing shape is not a trait readily responding to selective pressures optimizing aerodynamic performance of the moths in different environments. Instead, we believe that different wing shapes in geometrids should primarily be viewed as adaptations which contribute to the cryptic appearance of resting moths.

**Keywords:** Geometridae, wing morphology, morphometrics, phylogeny, comparative methods



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Pasi Sihvonen is Director of zoology unit at the Finnish Museum of Natural History, University of Helsinki. His research focuses on systematics, biodiversity and conservation, particularly on geometrid moths, a megadiverse insect radiation of 24 000 species. Sihvonen has worked in several non-academic positions also, and he advocates collaborative projects and promotes diversity, equity and inclusion <https://researchportal.helsinki.fi/en/persons/pasi-sihvonen>

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### Species delimitation in allopatry: a case study on African cycad moths (Geometridae: Ennominae)

The degree of differentiation between allopatric populations is variable, and it may concern phenotype, genotype, reproductive organs, and life history traits. Taxonomists have tried different methods to overcome the problem of classifying such populations. Recent attempts favor including more extensive molecular data, but repeatedly mitonuclear discordance appears, and hence even today the taxonomic delimitation of allopatric populations is largely opinion-based (authoritative) and hence arbitrary.

In Lepidoptera, species delimitation of allopatric populations has been studied rather extensively in Palearctic region (for instance between the Alps and Fennoscandia) and in Holarctic region (between Nearctic and Eurasia), covering vast geographical distances. In the northern Hemisphere, glaciations have played a significant role in shaping species distributions, but in the southern Hemisphere, where climatic history is different and includes drier and wetter periods, species delimitation examples are scarcer.

We present a case study from eastern South Africa on cycad feeding moths (Lepidoptera: Geometridae) in genus *Veniliodes*. These diurnal moths inhabit natural grasslands or forests in lowland and in a chain of allopatric populations, the extremes are only 700 kilometres apart. Using molecular species delimitation analyses and phylogenies, combined with wing patterns and reproductive organs, we demonstrate different species delimitation possibilities and how those could be transferred to formal classifications. Our study also shows the complexity of species delimitation decisions at the intersections of taxonomy and conservation.

**Keywords:** Molecular, DNA barcode, morphology, conservation, allopatry



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Hermann Staude has been studying the geometrid fauna of Africa for over 30 years and has authored 47 scientific articles on Lepidoptera. He recently completed the book Southern African Moths and their Caterpillars, illustrating over 1500 species.

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### Geometrid moths of southern Africa (GMSA) project, a monograph

The authors have been working on the southern African geometrid fauna for many years and decided to start with a synthesis of the gathered data. The aim of the project is to produce a monograph on the geometrid moth fauna of southern African (GMSA). This monograph will include the known basic knowledge of each taxon and an underlying narrative of how the authors interpret these data, as well as an attempt at gaining a better understanding of geometrids on the subcontinent, their diversity, ecology, origins and spatial distribution in the diversity of habitats across the highly variable topography.

Currently, 1608 described and known undescribed geometrid species are recorded to occur in southern Africa, but only a part of those have been treated in the modern literature allowing unambiguous identification. Primary data sources accumulated by the authors include: a geo referenced location database with 94156 records; a host association database with 2432 records, representing 554 geometrid species; a molecular library with 5890 DNA barcodes, representing 1115 geometrid BINS (barcode index numbers); an image library with 73311 images of live geometrid adults, early stages and museum specimens.

The aim is to produce a rough draft within three years and a more polished version in about five years. The project includes several collaborative smaller projects, primarily to address the alpha taxonomic backlog of over 200 known undescribed geometrid species in the region. We estimate the total species richness of geometrids in the region to perhaps exceed 2000 species.

**Keywords:** ecology, biogeography, morphology, taxonomy, phylogeny



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Claude Tautel is a former architect, urbanist specialist of the non-carbon city and professor. He is involved in many works on Geometridae in systematic or biology. He is participating to many actions to protect natural sites. He is Attaché of MNHN of Paris, helping on the curating of the Geometrid national collection. He has made more than 80 scientific papers (he has created more than 100 new species of Geometridae). He is participating to researches by an active collaboration with many "Geometrist" people of the world.

**Co-author:** Joël Minet<sup>1</sup>

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### The early stages and systematic position of *Gypsochroa renitidata* (Hübner, [1817]) (Lepidoptera, Geometridae)

Pierre Chrétien already described the biology and early stages of *Gypsochroa renitidata* in 1910 but his work, although accurate, did not include any illustration.

After rearing again this very particular species and studying in detail its larval chaetotaxy and pupal morphology, we can confirm that it belongs to the mainly tropical subfamily Desmobathrinae, as proposed by Axel Hausmann in 2001.

This systematic position of *Gypsochroa renitidata* also takes into account a number of imaginal characters and its larval foodplant, *Linaria repens* (Plantaginaceae), which belongs to the Lamiales, like the known hostplants of one of the two main desmobathrine lineages (which notably includes *Ozola* Walker, 1861 and *Derambila* Walker, [1863]).

While the important papers published in 2019 and 2021 by Leidys Murillo-Ramos and several co-authors define these two lineages (within Desmobathrinae) and a new subfamily called Epidesmiinae, they are mainly based on molecular phylogeny analyses despite taking also into account imaginal characters of several genera long held in the Oenochrominae sensu lato (essentially Desmobathrinae, Epidesmiinae and Oenochrominae sensu stricto).

Our work highlights the current lack of knowledge regarding the early stages of most of these genera, as well as the need to redefine the boundaries and imaginal characteristics of the Desmobathrinae and Epidesmiinae.

It also specifies the phenology, variability and distribution of *Gypsochroa renitidata* (in France mainly recorded from Ardèche but also known to occur in a wide area extending from Greece to the Near East and central Asia).

**Keywords:** Desmobathrinae, Epidesmiinae, cocoon, larva, pupa

# KEYNOTE SPEAKER



**Johanna Mappes**

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**ECOLOGY**

Johanna Mappes is an evolutionary ecologist and her research focuses on predator-prey interactions, aposematic signals and mimicry in chemically defended prey and the evolution of signal polymorphism. Her main study species is the polymorphic, aposematic wood tiger moth (*Arctia plantaginis*) and their bird predators. Her lab consists of researchers from the fields of molecular biology, sensory ecology, chemical ecology, behavioral ecology and evolutionary ecology. In 2003 The Academy of Finland awarded Mappes the 'Young Dynamic Researcher Award' for her research merits in developing the 'novel world method' to study the evolution of aposematism. She was elected as a Research Professor at the Academy of Finland from 2009-2013, and again from 2019-2023. Mappes served as a Professor of Evolutionary Ecology at the University of Jyväskylä from 2008-2019, where she headed the Centre of Excellence in Biological Interactions for the Academy of Finland from 2012-2018. In 2017 she was elected member of the Finnish Society of Sciences and Letters and in 2018 she became an honorary member of the American Academy of Arts and Sciences (AAAS). As of 2020, she is a Professor of Ecology at the University of Helsinki, Research Professor at the Academy of Finland.

### Ecology and evolution of colours: Predators, conspecific and other drivers of colour polymorphism

Ever since Darwin and Wallace, animal colours have been at the core interest of naturalists because coloration is involved in survival and reproduction of individuals. Coloration is easy to observe and accessible for experimental manipulation. Same time coloration of animals created evolutionary paradoxes for evolutionary biologists, that are still partially unresolved. In my research, I use colourful and distasteful wood tiger moths (*Arctia plantaginis*) and their bird predators to understand the interplay between phenotypic and genotypic variation on individual fitness. This moth species has many colour morphs (= polymorphism), which is puzzling because predators are expected to learn to avoid the most effective and common signal and thus wipe out other colour variants from the prey population, yet polymorphism is common among aposematic animals. I will show some recent developments to determine genetic basis of colour polymorphism and results of experiments that test ecological conditions that may drive and maintain phenotypic diversity in warning signals and mimicry.

**Keywords:** Warning colours, chemical defence, predation, balancing selection



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Currently I am investigating the origin of phenotypic convergences within a group of neotropical skippers (Eudaminae, Hesperidae) within the scope of my PhD thesis. I have spent almost a year running predator experiments in the Amazon. Generally, I am interested in evolutionary ecology and speciation. During my undergrad I have been working in species conservation within Europe but have now moved towards the Neotropics.

**Co-authors:** Daniel Linke<sup>1,2</sup>, Marianne Elias<sup>3</sup>, Johanna Mappes<sup>4</sup>, Jacqueline Hernandez Mejia<sup>5</sup>, Valery Nicole P. N. Eche, Pedro de Gusmão Ribeiro<sup>1,2</sup>, Pável Matos-Maraví<sup>1</sup>

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### Anti-predator defences of neotropical Skipper butterflies (Hesperiidae), more complex than previously thought

Prey organisms are under constant selective pressure by various predators, thus, multiple strategies have evolved to evade, to confuse or to mislead predator attacks. Skippers (Hesperiidae) are diurnal butterflies long suspected to utilise different strategies to evade visual predators (e.g., insectivorous birds). By using a laboratory protocol, we found that hindwing tails in artificially escaping, dummy Skippers can be learnt by a surrogate predator, thus, showing 'butterfly tails' can be effective morphological cues to advertise evasiveness, in addition to their role in deflecting predator attacks. In field experiments in Peru, we have uncovered an additional defence strategy in Skippers; some species are unpalatable for domestic chicks (a common surrogate model for testing palatability). This suggests that Skippers have multimodal defences, being highly evasive and highly unpalatable as other aposematic neotropical butterflies such as Heliconius or Ithomiini. Finally, by conducting aviary experiments across seasons and habitats using local insectivorous birds, we have gathered evidence suggesting that such predators are aware of the defences and significantly reduced their attack rate to Skippers compared to control palatable and slow butterflies. Altogether, by using a combination of lab and field experiments, we are shedding light upon the possible drivers explaining multimodal defences in Skippers.

**Keywords:** Predator avoidance, defensive strategies, Hesperiidae, unpalatability, evasiveness



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I am a post-doctoral researcher at the Centre for Ecological Sciences, IISc, Bangalore, India. I completed my PhD from the Wildlife Institute of India and Zoologische Staatssammlung Munich, Germany on the taxonomy and diversity of Geometrid moths in western Himalayan protected areas. I am largely interested in the evolutionary ecology of moths. Apart from science, I share my experiences through popular articles and public outreach aiming to improve the state of moth research in India.

**Co-author:** Rohini Balakrishnan<sup>1</sup>

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### A trait-based understanding of the vulnerability of a paleotropical moth community to predation by a sympatric bat with flexible foraging strategies

Prey profitability for a predator hunting diverse prey varies with species and seasons. Understanding prey selection in bats that adopt flexible foraging strategies (both gleaning and aerial hawking) thus poses a challenge.

In the Western Ghats of India, a global biodiversity hotspot, we investigated a sympatric moth community subjected to predation by Megaderma spasma, the Lesser False Vampire bat. Coupling measurable prey traits with availability in the foraging grounds, we aimed to characterize the vulnerability of prey species to predation.

We analyzed the discarded prey remains from several roosts, collected over three years. We also collected moth specimens from the foraging area of the bat in different seasons, in which the following traits were measured: forewing length, hindwing length, wingspan, and body length (a proxy for body size); forewing area, hindwing area, maneuverability, and wing loading (as a proxy for evasive flight capability), and forewing aspect ratio (as a proxy for wing shape).

Our results showed seasonal variation in prey diversity, with moths belonging to the Hepialidae family being preferred in the wet season, although Sphingidae moths were the most abundant in the overall diet. Sphingid moths have the lowest maneuverability and highest forewing aspect ratio; the Hepialidae moths have maximum body size followed by Sphingids thus confirming our hypothesis that larger moths with low evasive capabilities are more vulnerable to predation.

Through a trait-based approach, we establish a framework for future research on moth-bat interactions at the community level from the diverse and less-explored paleotropical communities.

**Keywords:** moths, megadermatid bats, morphological traits, prey-predator, Western Ghats



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I'm a PhD student at CEFE-CNRS (Montpellier, France) within Mathieu Joron's team. My work is interested in the phenotypic variation and the genomic bases of the characters involved in adaptation and diversification in alpine butterflies of the genus *Coenonympha*.

**Co-authors:** Paul Doniol-Valcroze<sup>1</sup>, Lucie Develay<sup>1</sup>, Bruno Buatois<sup>1</sup>, Laurence Després<sup>2</sup>, Mathieu Joron<sup>1</sup>, Anne-Geneviève Bagnères<sup>1</sup>

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#### Variation of chemical profiles and diversification in an alpine butterfly species complex

Deciphering the factors driving reproductive isolation and speciation is central to our understanding of the build-up of divergence between lineages and the shaping of biodiversity patterns. Reproductive isolation may be based on intrinsic factors (e.g. genetic incompatibilities) or extrinsic factors (e.g. strong ecological divergence). Here we study the interplay of ecological divergence and hybridization in diversification in the *Coenonympha arcania/gardetta* species complex (*Coenonympha*, *Nymphalidae*: *Satyrinae*). In the French Alps, this complex is composed of three species, a widespread low elevation, wood edge species, (*C. arcania*), a high elevation grassland specialist species, (*C. gardetta*), and a species of hybrid origin found in intermediate habitats and elevations (*C. cephalidarwiniana*). In this complex, species-specific chemical traits are of high interest as they could be linked with adaptation to altitude (e.g. involvement of cuticular hydrocarbons against dessiccation) and/or with reproductive isolation and speciation (e.g. pheromone-based mate choice) and therefore play an important role on its diversification. In the present study we first describe the three species' chemical profiles (volatile and cuticular components) using GC-TOF-MS analysis, pointing out the components or their proportions discriminating species and sex. Second, we compare the chemical profile of individuals of three possible contact zone modalities (gardetta-arcania; gardetta-cephalidarwiniana; arcania-cephalidarwiniana) in regard of known gene flow and therefore strength of reproductive isolation between each species pairs.

**Keywords:** *Coenonympha*, chemical profiles, diversification



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Zowi Oudendijk is a first-year PhD researcher at Helsinki University. He is interested in the evolution of chemical defence in insects and its variation across species. His current doctoral research explores the evolution of de novo synthesis of methoxypyrazines as a chemical defence in Tiger moth (Arctiinae) species. It involves sampling Arctiinae species from across the globe. He is looking for collaborators to help collect species and observe reflex bleeding.

