PROGRAMME AT A GLANCE

Monday, 6 June 2022

17.00	Welcome drink
18.00 – 19.30	Welcome and opening lectures

Tuesday, 7 June 2022

9.00 – 11.40	*Symposium* The ecology of Lepidoptera in anthropogenic landscapes
11.40 – 15.40	*Symposium* Analysis of time series from long-term moth monitoring projects
16.10 – 18.10	*Talks*: Conservation biology and miscellaneous

Wednesday, 8 June 2022

9.00 – 12.40	*Symposium* Genomic studies on Lepidoptera in the context of ecology
14.00	Poster session
15.00	Excursion

Thursday, 9 June 2022

9.00 – 10.20	*Symposium* The use of volunteer data in lepidopterology
11.00 – 15.40	*Talks*: Biogeography and miscellaneous
16.10	SEL general meeting/student discussions in parallel

Friday, 10 June 2022

9.00 – 12.40	*Talks:* Life history and ecology
14.00 – 17.30	*Talks:* Morphology and sytematics
19.00	Conference dinner

PROGRAMME

ORAL PRESENTATIONS

NB! presenting authors only are indicated, see abstracts for full author lists

Monday, 6 June 2022

17.00 – 18.00	**WELCOME DRINK**
18.00 – 18.15	Welcoming words *Toomas Tammaru*
18.15 – 18.30	Societas Europaea Lepidopterologica presidential address *Erik van Nieukerken*
18.30 – 19.00	How to manage biodiversity data? *Urmas Kõljalg*
19.00 – 19.30	Museomics: what have we learned so far for Lepidoptera? *Niklas Wahlberg*..14
19.30	**DINNER**

Tuesday, 7 June 2022

Chair Tiit Teder

9.00 – 9.40	Do Lepidoptera adapt to urban stressors? *Sami Kivelä*..15
9.40 – 10.20	City life, or how to deal with urban heat, habitat fragmentation and light pollution *Thomas Merckx*..16
10.20 – 11.00	**Coffee break**
11.00 – 11.20	Tropical forest restoration: are the lepidopteran communities being restored as well? *Sille Holm*..17
11.20 – 11.40	What happens to fruit-feeding butterfly communities and diversities during tropical forest restoration? *Eveliina Korkiatupa*...18

11.40 – 12.00	Are insects declining and at what rate? An analysis of standardised, systematic catches of aphid and moth abundances across Great Britain *Chris Shortall*..........19
12.00 – 12.20	Moth declines are most severe in broadleaf woodlands despite a net gain in habitat availability *Dan Blumgart*..........20
12.20 – 12.40	What is the Forestry Light Trap Network for? *Csaba Gáspár*..........21
12.40 – 14.00	**LUNCH**
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14.00 – 14.20	Rapidly expanding Dutch Moth Monitoring Scheme *Jurriën van Deijk*..........22
14.20 – 14.40	The Finnish moth monitoring scheme *Anna Suuronen*..........23
14.40 – 15.00	Predicting population dynamics: phylogenetic analysis reveals links between cyclicity and life history in moths *Ants Kaasik*..........24
15.00 – 15.20	Long-term moth monitoring in Estonia: southern invaders become increasingly abundant *Erki Õunap*..........25
15.20 – 15.40	Moth – grouse interactions in the north *Tuomas Kankaanpää*..........26
15.40 – 16.10	**Coffee break**
16.10 – 16.30	A unique population in a unique area: the Alcon Blue butterfly in the Białowieża Forest and its conservation *Marcin Sielezniew*..........27
16.30 – 16.50	Large Heath (*Coenonympha tullia*) in the Czech Republic, its situation and prospects *Zdenek Faltynek Fric*..........28
16.50 – 17.10	Just beautiful?!? – How to select species for conservation frameworks *Thomas Schmitt*..........29

17.10 – 17.30	A lingering flavour of biodiversity *Nils Ryrholm*...30
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Wednesday, 8 June 2022

Chair Marianne Elias

9.00 – 9.20	Genomic insights into ecological diversification of the charismatic *Hemileuca maia* complex (Lepidoptera: Saturniidae) in North America *Julian Dupuis*..33
9.20 – 9.40	The genomics and ecological drivers of diversification in *Coenonympha* butterflies *Laurence Després*...34
9.40 – 10.00	The conundrum of species delimitation in allopatry - Patterns of genetic divergence within and across the continent in Lepidoptera *Mukta Joshi*...35
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11.20 – 11.40	Revisited evolution of sex chromosomes in Lepidoptera *Petr Nguyen*..38

11.40 – 12.00	Neo-sex chromosomes in a common blue *Polyommatus icarus* (Lycaenidae) *Monika Kreklová*..........39
12.00 – 12.20	How to improve the assembly and the extraction of loci of interest from different types of genomic data *Pedro Ribeiro*..........40
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15.00	**EXCURSION**
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9.40 – 10.00	Towards a European Red List of larger moths *Jurriën van Deijk*..........43
10.00– 10.20	Effectiveness of community science in detecting new Lepidoptera introductions in New York State, USA *Jason J. Dombroskie*..........44
10.20 – 11.00	**Coffee break**
11.00 – 11.20	Blank spots in European biogeography: lesson from the Czech butterfly barcoding *Alena Sucháčková*..........45

16.10	SEL GENERAL MEETING/STUDENT DISCUSSIONS IN PARALLEL
18.30	**DINNER**

Friday, 10 June 2022

Chair Thomas Merckx

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9.20 – 9.40	A trait-based framework to predict phenological responses of temperate Lepidoptera to climate warming *Tiit Teder*..........56
9.40 – 10.00	Between-generation differences in life-history traits of a seasonally polyphenic butterfly: seasonal adaptations with some environmental modification *Toomas Esperk*..........57
10.00 – 10.20	Multilevel variation in body mass and thorax width in a natural butterfly population *Kata Pásztor*..........58
10.20 – 11.00	**Coffee break**
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11.20 – 11.40	Shape of evasive prey is an important cue that triggers learning in avian predators *Daniel Linke*..........60
11.40 – 12.00	Understanding the regulatory role of predators by following changes in Lepidopteran assemblages *Csaba Béla Eötvös*..........61
12.00 – 12.20	Habitat specialization of forest butterflies and moths along a tropical elevational gradient of Mount Cameroon *Fernando Gaona*..........62

12.20 – 12.40	Extraordinary range expansions in butterflies and their causes – the examples of *Papilio demoleus* and *Pieris mannii* *Martin Wiemers*..63
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15.00 – 15.20	Exploring imaging techniques in integrative insect systematics: case study on an undescribed African geometrid moth (Lepidoptera: Geometridae) *Mikael Englund*...67
15.20 – 15.40	New approaches for studying the functional anatomy of the phallus in Lepidoptera *Boyan Zlatkov*...68
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16.10 – 16.30	On the identity of *Argyria lacteella* (Fabricius, 1794) (Lepidoptera, Pyraloidea, Crambinae) and its synonyms based on the available type material's DNA and morphology *Bernard Landry*...69
16.30 – 16.50	The Gelechiidae of North-West Europe – a new handbook *Ole Karsholt*..70

16.50 – 17.10	Lepidoptera Iranica, a complete inventory and catalogue of the order Lepidoptera in Iran *Hossein Rajaei*..71
17.10 – 17.30	A new open access web portal integrates biodiversity and taxonomy data of geometrid moths *Pasi Sihvonen and Hossein Rajaei*.................................72
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Saturday, 11 June 2022

VISITING ARVO PÄRT CENTRE AT 10.00

DEPARTURE

POSTER PRESENTATIONS

ABSTRACTS

ORAL PRESENTATIONS

Museomics: what have we learned so far for Lepidoptera?

Niklas Wahlberg

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DNA sequencing technologies have advanced to amazing levels in the past decade, and now enable us to work with the DNA of ancient specimens, from sub-fossils to more recently collected specimens in natural history collections. Costs of sequencing are also coming down at a fast pace, making it economically feasible to sequence whole genomes of many groups of insects, including Lepidoptera. Acquiring genomic resources from museum specimens has come to be known as museomics. I review the current state of Lepidoptera museomics and compare the different methods of accessing genomic level data from old specimens. I end with a look to the future, what can we expect to happen in molecular systematics, especially for Lepidoptera?

Do Lepidoptera adapt to urban stressors?

Sami M. Kivelä[1], Thomas Merckx[2], Matthew E. Nielsen[1], Tomáš Kadlec[3], Tuomas Kankaanpää[1] and Mahtab Yazdanian[1]

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[2] Vrije Universiteit Brussel, Belgium
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Because of the growth of cities, more and more animal populations live in urbanized environments. These environments are characterized by factors that typically cause stress in animals: higher temperature than rural environments; chemical, light and noise pollution; and high mortality risk due to traffic, other human actions, and intense predation. Of these stressors, light pollution may be particularly detrimental to the many insects that use day length as a cue for diapause induction. Light pollution may increase the perceived day length, and postpone diapause induction until too late to survive winter. In the geometrid moth *Chiasmia clathrata*, simulated light pollution strongly averted diapause in both rural and urban populations, while urban populations did not show signs of adaptation to light pollution. Higher urban temperatures have selected for increased heat tolerance in some insects. Accordingly, *C. clathrata* from urban populations tolerated a heat shock better than those from rural populations as adults but not as larvae. If mortality risk is higher in urban than in rural environments, selection for a fast life history would be expected in urban populations. There was no life-history difference between urban and rural *C. clathrata* expressing diapause under common-garden conditions. However, increased expression of non-diapause development in urban environments effectively means a faster life history in urban than rural populations, because non-diapause development results in a faster life history than the diapause pathway. Yet, this seems more a consequence of selection on voltinism rather than a response to a high mortality risk. By using *C. clathrata* as a model, it seems that Lepidoptera adapt to some stressors in urban environment but not to all of them. Future research should focus on identifying the constraints that prevent adaptation to light pollution.

City life, or how to deal with urban heat, habitat fragmentation and light pollution

Thomas Merckx[1,2,3], Karl Gotthard[4], Aurélien Kaiser[2], Sami Kivelä[3], Matthew Nielsen[3,4] and Hans Van Dyck[2]

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[2] UCLouvain, Belgium
[3] University of Oulu, Finland
[4] Stockholm University, Sweden
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Urbanisation involves a ‘cocktail’ of stressors, such as habitat fragmentation, the urban-heat-island effect (UHI) and light pollution. For butterflies and moths, we first assess how this ‘cocktail’ is driving homogenisation by comparing communities along urbanization gradients. With increasing urbanization, abundance and diversity severely decline, with communities shifting towards generalist, thermophilous, and mobile species, and with some species shifting towards larger, more mobile individuals. Next, we assess the scope for urban evolution, with a focus on seasonal life-history plasticity, which mainly relies on photoperiod as a cue to predict future seasonal change. Settings where anthropogenic changes alter either the cue or the environment can create mismatches; previously adaptive plasticity can become maladaptive unless evolution corrects for the mismatch. In the case of urbanization, these mismatches can arise because the UHI raises temperatures (i.e. alters the environment) or because light pollution alters photoperiod (i.e. the cue) in urban settings, and we predict different evolutionary responses to these two changes. Using common-garden experiments with two widespread model species from urban and rural environments, we show that the photoperiodic reaction norm for diapause induction has evolved in the direction predicted by the UHI, and not in the direction predicted by light pollution. We discuss that despite some local adaptations, urbanization is heavily impacting Lepidoptera communities across the globe, but also that these impacts could be mitigated via multi-scale creation and improvements of urban green infrastructure and via implementing mitigation measures for outdoor lighting.

Merckx, T. and Van Dyck, H. (2019). Urbanization-driven homogenization is more pronounced and happens at wider spatial scales in nocturnal and mobile flying insects. Global Ecology and Biogeography, 28: 1440-1455.

Merckx, T., Kaiser, A. and Van Dyck, H. (2018). Increased body size along urbanization gradients at both community and intraspecific level in macro-moths. Global Change Biology, 24: 3837-3848.

Merckx, T., Nielsen, M.E., Heliölä, J., Kuussaari, M., Pettersson, L.B., Pöyry, J., Tiainen, J., Gotthard, K. and Kivelä, S.M. (2021). Urbanization extends flight phenology and leads to local adaptation of seasonal plasticity in Lepidoptera. Proceedings of the National Academy of Sciences USA, 118, 40: e2106006118.

Tropical forest restoration: are the lepidopteran communities being restored as well?

Sille Holm [1, 2], Geoffrey M. Malinga[1,3], Eveliina Korkiatupa[1], Saskia Wutke[1] and Anu Valtonen[1]

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The rapid decline of natural tropical forest ecosystems has caused severe changes and loss of different taxonomic communities. The first global priority is to conserve the still relatively intact tropical forests. The second priority is to restore the destroyed tropical forests (UN, 2021; IUCN, 2020). Yet, it is still poorly understood if and how communities can recover during restoration process.

We investigated the recovery patterns of lepidopteran communities across 35 study sites representing different-aged restored forests planted between 1995 and 2011 and compared these with 10 primary forest study sites in the Uganda Wildlife Authority – Forests Absorbing Carbon dioxide Emissions (UWA-FACE, 2015) tropical forest restoration project area in Kibale National Park, Uganda. At each site, we indiscriminately searched plants for caterpillars using standardized 5-person-work-hour-visual-search (i.e., if there were 5 persons, we searched visually for 60 mins). The collected caterpillars were individually placed in a container and the host plant information was recorded. In the laboratory each caterpillar was assigned a morpho-species name based on their external morphology. The validity of these morpho-species was subsequently re-checked by DNA barcoding.

In total 3247 caterpillars belonging to 279 morphospecies were sampled from 164 plant species during the field work in the period of 11.11 - 06.12.2019. Here, we will present the patterns describing the lepidopteran communities in different-aged restored forest and discuss our results in terms of lepidopteran community recovery. We will also briefly introduce our field work results from 2021 and our goal to construct plant-caterpillar-parasitoid networks for these restored and primary forest study areas.

IUCN (2020). The Bonn Challenge. Retrieved from www.bonnchallenge.org/
UN (2021). United Nations Decade on Ecosystem Restoration 2021-2030. Retrieved from https://www.decadeonrestoration.org/
UWA-FACE (2015). Natural high forest rehabilitation project on degraded land of Kibale National Park, Uganda. CCB Project Design Document. UWA & Face the Future. Retrieved from https://www.climate-standards.org/2015/04/20/natural-high-forest-rehabilitation-project-on-degraded-land-of-kibale-national-park-uganda/

What happens to fruit-feeding butterfly communities and diversities during tropical forest restoration?

Eveliina Korkiatupa[1], Geoffrey M. Malinga[1,2], Margaret Nyafwono[2], Perpetra Akite[3], Sille Holm[1,4] and Anu Valtonen[1]

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[3] Makerere University, Kampala, Uganda
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The alarming rate of deforestation of tropical humid forests has resulted in decline in biodiversity and has compromised ecosystem functioning. As a response, ambitious restoration targets have been set globally (e.g. UN 2021). Forest restoration is needed to aid the recovery of forest communities in case succession is halted, e.g., by a dense cover of grasses and shrubs or frequent fires (Chazdon 2014). The primary aim of forest restoration approaches has been to reinstate the original vegetation, while less emphasis has been placed on other aspects of biodiversity, such as insect communities.

We investigate the recovery patterns of fruit-feeding butterfly communities across a tropical forest restoration project area of Kibale National Park, Uganda. Study sites represent seven restoration areas planted between 1995 and 2011, as well as two primary forest areas. Altogether we had 40 different-aged study sites, 10 of which were reference sites in the primary forest. At each study site we used one cylindrical trap with fermented banana as a bait. The sites were first sampled in 2011-2012 (Nyafwono et al. 2014), and the sampling was repeated with five additional study sites in 2020-2021, allowing a direct comparison of how communities and diversities have changed in the nine years.

During the 2011-2012 census (40 study sites, restored forest aged 4 to 17 years) we captured a total of 4 588 fruit-feeding butterflies from 67 species, while during the 2020-2021 census (45 study sites, restored forest aged 10 to 26 years) 10 015 individuals from 98 species were captured. As a main result, we found that communities in restored forests were becoming more similar to the primary forest communities over time. We conclude that tropical forest vegetation also supports the recovery of fruit-feeding butterfly communities.

Chazdon R.L. (2014). Second growth. The promise of tropical forest regeneration in an age of deforestation. The University of Chicago Press, Chicago. 449 p.

Nyafwono M. et al. (2014). Fruit-feeding butterfly communities as indicators of forest restoration in an Afro-tropical rainforest. Biological Conservation 174: 75-83.