**Co-author:** Johanna Mappes<sup>1</sup>, Niklas Wahlberg<sup>2</sup>, Simeão de Souza Moraes<sup>3</sup>, Junia Yasmin Oliveira Carreira<sup>3</sup>, Kimmo Silvonon

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#### Evolution and prevalence of de novo synthesized pyrazines as a chemical defence in Tiger moth (Arctiinae) species

Pyrazines are volatile, nitrogen-containing heterocyclic compounds that are widely distributed in plants, insects, fungi, and bacteria, and act as an odour signal to repel predators. Herbivorous insects can obtain these compounds through sequestration from the host plant or de novo synthesis by the organism itself. While studies on de novo synthesis of defensive compounds within insects are well known among beetles and other insects, this mechanism has been less explored in moths and butterflies (Lepidoptera), with the exception of the wood tiger moth (*Arctia plantaginis*), which is known to produce methoxypyrazines de novo. In this study, we sampled Arctiinae species from a broad geographic distribution across their phylogeny to investigate whether they produce reflex bleeding when provoked, whether their defensive fluids contain pyrazines and whether methoxypyrazines are produced de novo. Our preliminary results suggest that reflex bleeding is widespread in this group, but pyrazine production appears to be limited to the *Arctia* genus, which includes the Holarctic species. We discuss the implications of these findings in the context of the ecological drivers that may have led to the evolution of such defensive strategies in this group.

**Keywords:** Arctiinae, De novo, methoxypyrazine, Reflex bleeding, Chemical defence



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I am an evolutionary biologist working on the ecology and evolution of butterflies. My main study group so far has been the neotropical mimetic butterfly tribe Ithomiini, where I investigated diversification patterns, community structure and trait evolution. On particularity of ithomiine butterflies is that many species have transparent wings, and I have on-going collaborations with physicists to unravel the properties of those wings and the selection pressures driving their evolution.

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### One ring to bring them all: community assembly and niche evolution of mimetic butterflies

Müllerian mimicry is a type of intraguild mutualistic interactions where individuals belonging to different defended species converge in warning colorations that are learned and avoided by predators. Here we take advantage of a nearly comprehensive phylogeny and an extensive distribution database for the largest known radiation of mimetic butterflies, the neotropical tribe Ithomiini (396 species), to assess the impact of mimicry on the structure of species assemblages throughout their entire distribution range and on the evolution of various facets of their ecological niches. We found that species with similar wing color pattern co-occur more often than expected at random. Moreover, we showed that species with similar color patterns have more similar climatic and microhabitat niches than expected under neutral evolution. This suggests that these species have converged in their climatic and microhabitat niches, as predicted by a theoretical model, thereby strengthening co-occurrence and protection against predators. Indeed, observations and experiments performed in a diverse community in Ecuador showed that predators incur selection on species microhabitat use and color pattern. Finally, we found evidence that mimetic interactions may also be linked to hostplant use. Mimetic interactions are therefore a strong driver of butterfly community structure and trait evolution. We hypothesise that divergent selection on those traits, namely color pattern, microhabitat preference, climatic tolerance and hostplant, has likely played an important role on the diversification of mimetic butterflies.

**Keywords:** mimicry, climatic niche, microhabitat, adaptive convergence



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Eric Toro-Delgado is a PhD student at the Institute of Evolutionary Biology of Barcelona (Spain). In 2019 he started to work with Roger Vila's and Gerard Talavera's labs, being involved in research projects on various topics of ecology and evolution, such as thermoregulation, DNA barcoding and plant-host-parasitoid interactions, using butterflies as a model system. He has recently started his PhD at Roger Vila's lab, aiming to study the prevalence and effects of *Wolbachia* in butterflies and its consequences for their diversification.

**Co-authors:** Gerard Talavera<sup>1</sup>, Dominik R. Laetsch<sup>2</sup>, Konrad Lohse<sup>2</sup>, Roger Vila<sup>3</sup>

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### Lack of evidence for co-cladogenesis suggests lateral and introgressive transfer of *Wolbachia* in European butterfly sister species

*Wolbachia* is an endosymbiont of arthropods and nematodes that can act as a reproductive parasite or as a mutualist. *Wolbachia* may influence host speciation, but the extent of this influence depends on the *Wolbachia* turnover rate, and therefore on the mechanisms of infection. Most studies up to date suggest introgressive and lateral symbiont transfer are common, which precludes the detection of the existence of co-cladogenesis across deep evolutionary times. Here, we address this problem by using a different approach: we assess the existence of co-cladogenesis in sister species of recent origin. In this work, we investigate the presence and phylogenetic relationships of *Wolbachia* strains in 18 sister species pairs of European butterfly species. We find that sister species pairs share strains more often than expected by chance. Also, the chances of sharing strains are higher with lower divergence times, and this effect is stronger for pairs with a high degree of sympatry. This suggests lateral and introgressive symbiont transfer are common enough to erase co-cladogenic patterns even in recently speciated taxa, limiting the potential effects of *Wolbachia* on host speciation.

**Keywords:** *Wolbachia*, endosymbionts, butterfly, coevolution



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I am a final year Ph.D. candidate under the guidance of Dr. Łukasz Przybyłowicz. I am interested in different aspects of evolution, taxonomy, phylogeny, biogeography and ecology of tropical tiger moths. My current research concerns Madagascan lineage of the tribe Syntomini, especially taxonomic revision of the genus Thyrosticta, as well as the Old World Arctiini genus Euchromia. I took part in a field expedition to Madagascar in 2020. I have collaborated with Prof. Niklas Wahlberg's lab in Lund (Sweden) starting from 2019.

**Co-author:** David C. Lees<sup>1</sup>

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### Madagascar, Moths & Mimicry – a new potential mimicry system in Madagascar, involving Syntomini tiger moths

Ever since Bates explored the Amazon, lepidopteran mimicry ring researches have focussed extensively on the model systems such as the butterfly genus *Heliconius*, largely neglecting Afrotropical moths. However, during a project on the phylogeny, systematics and biodiversity of the endemic Madagascan lineage of Polka-dot Moths (Syntomini), numbering 14 pre-existing genera and some 100 species, we found an intriguing distribution of apparently convergently similar body-wing patterns and colouration among the different evolutionary lineages of the group. This suggests the existence of mimicry rings in Madagascar within this remarkably diverse clade. Additionally, during a few decades of research there, supplemented by extensive research in collections and databases, we have recorded a number of Syntomini-like moths from other groups (such as Zygaenidae: Procridinae, one of the more diverse groups of potential Syntomini mimics, which resemble certain syntomine species most closely). Surprisingly though, some Trichoptera and even Coleoptera also share Syntomini-like colour patterns. Based on these findings, we are planning to test these presumed mimicry rings in Madagascar, i.e. checking for parallel patterns in phylogenies and by comparing wing patterns objectively. The results of the project are a potential springboard for future research e.g. in the fields of chemical ecology and genomics.

**Keywords:** Madagascar, Syntomini, endemism, mimicry



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I am an evolutionary biologist, interested in the evolution of phenotypic variations and their impact on speciation. I currently investigate feedbacks between ecological interactions and trait evolution in sympatric species, aiming at linking micro and macroscales of evolution. I used combinations of theoretical and empirical approaches, including both lab and field experiments.

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### Evolution of temporal niches in butterfly communities and consequences on sympatric speciation

The co-existence of closely-related species in sympatry often implies the partitioning of species into different ecological niches. Whether this partition is the result of sympatric speciation or of a secondary evolution of traits within species in response to ecological interaction in sympatry is an open question. Here we focused on closely-related species of *Morpho* butterflies that occur in sympatry for a large part of their Amazonian range and display parallel variations in their iridescent blue wing colour patterns. Using experiments carried out in the field, we recently showed that their striking resemblance may lead to substantial sexual interactions between species. In this talk, I will present results from mark-recapture experiments documenting the temporal segregation in the timing of daily activities between these species, in different South-American localities. I will then investigate the selective pressures acting the evolution of temporal patterns of daily activities in sympatric species using a mathematical model. Finally, I will use simulations to test for the effect of temporal segregation and genetic incompatibilities in the process of sympatric speciation. Altogether, this talk will highlight the key role of temporal pattern of reproductive activities in the assembly of species-rich communities and show the key determinants of sympatric speciation caused by such temporal segregation.

**Keywords:** mimicry, mate recognition, male-male competition, ecological niche, reproductive interferences

# KEYNOTE SPEAKER



**Eric Warrant**

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**ECOLOGY**

Warrant is Professor of Zoology and Head of the Lund Vision Group at the University of Lund in Sweden, Visiting Fellow at the Research School of Biology at the Australian National University and Adjunct Professor at the University of South Australia. Warrant leads an active research group studying vision and visual navigation in animals from extremely dim habitats (nocturnal and deep sea). Using electrophysiological, optical, histological, behavioral and theoretical approaches, Warrant studies how animals as diverse as nocturnal insects, deep-sea cephalopods and fast-swimming predatory fishes are able to see well at very low light levels, and his research has led to the discovery of neural principles that permit vision in dim light. In recent years Warrant's group has turned its attention to the sensory basis of long-distance migration in nocturnal insects, particularly the role of the Earth's magnetic field and the stars in migratory navigation. Warrant's work is funded by an Advanced Grant from the European Research Council, as well as from the Swedish Research Council. Warrant is Past President of the International Society of Neuroethology, Member of the German National Academy of Sciences Leopoldina, Fellow of the Royal Danish Academy of Sciences and Letters, Fellow of the Royal Institute of Navigation and Fellow of the Royal Physiographic Society, and sits on the Senior Editorial Board of the *Journal of Comparative Physiology A* and also on the Academic Advisory Board of the *Proceedings of the Royal Society B*.

## Australian Bogong moths use the stars and the Earth's magnetic field as compasses for long-distance navigation at night

Each spring, billions of Bogong moths escape hot conditions in different regions of southeast Australia by migrating over 1000 km to a limited number of cool caves in the Australian Alps, historically used for aestivating over the summer. At the beginning of autumn the same individuals make a return migration to their breeding grounds to reproduce and die. By tethering spring and autumn migratory moths in a flight simulator, we discovered that Bogong moths are able to sense the Earth's magnetic field and correlate its directional information with visual cues to steer migration. We also discovered that a critically important visual cue is the distribution of starlight within the austral night sky. Under natural dorsally-projected night skies, and in a nulled magnetic field (disabling the magnetic sense), moths fly in their seasonally appropriate migratory directions, turning in the opposite direction when the night sky is rotated 180°. Visual interneurons in the moth's optic lobe and central brain respond vigorously to identical sky rotations. Migrating Bogong moths thus use the starry night sky as a true compass to distinguish geographic cardinal directions, the first invertebrate known to do so. These stellar cues are likely reinforced by the Earth's magnetic field to create a robust compass mechanism for long-distance nocturnal navigation.



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**ECOLOGY**

PhD Anna Suuronen is ecologist and environmental scientist focused on biodiversity issues. She got her masters in ecology from University of Turku in 2011 and PhD from the University of Jyväskylä in 2017. Dissertation subject was ecological and social impacts of photovoltaic solar power plants and optimization of their locations in Northern Chile. After parental leave, she started her work at Finnish environmental institute (Syke) in 2021 focusing on statistical ways to describe species abundance trends, distributions, and estimates on biodiversity loss.

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## Outbreak probabilities of macro-moth species in warming high latitudes

The forest damages caused by moths and their outbreaks might change with climate warming. Here we focus on 7 macro-moth species that are considered as potential forest pest species in Finland. Four of them are polyphagous spring-feeding defoliators of deciduous trees and shrubs: Autumnal Moth (*Epirrita autumnata*), Winter Moth (*Operopthera brumata*) Northern Winter Moth (*Operopthera fagata*) and Scarce Umber (*Agriopsis aurantiaria*). Two species are monophagous on conifers Pine Beauty Moth (*Panolis flammea*) and Bordered White Moth (*Bupalus piniarius*), and one is coniferous preferring polyphagous species Black Arches (*Lymantria monacha*, Linnaeus, 1758). Our aim was to test if we can predict outbreaks of these species with logistic regression and define whether phenological phenomena or climatic variables explain outbreaks.

With the changing climate outbreaking species are moving towards northern regions. Autumnal Moth related outbreaks are normal phenomena in Northern Finland that occur repeatedly every 8-11 years. In our study, small values (i.e. cold summers) of growing degree day sums increased the probability of outbreaks with 3 other deciduous foraging species and warming environment might reduce outbreak events in the north. Species that have previously caused outbreaks might have already lost some of their potential to do so, meanwhile species with southern distribution are spreading towards the north. In our study, we discovered that all the studied species benefit from droughts. Also, temperature play a significant role in predicting outbreaks of moth species in high latitudes.

**Keywords:** Outbreaks, climate change, macro-moths, forest pests



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I am interested in macroecology, biogeography and systematics of species-rich moth communities; and also in the development of methods (light trapping and (UV) photography). My model groups are the species-rich moth clades of Geometridae (looper moths) and Arctiinae (tiger moths and woolly bears). The work has a focus on Central and South America, where thousands of species occur, many of them still undescribed. Current field work funded by DFG is carried out in Ecuador (pollinator networks) and Peru (elevational gradient).

### Five years LepiLED: Impacts on light trapping and moth monitoring

Light trapping is a common method that allows collecting large numbers of nocturnal insects, in particular Lepidoptera. LepiLED lamps were developed to facilitate the sampling (Brehm 2017) and they are used successfully in many projects all over the world. The light emitted by eight power LEDs contained in LepiLED directly corresponds to the three sensitivity peaks of most nocturnal insects (UV, blue and green in the electromagnetic spectrum). The small weight and size and low energy consumption (using powerbank batteries) have made it easy to collect in remote areas and when travelling. Recent experiments have confirmed that moths are indeed mostly attracted by ultraviolet and blue radiation. Field experiments showed that moth communities attracted by different types of UV lamps (i.e. UV only vs. mixed radiation) were very similar, and that effectiveness of lamps can depend on the habitat type. LepiLEDs can be used for manual sampling as well as in automatic traps. Light traps with (white) polypropylene vanes perform better than traps without vanes. For fieldwork in rainforests in both understorey and canopy in Peru and Ecuador, I developed lightweight bucket models with timers. LepiLEDs are also successfully used for the attraction of insects in automatic camera traps.

**Keywords:** light trapping, nocturnal insects, methods



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I am currently working as a researcher and monitoring scheme coordinator in the Finnish Environment Institute. In my work I coordinate the already 30-year-old Finnish moth monitoring scheme (Nocturna) and I also participate in coordinating the Finnish monitoring schemes for butterflies and other pollinators. Additionally, I do research work related to these monitoring schemes. My educational background is in ecology, and through an insect hobby I have gradually found my way into working with butterflies and moths. Lepidoptera are relatively new to me compared to some other insect groups, but I am eager to learn more and to continue working with monitoring schemes and conservation of butterflies and moths.

**Co-authors:** Juha Pöyry<sup>1</sup>, Anna Suuronen<sup>1</sup>

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### Distress of northern moths – population trends in the Finnish moth monitoring scheme (Nocturna)

With progressing climate change moth species with a northern distribution are expected to decline. We investigated the population trends of moth species with a northern distribution using the data from the Finnish moth monitoring scheme (Nocturna). The data included moth observations across 30 years (1993-2022) from 120 selected trap sites, comprising a spatially and temporally comprehensive representation of the monitoring sites. Cool-adapted moth species with a northern distribution were identified using European-wide moth handbooks including distributional maps. 84 northern species were observed in the selected trap sites during the 30-year study period. 61 of these species were abundant enough for calculating population trend indices by using TRIM-models (rtrim). Based on their distributional patterns the northern species were grouped into four classes in order of an assumed decreasing sensitivity to warming climate: boreal, northern boreo-montane, southern boreo-montane and boreo-temperate species. The proportions of population trends within the four distributional classes roughly followed the assumed order, and there was a notable surplus of declining species in all distributional groups except for the boreo-temperate group, where the numbers of increasing and declining species were equal. Around half of the 61 studied species showed declining trends and based on a geometric mean of population trends calculated across all species the northern species showed a significant overall decrease. The results indicate that the current level of warming, among other environmental changes, has already triggered wide-spread declines in populations of most cool-adapted moth species and their future seems highly uncertain also in their traditional strongholds in the northern regions of Europe.

**Keywords:** climate change, moths, northern species, population trend



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I am a Colombian biologist-entomologist from the University of Antioquia in Medellín, Colombia. I have a Master's in Biodiversity, Ecology and Evolution (BEE), focused on functional ecology from the University of Montpellier, France, and I recently started my PhD at the University of Jena, Germany. My research interests are the ecology, taxonomy and biogeography of tropical butterflies and moths, especially Sphingidae moths, and I am particularly interested in answering questions related to climate change and environmental change. I am also interested in conservation, conservation governance and citizen science in the tropics.

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### ANDIV: Exploring insect diversity in a global biodiversity hotspot

Tropical mountains are global biodiversity hotspots, with the tropical Andes being the most species rich region in the world. Most of their insect diversity has remained unexplored, and diversity patterns and functional traits of most organisms are still poorly understood. This is particularly true for the hyper-diverse groups of holometabolous insect which contribute more than three quarters of all described animal species, and perform key functions in ecosystems like herbivory, pollination, or decomposition. The DFG-funded project ANDIV started in September 2022, and we are investigating insect diversity in forest habitats along an elevational gradient between 250 and 3650 m in south-eastern Peru in 26 sites. We combine cutting-edge genetic and bioinformatic tools with ecological field work and experiments to investigate the patterns and drivers of insect biodiversity, and the project aims to contribute to a better understanding of the response of insects to climate change. Our sub-project focuses on Lepidoptera, including Geometridae, Erebidae-Arctiinae, Sphingidae, Saturniidae and Hedyliidae as model groups. For these groups, we will study functional traits such as size and colouration patterns and their change along the gradient. Primary results already show an extraordinary species-richness of the region, and we have already recorded more than 1500 species of Geometridae and more than 300 species of Erebidae-Arctiinae.

**Keywords:** elevational gradient, insect diversity, hotspot, tropical biology, Neotropics



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I am a doctoral student at Pavel Matos' Lab since September 2022 in the Czech Republic, focusing on biogeography and phylogenomics of Atlantic Forest butterflies.

I am fascinated by biodiversity evolution and how the present patterns have been generated. My previous master's thesis focused on the population structure of the Mediterranean coral *Cladocora caespitosa*. Currently, the aim of my PhD project is to explore the micro- and macro-evolutionary mechanisms that shape the diversity and distribution of Nymphalidae in the Brazilian Atlantic Forest.

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### Potential and limitations of Oxford Nanopore's MinION sequencing device as a tool for rapid biodiversity inventory in the field

Biodiversity loss is one of the major challenges we face, and conservation biology must cope with it at a much faster pace. Especial emphasis must be put in biodiversity hotspots, where anthropogenic impact is greatest and, therefore, effective conservation measures need rapid and accurate biodiversity assessments. In this context, we aimed at evaluating the efficiency of a portable DNA sequencing device (Oxford Nanopore Technologies' MinION) in generating genome-wide data in real time to be used for rapid phylogenetic analyses. We studied Lichen Tiger moths (Erebiidae: Arctiinae: Lithosiini) from the rainforest locality Sitio Bacchus, RJ, in Brazil's Atlantic Forest biodiversity hotspot. We prepared Rapid Barcoding libraries for 12 individuals from the genera *Cisthene*, *Aglylla* and *Pronola*, and sequence them in the field using a single R9.4.1 flow cell. This sequencing technology produces long reads, but the error rate is still higher than other approaches (e.g., Illumina sequencing). Therefore, processing with this kind of data obtained during the field work requires optimized workflows depending on the final quality and quantity of reads. Here, we present an assembly-free approach consisting of mapping demultiplexed, clean reads directly to reference loci of interest with the aim of inferring rapid and accurate phylogenetic hypotheses. We discuss the potential and limitations of this technology (e.g., quantifying precise genetic distances may be limited depending on the quantity of generated long reads), as a tool for rapid biodiversity inventory.

**Keywords:** Lichen Tiger Moths; Lithosiini; Brazilian Atlantic Forest; nanopore sequencing; conservation biology



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**ECOLOGY**

I'm an ecologist currently working as a doctoral researcher in the research project «Global change impacts on northern animal communities: from mechanisms to ecosystem-level implications», led by Docent Sami M. Kivelä at the University of Oulu. I study how the abundance and community dynamics of Lepidopteran moths have responded to global change over the past three decades in Finland. Further, whether and how the moth abundance changes are reflected in trophic interactions, specifically, bottom-up effect on insectivorous birds.

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### Ecological and life-history traits predict temporal trends in biomass of boreal moths

Dramatic insect declines, and their consequences for ecosystems globally, have received considerable attention recently. Yet, it is still poorly known if ecological and life-history traits can explain declines and whether insect decline occurs also at high latitudes. Insects' diversity and abundance are dramatically lower at high latitudes compared to the tropics, and insects might benefit from climate warming in high-latitude environments.

We adopted a trait- and biomass-based approach to estimate temporal change between 1993 and 2019 in Finnish macro-moth communities by using data from 85 long-running light traps. We analysed spatio-temporal variation in biomass of moth functional groups with Joint Dynamic Species Distribution Models while accounting for environmental variables.

We did not detect any declining trends in total moth biomass of moth functional groups, and most groups were stable over time. Moreover, biomass increased for species using coniferous trees, lichens, or mushrooms as hosts, multivoltine species, as well as monophagous and oligophagous species feeding on trees. We found that length and temperature of the growing season, winter climatic conditions, and habitat structure all partially explained variation in moth biomass.

Although boreal moth communities are rapidly changing due to species turnover, in terms of total biomass they seem to contradict the trend of dramatic insect declines observed globally. This may lessen the immediate possibility of negative bottom-up trophic cascades in boreal food webs.

**Keywords:** climate change, functional trait, insect abundance, Joint Dynamic Species Distribution Models, time-series analysis



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I am a PhD student in the INSECT DOCTORS ITN program studying diet-microbiota-pathogen interaction in Lepidoptera pests. My current focus is to understand how diet quality shapes gut microbiota and how this affects growth and immunity during pathogen challenge, and the mechanisms underlying these interactions. Find out more about my research on <https://www.insectdoctors.eu/en/insectdoctors/show/project-14-microbiota-mediated-food-protection-against-lepidopteran-pathogens-fr.htm>

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### The active and inactive gut microbiota of Lepidoptera: Effect of diet composition and implications for growth

In many insects, the gut microbiota has a functional role in nutrition. However, the situation is less clear in Lepidoptera. Field studies suggest that the microbiome may not be stable and is determined by diet, while in the laboratory lepidoptera are routinely reared on artificial diet containing broad-spectrum antibiotics with unknown effects on microbial communities. Methodological approaches may also bias the characterization of lepidopteran microbiomes and inflate estimates of variation between and within studies. Understanding the make-up and stability of microbial communities, and whether perturbation via diet and antibiotics affect insect growth, is important for understanding host-microbe interactions and optimizing insect rearing. In this study we assessed how alfalfa and wheat germ based artificial diets affected the growth and development of *Spodoptera exigua*, in presence and absence of streptomycin. Alfalfa diet improved larval growth, pupal mass, and survival, but antibiotics were only beneficial for the wheat germ diet. Further, to understand how sampling methods affect the way we characterize microbiomes, we evaluated the diversity of metabolically active (cDNA) and inactive (DNA) gut bacteria. Gut microbial diversity and composition, studied only in the alfalfa diet, showed that *Enterococcus* was the most dominant genus in the metabolically active cDNA subset while spore-forming *Bacilli* were very common members of the DNA community. Studies that exclusively use DNA-derived community composition may include environmental DNA, spores or dead bacteria, while RNA-derived communities are more likely to give an accurate representation of the diversity of active gut microbiota that are potentially interacting with hosts.

**Keywords:** cDNA metabarcoding, microbiome, diet interaction, antibiotics, gut bacteria viability



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I am doctoral student at Université de Bourgogne, within the Biogéosciences laboratory (CNRS, Dijon, France). Under the supervision of Philippe Louâpre, my research focuses on the collateral damages of fungicides on insects. Given Burgundy's renowned vineyards, I investigate the pest-related issues in this agricultural context. My particular interest lies in studying the response of the European Grapevine moth (*Lobesia botrana*, Lepidoptera: Tortricidae), a major pest affecting vineyards, to the principal fungicide used in both conventional and organic agriculture: Bordeaux mixture.

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### Side effect of copper-based fungicide on untargeted pest: a case study of European Grapevine Moth

Global use of pesticides is rising worldwide, together with increasing pest pressure under climate changes. Among pesticides, fungicides not only affect targeted pathogenic fungus but can also potentially impact all other organisms within agroecosystems. However, little is yet known about the way fungicides affect non-targeted pests. The purpose of this study was to determine the extent to which copper-based fungicide impacts the performance of the European Grapevine Moth (EGVM) *Lobesia botrana* (Lepidoptera: Tortricidae), attacking vineyards in Europe, the Middle East, and North and South America. Even if this major pest is not targeted by copper-based fungicides, it is chronically exposed to chemicals used during the vegetative growth of vines. Based on laboratory experiments, we explored the effects of copper consumed by larvae during their development on reproductive traits and behaviors. We found overall adverse effects of copper on the EGVM performance, both developmentally and reproductively. Copper consumed during the larval development negatively impacted almost all physiological traits (larvae survival, development time to emergence, fertility, fecundity, spermatophore size and quality). However, we did not detect effect of copper on any reproductive behaviors (mating success, pre-mating latency and mating duration). Despite this apparent beneficial effect of copper treatments in limiting EGVM populations, copper could however, affects other protagonists (predators, parasitoids, pollinators), generating adverse effects for integrated crop management.

**Keywords:** Copper – European grapevine moth – Pest – Fungicide – Viticulture

# SHORT TALKS

**Feza Can**

**SYSTEMATICS**

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### Geometrid Moths of Turkey, a complete inventory of the family

Geometrid moths with close to 24,000 known species constitute the second largest lepidopteran family. Koçak & Seven (2001) published an overview of the geometrid moths of Turkey, as a part of the Lepidoptera checklist of this country. This list was out of date even in its time being, containing many mistakes and without any detailed bibliographic data. The subsequent editions of checklists of Lepidoptera of Turkey by Koçak & Kemal (2006, 2007, 2009) still contain a large number of errors, misidentifications, unclear taxonomic status of some taxa, and many misspellings. Additionally, the bibliographic data did not cover all important works related to the fauna of Turkey and the phylogeny and classification of the geometrid moths are outdated. Okyar & Mironov (2008) published a more carefully researched up-to-date checklist of the geometrids of European Turkey. Additionally, many species of this family in Turkey were critically examined in the framework of the book series "The Geometrid Moths of Europe", as well as in numerous taxonomic revisions. A new catalogue on the Geometrid moths of Turkey is under preparation, aiming at providing a comprehensive overview and at updating nomenclature, taxonomy, and phylogeny in the catalogue. Data on distribution and endemism shall be presented as well. In this talk, we will introduce this project by presenting details and further perspectives.

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**LEPIDOPTERA IRANICA, call for the next update**

The most comprehensive and completed inventory catalogue of the order Lepidoptera in Iran is recently published as open access online version, as well as printed version. The catalogue summarized the data of all up to now published literature on the Lepidoptera fauna of the country. All together 4,812 species in 70 families regarded as present in Iran and 114 species regarded as error reports. The catalogue sorted all species phylogenetically and listed the synonym names that were reported from Iran, gave detailed information on provincial distribution of each species, listed the type localities when they were in Iran as well as the endemic species. Finally, whenever needed remarks were added to clarify misspellings and odder ambiguities. An update to this catalogue is in preparation and this short talk will call contribution of all lepidopterists, who publish new data on the fauna of Lepidoptera of Iran.

**Keywords:** Catalogue, Iran, Lepidoptera, Middle East, Palearctic

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**Zygaenidae of Turkey**

Our knowledge on the Zygaenidae fauna of Turkey has significantly increased during recent years. An application of newly synthesized sex attractants from the series EFETOV-2 has allowed us to find some species hitherto unknown in Turkey (for example Rhagades pruni and Jordanita globulariae) and clarify many distributions. So far 56 Zygaenidae species from two subfamilies, five genera and 14 subgenera are known from the territory of the country. Five species are endemic to Turkey, viz. *Jordanita (Jordanita) chloronota*, *Zygaena (Agrumenia) formosa*, *Z. (A.) peschmerga*, *Z. (Mesembrynus) lydia*, and *Z. (Zygaena) problematica*. Many species are subendemic (can be found only in Turkey and surrounding countries).

The aim of our project is summarizing all information on Turkish Zygaenidae, obtaining new data by targeted expeditions and creating distribution maps of all species.

A current overview of the data on the biology, ecology and main characters will be given. The possible steps for the conservation of endemic and rare species will be discussed.

The authors hope that this research will stimulate new investigations of this Lepidoptera group in Turkey and adjacent countries.

**Keywords:** Zygaenidae, Turkey, endemic species, conservation

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### Landscape-level determinants of butterfly species richness in northern Europe

Human-induced changes in habitat amount and quality form the key driver behind the negative trends in global biodiversity. Conservation actions must be based on solid knowledge of the factors affecting species richness in the remaining habitat fragments. Besides the proximate parameters of the habitat patches, it is critical to consider a broader spatial context when habitat quality is evaluated. Here we present an analysis of landscape-level determinants of butterfly species richness based on a country-wide survey in Estonia, representing the north European forest zone. This study compares favourably to previous research in its scope (over 1200 systematically selected sites), and provides a relatively 'natural' reference point for the analyses based on areas with higher human population density. The number of butterfly species locally recorded was sought to be explained by variables describing the surroundings of the study sites at four different spatial scales. The proportion of forest land was by far the strongest factor (positively) affecting the number of butterfly species recorded, followed by soil alkalinity. Notably, the effects of forest land area at the minimal (250 m) and the maximal (2,000 m) spatial scales were partly independent of each other. The first effect likely reflects immediate habitat quality while the latter should be related to the colonisation-extinction balance in the metapopulation context. The correlates of anthropogenic pressure had little effect. The results highlight the key role of designing responsible forestry practices in the regional context of nature conservation.