UN (2021). United Nations Decade on Ecosystem Restoration 2021-2030. Retrieved from https://www.decadeonrestoration.org/

Are insects declining and at what rate? An analysis of standardised, systematic catches of aphid and moth abundances across Great Britain

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Although we have known anecdotally that insects have been declining in Great Britain for more than 100 years, insect declines have only been statistically estimated over the last 20 years. Estimation of the rate of those declines is still hotly debated, fuelled by a lack of standardised, systematically collected data.

More than 24 million individual moths and aphids collected from 112 light traps and 25 12.2 m suction-traps, respectively, were analysed using mixed models. Our objective was to estimate the long-term trends in both groups based on annual totals recorded every year between 1969 and 2016.

The models showed that two paradigms existed: over 47 years, long-term linear trends showed that moths had declined significantly by −31%, but short-term trends indicated that there were periods of significant decline and recovery in most decades since the 1960s. Conversely, despite aphid annual totals fluctuating widely, this group was in a steady state over the long-term, with a non-significant decline of −7.6%. Sensitivity analysis revealed that moth trends were not driven by a group of abundant species, but the sign of the overall aphid trends may have been driven by three of the most abundant species.

The spatial extent of moth trends suggests that they are extremely heterogeneous. Uniquely, moth declines were different among several habitat types, with robust significant declines found in coastal, urban and woodland habitats, but notably not in agricultural, parkland and scrubland habitats. Conversely, aphid trends showed spatial synchrony extending to 338 km, albeit with local variation.

Moth declines are most severe in broadleaf woodlands despite a net gain in habitat availability

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While agricultural intensification and habitat loss are often cited as key drivers of moth decline, these alone cannot explain the declines observed in woodlands – a habitat which has expanded in area since 1968. Our aims were to quantify how moth communities have changed across habitats and regions and to determine how species traits interact with habitat and region in predicting moth abundance change. We hypothesised that, in woodlands, species more vulnerable to shading and overgrazing by deer (species that specialise on forbs, shrubs and shade-intolerant plants) had declined more severely than other species. We modelled how four moth community attributes had changed across time (1968 – 2016): abundance, biomass, species richness and diversity and how these interacted with habitat and region. We also modelled the interaction between habitat, region and two key moth species traits: larval feeding guild and the shade-tolerance of the hostplant. Moth declines were consistently highest in broadleaf woodland, and this was the only habitat in which species richness and diversity declined significantly. Abundance, biomass, species richness and diversity declined significantly by 51%, 52%, 14% and 15% in woodlands, respectively. This contrasted with an overall national decline in abundance and biomass of 34% and 39%, no significant change in species richness and an increase in diversity of 10%. Traits-based analysis found no evidence to support the hypothesis regarding shading and overgrazing by deer to explain moth declines in woodland.

What is the Forestry Light Trap Network for?

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The Hungarian Forestry Light Trap Network was originally established in the early 1960s in order to support the forest protection forecast and prognosis. The traps – emptied daily – operate from early March to late December. All macromoths and some other "pest species" are identified. Some traps have been operating at the same location for more than 50 years. The database built up on the catches of the traps is a supreme source for entomological research. The time series – on top of the well-known faunistic and prognostic purpose – can be used to study different recent ecological processes (i.e. related to the climate change and biological invasions). Just a few examples:

- Dramatic increase in the presence of a tropical/subtropical migrating noctuid (*Helicoverpa armigera*).
- Long term homogenization of moth communities in Central Europe (Valtonen et al., 2017).
- Weather-dependent population fluctuations of the oak processionary moth (*Thaumetopoea processionea*) (Csóka et al., 2018).
- Changes in Lepidoteran assemblages due to climate change.
- Long term trends in caterpillar availability for invertivorous birds in deciduous forests in Hungary (Eötvös et al., 2021).
- Potential impacts of the invasive oak lace bug (*Corythucha arcuata*) on the oak feeding lepidopteran assemblages, particularly of the oak specialists feeding in the late season (Paulin et al., 2020).

It is almost certain that the uninterrupted long time series provided by the traps will help to study and answer scientific questions not even emerged yet in the future.

Csóka, G. et al. (2018). Weather-dependent fluctuations in the abundance of the oak processionary moth, *Thaumetopoea processionea* (Lepidoptera: Notodontidae). European Journal of Entomology, 115, 249-255.

Eötvös, C. B. et al. (2021). No long-term decrease in caterpillar availability for invertivorous birds in deciduous forests in Hungary. Forests, 12(8), 1070.

Paulin, M. et al. (2020). Known and predicted impacts of the invasive oak lace bug (*Corythucha arcuata*) in European oak ecosystems – a review. Folia Oecologica, 47(2), 131-139.

Valtonen, A. et al. (2017). Long-term species loss and homogenization of moth communities in Central Europe. Journal of Animal Ecology, 86(4), 730-738.

Rapidly expanding Dutch Moth Monitoring Scheme

Jurriën van Deijk[1] and Martin Poot[2]

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Lepidopterists have been observing moths for more than 200 years in the Netherlands. Therefore, we now know a lot about the distribution and occurrence of the 860 larger moths in the Netherlands. Ellis et al (2013) published a provisional red list of larger moths in the Netherlands, in which they listed two-third of the species as threatened, one of the reasons why a national monitoring scheme had been set up for the larger moths. At the start of this scheme only traps at a fixed location with a fixed lamp operated at which the exact numbers were counted throughout the night. This was done primarily with bright mercury vapour lamps, but in the course of time a considerable shift to other type of traps was made, including energy-efficient LedTraps, which are now predominantly used in the Netherlands. As these run on a power bank, this allows the traps to be set up in, for Dutch standards, remote locations. Together with the relatively low price, this has led to an enormous growth in the number of sampling locations. Where in the early years about 60 locations were counted, in 2021 this had grown to more than 800 locations, operated by more than 400 volunteers. These locations are in recent years representatively spread throughout the country, with proportionally to general land use most points in the agricultural area, where within a special project also farmers themselves are involved in counting the moths. This monitoring scheme is already providing the first short-term trends for the 59 most numerous species with 2013 as a base year, but for 269 species we will be able to see how well they did compared to the previous year. This promises to provide an increasing knowledge about the status of the Dutch larger moths in the coming years. From 2022 onwards the Dutch scheme is part of the European wide eBMS (www.butterfly-monitoring.net), which will make it possible for everyone in Europe to join in standardised moth monitoring.

Ellis, W.N, Groenendijk, D, Groenendijk, M.M, Huigens, M.E, Jansen, M.G.M, van der Meulen, J, van Nieukerken, E.J and de Vos, R. (2013). Nachtvlinders belicht: dynamisch, belangrijk, bedreigd. De Vlinderstichting en Werkgroep Vlinderfaunistiek, Wageningen, Leiden.

The Finnish moth monitoring scheme

Anna Suuronen and Juha Pöyry

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The Finnish moth monitoring scheme (Nocturna) was launched in 1993 and 2022 will be the 30th season of monitoring moth populations. The scheme uses light traps that are run every night from early spring to late autumn. Traps are emptied weekly, and moth samples (macro-moths plus Hepialidae and Cossidae) are identified to species by volunteer lepidopterists and saved to a web-based database. Majority of trap sites (90%) are situated in forested biotopes. The number of trap sites has varied markedly over years being highest in 1996 (152 traps) and lowest in 2017 (ca. 45 traps), but the core of trap sites (ca. 15) has remained the same. In 2021 there were 91 traps situated across Finland. Old Jalas-type traps have been replaced with new freezer traps during 2020-2022.

Main trends of moth communities were analyzed for the period 1993-2016. Annual species richness of moths increased during the monitoring period with the greatest increase in the north. Total abundance and biomass of moths showed only a weak trend but notable year-to-year variation with abundance peaks occurring tentatively at 10-year intervals (1995-96, 2005-06 and 2015-16). TRIM-analyses (rtrim R-package) were used to analyze trends for individual species. Higher proportion of species showed decreasing than increasing population trends, but some species had increased strongly in abundance thus balancing changes in total abundance. Overall, we observed a high turn-over at community level so that more than half of northern moth species (56%) have decreased in abundance whereas numbers of southern species have increased. These changes mirror the recent climatic warming in the study area, but changes in habitats and soil eutrophication may also be in action.

Antão, L. H., Pöyry, J., Leinonen, R. and Roslin, T. (2020). Contrasting latitudinal patterns in diversity and stability in a high-latitude species-rich moth community. Global Ecology and Biogeography*, 29*(5), 896-907.

Hällfors, M. H., Pöyry, J., Heliölä, J., Kohonen, I., Kuussaari, M., Leinonen, R., ... Saastamoinen, M. (2021). Combining range and phenology shifts offers a winning strategy for boreal Lepidoptera. Ecology Letters*, 24*(8), 1619-1632.

Kohonen, I. (2020) No long-term change in macro-moth abundance and biomass in Finland. Unpublished Master's thesis, University of Helsinki.

Predicting population dynamics: phylogenetic analysis reveals links between cyclicity and life history in moths

Ants Kaasik[1], Cecilia Ronnås[1], Robert B. Davis[1], Erki Õunap[1], Juhan Javoiš[1], Anna Suuronen[2], Juha Pöyry[2] and Toomas Tammaru[1]

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Studies on causal links between species-specific life history and population dynamics have suffered from scarcity of comparable high-quality data on a sufficient number of species, and incompleteness of phylogenetic information. To fill this gap, we used data sets obtained by Finnish and Estonian long-term monitoring programs of night-active Lepidoptera spanning from 1993 to 2018. We derived parameters describing 1) variability and 2) cyclicity of population numbers for 142 species of north European Geometrid moths. Derivation of these parameters for each species consisted of two steps. First, the respective values and their error (typically, with double-step bootstrap taking into account both the size of yearly abundances and the length of the time-series) for individual study sites were estimated. Then meta-analysis was applied for aggregation of the time series parameters of the monitoring stations. Positive temporal autocorrelation in population numbers was found for most species, indicating the commonness of density dependent regulation. Variability and cyclicity were analysed as dependent on species-specific life-history traits such as body size, larval diet breadth and indices indicative of the degree of capital (vs income) breeding (dCB), reflecting the importance of larvally derived resources (as opposed to adult feeding) for reproduction (Davis et al., 2016). A phylogenetic GLM analysis, relying on an original phylogenetic reconstruction was used to derive correlation coefficients between the indices of population dynamics and life history traits. Of the traits analysed, dCB appeared to correlate with both variability and cyclicity parameters: capital rather than income breeding moths was found to have to display stronger density dependence. These results are consistent with predictions relying on the Phylogenetic Constraint hypothesis (Tammaru and Haukioja 1996, Price 2003): higher variation in population numbers of capital breeding insects is expected due to the typically simplified behaviour of females in such species, and the consequent lack of population regulation at the level of adult behaviour. In turn, regular cyclicity (potentially indicative of density dependence) may be characteristic of capital breeders due to the crucial role of the interactions of the larval stage in population regulation.

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Long-term moth monitoring in Estonia: southern invaders become increasingly abundant

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The list of Estonian Macrolepidoptera has been expanding continuously since the beginning of lepidopterological work here in the 19th century. During the last 20 years alone, more than 60 species have been reported as new to Estonia (Jürivete & Õunap 2008, 2020). In concordance with several studies (Parmesan et al 1999, Sánchez-Guillén et al 2013, Forsman et al 2016), the vast majority of new species recorded are of southern distribution, having extended their range northwards. Using data from the national moth monitoring programme, we studied how has changed the proportion of species that have colonised Estonia only recently, i. e. in 1990 or later. The overall abundance and diversity of moths have slightly increased since the beginning of the monitoring programme in 2003. The abundance and diversity of species recently added to the Estonian fauna, on the contrary, show clear trends of increase. The pattern remains qualitatively the same when the period considered to be ‘recent’ is shortened and includes only species that have been recorded as new to Estonia in 2000 or later. At a study site on southwestern part of the island Saaremaa, up to 4% of all species (5% of all specimens) recorded have colonised Estonia during the last 30 years. Several recently recorded species are now resident all over Estonia and rather numerous in parts of the country. On the other hand, boreal and boreomontane species that have their southern range boundary within Estonia or close to it, are only sporadically recorded in the moth monitoring programme.

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Jürivete, U. and Õunap, E. (2020) Eesti liblikad. Kataloog. Estonian Lepidoptera. Catalogue. Tallinn, 192 pp. [bilingual, Estonian and English]

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Sánchez-Guillén, R. A., Muñoz, J., Rodríguez-Tapia, G.,Feria Arroyo, T. P. and Córdoba-Aguilar, A. (2013) Climate-Induced range shifts and possible hybridisation consequences in insects. PLoS One 8: e80531

Moth – grouse interactions in the north

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Animal communities are facing many simultaneous pressures, of which climate change and habitat transformation are the most pervasive. While we might sometimes have detailed understanding how single species are affected by each stressor or a general idea of the overall biodiversity trends, we know much less about how species interactions are modified as a result and what is their importance for population dynamics.

The declining populations of grouse species have been extensively studied, yet no consensus has been reached on the consequences of either climate change or loss of old growth forest for these birds, due to contrasting results even within Fennoscandia. The grouse species are uniquely dependent on insect food for a very short time span in their lives, making them especially susceptible to phenological mismatches with their lepidopteran prey.

We assess the effects of climate change on species interactions between moths and grouse species in Northern Finland using long term monitoring datasets and joint species distribution modelling (JDSM). Specifically, we explore climate change effects on different functional groups of moths as well as their importance to the upper trophic level, relative to other factors affecting grouse population size or reproductive output. We infer trophic interactions based on moth species' larval traits affecting palatability, preferred strata in the landscape and temporal availability during the season. For estimating moth functional group abundances in grouse habitats, we use two long time series, stretching back to 1970's, from Värriö and Oulanka research stations, as well as data from the Finnish national moth monitoring scheme Nocturna, started in 1993.

A unique population in a unique area: the Alcon Blue butterfly in the Białowieża Forest and its conservation

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The Białowieża Forest is believed to be the best-preserved forest complex in temperate lowland Europe. Less common knowledge is that it is also considered to be one of the best explored and richest areas, as far as Lepidoptera are concerned. In 2016 we discovered an isolated population of Alcon blue butterfly *Phengaris alcon*, which had never been recorded there before. The site was located in an open anthropogenic habitat surrounded by woodlands. Larvae of the butterfly initially feed inside the flowerheads of *Gentiana* plants but complete their development as social parasites in the nests of *Myrmica* ants. We investigated this isolated population using the mark-release-recapture method. The seasonal number of adults was estimated at 1,460 individuals, and their density (850/ha) was the highest among all populations using *G. pneumonanthe* studied so far. The site is also unique due to the presence of the specific parasitoid, which as imago turned out to be three times more numerous than its host. The high abundance of both may be explained by favourable habitat characteristics, i.e., the abundance of host plants and the high density of nests of *Myrmica scabrinodis,* i.e., the only local host ant (Dziekańska et al. 2020). Their complicated ecological requirements make *P. alcon* a very sensitive species, and for the focal population the main threat is related to mowing in the wrong period. In 2020 we performed an unplanned experiment to save caterpillars present in freshly cut plants. We kept gentians bearing eggshells in water, to collect just-emerged larvae ready for adoption. They were transported to the site and put close to the nests of host ants. Next season we noticed that the majority of them had developed successfully and some of pupae were even infested by parasitoids, proving that such desperate actions can be fully effective.

Dziekańska I., Nowicki P., Pirożnikow E. and Sielezniew M. (2020) A unique population in a unique area: the Alcon Blue butterfly and its specific parasitoid in the Białowieża Forest. Insects, 11: 687.

Large Heath (*Coenonympha tullia*) in the Czech Republic, its situation and prospects

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Large Heath, *Coenonympha tullia* (Müller, 1764) (Lepidoptera, Nymphalidae, Satyrinae) is widespread in large part of Holarctic region. In Europe, it is not considered as being under serious threat on a scale of a whole Europe (Vulnerable, VU) or near threatened (NT) for EU27 (Maes et al. 2019) but disappeared from a vast area in NE Europe (Sommer et al. 2022). In the Czech Republic, it used to be locally distributed in all regions of the country. After the 1960s, the species underwent a rapid decline and now it survives only in two parts of South Bohemia. In 2021, we investigated its formerly known localities in National Park Sumava. We confirmed the species from 10 sites, only four sites host larger populations. We evaluated habitat affinities of *C. tullia* and its genetic pattern using COI. For the species, very important is a presence of a larval host plant, but also leeward structures and the amount of appropriate habitat. All Czech populations of *C. tullia* are very uniform in COI and do not differ from other populations in Europe.

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

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Just beautiful?!? – How to select species for conservation frameworks

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Biodiversity is strongly decreasing for many decades now, with butterflies being a prominent example (Van Swaay et al. 2010). Therefore, the European Union implemented conservation mechanisms as the Habitats Directive (92/43/EEC) including lists of species of special conservation interest. However, the selection of the species on these lists is often criticised (Cardoso 2012). We therefore established a scheme for a purely evidence driven selection of conservation priority species based on information on distribution, endemicity, threat and specialisation. We applied this method to all butterfly species existing in the 27 EU countries (but excluded Macaronesia as these islands biogeographically do not belong to the European continent). Following our selection criteria, we obtained 51 butterfly species of conservation priority (i.e. 12.7% of all butterfly species). Only four of these species were also listed on the annexes II and IV of the Habitats Directive. Then, we ranked the European butterflies according to their charisma using four external features (i.e. size, colour, shiny wings, conspicuous wing shape). 20 European butterfly species were ranked as particularly charismatic. None of these was selected by our selection procedure, but five of them are found on the Habitats Directive. In addition, 34 citizens (all non-lepidopterologists) ranked the charisma these butterflies. The highest values were given on average to the 20 species selected as most charismatic, the lowest to our conservation priority species; Habitat Directive species had an intermediate rank. It therefore has to be argued that not only arguments of nature conservation have driven the selection of these species, but partly also their beauty. This has pros and cons as nature conservation always has to be accepted by the people, which are more willing to accept conservation measures if these are for beautiful and charismatic species than in case of small and little attractive ones. This field of conflict in nature conservation is also discussed.

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A lingering flavour of biodiversity

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There is an urgent need for saving and protecting biodiversity all over the world. There is no exception in Europe where nitrogen downfall, intense forestry and agriculture as well as several other causes threaten the biodiversity. Despite the continuous decline, there are not sufficient resources in sight to halt or turn this development. Here I present a possibility to reduce the costs and enhance the quality for terrestrial habitat assessments. We are developing methods by which moth and beetle species, whose presence is often difficult to detect, can be monitored with the help of their sexual pheromones. I will give examples of how the methods can be used in both woodland and grassland habitats. We are focusing on indicator species, i.e. species whose occurrence indicate either high habitat quality, long habitat continuity or in many cases both these qualities. Many of these species are endangered and Red listed. If widely used, these methods can both simplify and reduce the cost for evaluation of habitat qualities and thus facilitate for safer and faster conservation assessments. When properly used, the monitoring can be made by nonexperts and parallelly on a number of sites by only one or a few persons.

In search of safe space: entomopathogenic fungi on folivorous Lepidoptera

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Natural enemies shape the fate of species at both ecological and evolutionary time scales. While the effects of predators, parasitoids and viruses on insects are well documented, much less is known about ecological and evolutionary role of entomopathogenic fungi. In particular, it is unclear to which extent may the spatiotemporal distribution patterns of these pathogens create selective pressures on ecological traits of herbivorous insects, determining where and when is life the safest. Overall, quantitative studies on the prevalence of pathogenic fungi in natural habitats are notably scarce (Gielen et al., 2021; Samson et al., 2013). As the food plant of a herbivore is often a crucial mediator of fungal-insect interactions (Cory and Hoover, 2006), we focused our experiments to folivorous Lepidoptera. We conducted semi-natural rearing experiments in Estonia and Argentina with the aim of estimating fungal mediated selective pressures on insect life histories. Fungal prevalence remained constantly below 10-15%; however, the diversity of fungi associated with Lepidoptera was unexpected – around 30 species from genera *Akanthomyces, Aspergillus, Beauveria, Cladosporium, Cordyceps, Fusarium, Samsoniella, Simplicillium* etc. were detected (Gielen et al., 2021, Gielen et al. unpublished). Interestingly, the communities of fungi infecting larvae differed from those found on pupae as these comprised more fungi from genera usually not considered to harbor obligatory entomopathogens. Some differences in the prevalence of entomopathogenic fungi were found between study sites and food plants which provide evidence for fungus-mediated selective pressures on habitat and host plant use.

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Ancient Mesopotamian omens concerning moths

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The movements and actions of animals formed a fertile field of divination in Ancient Mesopotamia. Omens predicted what was likely to happen if, among other things, certain insects appeared in a man's house or in the entrance of a city gate. Tablet 38 in the Akkadian omen series known as "If a city is set on a height" (*Šumma ālu ina mēlê šakin*) includes 105 omens taken from appearances and behaviour of moths, grasshoppers, caterpillars, crickets, worms and other crawling creatures. According to these omens, moths (Akkadian: UR.ME and *sà-a-sù*) generally bring good luck, while caterpillars, grasshoppers, crickets etc. were seen as bad augury. I present translations of these fascinating and little-known omens and discuss why not all ancient wisdom and prophecies should be disregarded as signs of mere superstition.

Genomic insights into ecological diversification of the charismatic *Hemileuca maia* complex (Lepidoptera: Saturniidae) in North America

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The charismatic, day-flying buck moths of the *Hemileuca maia* (Drury) species complex are among North America's most enigmatic groups of Lepidoptera regarding their evolutionary history, ecological specialization, and taxonomy. While the group is geographically widespread, populations are highly localized and stenotopic, exhibit considerable ecological and morphological variability, and display widely variable specificity to host, habitat, and sex pheromone attraction. As such, they are an ideal model for investigating patterns and constraints of local adaptation and the effects of ecological specialization on speciation. Here, I report on recent efforts to use genomics to understand the evolutionary history of this group. This work includes generation of a chromosome-scale genome assembly, population genomic and phylogenomic analyses using both reduced-representation sequencing and whole-genome resequencing, and transcriptomics. This genomic foundation provides a novel lens with which to assess host and habitat specificity, diversification of sex pheromone components, and taxonomy of the group, including several species of conservation concern.

The genomics and ecological drivers of diversification in *Coenonympha* butterflies

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Speciation with gene flow is more common than previously thought, but the mechanisms by which phenotypic divergence and reproductive isolation arise are poorly understood. Furthermore, the role of hybridization in species diversification and adaptive radiation is debated. The *Coenonympha* genus is a species-rich group mostly distributed in Eurasia. A recent genetic analysis found a divergence ~17 MYA for the genus with bursts of speciation during climate changes in mid-miocene and pleistocene. Larvae from all taxa feed on various grass and adults are easily distinguished by their hindwings (eyespot and colour patterns). However, some studies report occasional hybridization between species or even the formation of new hybrid species (Capblancq et al 2015; 2019; 2020). Distribution ranges of the different taxa are contrasted, some species being widespread and other restricted to specific habitats, latitudinal ranges, or altitudinal ranges, resulting in a large variety of situations from sympatry to allopatry between pairs of species. Based on occurrence datasets from 10 *Coenonympha* species we evaluate the climatic space occupied by each species in Europe, and based on simplified representation of whole genomes (ddRAD seq) we refine the evolutionary history of the genus. We investigate the intensity of gene flow among species and populations and question the role of hybridization and introgression in speciation. We discuss the possible ecological drivers of diversification along the altitudinal gradient in the Alps (*arcania-gardetta* species complex) and of local adaptation in *C. oedippus* acrosss its large but fragmented geographical range in Europe.

Capblancq, T., Després, L. and Mavarez, J. (2020) Genetic, morphological and ecological variation across a sharp hybrid zone between two alpine butterfly species. Evolutionary Applications

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The conundrum of species delimitation in allopatry - Patterns of genetic divergence within and across the continent in Lepidoptera

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Delimitation of allopatric populations into species is difficult and largely arbitrary. Differing species concepts together with variation in morphological characters create significant subjectivity in delimitation for allopatric taxa, thus creating taxonomic instability. Since a major part of species have uneven or patchy distributions, the problem is widespread. Many species found both in alpine and arctic habitats often fall into this category because their ranges are fragmented owing to the discontinuous distribution of habitats occupied by them (Mutanen et al, 2012). The same concerns Holarctic species which are many and which almost regularly show at least some differentiation between the continents. In this study, we analyze the high-throughput target enrichment data for 4 groups of species mainly occurring in alpine and arctic habitats - *Syngrapha hochenwarthi*, *Elophos vittaria*, *Xestia speciosa*, *Eudonia sudetica* and 6 groups of Holarctic species - *Agriades glandon*, *Arctia caja*, *Macaria brunneata*, *Xestia lorezi, Carsia sororiata, Coenonympha tullia*. We assess whether DNA barcode divergences reflect the genetic differences in the nuclear genome and whether the difference between population and species-level differences can be dissected using genomic data. We compared the phylogenetic trees obtained from target enrichment and the barcodes. We also calculated and compared the pairwise genetic distances between individuals from different populations using the two approaches. Additionally, we also computed pairwise Fst between different populations of these species groups. From the preliminary analysis of target enrichment data, we found that North American population is almost always differentiated, while the Palearctic alpine and arctic populations may or may not show the differentiation. Finally, we also discuss the benefits of target enrichment method in standardizing species delimitation.

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Evolutionary history of European *Agriades*: Implications for taxonomy and conservation

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A good knowledge of the evolutionary history of organisms and an accurate taxonomic framework are keys for efficient biodiversity conservation measures. This is particularly relevant for European butterflies, which include numerous model species for research and are often used as bioindicator organisms and umbrella species for conservation.

The Holarctic genus *Agriades* includes seven arctic-alpine species in Europe of which several have a debated taxonomic status. They are localized and allopatric and at least two of them are of high conservation value, namely *A. aquilo* (Habitats Directive) and *A. zullichi* (endemic to southern Spain). In the last decades, from two to four species have been recognized in the European *glandon* and *pyrenaicus* species-groups. Despite this taxonomic uncertainty and conservation value, detailed molecular studies on these taxa are lacking and most molecular data is limited to DNA barcodes. We investigated the evolutionary history and species delimitation of these species-groups using high-throughput double-digest RAD sequencing (ddRADseq).

While delimiting allopatric species is challenging due to the gradual nature of speciation, various analyses using genomic ddRAD data (phylogenetic inference, STRUCTURE, PCA, SNAPP) suggested the presence of one species in the *glandon* species-group and one or two in the *pyrenaicus* species-group. The differentiation within the *glandon* species-group (i.e. *glandon*, *aquilo*, *zullichi*) appears to be relatively recent, although *aquilo* and *zullichi* may still be regarded as evolutionary significant units (ESUs). Notable geographic structure was found within the *pyrenaicus* species-group, with four allopatric ESUs detected. Genomic data revealed the evolutionary trajectory of European *Agriades* and suggested some tendency of taxonomic oversplitting within this genus. These findings may aid conservation efforts by providing information to prioritize regions and organisms. While species are arguably still the most used units in conservation, considering ESUs as relevant units may represent a beneficial update in terms of efficiency and flexibility.

Does moth life on sloth please them both?

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The intriguing species of sloth moths have adapted to spending their lives in the fur of two- and three-toed sloths. Sloths are arboreal and very slow-moving mammals and are thought to be a mobile ecosystems due to a fact that many different organisms find their fur to be a suitable habitat. However, sloths come down from their tree to defecate on the ground about once a week and this is likely for the benefit of the moths, who lay eggs into the sloth excrement, where their larvae develop (Pauli et al., 2014). When the moth larvae develop and the adult moth emerges, it flies off in search of new habitat i.e. sloth. Drivers of adaptations to this unique habitat remain unexplored (Fountain et al., 2017; Pauli et al., 2014). I will infer a phylogeny of the subfamily Chrysauginae (Pyralidae), to which sloth moths belong. Chyrsauginae include 391 species across 133 genera (Regier et al., 2012). Inferring the phylogeny of this group will also enable me to examine the origin of Chrysauginae by carrying out timing of divergence analysis. Also, I am interested in testing for the coevolution between sloths and moths, owning to the fact that sloths have unusual behavior of risking their lives to leave the excrement in fitting environment for moth larvae to develop. Using museomics approach, I will extract the whole genome of samples from the largest Chrysauginae collection in the world at the National Museum of Natural History (USNM), Smithsonian Institution. This study will contribute to resolving the phylogeny of one of the most diverse groups of Lepidoptera, superfamily Pyraloidea. Also, using museum specimens I will bring awareness to the data being kept in the entomological collections and what an information treasure they really are.

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Revisited evolution of sex chromosomes in Lepidoptera

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Current reviews provide a clear picture of sex chromosome evolution in Lepidoptera, which along with their sister order caddisflies (Trichoptera) constitute the most species rich taxon with female heterogamety. According to the prevailing hypothesis, early diverging lepidopteran lineages together with their sister order caddisflies (Trichoptera) share an ancestral Z0/ZZ sex chromosome constitution. A WZ/ZZ system then supposedly evolved upon a Z chromosome–autosome fusion, which occurred in a common ancestor of the family Tischeriidae and the clade Ditrysia comprising vast majority of extant Lepidoptera.

However, this inference was drawn mostly from indirect cytogenetic evidence and some contradictory data were overlooked in the reviews. Here we revise the sex chromosome evolution in Lepidoptera considering our molecular cytogenetic and genomic studies of sex chromosomes in early diverging lepidopteran lineages. Our comparative analyses suggest the W chromosome evolved via a non-canonical mechanism such as B chromosome adoption. Moreover, the W chromosome most likely occurred independently in different clades, as its presence was recently confirmed in one of the earliest diverging lepidopteran families, Hepialidae. Together these results rebut most of our inferences on W chromosome differentiation in Lepidoptera, except for few studies of neo-sex chromosomes.

Evolution of the W chromosome from a B chromosome could be driven by acquisition of novel sex determining mechanism. Indeed, analysis of a B chromosome in a Mediterranean flour moth, *Ephestia kuehniella* (Pyraloidea), showed that it contains sequences of the intracellular bacterium *Wolbachia*, which is ovarially transmitted and can induce feminization. It is tempting to envision a scenario in which *Wolbachia* incorporated into a B chromosome, took over sex determination, and thus gave rise to a W chromosome.

Neo-sex chromosomes in a common blue *Polyommatus icarus* (Lycaenidae)

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Classic model assumes that sex chromosomes evolve from a pair of autosomes harbouring sex determining locus and their differentiation, i.e. gene decay and accumulation of repetitive sequences, is driven by sexually antagonistic selection for alleles beneficial to one sex but deleterious to the other. However, in Lepidoptera, the most species-rich group with female heterogamety (♀WZ/♂ZZ), the W chromosome probably evolved through adoption of a supernumerary B chromosome. The classic process of sex chromosome differentiation is thus limited to neo-sex chromosomes resulting from sex chromosome-autosome fusion and translocation. Recent studies revealed that neo-sex chromosomes are quite common in Lepidoptera. They occurred independently in various taxa and supposedly have a role in formation of reproductive barriers. We investigated sex chromosomes in blue butterflies with fragmented karyotypes using a common blue *Polyommatus icarus* (Lycaenidae) as an outgroup. We performed cytogenetic and bioinformatic analyses of *P. icarus* sex chromosomes and found out originate from sex chromosome-autosome fusion. Furthermore, we observed polymorphic neo-sex chromosomes, which differed by number of fused autosomes. Thus, there are two karyotype races in *P. icarus*, which differ in their sex chromosome and provide an opportunity to study the role of neo-sex chromosomes in speciation.

How to improve the assembly and the extraction of loci of interest from different types of genomic data

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Assessing genome wide data of butterflies have been increasingly cheaper in the last decade giving butterflies a "model" status for the study of ecology and evolution (Boggs et al., 2003; Jiggins, 2016). Nonetheless, there is still a gap in the access of flexible and user friendly bioinformatic tools that can process genome data, from raw DNA sequences to multi-species alignments, containing loci that are crucial for evolutionary analyses. Moreover, a guideline providing the most cost-effective sequencing approaches and the best strategies to process their resulting sequences is still missing. Here, we use the SECAPR (Andermann et al., 2018) bioinformatic tool to assemble genomes of 10 butterfly species and to extract a set of butterfly protein-coding loci of interest from them for their subsequent use in phylogenetic inference. Specifically, we test the performance of different assembly and loci extraction strategies within SECAPR on data of different genomic coverages and deriving from two different sequencing techniques: whole-genome sequencing (WGS) and target sequence capture. We demonstrate that WGS at a coverage of 5X is currently the most cost-effective approach for obtaining correct phylogenetic species relationships. We also provide a guideline for end-users of SECAPR on the assembly and loci extraction strategies that can generate the highest yields of extracted loci of interest for subsequent evolutionary analyses. Our results represent a step forward in establishing bioinformatic tools and its underlying strategies that are suitable even for less experienced end-users. We believe that using the strategies and cost-effectiveness guidelines provided here will increase the representation of butterflies in cutting-edge evolutionary studies for years to come.

Andermann, T. et al. (2018). SECAPR-A bioinformatics pipeline for the rapid and user-friendly processing of targeted enriched Illumina sequences, from raw reads to alignments. PeerJ, 2018(7), 1–15.

Boggs, C. L., Watt, W. B. and Erlich, P. R. (2003). Butterflies: Ecology and Evolution Taking Flight. The University of Chicago Press.