**Keywords:** landscape ecology, distribution mapping, forest, diversity, Papilionoidea

## KEYNOTE SPEAKER



**Sandra Schachat**

**SYSTEMATICS**

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I am a postdoctoral fellow in Dan Rubinoff's lab with interests in the fossil record, morphological evolution of Lepidoptera, and parthenogenesis in the context of sexual antagonism. I am particularly interested in the early fossil record of Pterygota and the early evolution of Lepidoptera. My research into both fossils and moths revolves largely around wings. During geologic intervals that predate major amber deposits, the fossil record of insects consists primarily of wings. When studying extant Lepidoptera my main focus has been on wing morphology: veins and color patterns. My university degrees are in Art History, Entomology, and Geology, and I enjoy conducting research that spans these disciplines. During the past few years I have been particularly interested in the question of whether we can pinpoint true evidence of absence in the fossil record, and more generally, what the fossil record can and cannot tell us.

### Evaluating putative fossil gaps for Lepidoptera and Pterygota: A comparative approach

The fossil record of winged insects (Pterygota) is famously incomplete; the fossil record of Lepidoptera, all the more so. The ages of both Pterygota and Lepidoptera remain contentious because both undoubtedly originated before their first known appearances in the fossil record. Time-calibrated molecular phylogenetic studies present an available but imperfect alternative to a direct reading of the fossil record for estimating clade ages. Certain age estimates suggest that both Pterygota and Lepidoptera evaded fossilization for tens of millions of years during their early histories. However, whereas Pterygota appear to have diversified rapidly following the origin of wings, Lepidoptera appear to have diversified more slowly. Pterygota are unknown from the fossil record until ~325 Ma, shortly after which the major groups such as Holometabola appear and quickly outnumber all other terrestrial arthropods. In contrast, the few dozen fossil Lepidoptera known from the first ~100 Myr of the group's history have all been assigned to Monotrysis.

There are several plausible explanations for why Lepidoptera appear so sporadically during the first ~100 Myr of their fossil history, including poor fossilization, rarity, and possible misidentification. The scales on the wings of Lepidoptera cause them to float, hindering fossilization. Monotrysis are not particularly diverse or abundant today, and there is no reason to expect that they would have been more abundant earlier in their history, before the diversification of angiosperms. Additional Monotrysis from this interval may have been confused for co-occurring enigmatic Amphiesmenoptera, such as Necrotauliidae.

None of these potential explanations apply to Pterygota as a whole, however. For example, the wings of Pterygota cannot be confused with wings of other invertebrates. In short, the appearance of Lepidoptera in the fossil record during their early history casts further doubt on the plausibility of a scenario in which Pterygota evaded fossilization completely for tens of millions of years.



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## SYSTEMATICS

I was born and brought up in England, inheriting an interest in Lepidoptera from my father Ian. My education was primarily classical (Latin and Greek literature) until I decided to take a degree in Biological Sciences at Exeter University from 1991 to 1994. I moved to Australia in 1995 to do my PhD at the Australian National University in Canberra on Nepticulidae systematics, supervised by Ebbe Nielsen and Penny Gullan. After John Dugdale's retirement, I came to New Zealand and started as lepidopterist at NZAC in 1998. I have been here ever since, revising parts of the Xyloryctidae and later Noctuidae, always with John as mentor and friend until his passing in 2020. I have now turned my attention to the strange, diverse and misunderstood New Zealand fauna of Tineoidea.

### Phantasmagoria unfettered: the astonishing *Eschatotypa* group of New Zealand (Lepidoptera: Tineoidea)

The pioneering Alfred Philpott illustrated the genitalia of many of the New Zealand 'Tineidae' back in 1927. He revealed some extreme morphological peculiarities, notably in the genera *Eugennaea* and *Eschatotypa*, but did not alter the classification. It has subsequently been suggested that these genera may belong to Dryadaulidae (formerly Tineidae: Dryadaulinae), but in many respects they are almost polar opposites of *Dryadula* in structure and do not fit the current definition of the family. Very little has been published on these moths since Philpott's day. New work on the biology and morphology of the '*Eschatotypa* group' shows it to be an unexpectedly diverse but probably relictual lineage with such bizarre structural modifications that Gaden Robinson referred to one species as a 'morphologist's nightmare'! My investigations of the morphology of the group, as well as the discovery of the previously unstudied fungivorous larvae, are pointing the way to a more robust systematic placement. This is supported by molecular phylogenetic work (by Niklas Wahlberg) in progress. The group appears to be nearly endemic to New Zealand, but some intriguing clues suggest that a few members may have been overlooked or misclassified elsewhere in the world.

**Keywords:** Tineoidea, Dryadaulidae, fungivory, asymmetry, classification



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## CONSERVATION

Sajad Noori is a PhD student at Hamburg University and currently conducting his research at the Nature History Museum in Stuttgart. He employs a biogeographical perspective to examine the distribution patterns of different insect groups in Iran. Utilizing machine learning approaches, Sajad investigates the environmental variables that have historically shaped biodiversity hotspots and centers of endemism. This work will allow him to assess the conservation gaps and evaluate the impacts of human-induced threats on insect groups both in the present and in the future.

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### Lepidoptera under human-induced threats: a case study on Iranian Lepidoptera

Insects are facing a tremendous population decline at a global scale. This decline has shown to be mainly the result of human-induced threats such as habitat destruction, agricultural intensification, and climate change. As part of this, Lepidoptera are affected significantly by anthropogenic pressures. Yet, our knowledge regarding the extent and magnitude of the insect decline is geographically and taxonomically biased toward developed countries and few iconic groups. Two of global biodiversity hotspots lie in Iran, signifying the importance of the country for global diversity. This is mirrored by Lepidoptera diversity: over 4,800 are known in Iran of which 19.7% are endemic. In this study, using the most comprehensive dataset derived from the recently published project of Lepidoptera Iranica, we shed light on distribution patterns of Lepidopteran species and explore the biodiversity hotspots in Iran. Machine learning approaches were applied to predict the range of species under different future climate scenarios. Moreover, we discuss the impact of different human-induced threats like drought, fire, and overgrazing on the biodiversity of the group. Our results illustrate that under pessimistic climate scenarios, most species will experience a dramatic decline and shift poleward or to higher elevations. The shift in species ranges is more profound in the mountainous areas in the central and southern parts of Iran. These regions are home to a high number of endemic species with extremely narrow distribution. Significant conservation gaps have been reported for vertebrates, therefore our results can provide an insight to conservation status of insects in Iran.

**Keywords:** Climate change, insect decline, butterflies, moths, species-range shifts



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Marta Vila is Associate Professor of Genetics at the University of A Coruña [Spain], where she earned her PhD in 2004. Her dissertation was focused on the phylogeography of *Erebia triaria* (Nymphalidae). During her postdoc she cooperated with Carlos Lopez-Vaamonde in a project about *Graellsia isabellae* (Saturniidae), while doing research in other animal species. She is currently supervising a PhD thesis on *Erebia palarica*, as well as actively contributing to the Butterfly (BMS) and the EU Pollinator (EUPOMS) Monitoring Schemes.

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### **Landscape genetics of the protected Spanish Moon Moth in core, buffer, and peripheral areas of the Ordesa y Monte Perdido National Park (Central Pyrenees, Spain)**

One of the conservation projects carried out by the Ordesa y Monte Perdido National Park is the monitoring of the protected Spanish Moon Moth, *Graellsia isabellae* (Saturniidae), in several sites within the actual park, buffer zone, and peripheral area. Here we studied the genetic diversity, geographical structure, and connectivity of this iconic insect in those areas with the aim of producing evidence-based recommendations that might help the National Park staff in their decision-making. For this, we non-lethally sampled 402 adult moths from 17 sites and worked at two geographic scales: Western/Central Pyrenees and the area monitored by the staff of the National Park. The multilocus genotypes obtained for nine nuclear microsatellite markers allowed us to quantify genetic variation, investigate population structure, and calculate recent migration rates. Our results revealed a large-scale (ca. 125 km) west-east cline in allele frequencies that causes low overall genetic differentiation ( $F_{ST} = 0.038$ ) and similar levels of diversity among sites. Habitat connectivity revealed as an important element determining dispersal for *G. isabellae*, given the patchy distribution of the host plant (*Pinus sylvestris*) in the study area. Gene flow within and outside the National Park was proved, with a particular site of the buffer zone (Bujaruelo) acting as a source of migrants to other localities within and outside the National Park. This finding underlines the importance of considering buffer zones to preserve genetic diversity within protected areas, and that safeguarding the connectedness of pine patches is key to the conservation of this iconic moth.

**Keywords:** *Graellsia isabellae*, *Pinus sylvestris*, Isolation by Distance, Least cost path analysis



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I am a 26-year-old PhD student from Belgium. In 10 years, my passion for moths has developed from catching them in my own garden to doing eco-evolutionary research in which moths serve as my study system to address eco-evolutionary and conservation-related issues. So, my dream of turning my hobby into my job has come true and now I investigate the effects of artificial light sources on moths, both in field studies and experiments in our lab.

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### **Impact of light pollution on the development of the diurnal caterpillars of the Garden Tiger Moth (*Arctia caja*): an experimental approach**

There is mounting evidence for strong alterations in moth communities, including many species and population declines. Multiple drivers have been put forward as causes, but recently, light pollution caused by artificial light at night (ALAN) receives growing scientific attention. ALAN has been shown to affect biological cycles, feeding and pollination behaviour, but it can also disturb organisms by attracting or repelling them. We study the impact of ALAN on moths across their life cycle combining both field studies in gardens [i.e., community-level responses] and controlled laboratory experiments [i.e., intra-specific responses]. For our field study, we sampled moth communities in gardens with either high or low skyglow levels and presence or absence of street lighting to obtain a full factorial design. Besides the effects on species diversity, also changes in species traits within these communities are investigated considering multiple environmental factors. In this talk we will mainly focus on our first results of controlled laboratory experiments using the Garden Tiger Moth (*Arctia caja*), a moth species with mainly diurnal caterpillars. We reared first and second-generation caterpillars under dark night and ALAN-conditions with a split-brood design. We monitored several life-history traits like caterpillar growth, survival and adult morphology. Preliminary results indicate that ALAN has negative effects on larval survival and leads to accelerated development, but with varying results for the impact on growth.

**Keywords:** Light pollution – Moths – Development – Survival – Lab experiment



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Laura Torrado-Blanco is a PhD student from Universidade da Coruña [Spain]. She showed a passion for lepidopterans since very early in her career, and her graduate and Master's dissertations already focused on nocturnal species. Recently, she completed an internship at Uppsala Universitet, where she worked on *Leptidea juvernica* using NGS approaches. Now, Laura is studying the phylogeographic pattern and population genetics of *Erebia palarica* as her thesis project. She is also an active collaborator of the Butterfly (BMS) and the EU Pollinator (EUPOMS) Monitoring Schemes.

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### Past, present, and future of the NW Spanish montane endemism *Erebia palarica* Chapman, 1905

Alpine and subalpine biodiversity is particularly vulnerable to the rapid oscillations in environmental conditions derived from climate change. Recent modelling showed that only three of the 19 species of *Erebina* (Nymphalidae, Satyrinae) currently present in the Iberian Peninsula would remain there in the worst-case scenario for 2070. One of them is *Erebia palarica*, endemic to the mountain ranges of Northwest Spain. We performed an integrative analysis combining genetic and morphometric approaches, using samples from the complete distribution range to determine the evolutionary history and current population structure of *E. palarica*.

We sequenced a 786bp fragment of the mitochondrial Cytochrome Oxidase I (COI) gene in 305 individuals and identified 24 haplotypes. The 95% statistical parsimony network revealed a double star-like pattern connected by a single mutational step. This result points towards a demographic expansion from two ancestral populations. This finding is congruent with the larger putative distribution area revealed by climatic modelling during the Last Glacial Maximum.

The current population structure was inferred after genotyping 262 individuals with seven microsatellite markers and a morphometric analysis of wings. Firstly, we detected a single cluster of 144 individuals (central-eastern part of the Cantabrian range) mostly affected by isolation by distance. Secondly, we found different levels of differentiation in the western localities. Actually, the westernmost site (Queixa, previously described as a subspecies), was recovered as a clearly separate unit by genetic and morphometric analyses. Lastly, the different effects of sex and locality on the variability of wing size, shape and pattern will be discussed.

**Keywords:** phylogeography, glaciations, microsatellites, mtDNA, morphometry



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I am a conservation biologist at the University of Liverpool, where I have built a research group starting in 2013. I research how the spatial arrangement of land use and management affects the viability of species. The amount and pattern of our nature reserves and green spaces will strongly affect whether species can survive under climate change. I use a mixture of empirical and modelling approaches to investigate how species are already responding, and what might happen in the future. Much of my work has focussed on Lepidoptera as case studies, using large-scale and long-term data sets. I have also developed new theory to describe whether, and how quickly, species will be able to shift their geographic range when their habitat is sparse and fragmented. This theory has been translated into the software Condatis ([www.condatis.org.uk](http://www.condatis.org.uk)), to help in targeting habitat restoration and additional protection. I previously worked at the Universities of York and Leeds, and have published over 50 peer reviewed papers with approximately 200 co-authors

### Where and why are species' range shifts hampered by unsuitable landscapes?

There is widespread concern that species will fail to track climate change if habitat is too scarce or insufficiently connected. Targeted restoration has been advocated to help species adapt, and a 'conductance' metric has been proposed, based on simulation studies, to predict effective habitat configurations. However, until now there is very little empirical evidence on how the configuration of habitat is affecting expansion at species' cool range margins. We analysed the colonisation events that have occurred in continuously monitored trap locations for 54 species of southerly distributed moths in Britain between 1985 and 2011. We tested whether the time until colonisation was affected by attributes of each species, and of intervening land cover and climate between the trap and the baseline distribution (1965-1985). For woodland species, the time until colonisation of new locations was predicted by the 'conductance' of woodland habitat, and this relationship was general, regardless of species' exact dispersal distances and habitat needs. This shows that contemporary range shifts are being influenced by habitat configuration as well as simple habitat extent. For species associated with farmland or suburban habitats, colonisation was significantly slower through landscapes with a high variance in elevation and/or temperature. Therefore, it is not safe to assume that such relatively tolerant species face no geographical barriers to range expansion. We thus elucidate how species' attributes interact with landscape characteristics to create highly heterogeneous patterns of shifting at cool range margins. Conductance, and other predictors of range shifts, can provide a foundation for developing coherent conservation strategies to manage range shifts for entire communities.

**Keywords:** Climate Change; Connectivity; Dispersal; Land Use; Lepidoptera



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Leading Laboratory of Biogeography and Diversification at Institute of Entomology, Biology Centre, Czech Academy of Sciences. Interested in various aspects of butterflies, from population biology and genetics to biogeography, evolution, and ecology.