Jiggins, C. D. (2016). The Ecology and Evolution of Heliconius Butterflies (1st ed.). Oxford University Press.

Has phylogenomics helped us to resolve the lepidopteran tree of life: an overview of progress in the past decade

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Next-generation sequencing technologies have revolutionized the field of molecular phylogenetics and we are now in the era of phylogenomics. In the past decade a number of phylogenomics studies focusing on Lepidoptera have been published, advancing our efforts to resolve the lepidopteran tree of life. However, despite having thousands of genes from representatives of more than 80% of the superfamilies in the order, the relationships among especially ditrysian superfamilies remain unresolved (Rota et al., 2022) and it appears that little progress has been made since the publication of the seminal studies based on Sanger sequencing (Mutanen et al., 2010; Regier et al. 2013). In this presentation, I will provide an overview of how our understanding of the lepidopteran phylogenetic relationships has changed because of the wealth of data coming from transcriptomes and genomes, which parts of the tree remain unresolved, and the potential reasons for this lack of resolution.

Mutanen, M., Wahlberg, N. and Kaila, L. (2010). Comprehensive gene and taxon coverage elucidates radiation patterns in moths and butterflies. Proceedings of the Royal Society B 277: 2839–2848.

Regier, J.C., Mitter, C., Zwick, A., Bazinet, A.L., Cummings, M.P., et al. (16 authors). (2013). A large-Scale, higher-Level, molecular phylogenetic study of the insect order Lepidoptera (moths and butterflies). PLoS ONE 8(3): e58568.

Rota, J., Twort, V., Chiocchio, A., Peña, C., Wheat, C.W., Kaila, L. and Wahlberg, N. (2022). The unresolved phylogenomic tree of butterflies and moths (Lepidoptera): assessing the potential causes and consequences. Systematic Entomology: early view 1–20.

Lepidoptera Mundi: an example of using volunteer data in lepidopterology

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Lepidoptera Mundi is an open project started in 2002, created and maintained by a single volunteer. The first, initial version was created as a local database for Lepidoptera of Poland only. In the following years the database has been changed, reconstructed and finally migrated to the Internet. The territorial range of the database has been extended from Poland to Europe, and finally to the whole world. Unlike other similar websites, *Lepidoptera Mundi* comes with a set of unique tools and features. One of them – observation module allows to add/browse sightings from any country of the world. Over the course of 20 years of the website history we've collected almost 400,000 records from 70 countries. Collected data is used for different kind of science projects like for example *European Moth Nights* (Jonko & Słowińska, 2022) or *Red Admiral Citizen Project* (Insect Migration & Ecology Lab) but also for many science publications. Part of our data has also been used as an initial analysis for the planned protected areas and as a support for few official checklists.

The most extensive and well-known usage of our data is the *European Moth Nights* project. It was initiated in 2004 by Swiss and Hungarian Entomological Societies. *European Moth Nights* is a recurring event that consists of observing and collecting information about moths (Heterocera, Macrolepidoptera) in the same time period throughout Europe. Each year the participants have 5 nights for the purposes of observation. Between 2004 and 2018 the *Lepidoptera Mundi* website (formerly known as *European Butterflies and Moths)* was a local event ambassador for EMN headquarters. In 2019 the founder of EMN – Dr. Ladislaus Rezbanyai-Reser decided to resign and announced that *Lepidoptera Mundi* will be the main organiser in the coming years. Participating in EMN event is now even easier than before. Data can be added online on any kind of device – from smartphones to computers, but it's still possible to use old, offline method. Dedicated Excel sheet to add data manually has been extended with GPS coordinates and example data. Since 2004, as part of the EMN project, 71,000 records from 28 countries have been collected. More info about the project and full results will be presented at the 22nd Congress of Lepidopterology.

Jonko K. and Słowińska I. (2022). Lepidoptera Mundi. Available at https://lepidoptera.eu/emn

Max Planck Institute of Animal Behaviour. Insect Migration & Ecology. Red Admiral migration. Available at https://insectmigration.wordpress.com/red-admiral-migration/

Towards a European Red List of larger moths

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Declines in moths have been identified, and in some cases quantified, in various European countries. For example, Valtonen et al. (2017) identified a dramatic rate of species loss and a homogenization of community compositions in Hungary. Antäo et al. (2020) reported that in Finland moth abundance had declined although species richness had increased and that this was accelerating towards the pole. In Great Britain, Bell et al. (2020) showed that moths had declined by 31% over 47 years with significant declines found in a range of habitat types. But moths remain relatively poorly studied in some parts of Europe, specifically in Southern and Eastern Europe, where both the data and the community of experts are more scattered than in other parts of the continent (like central and northern Europe). Producing a European Red List of Moths will therefore not only help identifying conservation priorities for this taxon, it could further raise the profile and encourage the recording of this fascinating group of insects particularly in under-sampled parts of the continent. Developing a Red List for this species group will provide an overview of the status of moths in Europe, identify the main threats to them and make recommendations for further research and conservation action needed. The compilation of spatial data collected for the range maps will also highlight areas of high endemism or areas of particularly high concentration of threatened species. It will help identify priority sites for conservation with moths acting as 'umbrella' species for other threatened taxonomic groups, as well as adding weight to existing priority sites for conservation as these species can occur alongside other threatened taxa. Finally, it will also contribute to increasing the coverage of invertebrate species on the European Red List and making it a better barometer of the status of biodiversity in Europe. This project would not be possible without the help and support of a wide range of experts across Europe.

Antão, L. H., Pöyry, J., Leinonen, R. and Roslin, T. (2020). Contrasting latitudinal patterns in diversity and stability in a high-latitude species-rich moth community. Global Ecology and Biogeography, 29(5), 896-907.

Bell, J.R., Blumgart, D. and Shortall, C.R. (2020). Are insects declining and at what rate? An analysis of standardised, systematic catches of aphid and moth abundances across Great Britain. Insect Conservation and Diversity.

Valtonen, A., Hirka, A., Szőcs, L., Ayres, M.P., Roininen, H. and Csóka, G. (2017). Long-term species loss and homogenization of moth communities in Central Europe. Journal of Animal Ecology, 86: 730-738.

Effectiveness of community science in detecting new Lepidoptera introductions in New York State, USA

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Approximately 5% of the Lepidoptera recorded in New York State, USA have been introduced from other continents with about 85% of these being introduced from the Palearctic. These introductions have been ongoing since earliest European settlement and continue to the modern day. Most of these species have had limited noticeable impact on our economy or natural ecosystems, but some of these species have had major impacts and resulted in costly interventions. In this talk we will examine the effectiveness of community science platforms like iNaturalist in first detections and monitoring the spread of non-native species versus more traditional collecting and government surveys.

Blank spots in European biogeography: lesson from the Czech butterfly barcoding

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The barcoding, i.e., sequencing a part of the mitochondrial gene cytochrome c oxidase, of European butterfly fauna seems to be nearly complete (Dinca et al. 2021). The overall patterns are well explored and we know that even the cryptic (genetic) diversity is highest in the south and declines towards the north. Still, the amount of database sequences decrease north-eastwards and biogeographic patterns specific for Central and Eastern European butterfly faunas might remain overlooked. We barcoded ~850 specimens from 141 species representing the full extant Czech butterfly fauna plus several recently extinct species. The fauna comprises species of high mountains, boreomontane bogs, wet and dry grasslands and alluvial and open forests. The Czech Republic is bordered by mid-altitude mountains, which mostly consist of Pre-Cambrian crystalline rocks. The populations of grasslands could be connected to the East through the Pannonian basin or the Moravian Gate. Moreover, isolation of populations and survival of many elements through the entire glacial cycles is proposed (Suchackova Bartonova et al. 2021). The montane elements, which likely survived Pleistocene glaciations in lowlands, should be related to those inhabiting the Alps, Carpathians, and Hercynian mountains of Germany (Schmitt 2017). Further, separate genetic lineages of species expanding to the north from the Mediterranean Peninsulas after glacial habitat contractions might meet in Central Europe and produce hybrid or secondary contact zones here. In our presentation, we will explore if these biogeographic hypotheses are valid on the example of the Czech butterflies.

Dinca, V. et al. (2021). High resolution DNA barcode library for European butterflies reveals continental patterns of mitochondrial genetic diversity. Communications biology, 4: art. no. 315.

Schmitt, T. (2017). Molecular biogeography of the high mountain systems of Europe: an overview. In: Catalan, J., Ninot J. M., Aniz M. M. (eds). High mountain conservation in a changing world, 63-74. Springer International Publishing. Cham.

Sucháčková Bartoňová, A. et al. (2021). Extremely endangered butterflies of scattered Central European dry grasslands under current habitat alteration. Insect Systematics and Diversity, 5: 6.

Tracing the invasion of a leaf-mining moth in the Palearctic through DNA barcoding of historical herbaria

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Herbarium specimens collected over the centuries in different biogeographic regions have a great value for science. They represent not only an important source of information for botanists, but they also provide entomologists with paramount evidences on past diversity, distribution, abundance, and trophic associations of insects (Lees et al 2011).

Here we focus on the lime leaf-miner, *Phyllonorycter issikii,* an invasive micromoth with an unusually higher number of haplotypes in the invaded area (Europe, Western Siberia) compared to its putative native region (East Asia) (Kirichenko et al 2011). The origin of the genetic diversity in the neocolonized region remains unclear. We surveyed over 15 thousand herbarium specimens of lime trees (Tilia spp.) collected across the Palearctic over a period of 252 years (1764–2016) looking for preserved larvae within the archival leaf mines. We found 203 herbarium specimens with leaf mines of Ph. issikii collected in East Asia, one of them dating back to 1830, i.e. 133 years before the description of the species. In contrast, only 22 herbarium specimens collected in the West Palearctic in the last three decades (1987–2015) carried leaf mines (Kirichenko et al 2022).

DNA barcoding of archival specimens revealed 32 haplotypes out of which 23 were novel (not known from modern populations) and found exclusively in East Asia. Six haplotypes are shared between both native and invaded areas and only two were responsible for the recent invasion of the Western Palearctic. The remarkable number of newly discovered haplotypes in archival populations supports East Asia as the native region and the source area of invasion (Kirichenko et al 2022).

Kirichenko, N. et al. (2017). From east to west across the Palearctic: phylogeography of the invasive lime leaf miner Phyllonorycter issikii (Lepidoptera: Gracillariidae) and discovery of a putative new cryptic species in East Asia. PLoS ONE 12, e0171104.

Kirichenko, N., Zakharov, E. and Lopez-Vaamonde, C. (2022). Tracing the invasion of a leaf-mining moth in the Palearctic through DNA barcoding of historical herbaria. Scientific Reports. 12: 5065

Lees, D. C. et al. (2011). Tracking origins of invasive herbivores using herbaria and archival DNA: the case of the horse-chestnut leaf miner. Front. Ecol. Environ. 9, 322–328

Dysauxes – an African conqueror of the Cold Lands

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The genus *Dysauxes* Hübner, 1819 is a small lineage of tiger moths belonging to the tribe Syntomini. According to the last review it contains 8 species distributed exclusively in Palaearctic (Ignatev, 2006). While most of the lepidopterists treat *Dysauxes* as a rather uniform morphologically West Palaearctic taxon, its true diversity can be assessed only by taking into account the much less known Asiatic species. Surprisingly, thorough analysis of the entire range of this genus implicates intriguing question on its evolutionary and biogeographic origin, that seems to be much more complicated and unclear. The newest discoveries resulted from the study of a wide range of taxa representing most of the Syntomini genera strongly indicate the Madagascar roots of this lineage (Przybyłowicz et al., 2019). Such hypothesis is confidently confirmed by both morphological and molecular data. To make the story even more complicated, *Dysauxes* appears to be even wider distributed across the Indian Ocean, by the existence of the omitted until very recently, endemic *D. florida* on a small oceanic island Mauritius, located about 900 km east from Madagascar (Przybyłowicz et al., 2021). The species differs in some characters from typical congeners however it is reasonable to ascribe it to the genus in question based on our present knowledge. Its presence on the remote, small oceanic island is not that improbable and can be confidently elucidated assuming the stepping-stones scenario. This seemingly unlikely distribution pattern gained important confirmation by the very recent unexpected finding from East Africa. A single male of unknown taxon deceptively similar to typical *Dysauxes* was collected in NE Tanzania. This discovery further corroborates the hypothesis that *Dysauxes* is not what it was thought to be. The European taxa are most probably only the youngest conquerors of the Cold Lands in which (wing-) veins still flows hot African blood.

Ignatev, N.N. and Zolotuhin, V.V. (2006). A review of syntomids (Lepidoptera: Syntomidae) of Russia and adjacent territories. Part 2. Genus *Dysauxes* Hübner, 1826. Eversmannia, 6: 27–51.

Przybyłowicz, Ł., Lees, D.C., Zenker, M.M. and Wahlberg, N. (2019). Molecular systematics of the arctiine tribe Syntomini (Lepidoptera, Erebidae). Systematic Entomology, 44: 624-637.

Przybyłowicz, Ł., Wiorek, M., Przystałkowska, A. and Wahlberg N. (2021). Alone on an island: The reassessment of an enigmatic species of Handmaiden Moth (Lepidoptera, Erebidae) endemic to Mauritius. Zoologica Scripta, 50: 752-768.

Capturing the species diversity of pyraloid moths from the Philippines

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The Philippines archipelago is one of the most threatened biodiversity hotspots in South-East Asia. While its butterfly diversity is fairly well-known (Treadaway 1995, 2012), the Microlepidoptera fauna remains largely unexplored until now. The collections of the Museum für Naturkunde, Berlin, host a large amount of material from the archipelago, making them one of the most significant collections worldwide for this region. We tackle the pyraloid diversity of the archipelago using an integrative approach combining morphological and molecular characters. Presently, 768 DNA barcode sequences were generated and analyzed. Preliminary results from comprehensive revisions of the subfamilies Crambinae, Lathrotelinae and Scopariinae reveal an endemism rate ranking from 60 to 85%. The undescribed diversity in these groups is estimated to be roughly 60%. DNA barcodes reveal high cryptic diversity in several montane species. Areas of endemism and future areas to prospect on the Philippine archipelago are discussed.

Divergence history and high-altitude adaptations in Alpine geometrid moths

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Many unique high-altitude mountain habitats have been declining due to climate change, threatening their flora and fauna, which have adapted well to these ecosystems. We study how high-altitude adaptations such as wing degeneration in females and the shifts to diurnal flight activity have evolved in the European Alps using geometrid moths in the tribe Gnophini (e.g., genera *Crocota*, *Elophos*, *Psodos*, *Sciadia*, and *Yezognophos*) as the study group. These moths are a well-researched group as regards life histories and taxonomy, inhabit narrow ecological niches, and have short life cycles, providing an ideal material for studying evolutionary questions (Müller et al. 2019). Using a multi-gene analysis approach, we built a phylogenetic hypothesis for Gnophini to understand whether various high-altitude habitats have been colonised by a single moth lineage sharing a common ancestor, or whether there has been multiple convergent evolution by non-related lineages. Our results also provide a robust basis for classification of these moths and we demonstrate how phylogenies can be used to make more informed conservation prioritization decisions.

Müller B., Erlacher S., Hausmann A., Rajaei H., Sihvonen P. and Skou P. (2019). Ennominae II. In Hausmann A, Sihvonen P, Rajaei H, Skou P (eds), Geometrid Moths of Europe, vol. 6. Brill, Leiden. 906 p.

Moths and butterflies on alien shores – global biogeography of non-native Lepidoptera

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The global trade of plants and plant-based goods facilitates the transport of a considerable number of Lepidoptera species to outside their native range. Analogous to island disharmony, we examine invasion disharmony, where species filtering during invasions increases systematic compositional differences between native and non-native species assemblages, and test whether some families are more successful at establishing in non-native regions than others. We compared non-native Lepidoptera species numbers with the land area of 11 regions worldwide: Hawaii, North America, Galapagos, Europe, South Africa, South Korea, Japan, Nansei Islands, Ogasawara Islands, Australia, and New Zealand. We used ordination analysis to investigate differences among native and non-native assemblages in the distribution of species among families, and tested whether invasion disharmony is explained by propagule pressure (proxied by species richness in border interceptions). We found 742 non-native Lepidoptera species (0.47% of the global Lepidoptera diversity) to be established in at least one of the 11 regions. Crambidae, Pyralidae, Tineidae and Gracillariidae were particularly successful invaders, whereas Erebidae and Geometridae were under-represented among non-native Lepidoptera. Much of the variation in species numbers in the native, and less so in the non-native assemblages could be attributed to land area. Although native assemblages were similar among nearby regions, non-native assemblages were not, suggesting geography had little effect on invasion disharmony. Macromoth families were generally under-represented in establishments, whereas several micromoth families were under-represented in interceptions. This discrepancy may relate to greater detectability of larger species or high propagule pressure via associations with specific invasion pathways. Invasion disharmony in Lepidoptera appears to be driven by processes unrelated to the success of native assemblages. While native assemblages developed through long-term evolutionary radiation, non-native assemblages arise through their tendency to associate with invasion pathways followed by establishment of founder populations, which depend on life history traits that vary among families.

A journey between worlds: genus *Euchromia* Hübner, 1819 as an excellent group for research on dispersal and colonisation of the Old World by the Neotropical fauna (Lepidoptera: Erebidae: Arctiinae)

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In zoogeography there is a need for comprehensive studies on long distance dispersal, that are based on larger groups of animals and a broader geographic scale. This applies also to the colonisation of the Old World, and especially the islands of the Pacific Ocean, from the Neotropics. An excellent group for such studies is the tiger moths genus *Euchromia* Hübner, 1819. The genus comprising ca. 50 valid species is widely distributed in the tropics of the Old World, from Africa to Fiji, but it certainly dispersed from the Neotropics (Zenker et al. 2017) over ocean, as it evolved in the late Oligocene at the earliest (Wahlberg et al. 2013). In the talk I will present the main objectives of the project which will be the first complex elaboration of a widely distributed Old World group of flying insects of a neotropical origin, with the reconstruction of dispersal and colonisation routes. Several biogeographical hypotheses will be tested with the use of combined morphological and molecular data, obtained from both regular PCRs and NGS "museomics" methods (Twort et al. 2021). Contrary to the traditional approach of fundamentally Asian origin of the SW Pacific Ocean islands fauna, a transpacific dispersal route is proposed for the ancestor of *Euchromia*. Dated phylogeny compared with the timing of geological events will allow to indicate the most probably routes of its further dispersal in the Old World, contributing to a better understanding of the patterns of fauna exchange between Asia and Africa. The project also combines the developing studies on the importance of New Guinea as a source of biodiversity, and the influence of neighbouring Wallacea as a hypothetical barrier in its propagation. Finally, the project will contribute to a taxonomic revision of the genus *Euchromia* and revelation of the relationship with its sister neotropical genus *Syntomeida*.

Zenker, M.M., Wahlberg, N., Brehm, G., Teston, J.A, Przybyłowicz, Ł., Pie, M.R. and Freitas, A.V.L. (2017). Systematics and origin of moths in the subfamily Arctiinae (Lepidoptera, Erebidae) in the Neotropical region. Zoologica Scripta, 46: 348-362.

Wahlberg, N., Wheat, C.W. and Peña, C. (2013). Timing and Patterns in the Taxonomic Diversification of Lepidoptera (Butterflies and Moths). PLoS ONE, 8: e80875.

Twort, V.G., Minet, J., Wheat, C.W. and Wahlberg, N. (2021). Museomics of a rare taxon: placing Whalleyanidae in the Lepidoptera Tree of Life. Systematic Entomology, 46: 926-937.

Evolution and diversification of *Catocala* underwing moths

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Striking hindwing coloration occurs in numerous families of Lepidoptera. Underwing moths in the genus *Catocala* possess classic examples of this adaptation. Some species of *Catocala* have orange hindwing patterns; others are yellow, red, pink, white, purple or entirely black. It is thought that differences in hindwing coloration interfere with the predator's ability to habituate to the startle stimulus (Ingalls, 1993), and hindwing color has been hypothesized as a driver for speciation in *Catocala* by this mechanism (Sargent, 1969). However, a phylogenetic study of *Catocala* by Ishizuka et al. (2015) found hindwing color to be conserved in many *Catocala* groups that share larval host plants. To better understand the evolutionary processes that led to the diversity of species and hindwing colors in this genus, we obtained sequence data from 164 *Catocala* species, including 80 pinned museum specimens, to construct a robust phylogenetic hypothesis for *Catocala.* Hindwing color data were extracted from digitized museum specimens, and evolutionary histories were estimated for hindwing color, larval host plant and biogeographic traits. Diversification rate analyses revealed that faster rates of hindwing hue evolution did not correspond with higher diversification rates. While we found links between some larval host plant family, geographic distribution, and wing color character states and increased diversification rates, we were unable to conclude whether any of these character states are driving diversification in *Catocala.* Lastly, we tested the role of hindwing color in mediating the assembly of 70 *Catocala* communities across North America. While few communities exhibited greater hindwing diversity than expected by chance, we found that hindwing color tends to exert more influence on community assembly as species richness increases and as phylogenetic and larval host plant diversity decreases, but only in regions with high diversity.

Ingalls, V. (1993) Startle and Habituation Responses of Blue Jays (*Cyanocitta cristata*) in a Laboratory Simulation of Anti-Predator Defenses of *Catocala* Moths (Lepidoptera: Noctuidae). Behaviour, 126, 77-96.

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So familiar, yet so unknown: Taxonomy and DNA barcoding of the Palearctic *Papilio machaon* species-group

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Swallowtail butterflies of the *Papilio machaon* species group provide a diverse and ideal model system to study hybridization. Species limits and systematic relationships have been notoriously difficult to resolve in this group in part due to a plethora of ecological races, color morphs, and incomplete reproductive barriers, as well as abundant natural hybridization. Although the evolution of the North American species has been studied extensively, studies on the Old World species are lacking. In the Palearctic region, four species are currently recognized within the *P. machaon* species complex: *P. machaon*, *P. saharae, P. hospiton* and *P. xuthus*. Their distributions vary, some are widespread while others are more localized. Some of the species hybridize while others do not. Current environmental changes are modifying species distributions and consequently their biotic interactions. Studies have shown that, under future climate scenarios, species distributions will shift and shrink considerably. This can alter the gene flow between species and even cause extinctions. An adequate understanding of the hybridization processes is of utmost importance in predicting the effects of rapid environmental changes to species survival. In order to shed light on the taxonomy and evolution within the *P. machaon* species group, we sampled 258 new specimens from across their range in Eurasia, and are currently in the process of sequencing their mtDNA cytochrome oxidase (COI) barcoding region. Initial results reveal a complex genetic pattern consistent with the response of the species-group to the last glacial periods. A taxonomic revision of the species-group is proposed.

Contribution to the knowledge of the butterflies of Albania with notes on the family Nymphalidae and Pieridae (Lepidoptera: Papilionoidea)

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Studies on the Lepidoptera fauna of Albania started no earlier than 1913 (Rebel, 1913), followed by several other studies. A recent checklist of the superfamily Papilionoidea has listed 196 species documented for Albania till now (Cuvelier et al., 2018). The results of our faunistic survey give considerable data on the occurrence and distribution of some daily-flying species of five families: Hesperiidae, Lycaenidae, Nymphalidae, Papilionidae, and Pieridae (Lepidoptera: Papilionoidea). The field expeditions were realized in June 2019 and May - June 2021, revealing a total of 31 species collected randomly during the fieldwork from southern (Gjirokastër County) to northern Albania (Dibër and Kukës Counties).

The species of the family Pieridae and Nymphalidae are described in detail. The analyses of the genus *Melitaea* Fabricius, 1807 (Nymphalidae) include four species from this study, *M. athalia* (Rottemburg, 1775), *M. didyma* (Esper, 1778), *M. ornata* Christoph, 1893, and *M. phoebe* (Denis & Schiffermüller, 1775).

All the specimens are mounted and preserved in the scientific fund of the Museum of Natural Sciences, Tirana, Albania.

This faunistic study gives considerable data on the occurrence and bio-ecology of some butterflies, thus enriching their distribution map in Albania and raising awareness to protect their habitats.

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Evolution of seasonal plasticity in response to climate change differs between life-stages of a butterfly

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Many insects and other organisms rely on photoperiod as a seasonal cue to predict future weather conditions and make appropriate plastic decisions, such as choosing when to enter diapause. Anthropogenic climate change poses an added challenge for these species because although temperatures are rising, changing many different aspects of the abiotic and biotic environment, photoperiod isn't changing, creating a cue-environment mismatch with potentially severe consequences for many species. Evolution could potentially correct for this mismatch by altering the photoperiodic reaction norm, but evolutionary responses to climate change have been quite difficult to identify (Merilä and Hendry 2014). We tested for this evolution in *Pararge aegeria* (Speckled wood butterfly) by recreating past experiments. This butterfly uses photoperiod as a cue for life history plasticity in two different life stages: larval development time and pupal diapause. Reaction norms for plasticity in these traits were first measured over 30 years ago for two different Swedish populations (Nylin et al. 1989, 1995). To determine if photoperiodic plasticity has evolved in response to the climate change that has occurred during this time, we replicated the original experiments which measured these reaction norms but using the contemporary populations. We found evidence for evolution of the reaction norm for larval development time, but the change was in opposite directions in the two populations. In contrast, we found no evidence for evolution of the reaction norm for pupal diapause. Our results show that different life stages may evolve differently in response to climate change and that climate change can have very different evolutionary consequences in different parts of a species' range. They also show the power of replicating past experiments to identify evolutionary responses to climate change.

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Nylin, S., Wickman, P.-O. and Wiklund, C. (1989). Seasonal plasticity in growth and development of the speckled wood butterfly, Pararge aegeria (Satyrinae). Biological Journal of the Linnean Society, 38(2), 155–171.

Nylin, S., Wickman, P.-O. and Wiklund, C. (1995). Life-cycle regulation and life history plasticity in the speckled wood butterfly: are reaction norms predictable? Biological Journal of the Linnean Society, 55(2), 143–157.

A trait-based framework to predict phenological responses of temperate Lepidoptera to climate warming

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Many lepidopterans in temperate environments have responded to climate warming by increasing the number of generations per year (voltinism). By contrast, numerous species have maintained a univoltine life cycle (one generation per year) throughout their range, indicating the operation of phylogenetic, ecological or other constraints against such phenological change. In this study, I examined geographic variation in voltinism in moths and butterflies of northern and central Europe to identify traits that might predispose species to an obligately univoltine life cycle. My focus was on species with a wide latitudinal distribution range (15 degrees as a minimum), making it unlikely that constraints imposed by season length alone could preclude multivoltinism across their entire range. Instead, a univoltine life-cycle across this wide thermal and day-length gradient implies that certain species traits make multiple generations per year either impossible or strongly disadvantageous, which will unlikely change with future climate warming. Nearly half of the 731 lepidopteran species examined appeared to have a single generation throughout their entire European range. Univoltine and multivoltine phenologies were widely distributed across the lepidopteran phylogeny, indicating that phylogenetic constraints on changes in voltinism are generally weak, and the trait is open to ecologically-driven adaptive evolution. Although univoltine species tend to be generally larger than multivoltine species, size forms no strong constraint to having multiple generations per year. Life-histories that predispose species to overwinter as eggs or adults are strongly associated with univoltinism, whereas most species overwintering as pupae have a capacity for multiple generations. Obligately univoltine life-cycles also dominate among grass-feeders, particularly in endophagous species. Somewhat surprisingly, however, larval diet breadth sets no discernible constraint on voltinism. Given the diverse ecological consequences of voltinism and its changes, accounting for the species' capacity for multivoltinism may be a key to addressing future challenges in biodiversity conservation and pest management.

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Between-generation differences in life-history traits of a seasonally polyphenic butterfly: seasonal adaptations with some environmental modification

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Seasonal polyphenisms are cases in which individuals representing generations occurring in different times of the year systematically differ in the values of traits closely related to fitness. Such differences are often assumed to constitute adaptive responses to seasonally varying environments, but the evidence for this is still scarce. The adaptive character of the response would be corroborated by the pattern in which the decision about choosing a particular seasonal phenotype is made before the onset of respective environmental conditions (anticipatory plasticity). Alternatively, the between-generation differences can be caused by immediate effects of seasonally varying environments (responsive plasticity). In the series of laboratory experiments we reared the larvae of the seasonally polyphenic map butterfly *Araschnia levana* under two different photoperiodic regimes, inducing direct development and diapause pathways, respectively. Replicating the experiment at different temperatures and levels of host plant quality allowed us to evaluate both the anticipatory and the responsive components of the associated plastic changes in life-history traits. To complement the laboratory-retrieved data with the evidence from the field we also collected late instar larvae of both generations from the field. Larvae representing the direct development pathway invariably had higher growth rates and shorter development periods, although the difference between the developmental pathways was smaller at inferior host quality. Body size differences between the developmental pathways turned out to be less consistent. Both in laboratory experiments and in the field, last instar larvae heading towards the diapause (overwintering) had higher levels of both phenoloxidase (PO) activity and lytic activity than directly developing individuals. Though being considerably modified by immediate environmental effects, the between-generation differences in size, growth rates, duration of larval period and immune activity are largely based on anticipatory plasticity (= responses to photoperiodic cues) and should be treated as seasonal adaptations in *A. levana*.

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Multilevel variation in body mass and thorax width in a natural butterfly population

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The condition of animals is a widely used proxy to assess potential reproduction and survival. Standardized condition estimates are regularly measured in natural populations of vertebrate taxa. Much fewer condition proxies, e.g. measurements of body size, are used in invertebrates which are mostly examined under laboratory conditions. Here we assessed variation in body mass and thorax width in a natural butterfly population at multiple levels: within individuals during their life, among individuals during the flight period and among different years.

We studied a population of the univoltine Clouded Apollo (*Parnassius mnemosyne*) in Hungary from 2014 to 2020 using mark-recapture during the whole flight period each year. Repeated measurements on body mass and thorax width were performed on individually marked butterflies.

Both body mass and thorax width declined significantly with age in all years. The rate of change was significantly different for males and females only in 2016 for body mass. Every year (except 2020 for body mass), individuals that entered the population later in the flight period had significantly smaller initial body mass and thorax width. We found a sexual dimorphism in each year with a higher initial body mass and thorax width in females. Initial thorax width showed higher inter-annual variation than initial body mass.

Our study is among the first with repeated measurements on temporarily changing body sizes in a wild butterfly population. Our results imply that both body mass and thorax width may be suitable condition estimates. Uncovering variation in body size in natural populations may enable us to reveal potential pathways of adaptation to environmental changes.

Wing transparency in butterflies: ecological relevance and challenges

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Colours of butterflies are involved in anti-predator defences such as deflection of predator attacks, camouflage, and aposematism, whereby chemically-defended prey advertise their distastefulness to predators by the means of conspicuous wing colour patterns. Surprisingly, many aposematic butterfly species harbour transparent or translucent wings, a feature generally associated with camouflage. Why has transparency evolved in aposematic butterflies? How is transparency produced in these butterflies and does it incur costs for other function that involve wing patterns or structures, such as hydrophobicity and thermoregulation? We explored these questions using the neotropical butterfly tribe Ithomiini, representing the largest described radiation of aposematic butterflies encompassing a large range of transparency degrees, as a study system. Vision modelling and detection experiments involving avian and human predators show that transparency is associated with a lower detectability (McClure et al. 2019, Arias et al. 2019), suggesting that transparency might be part of a camouflage strategy. However, we found that transparent species are no less distasteful than opaque species (McClure et al. 2019). We revealed that transparency is primarily produced by a variety of scale modifications resulting in incomplete coverage of the wing membrane by scales, and enhanced by the presence of nanostructures on the wing membrane with anti-reflection effect (Pinna et al. 2021). Scales strongly contribute to making wings superhydrophobic, and their pigments are involved in thermoregulation. We examined whether transparency and associated scale modifications impacted those two functions, and found that transparency reduces both hydrophobicity and heat accumulation by wings. Finally, puzzled by the fact that the proportion of transparent species increases with altitude in the Andes, we compared thermal tolerance of transparent and opaque ithomiine species and found that opaque species were more tolerant to heat, but this effect is likely explained by the phylogeny of species.

Arias, M. et al. (2019). Transparency reduces predator detection in mimetic clearwing butterflies. Functional Ecology 33:1110-1119.

McClure, M. et al. (2019). Why has transparency evolved in aposematic butterflies? Insights from the largest radiation of aposematic butterflies, the Ithomiini. Proceedings of the Royal Society B, 286: 20182769.

Pinna, C. et al. (2021). Mimicry can drive convergence in structural and light transmission features of transparent wings in Lepidoptera. eLife, 10:e69080.