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### Population size, behaviour, and dispersal of *Coenonympha tullia* (Lepidoptera, Nymphalidae, Satyrinae)

Large Heath, *Coenonympha tullia* (Müller, 1764), despite its large Holarctic distribution strongly declines over Central Europe. From 49 faunistic squares known from Czechia before 1980, distributed all over the country, the species is currently found in 7 squares only, all of them in South Bohemia. In 2022 we conducted a study to compare population and demography structures, behaviour, and dispersal abilities on two sites, one isolated in the lower part of the Třeboň basin, the second interconnected with other sites in the submontane part of Šumava Mts. Using mark-release-recapture (MRR) methods, we found that the estimated population in both sites is 2965 and 1681 individuals, respectively, biased towards females. The species display different behaviour patterns throughout its flight season and the species is capable of dispersal between suitable patches through a matrix of non-habitats. The currently inhabited sites suffer from the absence of nectar plants.

**Keywords:** butterfly; conservation; Mark-release-recapture; Czech Republic

**Acknowledgments:** The study was supported by National Park Sumava (contract F 164 B/S02).



## Caroline Kebaili

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## CONSERVATION

I am a third PhD student working for the Regional Natural Park of Haut-Jura, aiming at informing managers of peatland butterflies conservation. During my master degree, I specialized in population and landscape genetics, studying the Apollo butterfly *Parnassius Apollo*. I am currently part of a conservation project for four peatland butterflies, which also participates to a European LIFE program in favour of Franche-Comté peatlands.

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### Human and climatic impact on four emblematic species of butterflies in Franche-Comté and implications for conservation management

Peat bogs butterflies are characterized by their high level of habitat specialization, depending on peatlands complex hydrological functioning and natural fragmented distribution. Many of these species are declining and protected in Europe. To inform conservation measures in the context of climate and land-use change, it is essential to identify the importance of each of these factors in population declines. The Jura massif is the last French area where the Large heath (*Coenonympha tullia*), the Violet Copper (*Lycaena helle*), the Scarce heath (*Coenonympha hero*) and the Cranberry fritillary (*Boloria aquilonaris*), are co-distributed. Based on a non-lethal sampling of local populations, we used SNP markers and SDMs to study their demographic responses to past climate changes since the Last Interglacial to current days. We showed that despite important degradation of climatic conditions between the Last Glacial Maximum and Holocene, they have succeeded in limiting their ancestral population contraction. Besides, the dramatic decline they are currently experiencing corresponds to an improvement in the climatic conditions these species require, therefore supporting the hypothesis that habitat and landscape connectivity degradation is the main driver of population decline. We now study each species landscape connectivity within the massif to identify features influencing gene flow, using both Mixed Linear Population-Effect models and graph theory. The impact of the restoration or loss of habitat patches and ecological corridors on genetic diversity is also assessed in specific sectors using genetic simulations. All results are discussed with local field experts to propose specific management measures for each species.

**Keywords:** Population genomics – Species distribution modeling – Landscape genomics – Connectivity – Graph theory



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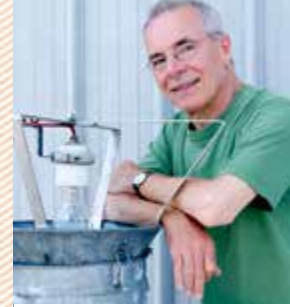
Dirk Maes is senior researcher at the Research Institute for Nature and Forest (INBO) in Brussels and is a part-time professor in Insect Conservation at the Radboud Universiteit in Nijmegen (the Netherlands). He is an advisor to Butterfly Conservation Europe and is also Editor-in-Chief of the scientific journal *Journal of Insect Conservation*. His research focuses on the conservation of insects, for example, by compiling Red Lists for a wide variety of insect taxonomic groups in Flanders and in Europe (butterflies, macro-moths, hoverflies, dragonflies, carabid beetles ...). He also studies strongly declining butterfly species (both ecologically and genetically) such as the Alcon Blue butterfly *Phengaris alcon*, the Silver-studded Blue *Plebejus argus* and the Grayling butterfly *Hipparchia semele*. With the results of these studies, he compiles species action plans and translocation or reintroduction projects to safeguard the presence of these threatened insect species in Flanders.

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**Species traits as a guidance for moth conservation in a highly anthropogenic European region**

Insects are declining rapidly during the last decades, but some species groups such as moths, however, remained under the radar because they are almost exclusively active at night and are, therefore, not readily observable by the general public. We recently compiled the first Red List of macro-moths in Flanders (northern Belgium), a highly anthropogenic region suffering from intensive agriculture, industrialization and urbanization. To do so, we used quantitative IUCN criteria and calculated changes in the distribution of 717 macro-moth species between the period 1980-2012 and 2013-2022. Thirty-nine species are Regionally Extinct in Flanders and a further 165 (23%) are threatened (41 Critically Endangered, 82 Endangered and 42 Vulnerable). By correlating the obtained trends for the Red List compilation with ecological or life-history traits using so called multi-species change indices, we were able to extract some general patterns from the Red List of macro-moths. Species of nutrient-poor habitats (such as marshes, heathlands, nutrient-poor grassland and coastal dunes) declined between the two compared periods, while generalist species and woodland species did not show a significant change in distribution. Species from cold and wet habitats significantly declined in distribution while species of hot and dry habitats increased. Species feeding on grasses strongly declined in distribution while species feeding on lichens, mosses and dead leaves strongly increased. Day-active species significantly expanded their distribution, while night active species did not show a significant change in distribution between both periods. Finally, species with a Mediterranean distribution and migrant species significantly expanded their distribution between both periods. These findings allowed us to formulate management and policy measures to protect macro-moths in Flanders more efficiently and to focus on the protection of the most endangered species and habitats.



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**The Lepidoptera of the Faroe Islands – a dynamic fauna**

The Faroe Islands are located about 285 km north-west of the Shetland Islands and 600 km west of Norway. They consist of 18 islands and numerous islets and have an area of 1,400 km<sup>2</sup>. The islands are of volcanic origin and mountainous with the highest point 882 m a.s.l. They were, at least partly, covered by ice during the last glaciation, and the present Lepidoptera fauna has arrived since. There is no endemic species. The climate is characterized by mild winter and cool summers (about 10 °C), strong, mostly western winds and frequent rain.

183 species of Lepidoptera have been mentioned from the Faroe Islands. Ten of these are due to misidentification or other errors, the occurrence of five species are unconfirmed (mostly "sightings"), and 31 species have with high probability occurred there after being introduced with trade from abroad. The remaining 137 species are either residents or migrants.

The number of resident species is low, probably less than 50 species have been able to maintain populations on the Faroe Islands for several decades or even centuries. Still the number of species on the list of Faroese Lepidoptera is growing, both from migration and introduction, supported by global trade and warmer climate.



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I am the Head of Ecology and Curator of Lepidoptera at the Senckenberg German Entomological Institute in Müncheberg. I obtained my PhD at Bonn University working on a molecular phylogeny of the butterfly subgenus *Agrodiaetus*. Before and after my PhD thesis I worked several years as an entomologist in Papua New Guinea and then became Assistant Professor at Vienna University for six years and afterwards researcher at the Department of Community Ecology of the Helmholtz Centre for Environmental Research - UFZ in Halle (Saale).

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### Conserving Madeira's threatened endemic butterflies

Madeira is a hotspot of threatened endemic butterflies in Europe. According to the most recent European Red List of Butterflies, two species, the Madeiran Speckled Wood (*Pararge xiphia*) and the Madeiran Brimstone (*Gonepteryx maderensis*), are listed as endangered, and one, the Madeiran Large White (*Pieris wollastoni*) even as Critically Endangered (Possibly Extinct).

In the course of a LIFE4BEST-funded project, intensive surveys along 534 km of survey routes across the whole island were carried out in 2021 and 2022 with the help of volunteers.

*Pararge xiphia* turned out to remain one of the most common species, despite its decline after the introduction of the Speckled Wood (*Pararge aegeria*) in the 1960s. However, its main strongholds are confined to undisturbed laurel forests in the centre of the island, whereas the invasive congener predominates in coastal areas. In contrast, *Gonepteryx maderensis* has become a low density species, and only a few major breeding sites remain near steep cliffs within the laurel forest, which harbour its larval foodplant, *Rhamnus glandulosa*. No sign was seen of *Pieris wollastoni*, which is now presumed extinct and thus becomes the first globally extinct European butterfly.

The talk discusses the reasons for the declines and possible steps to improve the conservation status of Madeira's endemic butterflies. Further monitoring is facilitated by newly set up transect routes, a recording app and training resources in multiple languages, which enable the involvement of citizen scientists, both from the local population and tourist visitors to the island.

**Keywords:** Islands; Madeira; hotspot; endangered butterflies; conservation



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**CONSERVATION**

I study the evolution of insect biodiversity at the population level. Thanks to hybridization capture methods it is now possible to obtain genetic information from museum samples. To analyse these data, I use and develop bioinformatics methods that allow to trace the evolutionary history of populations.

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### Museomics to retrace the decline of butterfly populations throughout the 20th century

The large-scale decline of insects in the past decades starts to be widely documented. The mechanisms, the kinetic and the causes of this decline, and in particular the role of anthropogenic activities, remain poorly understood. Indeed, studies documenting this decline are based on recent trends, since the 1970s, and rely on biomass estimations that do not fully reflect the state of populations. However, samples are available to undertake a large-scale study, both spatially and temporally (throughout the 20th century). The museum collections contain insects collected throughout this period and form real time series. Thanks to recent developments in museomics, it is now possible to access the genetic information carried by these samples and thus to study their demographic evolution over time. Through two studies, we will show that museum collection specimens constitute an invaluable sample source, potentially providing direct access to genetic variation over time. The first study used large time series of two butterfly species in Finland, *Erebia embla* and *Lycaena helle*, and showed that despite local variations, overall genetic erosion has increased across the last hundred years, as revealed by signatures of allele extinction and heterozygosity decrease. In one of the two butterflies, isolation by distance also increased through time, suggesting an increase in habitat fragmentation. The second study is a large study across Switzerland including two common butterfly species, *Polyommatus icarus* and *Pieris napi*, and aims to track specific responses to global changes.

**Keywords:** Museomics, Insect decline, Time series, Genetic diversity, Anthropic activities



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Nils Ryrholm is presently working as professor at the University of Gävle in Sweden. He is working on the development of sexual pheromones as a tool in insect conservation. He is also studying climatic impact on insects, in recent years mainly changes due to global warming. Nils is furthermore strongly involved in several conservation projects like enhancing biodiversity in infra-structural habitats and the red-listing of butterflies and moths – on both national and European level.

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### In search of unknown biodiversity – and their resources

EU has initiated the construction of a Red List for European macro moths, including species from the families clearwings (Sesiidae) and burnets (Zygaenidae). Most species in these two families are day active and particularly good indicators on habitat quality and -continuity. One advantage is that most species are specialized on hostplants found on high quality grasslands of various types. However, especially the clearwings are difficult to detect with classical entomological methods. Likewise, burnets may be difficult to discover in declining and fragmented habitats and sometimes also difficult to distinguish. Older distribution maps show that most these taxa were widespread in the pre-industrial landscape. When looking at recent distribution maps for these species, it becomes evident that both our present knowledge, as well as the actual occurrences unfortunately are considerably more restricted. In addition, within both families there are several complexes of sibling species which are hard to determine in the field by nonexperts.

Here we review our knowledge on the pheromones used by both these families and highlight the needs for creating new attractants for several European clearwings and burnets. Monitoring of such key species would effectively facilitate the evaluation, protection, monitoring and upholding of valuable grasslands in Europe. We highlight the use of pheromones in citizen science programs such as the French project SESIF, as a cost-efficient way to increase the knowledge of the present situation of these important indicator species.

**Keywords:** Red listing of Moths, EU conservation strategy, pheromone attraction, Zygaenidae, Sesiidae



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Born in Innsbruck (Austria) in 1950. Studies in biology and earth sciences (master) and zoology and botany (PhD) at University of Innsbruck. 1974–2015 Head of Department of Natural History at Tiroler Landesmuseum, Ferdinandeum. 2005–2006 director of Ferdinandeum. Main work of life has been the creation and establishing of an international centre for documentation of the Lepidoptera of the Alps in the Ferdinandeum. Special interest in taxonomy: Zygaenidae (orbis terrarum). Organisation of meetings, symposia and congresses in Austria and other countries. Lecture activities at University of Innsbruck and Crimean State Medical University, Simferopol, Crimea, Ukraine. Hon. Prof. 2006 (CSMU, Simferopol). Ca. 300 publications, amongst these various books, e.g. Revision of the American Zygaenidae, Zygaenid Moths of Australia. Since 2000 head of the Conservation Committee of S.E.L. (Societas Europaea lepidopterologica), 2007–2016 president of S.E.L. Since 2008–2016 member of the National Committee of ICOM Austria. Retired since 2015.

### Promising developments in the upper Vinschgau valley/Val Venosta and in the SEL Study Area Sesvenna (Südtirol/Alto Adige, Italy) regarding the distribution and diversity of Zygaenidae

Since 1972, Zygaenidae have been used as a model group to study changes in the biodiversity of the Obervinschgau/Upper Val Venosta in Südtirol/Alto Adige in Italy. For half a century these studies target on the influence of agricultural poisons used in the apple industry on Zygaenidae populations. After many years of dramatically declines of biodiversity, the communities try to stop pesticide use in their territories. The citizens of Mals/Malles have undertaken a referendum in 2014 where a strong majority of the local population voted for a complete stop of use of chemical poisons in agriculture on their territory. This referendum has been strongly counteracted by the government of the province and, of course, by the fruit companies and the chemical industry. However, the local people did not give up and changed agriculture. With success! In 2021 for the first time after decades, Zygaenidae species could be observed on the wing again on flowery meadows in close vicinity of intensively used apple orchards that were still sprayed several times during the year. But these orchards are now maintained with special organic methods and with special care on the surrounding biodiversity. Six Zygaenidae species have already re-invaded meadows that were for a long time completely free of members of this Lepidoptera family. Moreover, an international project to support ground nesting birds was started in 2021 in Mals/Malles and some contract-farmers are now cutting the grass in mosaic clusters slightly later or some even much later than in the earlier years. This led to an immediate re-invasion of these meadows by Lepidoptera and by Zygaenidae. Many of the Lepidoptera that re-invade these meadows are coming from the SEL Study Area Sesvenna. An important part of our Study Area is situated on the territory of the community of Mals/Malles. Since 2004, SEL has a written contract with the three communities Taufers/Tubre, Mals/Malles and Graun/Curon. Now, our effort is bringing benefit to the re-naturalized land nearby. The communities have even plans for an ambitious project to re-introduce strictly controlled grazing with some sheep and goats on the extremely biodiverse steppe-slopes within the Study Area to keep invading bushes (mainly *Prunus spinosa*) out from the valuable steppe environment.