Shape of evasive prey is an important cue that triggers learning in avian predators

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Predator selection has influenced the evolution of wing shape and colouration patterns in butterflies. Although signalling unprofitability associated with secondary defences (e.g., unpalatability) has comprehensively been studied, signalling of evasive capabilities of prey remains poorly investigated. Advertising elusiveness is a prey strategy that reduces predatory attacks by relying on predator cognitive abilities (i.e., learning and memorizing aposematic cues). However, it is yet unknown how different phenotypic cues, including colour, body size and shape, differ in effectiveness and memorability. During the past two years, we conducted behavioural experiments using wild blue tits and butterfly models to understand how certain cues (hindwing tails and forewing white bands) are learnt and generalized by predators when associated with prey evasiveness. We constructed custom boxes to offer blue tits two butterfly models simultaneously. By pulling the evasive form out rapidly once approached by the bird we simulated evasiveness. The birds were trained until they attacked the control (reward – non-evasive) in 10 out of 12 consecutive trials, birds were given 80 trials to achieve this. The learning success was then evaluated by offering a factorial combination of the used cues (tails and bands). For two years we tested different cue combinations and recorded the learning and generalisation behaviour of ~120 birds. We uncovered a highly dynamic generalisation pattern that depended on initial predatory preferences prior to the experiments. Our results suggested that learning evasive phenotypes was possible and that both the wing shape and colour were effective cues in signalling evasiveness. We are hoping to present these results during the 22nd Congress of Lepidoptera.

Understanding the regulatory role of predators by following changes in Lepidopteran assemblages

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Predation is one of the most important ecological processes because of its community-structuring effects (Shochat et al., 2006). As prey animals, caterpillars are the most abundant herbivores in Hungarian oak forests and the occasionally severe defoliation they cause may have significant effects both on acorn crop (Koenig et al., 2013) and forest health. However, diversity may increase where predation limits competition (i.e., *keystone predation*; Paine, 1966). According to our hypothesis the presence of predators, such as red wood ants and insectivorous birds can result in a healthier forest, where the diversity of prey animals will increase as well. We used sticky belts and funnel traps to monitor the lepidopteran community at our study sites. We investigated the forest health status and both quantity and quality of acorn crop to follow the effects of the changes of lepidoptera larva abundancies in two Hungarian sessile oak (*Quercus petraea*) dominated stands. At one sample site we were able to investigate the presence-absence of a red wood ants (*Formica rufa*), while at the other sample site we placed nest boxes to maximize the density of insectivorous birds. According to our results the presence of predator species can reduce the abundance of lepidopteran larvae, however the community becomes more diverse and specialized. Considering the health of the forest, we can observe an improvement in the quality of acorn crop. Our research was supported by the OTKA-128008 research grant (Quantifying forest-health-related ecosystem services in Hungarian oak forests) provided by the National Research, Development and Innovation Office.

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Shochat, E., Warren, P. S., Faeth, S. H., McIntyre, N. E., Hope, D. (2006). From patterns to emerging processes in mechanistic urban ecology. Trends in Ecology and Evolution, 21, 186–191.

Habitat specialization of forest butterflies and moths along a tropical elevational gradient of Mount Cameroon

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Understanding the causes and consequences of insect diversity patterns along elevational gradients is a longstanding problem in ecology, especially in the species-rich tropics. Ecological specialization (*aka* niche breadth) has been considered among the key drivers of the patterns (Forister et al., 2015). Following the elevational niche-breadth hypothesis (Rasmann et al., 2014), species' niche-breadth should decrease (i.e. higher specialization) with decreasing elevation because of an increased role of biotic interactions and more stable environments. Nevertheless, it has not been studied sufficiently yet.

We assessed the habitat specialization (based on descriptors of forest structure) of 138 species of fruit-feeding butterflies and 396 species of fruit-feeding moths along the elevational gradient on Mount Cameroon from 350 to 2200 m a.s.l. (Maicher et al., 2020). Unexpectedly, we found decreasing niche breadth along elevation for most groups, suggesting that species tend to be more specialized at higher altitudes. Nevertheless, geometrid moths showed highest specialization at the mid elevations, whereas satyrin butterflies did not show any significant elevational pattern. Overall, our findings did not support the elevational niche-breadth hypothesis.

Forister, M. L., Novotny, V., Panorska, A. K., Baje, L., Basset, Y., Butterill, P. T., ... and Dyer, L. A. (2015). The global distribution of diet breadth in insect herbivores. Proceedings of the National Academy of Sciences, 112(2), 442-447.

Maicher, V., Sáfián, S., Murkwe, M., Delabye, S., Przybyłowicz, Ł., Potocký, P., ... and Tropek, R. (2020). Seasonal shifts of biodiversity patterns and species' elevation ranges of butterflies and moths along a complete rainforest elevational gradient on Mount Cameroon. Journal of Biogeography, 47(2), 342-354.

Rasmann, S., Alvarez, N. and Pellissier, L. (2014). The altitudinal niche-breadth hypothesis in insect- plant interactions. Annual plant reviews, 47, 339-359.

Extraordinary range expansions in butterflies and their causes – the examples of *Papilio demoleus* and *Pieris mannii*

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Range expansions and retractions are a common natural phenomenon in Lepidoptera, but appear to have increased in frequency and extent due to climatic and anthropogenic changes. In butterflies, two species have demonstrated extraordinary range expansions in recent years on a global or a European scale (*Papilio demoleus* and *Pieris mannii*, respectively). The original disjunct distribution of the Lime Swallowtail (*Papilio demoleus*) was confined to (1) continental South and Southeast Asia and to (2) Australia and few nearby islands, but Asian populations have rapidly extended their range to the northeast and the southeast, now completely closing the former distributional gap in the SE Asian islands, as well as in the Caribbean after their accidental introduction (Riaz et al. 2020). Whereas the invasive populations constitute a pest on *Citrus* trees (Rutaceae), the indigenous populations in the Australian region only feed on *Cullen* (Fabaceae). Most recently, the species has also extended its range into the Mediterranean region, reaching Cyprus (John et al. 2022). The Southern Small White (*Pieris mannii*) used to be mainly restricted to the Mediterranean region, with only isolated and often threatened populations further north. Since 2008, however, this species has expanded its range continuously across Switzerland to Germany and the Netherlands up to the North Sea and the Baltic coast, mostly confined to anthropogenic habitats such as urban gardens with the evergreen candytuft (*Iberis sempervirens*). Recent research indicated that this range expansion is not mainly caused by climate change but possibly by adaptations to new larval foodplants (Neu et al. 2021). However, recent observations question this assumption, and a collaborative genomics approach is currently under way to elucidate the causes. This talk will present an up-to-date overview of these two range expansions, also considering molecular data, and discuss possible causes and consequences, e.g. for indigenous populations in the invaded territories.

John, E. et al. (2022). Confirmation of the presence of nominotypical *Papilio demoleus demoleus* Linnaeus, 1758 (Lepidoptera: Papilionidae) in Cyprus, with additional notes on breeding and potential colonization. – Entomol. Gaz., 73(2): *in press*.

Neu, A. et al. (2021). Reduced host-plant specialization is associated with the rapid range expansion of a Mediterranean butterfly. – J. Biogeogr. 48(12): 3016-3031.

Riaz, S. et al. (2020). Morphology, life cycle, and management of two invasive subspecies of *Papilio demoleus* (Lepidoptera: Papilionidae): A review. – J. Appl. Entomol. 144(10): 845-856.

Morphology and distribution of the wing margin campaniform sensilla in the Lepidoptera and other amphiesmenopterans

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The wings of pterygote insects have a rich complement of proprioceptors, comprising primarily chordotonal organs and campaniform sensilla. The latter form conspicuous aggregations on the proximal sectors of some of the principal longitudinal veins and their structure and function has been subject of study in not few representatives of some insect orders (Aiello et al., 2021). Relatively little attention has been paid to the campaniform sensilla associated to the apices of the longitudinal veins in the Lepidoptera, the "Randkuppeln" of early workers (Vogel, 1911). We here survey the campaniform sensilla on the wing margins in a major subset of Lepidoptera and Trichoptera, and discuss its autapomorphic condition and phylogenetic implications for the groundplan of the superorder Amphiesmenoptera (Kristensen, 1984).

Aiello, B. R., Stanchak, K. E., Weber, A. I., Deora, T., Sponberg, S. and Brunton, B.W. 2021. Spatial distribution of campaniform sensilla mechanosensors on wings: form, function, and phylogeny. Current Opinion in Insect Science, 48: 8-17.

Kristensen, N. P. 1984. Studies on the morphology and systematics of primitive Lepidoptera (Insecta). Steenstrupia, 10(5): 141-191.

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Morphology of the male hindwing costal roll in Cochylini (Lepidoptera: Tortricidae) with an ecological and evolutionary perspective

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Secondary sexual characters in the Lepidoptera, such as those associated with male pheromone production and dissemination, are not directly involved in copulation, but they usually play an exceedingly important role in intraspecific communication, particularly at relatively short distances. The hindwing costal roll is a scent organ restricted to the Cochylina subtribe of the Tortricidae family. In this research, we have examined the structure of the costal roll, its variation and phylogenetic distribution as well as its evolutionary significance. The costal roll appears as a complex structure that involves modifications of the wing membrane and may include several types of sex scales including a hair pencil and microscales. Optical and scanning electron microscopy (SEM) are used thoroughly to explore these structures in a sample of 653 specimens of more than 250 species. Data are analysed in an evolutionary context. Scent organs are supposed to have evolved primarily because of sexual selection but habitat sharing contributes to maintain these expensive organs. By using food plants as a proxy of habitat use we have analysed if the costal roll may have evolved in this context. Network analysis helps us to understand how sexual and habitat selection have contributed to the evolution of the character. Moreover, the organ has evolved in a phylogenetically restricted clade. Gains and losses may be traced across the phylogeny of the group. Prevailing ideas predict that sexually selected characters are labile and lack the adequate phylogenetic structure, but the costal roll reveals a strong phylogenetic signal more compatible with a stable character.

Ustyurtiidae (Urodoidea), the recently discovered new family of Lepidoptera

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In 2013 and 2014, Kari Nupponen and Pavel Gorbunov collected some mysterious moths in the Ustyurt Nature Reserve in SW Kazakhstan. The phylogenetic affinities of these moths were studied using morphological and molecular methods leading to the description of a new family of Lepidoptera, Ustyurtiidae Kaila, Heikkilä & Nupponen in 2020 (Kaila et al. 2020). The obtained results placed these moths as the sister-group of Urodidae. Affinities of Ustyurtiidae with other Urodoidea and Lepidoptera and reasons for erecting a new family are explained.

Ustyurtiidae include two described species from Kazakhstan. Subsequently a third species from Iran, previously thought to belong to Gelechiidae, was moved to this family (Amsel, 1958; Kaila et al., in press). Information on the habitat and biology of these interesting moths will be given.

Amsel, H.G. (1959). Microlepidoptera aus Iran. Stuttgarter Beiträge zur Naturkunde, 27:31.

Kaila, L., Karsholt, O. and Rajaei, H. *In press*. Family Ustyurtiidae Kaila, Heikkilä & Nupponen, 2020. -in: Rajaei, H. & Karsholt, O. (eds.). *Lepidoptera Iranica*.

Kaila, L. Nupponen, K. Gorbunov, P. Yu., Mutanen, M. and Heikkilä, M. (2020). Ustyurtiidae, a new family of Urodoidea with description of a new genus and two species from Kazakhstan, and discussion on possible affinity of Urodoidea to Schreckensteinioidea (Lepidoptera). Insect Systematics & Evolution 51: 444–471.

Exploring imaging techniques in integrative insect systematics: case study on an undescribed African geometrid moth (Lepidoptera: Geometridae)

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State-of-the-art imaging techniques are useful in taxonomy, providing unambiguous illustration of structures and diagnoses, often being more informative than written descriptions. Non-destructive imaging techniques are particularly valuable when internal structures of rare species or type specimens need to be examined.

We present a case study, demonstrating how integrative approach can be applied in systematics to describe a new species and genus. Our study taxon is a large and conspicuous geometrid moth from South Africa, which we will classify to subfamily Larentiinae. The species has been present in collections at least 128 years but it has not been formally described.

Based on DNA barcodes from mitochondrial COIa and several nuclear markers, we determine the taxonomic position of this species through molecular phylogeny. Based on DNA barcode, the genetic distance to nearest available reference species is more than 11%. The presence of the intracellular bacteria *Wolbachia* will be analysed to control for any potential instability of the molecular analysis, and to contribute to the general knowledge of this incompletely understood arthropod endosymbiont.

We provide images to illustrate diagnostic characters using microscope and macro photo stacking, as well as scanning electron microscope (SEM). Micro-CT imaging will be experimented to yield 2D and 3D images of the wing venation, genitalia, and other internal structures without destroying or detaching body parts from the target specimens. Finally, we provide a description of the known distribution, habitat, host plant, immature stages, and parasitoids of the new species.

Our study species appears to belong to an isolated lineage being sister to Scotopterygini Warren, 1895 (Viidalepp 2011). We place the species in wider framework and discuss the potential need to reclassify the current Xanthorhoini *sensu lato* lineage (Hausmann & Viidalepp 2012, Õunap et al. 2016).

Viidalepp, J. (2011). A morphological review of tribes in Larentiinae (Lepidoptera: Geometridae). Zootaxa 3136: 1–44.

Hausmann, A. & Viidalepp, J. (2012). The Geometrid Moths of Europe 3. Larentiinae. Apollo Books, Stenstrup, 743 pp.

Õunap, E., Viidalepp, J. & A. Truuverk. 2016. Phylogeny of the subfamily Larentiinae (Lepidoptera:Geometridae): integrating molecular data and traditional classifications. Systematic Entomology 41: 824–843.

New approaches for studying the functional anatomy of the phallus in Lepidoptera

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The existing techniques for studying the everted vesica (endophallus) of Lepidoptera are based mainly on cuticular preparations macerated with caustic solution for taxonomic purposes, which practically eliminate the possibility to study the functional anatomy of the skeletomuscular apparatus of this structure. Injection of formaldehyde solution into the cavity of the phallus of fresh material is proposed as a new approach for studying the intact anatomy. The new technique results in simultaneously everted and fixed phallus, which better approximates its functional shape. The injection produces properly fixed tissues and the whole structure can be processed for various further studies, including histology sectioning, scanning electron and confocal laser scanning microscopy, allowing three-dimensional reconstructions. Moreover, the commonly used stubs for scanning electron microscopes do not allow observation of the sample from all aspects. This problem was solved by modification of a commercially available stub. The device allows 360° rotation of the phallus and certainly can be used for observation of other objects as well.

On the identity of *Argyria lacteella* (Fabricius, 1794) (Lepidoptera, Pyraloidea, Crambinae) and its synonyms based on the available type material's DNA and morphology

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The name *Tinea lacteella* Fabricius, 1794 has been applied to small white *Argyria* (Pyraloidea, Crambinae) moths collected widely, from the United States of America south to Brazil. Five synonyms or putative synonyms are presently ascribed to *A. lacteella* and no taxonomic revision is available for them. Because morphological variation and several DNA barcode lineages unassociated with verified names are observed in *Argyria* specimens that, like *A. lacteella*, share a similar 11 mm wingspan and few forewing markings, we aim to properly associate the available names to the species involved and to better understand their morphological variation and geographical distribution. We used hybridization capture adapted from Suchan et al. (2016) on the holotype of *A. lacteella*, likely collected between 1784 and 1789, as well as on the holotypes of two putative and one published synonyms, and that of a similar species. Based on the sequence of a specimen collected in Florida we designed 21 synthetic oligonucleotides of 108 bp to cover the COI barcode for comparison with the 230+ COI barcode sequences available for *Argyria* specimens in the Barcode of Life Data System (www.barcodinglife.org). We transcribed the synthetic oligonucleotides into RNA probes, used them to capture the DNA extracted from the holotypes (Patzold et al., 2020), and sequenced them. These innovative methods allow the recovery of genetic information from old and degraded samples offering new perspectives in the systematics of complex species groups such as that of *A. lacteella*.

Patzold, F., Zilli, A. and Hundsdoerfer A. K. (2020). Advantages of an easy-to-use DNA extraction method for minimal-destructive analysis of collection specimens. PLOS One, https://doi.org/10.1371/journal.pone.0235222

Suchan, T., Pitteloud, C., Gerasimova, N. S., Kostikova, A., Schmid, S., Arrigo, N., Pajkovic, M., Ronikier, M. and Alvarez, N. (2016). Hybridization capture using RAD probes (hyRAD), a new tool for performing genomic analyses on collection specimens. PLoS ONE.

The Gelechiidae of North-West Europe – a new handbook

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The Gelechiidae are among the most diverse families of smaller Lepidoptera. 269 species in 63 genera are known from North-West Europe, defined here as the region limited eastwards by the Russian border and southwards approximately to the 52nd northern latitude. Gelechiidae are rather small, often dull coloured moths, and they are considered as difficult to identify. There are many similar looking species, which may even belong to different genera. It is often necessary to dissect the genitalia to obtain a correct identification. Especially the male genitalia are more or less three-dimensional, and therefore the unrolling technique is recommended for preparing genitalia slides of male Gelechiidae.