# POSTERS

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## Diversification of phyto-predaceous lycaenid butterflies (Polyommatae, Lycaenidae) during the Miocene aridification of the African continent

Over the past 20 Myr, Africa became increasingly arid, leading to both radiation and extinction of species. The mechanisms behind this are poorly understood. Phyto-predation, a rare life history where caterpillars feed first on plants, then on ant brood, may have favored the explosive diversification of the afro-tropical genus *Lepidochrysops*. It is hypothesized that ant nests provide shelter from fire and drought, and a stable food source in arid environments. A study of *Lepidochrysops* and relatives (Espeland et al. submitted) supports the hypothesis that massive diversification occurred through the evolution of phyto-predation (6.5 Mya), as an adaptive response to the aridification. This allowed the species to survive in changing environments and disperse to drier regions.

My PhD project investigates this hypothesis on a broader scale.

A phylogeny of the genus *Lepidochrysops* and relatives (*Euchrysops* section) will be generated using a museomics approach. Samples from >200 of the ~210 species are available. Distribution data is collected by georeferencing label data (>20.000 specimens). This data coupled with morphometric data will be used to test the following hypotheses: 1) Ant parasitism evolved only once in the *Euchrysops* section; 2) The high species diversity in the phyto-predaceous *Lepidochrysops* is real, not a taxonomic artefact; 3) Ant parasitism is a key adaptation for survival in dry habitats; 4) Diversification of the group started in wetter, older habitats and shifted several times to available drier habitats; 5) Ant association affects niche, molecular and morphological evolution.

All collected data will be used for an integrative taxonomic revision.

**Keywords:** butterfly-ant interactions, *Lepidochrysops*, myrmecophagy, phyto-predation

SYSTEMATICS

1

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## Floral preference of *Parnassius apollo* (Linnaeus, 1758) in a Mediterranean habitat

The endangered butterfly *Parnassius apollo* (Linnaeus, 1758) is restricted in Southwestern Europe to isolated areas at relative altitude where it finds adequate breeding conditions. The butterfly frequently prefers open lands, in which the adult males make long patrolling flights, and the females disperse the eggs. The presence of flowers greatly conditions these movements. During the adult life, which can last between days and weeks, the nectar represents the only sustenance for the butterfly. However, the butterfly does not seem to exploit all the nectar resources at its disposal, concentrating on only some types of flowers that do not respond to a taxonomic bias. During the monitoring of a metapopulation of the species in the province of Castellón (Spain) between the years 2015 and 2022, we have surveyed the use of the nectar-bearing species present in the area. We have identified them and studied the predominant morphological characteristics and their coloration. The Apollo butterfly seems to prefer bluish to purple flowers arranged in inflorescences, ignoring yellowish or white species, even if they are abundant. Among his favourite flowers are some Compositae and Caprifoliaceae. Since the availability of water and nitrogen seems to condition the presence of these flowers, which are usually biennial, it is important to take these preferences into account in relation to any strategy for habitat management and conservation.

**Keywords:** Apollo butterfly, flower colour, nectar, conservation, pollinator

ECOLOGY

2

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### Monitoring butterflies by transect count in the Őrség region (West Hungary)

The efficiency of grassland management along the local population trends of butterflies of the Őrség National Park have been monitored by transect counts since 2017. Our poster presents the first five years of sampling carried out on humid meadows that were utilized by mowing. The study focused on ten different locations, with a km long transect at each site. We detected a total of 82 species that represented 77% of the local fauna. The most abundant species was *Melitaea athalia* followed by *Maniola jurtina*. Generalist grassland species were also frequent. In contrast, species of woodlands and scrubs, (e. g. *Satyrrium* sp., *Boloria euphrosyne*) along some local rarities (e.g. *Erebia aethiops*, *Charcarodus flocciferus*) were detected a single time only. The number of protected species was fairly high of which, the most abundant were *Boloria selene* and *Maculinea teleius*.

In spite of the specific habitat management (butterfly friendly) on meadows, the populations showed a decreasing trend. The medians between each sampling year did not differ significantly (Kruskal-Wallis test  $p=0.8895$ ) while the linear trend lines showed decreasing species richness and abundance of butterflies. However, the population of *Maculinea teleius*, which is a flagship and umbrella species of the local humid meadows, stayed fairly stable over time.

Transect count will be continued in order to monitor the recent population trends of butterflies and efficiency of habitat management in the Őrség National Park. In addition to the current method, we intended to implement supplementary measures on environmental variables in the near future.

**Keywords:** Lepidoptera, conservation, grasslands, decline, management

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### An online platform to access the Lepidoptera collection database of the Muséum national d'Histoire naturelle, Paris (MNHN)

We present the online platform designed to access the Lepidoptera collection database of the MNHN. Since its creation over 10 years ago, it has been significantly improved and developed by the scientific and technical team of the Lepidoptera division. As of today, it includes several thousands of individual specimen records, many of which are type specimens with standardized images of both upper- and under-side views, labels and scale. The process of digitizing entire drawers has been initiated in multiple families, including those containing accession material, and is currently in progress. This database is freely available to the entire scientific and amateur community. Here, we present its interface, research tools and options that help you navigate and access its contents.

**Keywords:** Website ; Moths ; Butterflies ; Specimen ; Type specimens

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### An integrative taxonomic revision of Gelechiidae of Southern Africa

This project is a part of the long-term study of the Afrotropical Gelechiidae by the first author, aims to revise several groups of Gelechiidae of southern Africa using an integrative approach, especially based on morphological and genetic data. In particular, the integrative revision of the tribes Gnorimoschemini and Litini will be provided, and the generic concept of some other taxonomic groups will be reconsidered based on modern knowledge on Gelechiidae taxonomy. Several genera of Gelechiini and Apatetrini will be revised accompanied with description of new species, establishing new synonyms and providing other taxonomic and nomenclature changes. A checklist of the South African Gelechiidae and online resources such as Afromoths will be updated in accordance with new taxonomic changes and new faunistic records proposed in recent decades and results from the proposed studies.

**Keywords:** Afrotropical, Gelechiidae, revision, taxonomy

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### Measuring the impact of forest management on the structure and composition of moth communities using automatic and manual light traps

Human-induced environmental impacts threaten global biodiversity, including temperate forests which have been highly altered and reduced. Despite these disturbances, temperate forests serve as biodiversity hotspots and play an important role in the conservation of declining species. Insect decline, often overlooked, is of significant concern due to its consequences on ecosystems and human health. To reverse insect decline, we first need to understand the influence our activities have on their populations. In this regard, our study focused on the impact of the French «futaie régulière» forest management method on moth communities.

First, we chose to evaluate the effect of forest management on species richness and diversity. Sampling took place using two types of automatic light traps (T-traps LepiLED and Skinner Actinic) in the forest of Tours-Larçay-les Hâtes, focusing on two contrasting plots: a naturally evolving plot and a managed plot. Contrary to our hypothesis, we found that forest management does not appear to have a significant impact on the moth communities we studied.

However, to confirm our results, we first had to improve upon our current biomonitoring protocol, focusing on increasing the sampling effort of micro moths which was initially insufficient. This was our second step. To do so we chose to use Bioform towers along with our automatic traps.

By doing so, we concluded that the “futaie régulière” forest management method has no effect on the richness and diversity of both the macro moth and the micro moth communities located in the forest of Tours-Larçay-les Hâtes.

**Keywords:** biomonitoring, community ecology, moth decline, forest disturbance

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### A shared taxonomic register as backbone for a knowledge database on Lepidoptera in France

The research support unit PatriNat (OFB, MNHN, CNRS, IRD) is responsible for managing and updating the national taxonomic register of all living organisms occurring in France, untitled TaxRef. It constitutes the backbone for the development of a knowledge database on species. This database includes the conservation status, distribution and life traits of Lepidoptera species, together with interactions with other species, in particular host plants and parasitoids. The taxonomic register for Lepidoptera and the associated knowledge database are updated mainly based on an associative network of amateur experts. Those data are subject to various processes ensuring its quality, particularly in terms of accuracy. They are available to the community, naturalists or researchers via an internet portal (<https://taxref.mnhn.fr>). It is planned to be available through a Restful API and the associative network can rely on the numeric diffusion of these data to build their own tools at the taxonomic and geographical levels specific to their field of action. Regarding Lepidoptera, the numeric diffusion is used by the portal Artemisiae designed by the association oreina, in which GIRAZ-Zygaena plays a joint role in validating observation data and photos. Artemisiae aggregates about 1,5 million data, regarding 5200 species of the 5600 species living in France (Palearctic part).

**Keywords:** Lepidoptera, taxonomic register, knowledge database, open data

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### Moth communities in natural, seminatural and agricultural habitats within semi-arid landscapes of Morocco

Moths are an important and diverse group of insects that play a significant role in the functioning of ecosystems by serving as pollinators and also as prey for a wide range of predators. In addition, moths are also considered important bio indicators by providing valuable information on the parameters of the ecosystems and the impacts of environmental change. In this study, we investigated the impact of different habitat types on moth communities in the semi-arid landscapes of High Atlas Mountains of Morocco, comparing natural, semi-natural, and agricultural habitats typical of the region. We conducted our study in six villages from September to November 2022, surveying moth populations in each of the three habitat types using automatic sugar bait traps. We collected more than 2200 individuals of Macroheterocera representing Noctuidae, Erebidae and Geometridae. Identifying the material is an ongoing challenge which must rely on a combination of methods as no comprehensive reviews or even just checklists of moths of Morocco are currently available. By examining the effects of habitat on moth populations, we are seeking to better understand the ecology of these insects in arid environments, something which is urgently needed to inform conservation efforts. This is of primary importance as these habitats are facing increasing pressure from human activities such as agriculture and urbanization. Besides the ecological and conservation-biological context, our study is bound to substantially contribute to the knowledge on the taxonomic diversity and composition of moth communities in the study region.

**Keywords:** moth community, sugar bait traps, semi-arid landscapes, Morocco

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### Mapping ignorance: Updating the information on the geographic distribution of the Iberian and Balearic butterflies (Lepidoptera, Papilionoidea)

Gaps in our knowledge of the geographic distribution of organisms represent a problem for the identification of biodiversity patterns as well as for planning biodiversity conservation strategies. The objective of this work is to determine the real coverage of present butterfly (Lepidoptera, Papilionoidea) distribution data in the Ibero-Balearic area in order to identify the most poorly-studied areas, which should help to plan future field work on butterflies in this area. Available presence data were updated to 2022. On this basis completeness (the number of species observed expressed as a percentage of the expected number) was calculated, both from accumulation curves and by regression modelling techniques. The results indicate that less than a quarter of the territory (22.8%) can be qualified as reasonably well known, with only 11% showing high completeness scores (>90%). Observed richness values suggest a gradient in favor of mountainous areas, with the highest number of insufficiently studied areas concentrated in inland territories of the southern half of the Peninsula. Most of these areas are not attractive from a landscape or lepidopterological point of view; however, these gaps are probably conditioning our ability to interpretate the geographic patterns of species richness.

**Keywords:** Butterfly, faunistics, geographic distribution, Spain, Portugal

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### Bioregionalization of the World – insights from diversity and distribution data of moths

Pioneer works in the field of biogeography have sought to delineate bioregions as spatial areas occupied by distinct assemblages of organisms. First conceived as a descriptive approach, bioregionalization is now based on quantitative analyses producing a robust spatial structure that can be used in evolutionary or conservation biology for its explicative or predictive value. At global scale, bioregions were all delimited from data of vertebrates or plants, and to the best of our knowledge there was no attempt so far to delineate global bioregions using insect data.

Here, we propose to fill this gap by carrying out the first quantitative global scale bioregionalization analysis in insects, using a comprehensive species-level database for Hawkmoths (Sphingidae) and Wild-Silkmoths (Saturniidae). To account for uncertainties in species identifications in existing databases, we restricted our analyses to a set of nearly 32,000 records with DNA barcodes and we used Barcode Index Numbers (BINs) as proxy for species. Occurrences were converted into species ranges whose overlaps were used to produce a presence-absence matrix representing species assemblages in a grid of 200x200km cells. Non-hierarchical and network clustering analyses were used to delimit bioregions and investigate methodological uncertainties, as well as the existence and position of transition zones characterized by intermediate compositions of their species assemblages.

Our results reveal that bioregions and transition areas delineated from insect data are overall highly congruent with those derived from vertebrate distribution, with the recovery of the following seven bioregions: Nearctic, Neotropical, Afrotropical, West-Palaearctic, East-Palaearctic, Oriental and Australian.

**Keywords:** biogeography, lepidoptera, macroecology, Saturniidae, Sphingidae

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### Biogeography and population genomic structure through time of an extremely endangered European butterfly, *Hipparchia statilinus*

By studying the phylogeography of butterflies in the Palearctic region, we can clarify the intraspecific relationships and the impact of Quaternary climate changes on the species. Additionally, it can provide valuable insights for future conservation. *Hipparchia statilinus* used to be commonly found in xerothermic habitats that are progressively diminishing in Central European countries, leading to the decline and extinction of the species. Our objective was to examine genetic data and reconstruct the species' history, including identifying genetic patterns, refugia, colonization routes, and population dynamics. To investigate the long-term history of the species, we employed the mitochondrial COI gene and the nuclear EF1a. We constructed haplotype networks and complemented them with gene trees (ML) and hierarchical Bayesian analysis of population structure (hierBaps). *Hipparchia statilinus* forms three genetic lineages corresponding to the major European glacial refugia in the Iberian, Apennine, and Balkan peninsulas, with possible extra-Mediterranean refugia. In the future, we will employ whole-genome sequencing to obtain genomic data from both museum specimens (museomics) and current specimens belonging to the same populations. This will allow us to investigate short-term changes in population dynamics within the most threatened populations. We expect that the current populations will exhibit reduced genetic diversity and higher levels of differentiation compared to the past. Isolated populations are likely to experience increased genetic drift. Furthermore, we will construct species distribution models to predict the species' past, current, and future distribution. We hypothesize that the present distribution of the species is primarily constrained by land use rather than climatic conditions.

**Keywords:** phylogeography; genomics; species distribution models; temporal study; museomics

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### A glimpse of the species and their hostplant data from Afrotropical rainforest

Tropical regions, particularly rainforests, are renowned for their remarkable biodiversity. However, data on the ecology of tropical insects, including Lepidoptera, remains insufficient. The existing body of knowledge on hostplant specificity in tropical Lepidoptera represents only a fraction of the intricate hostplant relationships within this taxonomic group. Many Lepidoptera species still remain poorly studied, largely due to the elusive nature of caterpillars and difficulties in conducting comprehensive fieldwork in remote and diverse tropical environments.

Since 2011 we have been carrying out fieldwork in Kibale National Park in Uganda, East Africa with the aim to study the regional Lepidoptera fauna. The National Park represents medium-altitude (900-1590 m a.s.l.) tropical moist forest and also comprises a 10 000 ha restoration project area, where restoration planting with native trees, and protection from fire, has taken place since 1995 by the Uganda Wildlife Authority (UWA) and Forests Absorbing Carbon dioxide Emission (FACE) the future foundation. Here, we will present a glimpse of the data on the Lepidoptera and their hostplants we have been collecting during rigorous field collection and controlled laboratory rearing experiments. In addition to allowing us to study evolutionary-ecological patterns in a comparative perspective of tropical species and their temperate relatives, this data on the hostplant relationships also helps to identify the key plant species that are vital for the survival and reproduction of these tropical Lepidoptera. This knowledge aids in the restoration and conservation of both Lepidoptera and their associated plant communities.

**Keywords:** Afrotropical rainforest, hostplant, caterpillars, conservation, restoration

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## Size spectra of fruit-feeding butterflies in actively restored tropical rainforest

Previous studies suggest that the community size spectra may be used as an indicator of environmental conditions because larger-bodied individuals typically suffer more from disturbances than smaller-bodied individuals. However, the phenomenon is poorly known among insects. For example, the recovery of fruit-feeding butterfly (FFB) community size spectra during tropical rainforest restoration is inadequately investigated.

Here we ask, do the community size spectra of FFBs (Nymphalidae) differ among younger and older restored tropical rainforests and primary forest control sites? The study was conducted at Kibale National Park, Uganda between 2020–2021. Study sites (45) were categorized into three age groups: younger restored forests (planted 2005–2011), older restored forests (planted 1995–2000), and primary forests. Butterflies were caught with fruit traps, and their forewing lengths were measured for three consecutive days of each month, during six study months. The individuals were categorized into three size groups: small (forewing length 0–25 mm), medium (25–40 mm), and large (40–60 mm). The frequencies between the age groups were compared with the chi-square test.

The relative abundance of large butterflies increased, while the relative abundance of smaller butterflies decreased from younger to older restored forests and to the primary forests. Apparently, the gradual arrival of larger butterflies to older restored forests could indicate that environmental conditions have become more similar to those found in the primary forests. We conclude that the size spectra of FFB communities could be used as one indicator when evaluating the recovery of restored forests.

**Keywords:** restoration, Nymphalidae, community, Afrotropical rainforest

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## Moths in space: the below-canopy structure of forest drive abundance and mobility-related traits of moth communities

Spatial distribution of species within the ecosystem is mostly driven by the presence of trophic resources. In each forest type, insects trophically related to dominant trees are expected to be evenly distributed due to the presence of their foodplant. However, individuals and species distribution within a forest ecosystem is driven also by more complex relationships with biotic/abiotic parameters. We investigated how the three-dimensional structure of space below the canopy may affect the composition of nocturnal lepidoptera communities on a micro-spatial scale. To synthesise the complexity of dispersal behaviour of moths, we evaluated measurable traits (wingspan, tympanic organs) connected to their mobility and thus potentially influenced by the structure of the available flight space. Study area was in the Sila National Park (Italy). 12 sampling sites were selected for both forests (*Pinus nigra* subsp. *laricio* and *Fagus sylvatica*). Forest spatial structure was investigated using a laser scanner. Moths monitoring was realised using UV-LED light traps that were activated one night per month in 2019 and 2020, respectively in pine and beech forests. The space available upwards from 3m above the ground is the only one that influences community composition. Here, larger species with tympanic organs prefer forests with less space below tree canopies, possibly as a defence strategy against nocturnal predators. Tympanate and larger species actively avoid chiropter predation and seem to actively choose denser forests where bat predation is lower. The micro-spatial distribution of species and their abundance thus appear to be significantly influenced by the spatial structure of forests.

**Keywords:** Lepidoptera, Community, Sila

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### Conservation genetics of the protected moth, *Gortyna borelii* (Noctuidae) in France

Accurate species delimitations are essential for establishing efficient conservation programs. *Gortyna borelii* (Noctuidae) is a threatened and protected moth, with a widespread, but localised in a range of meadows, forest clearings and edges in Europe. Larvae are internal feeders on a limited number of *Peucedanum* species, that are heavily impacted by intensive mowing regimes. Preliminary DNA barcode data from a few individuals showed a deep mitochondrial split in France suggesting a possible cryptic species complex. We DNA barcoded an additional 43 individuals sampled across France that confirmed the existence of two BINs, with a genetic divergence of 2.79%, one in Southeastern France (Maritime Alps) and Corsica and another in Western, central France and Eastern Pyrenees. RADseq data (9961 SNPs) from 34 individuals confirmed the existence of two clades but also revealed a substructure in five populations in France. The estimation of population genetic indices such as genetic diversity and inbreeding coefficient enabled us to assess the genetic status of these populations. This new insight into the genetic composition of *G. borelii* must be integrated into the conservation strategies to save this flagship species from extinction.

**Keywords:** barcode COI, RADseq, species delimitation, conservation genetics

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### CPopulation genomics and niche modeling of the Alpine populations of *Graellsia isabellae*

*Graellsia isabellae* (Lepidoptera, Saturniidae) is an emblematic threatened Lepidoptera species, found in mountain ranges of Spain and Alps. This moth is potentially impacted by climate change and dieback of its main host plant Scots pine (*Pinus sylvestris*). Our study was focused on the French Alpine population, because of its isolation and low genetic diversity as shown in a previous analysis based on mitochondrial DNA and microsatellite data. In order to better characterize the French population for conservation, a RADseq approach was used for 62 individuals, making it possible to obtain a large number of nuclear loci. The genetic variations analyzed (3,644 SNPs) confirm the strong isolation between the Pyrenean (n=8) and the Alpine (n=53) populations, but also reveal a sub-structure in the Alps. Basic genetic statistics also confirmed the low genetic diversity of the French population. To assess the environmental constraints affecting its distribution, a niche modeling approach was used, by incorporating climatic variables as well as the distribution of its host plant. This revealed that the potential distribution area is currently relatively limited. Projections of the evolution of its niche in the future, up to 2050, show a change in niche suitability that could have negative consequences for the survival of the French population and implications for the conservation strategy.

**Keywords:** RADseq, population genomics, moth, niche modeling

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**Now published: The second volume of the catalogue on the Jacques Plante collection of Noctuidae at the Muséum d'histoire naturelle, Geneva, Switzerland**

We present the second volume of our Catalogue on the Jacques Plante collection of Noctuidae, deposited in the Muséum d'histoire naturelle in Geneva, Switzerland. While volume 1 of the Catalogue treated all of the species of the Hadeninae and Noctuinae and roughly 33'000 specimens, volume 2 treats the new taxa only in the Amphipyridae, Psaphididae, Cucullidae, Oncocnemididae, Acontiidae, Pantheinae, Dyopsidae, Raphiidae, Acronictidae, Bryophilidae, Heliethidae, Condiciidae and Xylenidae. Volume 1 included 4 new genera, 21 new species and 21 new subspecies while the novelties of the second volume amount to 20 new genera, 5 new subgenera, 128 new species, and 39 new subspecies. These new taxa are illustrated on 80 colour plates displaying 640 magnified images of moths and 462 black and white photos of genitalia on 154 plates. The new species are described in 45 genera; 44 of them in *Athetis* Hübner, followed by *Callyna* Guenée (7 species) and *Mudaria* Moore (6 species). The genera for which new European taxa are described are *Amphipyra* Ochsenheimer, *Dasypolia* Guenée, *Mniotype* Franclemont, and *Omia* Hübner. The species are described from 19 countries (excluding Taiwan as separate); the highest numbers of species being described from Thailand (26), then China incl. Taiwan (25), Indonesia and Vietnam (12 each), Nepal (11), India (10), and Pakistan (9). A third volume, to be published later in 2023 will provide a checklist and illustrations of specimens in colour for all of the species of Noctuidae of the Plante collection, except the Hadeninae and Noctuinae.

**Keywords:** Lepidoptera, Noctuoidea, new taxa, Europe, East Palearctic

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**Impact of different human pressures on diurnal Lepidoptera of the Aspromonte National Park**

The use of insects as biological indicators for assessing environmental health is a valuable tool for understanding the modifications occurring in the environment under different anthropogenic pressures. Diurnal Lepidoptera, due to their high association with plants and susceptibility to environmental changes, are commonly used for this purpose.

In this study, we carried out a monitoring program within the Aspromonte National Park (Calabria, Italy) to evaluate the impact of various anthropogenic pressures on the qualitative and quantitative composition of these pollinators. Monitoring activities were carried out twice a month from May to September along ten 500m long transects situated in different environmental contexts, such as intensive and extensive grazing, cultivated fields, burned areas, and natural environments.

Butterflies flying within each transect were identified at species level. Additionally, the abundance of flowering plants and the main climatic parameters, including temperature, cloudiness, and windiness, were also recorded.

The results obtained from the study indicate that human activities have a negative impact on the structure and composition of this group of pollinators. A total of 43 species belonging to 5 families were surveyed during the monitoring activity. In the most degraded environments, such as grazed and burned areas, which had low abundance of flowering plants, butterfly biodiversity was lower than in environments with limited or absent human pressure.

**Keywords:** Pollinators, anthropic activity, biodiversity, butterfly

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### Population study on the newly discovered Marsh Fritillary (*Euphydryas aurinia*) colony of the Hanság area (NW-Hungary)

3. Abstract (maximum 250 words):

The “wetland ecotype” of the Marsh Fritillary is seriously retreating all over its area in Europe, including Hungary. The main causes of the decrease is supposed to be habitat loss, change of land use, drought and climate change.

In Hungary there were populations only on the West (Őrség, Balaton Upland), but recently some of them extinct or declining. It was never known from the Hanság area (Fertő-Hanság National Park), where strong colony was discovered in 2021.

In 2022. intensive CMR study was conducted with along the flying season (2022.05.11-2022.06.01.) involving 1065 individuals with 14 % recapture rate (1239 capture events). The Jolly-Seber method estimated the population size of males 4484 and females 1257 (together 5741).

The land management is made by summer mowing with unmowed stripes, for the preference of the highly threatened meadow viper living here too.

The mowing is supposed to be harmful for the young nests of the Marsh Fritillary caterpillars. One hundred nests were marked after the mowing to follow up the survival of the caterpillars. Despite of the expectations reasonable rate of marked nests could be found, some of them managed to successfully overwinter.

The survival is speculated to be successful due the “late” mowing when the nests were lower, close to ground level and they were not all or not completely destroyed.

There are new CMR study planned to estimate the abundance change and comparative studies between the managed and unmanaged sites so that to determine the most suitable land use of the site.

**Keywords:** habitat management of Marsh fritillary, mowing, CMR studiest

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### Biodiversity of leaf-mining insects in a dry Mexican tropical forest and their responses to anthropogenic and natural disturbances

Tropical dry forests are an essential habitat for many endemic and threatened insects. Mexico has one of the best examples of this habitat in the neotropics which is severely under threat. Despite the ecological importance of insects, they are very rarely taken into account in conservation programs.

Tropical leaf-mining insects are species diverse and easily sampled at larval stage within their leaf mines and immature stages can be identified using DNA barcoding. This makes leafminers ideal for understanding how plant-insect interactions vary along forest disturbance gradients and subsequent successional stages.

Our aim is to explore and describe the diversity of leaf-mining insects and their interactions with their host plants and their responses to anthropogenic and natural disturbances in the Chamela-Cuixmala Biosphere Reserve and Huatulco National Park.

We collected tenanted leaf mines along several disturbance and succession gradients. Immature stages were dissected out of the leaf mines and DNA barcoded. In addition, we analysed metabarcoding data from Malaise trap samples and pooled out any sequences belonging to insect genera with leaf-mining species.

We found 509 OTU in the Chamela-Cuixmala Biosphere Reserve and 472 OTU in Huatulco National Park. Preliminary results suggest that species richness and abundance is higher in sites with an early forest succession in comparison with last forest succession. We found differences according to species composition related to successional stages. These differences were significant for sites in the Chamela-Cuixmala Biosphere Reserve. Our results show relation between leaf-mining insects in tropical dry forests and their possible importance in succession pathways.

**Keywords:** community ecology, DNA barcoding, Neotropics, plant-insect interactions

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### Towards an update of the checklist of the Lepidoptera of São Tomé and Príncipe

During six trips to São Tomé and Príncipe from 2019 to 2023, we performed many nights of Lepidoptera sampling. We present here a provisional checklist from the literature and from our own observations.

Several endemic species, some of which described by Herbulot, were still found close to their type localities, highlighting the need for the continuing protection of their habitat in their very restricted range.

**Keywords:** Lepidoptera, Checklist, Africa, São Tomé and Príncipe

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### A network based-method reveals twelve bioregions in Iran: A study based on geometrid moths

Iran is a country with a high environmental heterogeneity, which is reflected in the complex biodiversity of different plant and animal groups. Recently published data confirm the presence of 4812 Lepidoptera species in this country, of them 539 species belong to the family Geometridae. This family show a high rate of endemism in this country (24%). Here we used distribution data of all known geometrid moths of Iran, to identify the bioregions of this group and uncover areas with unique faunal elements and find regions with significant species richness and endemism. Using a network-based method we were able to define bioregions of the geometrid moths across the country. This showed an outstanding species richness along the mountains, mainly the two main mountain ranges: Zagros in the west and south, and Alborz in the north. We found the southern mountainous areas harboring the most endemic species. The analysis identified six main bioregions, some of those reflecting a specific local faunal composition. These findings support previous studies on the biodiversity of the country and highlight the complex species composition there, exceptionally on the transition zone between zoogeographical realms. Furthermore, as three of the six zoogeographical realms defined by Wallace meet in the southern part of Iran our results confirmed the occurrence of two melting points between these realms. On the one hand between the Palearctic and Saharo-Arabian, along the southwestern and southern foothills of the Zagros Mountains and on the other hand between the Palearctic and Oriental in southeastern Iran.

**Keywords:** Bioregionalization, Geometridae, Infomap, melting point, Lepidoptera

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### Molecular phylogeny of North European Geometridae (Lepidoptera, Geometroidea)

Phylogenetic relationships between Geometridae of Northern Europe were studied using two-step approach. First, a phylogenomic backbone was created for the subset of local fauna, using more than 600 loci from nuclear protein-coding genes for 117 species of Geometridae and 35 species of outgroup taxa from different families, totalling more than 200,000 bp. Second, up to 11 'traditional' markers totalling more than 7,800 bp were sequenced for all 376 species of North European geometrids, complemented by nearly 100 taxa belonging to taxonomic key groups of Geometridae from other parts of the world in order to put the results into a global context. Phylogenomic backbone created in the first analysis was used as a topological constraint in the second step of the study. Results are compared to earlier phylogenetic studies and current classification of Geometridae. Taxonomically important findings including new tribe descriptions, new tribe associations, revised statuses of tribes and genera, and new synonyms are discussed.