Larvae of the Gelechiidae feed on a variety of different plants, but none of the North-West European species are polyphageous. Therefore gelechiids occur in a wide range of habitats, mostly in open landscapes on dry soil, but they can also be found in forests or in wet meadows. In North-West Europe there are more species in south-east than towards north-west, but some species are only distributed in the high north up to the Barents Sea. Based on own research and help from many colleagues we have compiled data on the taxonomy, biology and distribution of the 269 species for a book, which is now in print.

Gregersen, K. and Karsholt, O. in print. *The Gelechiidae of North-West Europe*. Norwegian Entomological Society, Oslo. 939 pp.

Lepidoptera Iranica, a complete inventory and catalogue of the order Lepidoptera in Iran

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Iran, with an area of 1,648,195 km^2, is surrounded by two large water bodies to the south and north and has a very complex topography: over 65% of the country's surface area is above 1000 m altitude and structured by two major mountain ranges (Alborz and Zagros) in the northern and central parts of the country. Additionally, two large deserts (Dasht-e Kavir and Lut) cover the central and eastern parts of the country. The geographic location of Iran and its contact with different zoogeographical regions (the Indo-Malayan Region in the southeast, the Afrotropical Region via the Hormuz Strait, the Arabian Peninsula in the southwest and the Mediterranean in the north) makes it one of the most complex Palaearctic faunal regions. Despite lots of taxonomic research on the Iranian Lepidoptera fauna, it remains largely unknown. To accelerate taxonomic studies on this insect order, we ran a mega project and invited 64 taxonomists from around the world to analyse and summarise the hitherto published data on the lepidopteran species of the overall 70 families known from the country. Records extracted from close to 2000 published literature sources are completed by previously unpublished records from 49 collections. From overall more than 5500 reported species names in Iran, 4395 species are confirmed to occur in Iran, and 278 species need further confirmation. In total 111 species are regarded as having been erroneously recorded for the country. In total, 169 species are reported as new for the Iranian fauna. For each species, we present the provincial distribution, a list of recorded synonymies from Iran and, where relevant, remarks clarifying misspellings or other ambiguities.

A new open access web portal integrates biodiversity and taxonomy data of geometrid moths

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Much of our core knowledge of biodiversity is found in collections of natural history museums, in records scattered across taxonomic publications (checklists, catalogues, reviews and revisions) and increasingly in internet databases. Up-to-date catalogues of global fauna are essential for taxonomists. With regard to the megadiverse family Geometridae, the recent knowledge is summarised in a print Catalogue (Scoble 1999) and a Checklist, which is partially online (Scoble & Hausmann 2007).

Because the taxonomy, nomenclature, species richness, genetic data and distribution patterns of geometrids is growing constantly and becoming more accurate, continuous updating of existing global Catalogue is necessary to reflect the latest knowledge. Moreover, providing an open access single-entry point is essential to both promote taxonomic research and make it widely accessible. We present the result of the first attempt at realizing this. The portal will include a wider body of information relating to species richness and taxonomy, with links to specimen photographs, DNA barcodes, original descriptions and, potentially, other species-specific data. The taxonomic element of the online database will be semi-dynamic and released every few years as a fixed version with a unique DOI, allowing unambiguous reference points to enable standard citation of the data.

We present the current state of this project, which covers ~35 000 validated species and subspecies of Geometridae. We summarise the global species richness of Geometridae by biogeographical region and by subfamily, and present the website that is used to search the database. The first online update is expected to be released by the end of 2022. Future updates will cover additional Geometroidea families (i.e. Epicopeiidae, Pseudobistonidae, Sematuridae, Uraniidae).

Scoble, M. J. (1999) Geometrid Moths of the World: a catalogue (Lepidoptera, Geometridae). Vol 1 and 2. CSIRO Publishing and Apollo Books, Stenstrup, 1016 pp. + 129 pp. of Index.

Scoble, M. J. and Hausmann, A. (2007) Online list of valid and available names of the Geometridae of the World. http://www.herbulot.de/globalspecieslist.htm

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Population recovery of *Parnassius apollo* (Linnaeus, 1758) in Mediterranean habitats: the case of the Penyagolosa Nature Reserve (Spain) (Lepidoptera: Papilionidae)

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The populations of the endangered Apollo butterfly (*Parnassius apollo* Linnaeus, 1758) in moderately low altitudes in Mediterranean habitats are specially threatened because of climate change. These populations survive at the limit of their biological possibilities. In 2006, the last individual in the population of the Penyagolosa Nature Reserve (Castelló, Spain) was seen. After years of monitoring, the population was considered definitely extinct in 2010. A recovery program for the species is being currently developed since 2018 based on translocation from nearby populations, including captive breeding and habitat restoration. Habitat restoration has focused on facilitating the proliferation of *Sedum album* and *S. sediforme* – the food plants for the larvae – and nectar plants for adults, as well as removal of tree barriers, among other actions. Specimens are bred in captivity from eggs and released as fourth-instar larvae. In 2021, we monitored for the first time since extinction the presence of butterflies in flight product of natural mating. This confirms the reintroduction has been potentially successful. However, the low performance of the breeding and the low level of recovery of the population suggest that a long-term strategy will have to be maintained. At the same time, a monitoring strategy for the population origin of translocation has been implemented to control the effects of extraction. We present our goals and the preliminary results (successes and failures) of this novel experience in Spain.

Identification of *Bombyx mori* L. Hatay yellow strain (Lepidoptera: Bombycidae) by morphological and molecular methods

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Throughout the history, silk fiber is one of the indispensable and most valuable textile products. The silkworm, *Bombyx mori* (Linnaeus, 1758) (Lepidoptera: Bombycidae), is one of the best characterized insect in the order Lepidoptera, is in the mulberry-fed group and is the only domesticated insect that depends only on humans to survive. Hatay yellow strain, indigenous to Turkey, was domesticated about 5000 years ago. In sericulture, the only hybrid strain that weaves white coccon has been bred for many years and Hatay yellow hasn't been bred for nearly 45 years in Turkey. In this study, it is aimed to investigate some morphological and molecular characteristics of the Hatay yellow which is facing the danger of extinction.

The morphological characteristics of the silkworm, especially the 5th instar, the late stage larvae, are very important. The yellow colour of the abdomen legs in this stage is an important distinguishing feature of the Hatay yellow. For this reason, all the morphological features of the last larval stage were examined in detail under the microscope. In this study, as well as the new morphological features of the adult and pre-mature stages, the ones known before were also updated. It is determined that its cocoon has about 20 different shades of colour from cream to light yellow to very dark yellow, even orange.

Hatay yellow strain and the hybrid strain of *Bombyx mori* were used for identification of their phylogenetic differences via molecular methods. Macherey Nagel Nucleospin Insect DNA Isolation kit was used for DNA extraction and LCO1490/HCO2198 primer pair was used to amplify mtCOI gene region in PCR analysis. The two strains were phylogenetically compared with the different strains from the world. As a result, it was determined that these two strains were separated from each other in the phylogenetic tree.

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A supertree of Northern European macromoths

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Ecological and life-history data on the Northern European macromoth (Lepidoptera: Macro- heterocera) fauna is widely available and ideal for use in answering phylogeny-based research questions: for example, in comparative biology. However, phylogenetic information for such studies lags behind. Here, as a synthesis of all currently available phylogenetic information on the group, we have produced a supertree of 114 Northern European macromoth genera, providing the most complete phylogenetic picture of this fauna available to date. In doing so, we have assessed those parts of the phylogeny that are well resolved and those that are uncertain. Furthermore, we comment on the current completeness of phylogenetic information in this group. With phylogenies playing an ever more important role in the field, this supertree should be useful in informing future ecological and evolutionary studies.

Davis, R.B., Õunap, E. and Tammaru, T. (2022). A supertree of Northern European macromoths. PLoS One 17(2):e0264211

Effect of patterns of land use on moth community in High Atlas Mountains of Morocco

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Insects are subject to a drastic decline across landscape level, with human actions being major drivers of species loss in urban and agricultural landscapes (Newbold et al., 2016; Uhl et al., 2021). Lepidoptera witnessed a rapid decline in regions with high human pressure due to habitat loss (Després et al., 2017). Several studies have investigated the effect of land use on Lepidoptera in Europe, North America and Japan while many regions have not been covered, including Morocco. The aim of our study is to assess how land use affects moth communities in Moroccan agricultural landscape. From mid-June to mid-October 2021, automatic sugar bait traps were used to quantitatively sample macromoths at 20 localities in an area covering about 45 ha. In total, 2237 individuals of 113 species were recorded, mostly representing Noctuidae and Erebidae.

We studied how abundance and species richness of moths depended on the area covered by agricultural crops, buildings and natural habitats. We found that moth abundance was influenced positively by agricultural field crops and negatively by urbanization, however, no significant effects were found for species richness. Our results also showed that the share of natural habitats in the surrounding area has no effect on moth diversity and abundance. We also tested the effects of agricultural crops and urbanization on abundance of two dominant species and found that agricultural crops are affecting positively *Catocala nymphaea* with no significant effect on *Agrotis segetum*, while urbanization has a negative effect on both species.

Our study revealed a species-rich community of nocturnal moths in Moroccan agricultural landscape, with little evidence of negative effects of human presence on either abundance or diversity of moths. Traditional irrigation practices used in Moroccan mountain villages might be a reason for high moth diversity in the otherwise predominantly arid landscape.

Newbold, T., Hudson, L.N., Arnell, A.P., Contu, S., de Palma, A., et al. (18 authors). 2016. Has land use pushed terrestrial biodiversity beyond the planetary boundary? A global assessment. Science, 353: 288–291

Després, L., Ficetola, GF., Baillet, Y. and Gallou, A. (2017). Elevational gradient and human effects on butterfly species richness in the French Alps. Ecol Evol, 7:3672– 3681

Uhl, B., Wölfling, M. and Fiedler, K (2021). From forest to fragment: compositional differences inside coastal forest moth assemblages and their environmental correlates. Oecologia, 195, 453–467

You do not need a scale to weigh a Geometridae moth: applying allometric relationships to predict dry body weight at maturation stage

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Specious clades, such as the Geometridae family (~24,000 species), provide a fruitful opportunity for exploring the role of body size on the determination of many other traits, often associated with reproduction and population dynamics (Tammaru et al. 2018; Murillo-Ramos et al. 2019). In insects, the dry body weight (DBW) is a well-known proxy of body size, used to estimate the amount of non-water resources allocated to the body. As body size changes throughout life, it becomes necessary to establish an ontogenetic reference point at which the trait is measured, and in insects, the time at maturation appears as a useful baseline for such purpose. An additional issue to be considered is that rearing a sufficient number of individuals of several species is methodologically challenging. Therefore, a more handy method based on the allometric relationships between DBW and simple linear measurements of body structures is a plausible and necessary alternative to generate estimates of DBW. The aim of this study is to provide simple and accurate models to predict DBW at maturation stage in Geometridae species, based on linear measurements of body parts. Individuals of 109 species from temperate (n = 69) and tropical (n = 40) forests were reared in laboratory conditions in order to obtain measures of DBW. Five linear measurements were digitally taken from additional specimens based on images of pinned individuals extracted from the Lepiforum database (https://lepiforum.org/). The predictive capacity of each linear measurement was accessed through linear models. For both sexes, the widest distance between the two wings was the best predictor of DBW. Such finding contrasts with the literature, where wing length is one of the most widespread proxy of body size in Lepidoptera, although the relationship between this trait and DBW is still ambiguous.

Tammaru , T. Johansson, N.R. Õunap, E. and Davis, R.B. (2018). Day-flying moths are smaller: evidence for ecological costs of being large. Journal of Evolutionary Biology, 31: 1400-1404.

Murillo-Ramos L., Brehm G., Sihvonen P., Hausmann A., Holm S., Reza Ghanavi H., Õunap E., Truuverk A., Staude H., Friedrich E., Tammaru T. and Wahlberg N. (2019). A comprehensive molecular phylogeny of Geometridae (Lepidoptera) with a focus on enigmatic small subfamilies. PeerJ 7:e7386

Lack of correlation between wing darkness and climate in SW European butterflies (Papilionoidea)

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Recent work has provided evidence for significant relations between wing colour shade and broad thermal preferences in insects including butterflies (Zeuss et al, 2014; Kang et al., 2021), which might have a bearing regarding climate warming trends (Zeuss et al., 2014). We tested the relationships between darkness/lightness and two climate variables (temperature and precipitation) for the Iberian butterflies. Reflectance in the visible light spectrum was estimated form 10 measurements per individual from at least one male and one female for 220 species. All measurements were calibrated as the mean RGB saturation (scale 0-255). The species mean reflectance was compared with the corresponding temperature and precipitation means derived from their known geographic distributions using both the European range and the regional (Iberian) data. The meaning of the strength and direction of the relations derived from the local data is described and discussed.

Kang, C., Im, S., Lee, W.Y., Choi, Y., Stuart-Fox, D. and Huertas, B. (2021). Climate predicts both visible and near-infrared reflectance in butterflies. Ecology Letters, 24: 1869–1879.

Zeuss, D., Brandl, R., Brändle, M., Rahbek, C. and Brunzel, S. (2014). Global warming favours light-coloured insects in Europe. Nature Communications, 5: 3874.

Does sexual dimorphism in wing colouration relate to sphragis shape in Apollo *(Parnassius)* butterflies?

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Apollo butterflies is a morphologically diverse group with at least 60 described species. Most of them may bear sphragides which are copulatory plugs with extremely elaborated structures produced by the males during mating to prevent females from further mating and to secure paternity. These sphragides show a high degree of diversity in shape, size, colour and the means of attachment. In parnassian butterflies a species-specific sexual dimorphism can also be observed. We aimed to reveal whether the shape of sphragides and sexual dimorphism are connected through evolutionary changes, since both are partly or fully the result of sexual selection. We expect that larger sexual dimorphism involves more complex sphragis shape due to stronger sexual selection.

We distinguished nine sphragis shape types and calculated the degree of sexual dimorphism with linear discriminant analysis according to the ventral and dorsal wing pattern elements, based upon photographs taken in the Eisner Collection, Natural History Museum (Naturaalis), Leiden. We used the most recent and comprehensive phylogenetic tree of the *Parnassius* clade based on Condamine *et al.* 2018, built with four mitochondrial (COI, ND1, ND5, 16S) and one nuclear genes (EF-1α) to trace the aforementioned characters utilizing Mesquite, a software for evolutionary analysis.

Although the phylogenetic tree and the evolutionary history of sphragis shape coincide, we found no relationship between the shape of sphragides and sexual dimorphism in wing colouration. This lack of relationship implies that the diversity of the sphragides may depend on other drivers, such as ecological traits, biogeographical impacts or the diversity in the shape of male and/or female genitalia.

Condamine, F. L., Rolland, J., Höhna, S., Sperling, F. A. and Sanmartín, I. (2018). Testing the role of the Red Queen and Court Jester as drivers of the macroevolution of Apollo butterflies. Systematic Biology, 67(6), 940-964.

A comparative perspective on lifespan in tropical and temperate region geometrid moths

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Lepidoptera can significantly contribute to understanding the evolution of lifespan as the trait can feasibly be measured in a high number of species from different environments. If the evolutionary determinants of longevity were mainly extrinsic (ecological), related species from different habitats should systematically differ in individual lifespans. We recorded adult longevities for 110 species of geometrid moths from a tropical community and paralleled the lifespans in this tropical assemblage with 43 species from a temperate community (Holm et al. 2016; Holm et al 2022). A comparative analysis based on an original phylogenetic reconstruction showed that larger moth species tended to live longer in both regions. Average adult lifespans were found to be highly similar for the tropical and temperate relatives. These patterns lead to the conclusion that intrinsic (physiological) determinants of longevity dominate over extrinsic (ecological) ones: the contrasting environments of tropical and temperate forests have hardly produced differences in moth longevities.

Holm, S., Davis, R.B., Javoiš J., Õunap, E., Kaasik, A., Molleman, F. and Tammaru, T. (2016) A comparative perspective on longevity: the effect of body size dominates over ecology in moths. Journal of Evolutionary Biology, 29: 2422–2435.

Holm, S., Kaasik, A., Javoiš, J. Molleman, F., Õunap, E. and Tammaru. T (2022). A comparative study on insect longevity: tropical moths do not differ from their temperate relatives. Evolutionary Ecology, 36: 251–262.

A glimpse of the species and their ecological data from Afrotropical rainforest

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Describing fauna is an urgent task due to the current rapid destruction of natural tropical forest ecosystems. However, the majority of tropical insects still remain insufficiently explored in terms of their taxonomy and ecology due to the difficulties in obtaining the data. 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. We have two broader aims: 1) to study evolutionary-ecological patterns in a comparative perspective of tropical species and their temperate relatives; 2) to study the recovery of lepidopteran communities in different-aged restored forests in the Uganda Wildlife Authority – Forests Absorbing Carbon dioxide Emissions (UWA-FACE, 2015) tropical forest restoration project area. Here, we will present a glimpse of the type of ecological data we have been collecting. We will use some most common geometrid moths (Geometidae) as our example species and we will present data on their host-plant usage, habitat preference, phenology and illustrate the data with images of their larval stages.