**Keywords:** phylogenomics, hybrid enrichment, taxonomy, systematics

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### Conservation and Protection of Family Pieridae of Lepidoptera from Larkana Sindh Pakistan

One of the biggest group of insects is called the Lepidoptera. These insects' systems have seen tremendous alteration in recent years. Every year, hundreds of new species from all around the world—including Europe—are described. Many Lepidoptera species are significant pests, while others, like the silkworm, are economically significant, and yet others are uncommon species that embellish our fauna. Their multicolored wings make them incredibly lovely and beautiful. They typically consume other sugary liquids and floral nectar as food. Their life cycle consists of four stages: egg, larva, pupa, and adult. They frequently can be observed flying around flowers and are very important in pollination. The majority of the pieridae family's butterflies are tiny to medium-sized and are widespread around the globe. They typically have wings with black dots, rear margins, and white or yellow colouring. The majority of Pieridae species have green or yellow caterpillars with black and white striped wings. Several types of mustard plants (family Brassicaceae), legumes (family Fabaceae), and other plants are consumed by caterpillars. During our study period we have surveyed Larkana and Qamber-Shahdakot regions of the province Sindh, Pakistan and over 1200 specimens have been collected. It was observed that during this period 4 species of butterflies found. Three species are genus *Anapheis*, *A. aurota* and one species from genus *Catopsila*, *C. pomana*.

**Keywords:** Butterflies, Lepidoptera, Lifecycle, Conservation

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### Moth monitoring network in the Balearic Islands, Spain and a regional catalogue of Lepidoptera with the historically reported species

Under the frame of the project "Diversity and community structure of moths as bioindicators of habitats quality of natural areas at the Balearic Islands", a moth monitoring network has created. The network is composed by 10 monitoring stations distributed all over the archipelago: five stations at Mallorca, two at Menorca, two at Eivissa and one at Formentera islands. Each station is visited monthly during a period from March to November and a moth trap is activated during all night long. Richness of moth species and abundance is recorded for each sampling night. The moth monitoring network constitutes a baseline of the community structure of the main natural habitats at the Balearic Islands. Additionally, a regional catalogue of Lepidoptera with the historically reported species has been done. A total of 870 taxa distributed in 21 superfamilies and 53 different families.

This work has been partially sponsored and promoted by the Comunitat Autònoma de les Illes Balears through the Servei de Recerca i Desenvolupament and the Conselleria de Fons Europeus, Universitat i Cultura and by the European Union- Next Generation EU (BIO/020). Nevertheless, the views and opinions expressed are solely those of the author or authors, and do not necessarily reflect those of the European Union or the European Commission. Neither the European Union nor the European Commission are to be held responsible.

**Keywords:** Lepidoptera, Diversity, Community structure, monitoring network, Illes Balears

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### Long term monitoring of suburban nocturnal macrolepidoptera in southern Italy: results of the years 2019-2021

Long-term monitoring programs (LTMPs) are increasingly demanded to facilitate early detection of ecosystem changes as a result of habitat alteration and to study their relationship to climate change. Continuous fauna monitoring can highlight changes occurring in species composition and abundances of indicator taxa useful to assess abrupt changes in animal communities, but also changes in communities occurring as a response to slow ecological trends. Detection of phenological changes is facilitated by daily sampling as well as detection of rare species of conservation interest, the observation of migratory events, and the detection of alien species. In 2019, two light traps for nocturnal macrolepidoptera monitoring were installed in Rende, Italy. The traps were placed in a site located in the middle of the Mediterranean Basin, where climate warming is stronger than elsewhere, and in a suburban area with increasing anthropogenic pressure. They were activated every night, with few exceptions, and after two years a total of 12,164 individuals belonging to 297 taxa were detected. Interesting was the presence of *Xanthia ocellaris* and *Leucania obsoleta*, never found in Calabria before, and *Utheteisa pulchella*, which periodically migrates to Southern Europe from North Africa. The timespan encompassed during this study was enough to add 177 species to the Crati Valley fauna but was too short to capture population changes in response to environmental changes. Nevertheless, our results provided a solid basis for studying ecological dynamics occurring in an area subjected to anthropogenic pressures and climate change acting in the short and long term, respectively.

**Keywords:** Agroecosystem, Biodiversity, Traps, LTMPs

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### The internal phylogenetic relationship of Epionini (Geometridae, Ennominae) with special reference to the homology of furca of male genital

Recent phylogenetic studies on the phylogeny of Ennominae reveal that Hypochrosini, Epionini, Scardamiini, Anagogini and Apeirini form a tribe complex (here termed EHSAA), and the African Drepanogynini is recovered to be the sister group. It is therefore necessary to examine the monophyly and internal relationships of this tribe complex before any taxonomic suggestion is proposed. We first selected 49 geometrid species from 28 genera and 5 tribes to represent EHSAA. Six species belonging to 3 tribes of Drepanogynini were used as the outgroups for comparative morphological study. We especially focused on the homology assessment of wing pattern and furca and carried out character coding for all the characters of interest. We then used DNA sequence data integrated from 8 markers (CO1, EF-1a, Wingless, RpS5, CAD, MDH, GAPDH and IDH, 4300 bps in total) and obtained from 121 species belonging to 115 genera and 28 tribes to reconstruct the phylogeny using Maximum Likelihood and Bayesian Inference strategies. The results show that: (1) EHSAA is monophyletic, while none of the included tribes except Apeirini is monophyletic. We therefore suggest combining all the tribes into Epionini; (2) previous study argued that the presence of furca in Hypochrosini (or Anagogini) and Ourapterygini (now Ennomini) is due to convergence. However, we consider that the similarity is due to misinterpretation of the character; (3) host plant specificity is obviously much higher in the Oriental region and this observation agrees with the classical prediction that climate and hostplant breadth are correlated; (4) EHSAA is probably originated in Ethiopian region, and then entered southeast Asia and Australia via Asian continent.

**Keywords:** male genitalia, diurnality, phylogenetics, aposematism, crypsis

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### Phylogeography of the subspecies of *Sasakia charonda* (Nymphalidae) and its implications on management of specimen trade of endangered butterflies

Among all the butterfly species protected by the Wildlife Conservation Law (WCL) in Taiwan, *Sasakia charonda* is the only species that has multiple geographical populations, wide distribution in E. Asia, and distinct hunting pressures from trade in different areas. *S. c. charonda*, the nominotypical subspecies in Honshu (Japan) is common and collecting for trade is not prohibited. *S. c. coreana* from Korean peninsula and NE China and *S. c. yunnanensis* from Vietnam and SW China are currently heavily harvested for butterfly taxidermy. The Taiwanese *S. c. formosana*, of which the hunting is now strictly prohibited by WCL since 1989 was heavily harvested for specimen trade since 1900s. Identification of the butterfly taxidermy using this species circulated in trade has recently become important in the aspect of verification of the legal status of the specimens in trade. However, most of the *Sasakia* specimens in trade are not labelled with locality and the wing patterns are not reliable for subspecies identification. It is therefore necessary to investigate the validity and relationship among the subspecies and verify the utility of morphological characters in defining subspecies identity. We attempted to extract mitochondrial DNA from multiple individuals of every subspecies from Hokkaido, Honshu, Taiwan, China and Vietnam to clarify the phylogenetic relationship among them. The results suggest that all the specimens being traded in recent years were collected from NE China, SW China and N. Vietnam. The Taiwanese subspecies was once used for butterfly artwork, but there is no sign that this subspecies is still circulated in trade. We also found that some subspecies have subtle differentiation in both morphology and genetics so the subspecies classification of this species is in need of a major revision.

**Keywords:** wildlife trade, Apaturinae, endangered species, Celtis, Oriental region

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**Phylogeny of the tribe Macariini (Geometridae, Ennominae) from Korea**

The tribe Macariini is one of the ennomine tribes with over 23 genera and 700 species worldwide. The monophyly of the tribe is defined, and a few diagnostic characters are recognized: the uncus with the enlarged setae and the divided valva in the male genitalia, and the modified male sternum on A8. Unlike African, Bornean, and European fauna, the revision of the tribe is rarely attempted in East Asia. In Korea, there are 18 species in seven genera. In this study, we compiled a list of species of the Macariini in Korea and confirmed whether they form the monophyly based on the adult morphology and molecular analysis.

**Keywords:** Geometridae, Ennominae, Macariini, South Korea

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**Reconstructing the phylogeny of two sibling butterflies: the case of *Erebia palarica* and *E. meolans***

*Erebia palarica* and *E. meolans* are two closely related montane species coexisting in Northwest Iberia. Highly similar in morphology and phenology, they are quite difficult to tell apart. However, *E. palarica* is endemic to this territory, while *E. meolans* extends its distribution along the mountain ranges of Central Europe. To provide an insight on the evolutionary relationship between these two sibling butterflies, we used genetic, cytologic and morphological analyses.

First, we sequenced one mitochondrial (COI, 786bp) and one nuclear gene (wingless, 400pb) in 305 *E. palarica* and 168 *E. meolans* individuals, accounting for the complete distribution range of both species. We found no evidence of recent hybridization between both taxa, as the Maximum Likelihood and Bayesian phylogenetic reconstructions yielded two clear clades corresponding to each species. The 95% statistical parsimony network further supports this separation while also revealing a differentiated group of *E. meolans* in the central Apennines.

Second, we investigated chromosome number of both species, providing further evidence for the karyotype of *E. meolans* and the first data regarding that of *E. palarica*. The diploid number in both species is  $2n=28$ . This result can be interpreted as a cytological synapomorphy of these species, given the ancestral number for Lepidoptera ( $2n = 62$ ) and the modal number for *Erebia* ( $2n = 58$ ).

Finally, as a complement to the molecular analyses, we dissected the female genitalia for 10 individuals of each species and prepared high quality illustrations describing and comparing their consensus anatomies.

**Keywords:** speciation, karyotype, genitalia, integrative taxonomy, introgression

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**The butterfly monitoring scheme in Spain: network status and preliminary results**

Spain is one of the European countries supporting more biodiversity due to its location in the Mediterranean basin, topographical complexity and historical preservation of traditional land uses. Consequently, it is a major priority area for the study and conservation of butterflies. The Spanish Butterfly Monitoring Scheme, part of the European scheme, has shown a steady increase in the number of recording sites since its setting in 2014. Currently, a total of 211 transects are active throughout the entire country (except for Basque Country, Navarra, La Rioja and Catalonia, which have independent schemes). Half of these transects are placed in natural protected areas (Biosphere Reserves, National Parks and others). Here, we present some preliminary data analyses for the 9 first years of monitoring based on more than 8,200 field visits that resulted in more than 600,000 butterfly records and 210 species. We also summarize the ongoing work in terms of monitoring, communication and dissemination of results.

**Keywords:** conservation, citizen science, BMS

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**Bauplan of the endophallus in Lepidoptera: in how many ways can the vesica work?**

The vesica (endophallus) in Lepidoptera demonstrates immense diversity in shape and development. Nevertheless, there seems to be a relatively low number of elements that are repeated in different combinations in non-related groups suggesting similar selective pressures. In this work we survey functionally different groups of cornuti: hollow projections of the vesica incapable of independent movements, long spines attached to partially eversible diverticulum with muscles attached to its base, combs and elongated areas of cornuti, deciduous cornuti, among others. In contrast large areas of the vesica are non-eversible in intact phalli and function as internal structures. Various degrees of sclerotisation can form plicated areas and endophallites. All these structures may be engaged in various putative functions, namely transportation of ejaculates, internal stimulation of the female or sensorial information.

**Keywords:** functional morphology, cornuti, muscles, sexual selection

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ECOLOGY

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**Contribution to the knowledge of four species of Ennominae (Geometridae) in central Spain: *Lycia zonaria* (Denis & Schiffermüller, 1775), *Isturgia famula* (Esper, 1787), *Nychiodes notarioi* Expósito, 2005 and *Adactylotis gesticularia* (Hübner, 1817)**

*Lycia zonaria* is confirmed from the province of Madrid from material collected in 2001 which adds to its known presence in Spain from Cantabria (Northern Spain); *Isturgia famula* is the commonest representative of the genus *Isturgia* Hübner in Spain with recent phenological data from March rather than May, additionally we provide simple images of its ova (female, Tres Cantos, Madrid); *Nychiodes notarioi*: images are given of its ova (female, Lagunillos, Cuenca) and the initial larval stages (L1, L2) which are not known, as well as detail as to its rearing; *Adactylotis gesticularia*: endemic to Spain with later larval stages known but not the ova or positioning (female, Tres Cantos, Madrid).

**Keywords:** Ennominae, *Lycia zonaria*, *Isturgia famula*, *Nychiodes notarioi*, *Adactylotis gesticularia*

ECOLOGY

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**Puss and Kitten moths in Madrid (central Spain) *Cerura iberica* (Templado & Ortiz, 1966); *Furcula bifida* (Brahm, 1787) (Notodontidae: Cerurinae): a brief contribution to their biology**

Brief biological detail is provided on the Iberian endemic *Cerura iberica* (Templado & Ortiz, 1966) and the more widely-distributed *Furcula bifida* (Brahm, 1787) from ova or larvae collected from *Populus nigra* L. (Salicaceae) on the outskirts of the Spanish capital (El Goloso, Madrid)

**Keywords:** conservation, citizen science, BMS

Marta Vila

CONSERVATION

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**Census and contemporary effective population size of a population of *Erebia palarica*, Chapman, 1905**

Butterflies are highly sensitive to oscillations in environmental conditions, particularly those with restricted habitats or narrow ecological requirements. Such is the case of the endemic *Erebia palarica*, limited to the mountain ranges of Northwest Spain and classified as “data deficient” by IUCN. In the present work, we studied *E. palarica* from Serra do Courel (Lugo province, Galicia region), a relatively isolated area, to shed some light on the conservation status of the species.

We firstly conducted a mark-release-recapture (MRR) study during summer of 2021, gathering data regarding mobility, behaviour and phenotypic variation for 707 butterflies. We surveyed two localities of Serra do Courel separated by 3.26 km (Alto do Couto and A Cabeza Grande) and obtained census (Nc) estimates of 565 and 303 individuals, respectively. The extrapolation of our results to the complete distribution area confirms the status of *E. palarica* as of “least concern” following IUCN standards.

Secondly, we produced a fine-scale distribution map in Serra do Courel. We confirmed the presence of the species in various localities cited in the literature, and detected the butterfly in new nearby areas with favourable habitats. Additionally, our field observations suggest low dispersal rates in *E. palarica* as well as territorial behaviour in males.

Lastly, we will next look at genetic variation as revealed by seven microsatellites for a time series of 138 samples obtained between 1999 and 2021 in Alto do Couto. These data will allow the calculation of contemporary effective population size (Ne) using both single-sample and temporal approaches.

**Keywords:** effective size, census size, conservation, MRR, Iberia



**NOTES**

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2023

Dr Patricia Silva Gôlo & Dr Foteini Koutroumpa  
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## LE STUDIUM

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