UWA-FACE (2015). Natural high forest rehabilitation project on degraded land of Kibale National Park, Uganda. CCB Project Design Document. UWA & Face the Future. Retrieved from https://www.climate-standards.org/2015/04/20/natural-high-forest-rehabilitation-project-on-degraded-land-of-kibale-national-park-uganda/

Flash coloration as the adaptive significance of hindwing pattern in *Catocala*

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While wing colouration in Lepidoptera provides an excellent model system for evolutionary-ecological research, our knowledge is still fragmentary. Here we focus on selective pressures on wing pattern in *Catocala* (Lepidoptera: Erebidae). *Catocala* moths are characterised by bright colours on the upperside of hind wings, accompanied by contrast-rich pattern of the ventral side. Kang et al. (2018) suggested that the function of the bright colours is to startle off predators when the hind wings are displayed in response to an attack. Indeed, such a behaviour is typical of some sphingid and saturniid moths but we have never observed it in *Catocala*. Instead, we believe that the bright hindwing colouration of *Catocala* is explained by the flash coloration effect. This implies that the moths get survival advantage by abrupt change in their appearance when they sit down after an escape flight: the predator which has developed a search image to the flying moth loses its sight. While we are unable to prove this hypothesis directly, we are collecting indirect evidence in its support. First, we present evidence that *Catocala* moths are more prone to be engaged in daytime escape flight than other size-matched nocturnal Lepidoptera. This was confirmed in an experiment in which we gently touched the resting moths and observed their behaviour. Second, we show that ventral side of *Catocala* has a higher degree of contrast than in other nocturnal moths, and the degree of contrast positively correlates with brightness of hindwing upperside. In a way or another, this must be an adaptation to daytime flight as wing underside is not displayed in any other situation. For the analysis of wing pattern, we apply an empirical photography method with a full spectrum camera. The moths are photographed using UV and regular filters and analysed with Mica Toolbox program.

Kang, C., Zahiri R. and Sherrat, T.N. (2017). Body size affects the evolution of hidden colour signals in moths. Proceedings of the Royal Society B, 284: 20171287.

Small size and short larval period as responses to chemically-perceived signals of high conspecific and congeneric larval density in a geometrid moth

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Larval density is an important determinant of insect life histories, as it is shown to affect a diverse array of fitness-related traits such as size, development time, fecundity, and immune reaction. However, we still lack a coherent understanding of ultimate causes, mechanisms and consequences of larval density effects in insects. By rearing the *Hypomecis atomaria* larvae at two different densities (one vs four larvae per container) we here examined the effects of intraspecific density on pupal mass development time and fat content in this widespread moth species. To determine if caterpillars perceived the density related signals primarily mechanically or chemically, two additional treatments (larvae occurring in the same container but separated with a mesh and mechanical disturbance) were introduced. To further specify the density effects and to elucidate the sensory abilities of caterpillars in discriminating between conspecifics and larvae of other moth species, we recorded life history traits of *H. atomaria* larvae reared together with either the larvae of geometrid *Hypomecis punctinalis*, geometrid *Cepphis advenaria* or noctuid *Acronicta rumicis*. We found that at higher densities *H. atomaria* had shorter larval period and remained smaller as pupae when compared to the solely reared conspecifics. Similar high density effects also appeared in the treatment when larvae were separated by mesh (only chemical, but not mechanical signals of high density allowed) and when *H. atomaria* larvae were reared together with the larvae of congeneric species (*H. punctinalis*). These results suggest that larval density has a specific influence on *H. punctinalis* life history traits, caterpillars perceive the density signals mainly chemically and the response to high densities caused by the larvae of closely related species is similar to that caused by conspecifics.

Vellau, H. and Tammaru, T. (2012). Larval crowding leads to unusual reaction norms for size and time at maturity in a geometrid moth (Lepidoptera: Geometridae). European Journal of Entomology, 109, 181–186.

Automating the reading of insect labels: an automated text search-based approach to extract collecting informations

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Natural history collections are home of billions of insect specimens worldwide. To ensure their sustainability and facilitate knowledge transfer, large-scale digitization initiatives are undertaken in several museums around the world. This process includes the acquisition of specimen photographs along with their associated labels. While image datasets are piling up, a time-effective way to extract label information from pictures and integrate it to a database is currently missing. Here, we present the “collecting event approach”, a semi-automated pipeline that extracts key elements from verbatim label text or outputs from optical character recognition (OCR) engines, and looks for the respective collecting event in a curated database. The collecting event database is built incrementally by the new collecting events that are added after being human proofed. This approach enables to efficiently recognize previously seen labels and get around the need to transcribe similar labels repeatedly. We test our approach on three kinds of datasets: the set of labels used to design the script (“control_dataset”), similar labels representing the same collecting events (“mapping_dataset”) and labels not used to design the script (“denovo_dataset”). We discuss the potential of this approach as the first stone to pave the way to future AI-based approaches.

The 83 million year old family tree of burnet moths

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To have a better understanding of the evolutionary history of Zygaenidae, a comprehensive molecular dataset was needed to infer the relationships among the five subfamilies. I present the first comprehensive molecular phylogentic study of 189 species from 39 genera of zygaenid moths, represented by data from 30 gene fragments. In addition to eight newly sequenced genes, we gathered all publicly available sequences. I also carried out a timing of divergence analysis to infer the age of the different lineages. I recovered strong support for the monophyly of Zygaenidae. All subfamilies for which we sampled multiple species were recovered as monophyletic, except for the newly described Inouelinae for which we have only sampled one gene fragment. The subfamily Zygaeninae is strongly supported as monophyletic and is recovered as sister to the clade comprising of all the remaining subfamilies (Callizygaeninae (Chalcosiinae, Procridinae). Our timing of divergence analysis suggests that the lineage leading to the extant Zygaenidae diverged in Late Cretaceous (ca. 83 Ma), which was before the Cretaceous–Paleogene (K-Pg) mass extinction event (ca. 66 Ma). The first split within the family happened in the Late Cretaceous (ca. 75 Ma), where Zygaeninae diverged from the rest of the family, i.e. Callizygaeninae, Chalcosiinae and Procridinae. In the Paleogene (ca. 61 Ma), Procridinae diverged from the lineage leading to the extant Callizygaeninae and Chalcosiinae. The divergence of Callizygaeninae from Chalcosiinae happened in the Eocene, ca. 51 Ma. The first splits within the subfamilies, i.e. divergence of genera, were in Zygaeninae in the Paleocene, followed by Procridinae in the Eocene. Our results form a strong basis for future studies of zygaenid evolutionary history, including historical biogeography and diversification dynamics.

Phylogenomics of North European Noctuinae based on anchored hybrid enrichment technology

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Noctuidae are one of the most diverse and economically important families of Lepidoptera, comprising over 12,000 species in ~1,150 genera. Though the number of studies addressing the phylogeny of Noctuidae is increasing (Keegan et al., 2021 and references therein), many genera have not been sampled in any phylogenetic studies. These gaps are primarily found in the largest subfamily Noctuinae, in which some large tribes like Noctuini, Hadenini and Orthosiini have so far received little attention in phylogenetic studies (Davis et al., 2022).

In the present study we used anchored hybrid enrichment method to sequence 589 loci (totalling 207,400 bp from single-copy nuclear protein-coding genes) for 68 species of Noctuinae collected from Northern Europe. Representatives of 12 additional species from families Notodontidae and Erebiidae were used as an outgroup in the phylogeny reconstruction. Phylogenetic analysis has been carried out using IQ-TREE on XSEDE (Nguyen et al., 2015) in CIPRES portal (Miller et al., 2010).

The resulting well-supported phylogenetic tree is largely concordant with the current system of Noctuinae, as almost all tribes have been recovered as monophyletic clades. The only exception is Hadenini, as the genus *Polia* clustered together with Leucaniini instead of other Hadenini genera. Some conflict with the current system was found in the genus level as well: *Cryptocala chardinyi* and *Anorthoa munda* were recovered within the genera *Noctua* and *Orthosia*, respectively. Surprisingly, *Cerapteryx graminis* was found to be sister to *Tholera decimalis*, thus rendering the latter genus paraphyletic.

The initial phylogenomic results reported here are the first step of research that will help to fill the vacuum in our knowledge about the phylogeny of Noctuidae.

Davis, R.B., Õunap, E. and Tammaru, T. (2022). A supertree of Northern European macromoths. Plos ONE, 17(2): e0264211.

Keegan, K.L., Rota, J., Zahiri, R., Zilli, A., Wahlberg, N., Schmidt, B.C., Lafontaine, J., Z. Goldstein, D.P. and Wagner, D.L. (2021). Toward a stable global Noctuidae (Lepidoptera) taxonomy. Insect Systematics and Diversity, 5(3): 1; 1–24

Nguyen, L.T., Schmidt, H.A, von Haeseler, A and Minh B.Q. (2015). IQ-TREE: A fast and effective stochastic algorithm for estimating maximum likelihood phylogenies. Molecular biology and evolution, 32: 268-274.

Miller, M. A., Pfeiffer, W and Schwartz, T. (2010). Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In 2010 gateway computing environments workshop (GCE). pp: 1-8.

Larval density effects on black soldier fly life history traits

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Larval density (i.e., crowding) is an important biotic factor but its impact on organisms has often been overlooked. This study explored the effects of larval density and its interactions with temperature on life history traits of economically important *Hermetia illucens* or black soldier fly (BSF). BSF larvae were reared at three different larval densities (1, 5 and 10 larvae/cm²) and at three temperature treatments (23, 27 and 30 °C). The results revealed an increase in prepupal mass, pupal mass, prepupal-to-pupal mass loss, survival, prepupal fat content, adult mass, adult longevity and a reduction in larval and pupal development time at low larval density. Temperature significantly affected all studied traits except phenoloxidase activity (PO), survival, prepupal fat content and adult longevity. BSF larvae reared at high larval densities had significantly higher PO activity compared to larvae reared at low larval density. We conclude that density and temperature and their interaction-related effects during larval development considerably affect BSF larval life-history traits. Higher immunity at high densities suggests that larvae are better protected against pathogens, but this comes at a cost of remaining smaller and growing for a longer time.

Opare, L. O., Holm, S., and Esperk, T. (2022). Temperature-modified density effects in the black soldier fly: Low larval density leads to large size, short development time and high fat content. *Journal of Insects as Food and Feed*, 1–20.

Opare, L. O., Meister H., Holm, S., and Esperk, T. (2022). Black soldier fly larvae exhibit higher immunity at high larval densities. In preparation.

Progress on the Sterrhinae moths of Iran (Lepidoptera: Geometridae)

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Due to its geographical location, Iran is one of the most important biodiversity hotspots in the world. A region in which different faunal elements from the Mediterranean, Caucasus, Central Asia and Arabian Peninsula come into contact, creating the conditions for high diversification. Unfortunately, this unique diversity is under threat due to direct human impact on habitats and climate change, which particularly affects insects.

Although research has been done on the Iranian geometrid moths, the Sterrhinae subfamily is still not fully known. To fill these knowledge gaps, a comprehensive literature review was conducted to gain information on the Iranian fauna, followed by an integrative taxonomic review of the Sterrhinae species based on already collected material from various collections and type specimens (where available). Ongoing work includes a comprehensive morphological examination of wing venation and male and female genitalia, as well as DNA barcodes as a tool for clarifying species delimitations and justifying taxonomic decisions. Here, we provide first insights into the taxa of this subfamily in Iran. In this poster we will give the first results of this project, including updates on the systematic position of 127 known Iranian species of Sterrhinae, which are placed in 17 genera. Up to now, we have found four new species and five new synonymies, which are in the process of being published as part of individual taxonomic revisions (Wanke et al. 2021, Wanke et al., in prep.).

Wanke, D., Krogmann, L., Murillo-Ramos, L., Sihvonen, P. and Rajaei, H. (2021) Systematics of *Problepsis wiltshirei* (Prout, 1938), comb. nov. (Lepidoptera, Geometridae, Sterrhinae) – an endemic species to the Zagros Mountains in the Middle East. – Nota Lepidopterologica 44: 175–192.

A riddle in the Middle East and Central Asia: the taxonomic status of two *Phaselia* moths, *P. serrularia* and *P. narynaria* (Lepidoptera: Geometridae: Ennominae)

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In 1858, French entomologist Achille Guenée described the genus *Phaselia*, a geometrid moth belonging to the tribe Boarmiini in the subfamily Ennominae. Up to now, nine described species were included in this genus, mainly from the Middle East. The high intraspecific variability between the described species of *Phaselia* has led to difficulties in their diagnosis. In a recent taxonomic revision of the genus in the Middle East and Central Asia, the authors found confusing data in the literature and identified specimens of *Phaselia serrularia* (Eversmann, 1847) from different collections. This species was described from Saissan Lake in east Kazakhstan, and is found also in Turkey and the southern Urals in Russia. *Phaselia narynaria* (Oberthür, 1913) was described from Kyrgyzstan, is widespread from western Mongolia through the east side of Kazakhstan to east Uzbekistan, and is regarded as the most abundant species in this area. After comparison of the lectotype of *P. serrularia* with *P. narynaria* and additional large set of specimens from Central Asia we found strong evidence for a potential synonymy between these two species. Here, we applied an integrative taxonomic approach to revise the genus *Phaselia* using external and internal morphological characters (wing pattern and male and female genitalia), DNA barcoding, and distributional data. Our results confirmed our assumption that *P. narynaria* should be regarded as a junior synonym to *P. serrularia* and that the species considered to be *P. serrularia* over the last decades is a so far undescribed species (Werner et al. in prep.).

Werner et al. (2022) An integrative taxonomic revision of the genus *Phaselia* (Lepidoptera: Geometridae: Ennominae) in the Middle East and Central Asia (in prep).

Back to the future: Climate change effects on habitat suitability of *Parnassius apollo* in the past, present, and future

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Alpine ecosystems, especially open areas above the tree line, are one of the most threatened by climate change, mainly due to forest expansion driven by warmer conditions. To address how climate-change-induced effects impacted open-areas insects, we chose a representative alpine grasslands species, *Parnassius apollo*. The overarching goal of this study is to unravel how climate change influenced the habitat suitability of the butterfly across the Palearctic region back to the Last Interglacial (130 kya), present, and future (2050 and 2070) under medium and high greenhouse gas emission rates. To do so, we combined bioclimatic variables (Worldclim) and occurrence data of *P. apollo* and its most used host plants (*Sedum album*; *Hylotelephium telephium*) from GBIF and iNaturalist as predictors to calculate SDM (species distribution models) through Maxent. The results reveal a significant increase in habitat suitability during cold periods, especially during LGM (Last Glacial Maximum, 22kya). We also found that adding the host plants as predictors into the models, allowed us to better define suitable areas for the butterfly. Future projections of the habitat suitability for the butterfly are surprisingly better than expected considering a future warming scenario. However, afforestation and overgrazing remain the main threats to *P. apollo*. We thus encourage enhancing habitat management measures in Europe and Asia and increasing the amount of available occurrence data to perform more accurate SDM.

Nadler, J., Bonelli, S., Dapporto, L., Karaçetin, E., Lukhtanov, V., López Munguira, M., Micevski, N., Settele, J., Tzortzakaki, O., Verovnik, R., Warren, M., Wiemers, M., Wynhoff, I. and van Swaay, C. (2021). *Parnassius apollo*. The IUCN Red List of Threatened Species 2021

Nakonieczny, M., Kędziorski, A. and Michalczyk, K. (2007). Apollo butterfly (*Parnassius apollo* L.) in Europe–its history, decline, and perspectives of conservation. Functional Ecosystems and Communities, 1(1), 56-79.

Extreme importance of shelters for populations of the Violet Copper *Lycaena helle* butterfly

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Violet Copper *Lycaena helle* is a butterfly species endangered in Europe and listed in the Annexes of Habitats Directive. It shows a boreo-mountainous type of distribution, and inhabits wet meadows with an abundance of its larval food plants e.g. *Bistorta officinalis* (=*Polygonum bistorta*) and in the north also *B. vivipara*. Violet Copper is considered an extremely sedentary species. Males are territorial and they show lekking behaviour. In eastern Poland the butterfly is still widespread and locally common, occurring in two broods. We used transect counts for studies of local distribution of the butterfly on the site near Bialystok (NE Poland). Four meadows covered by *B. officinalis*, separated by stripes of trees and bushes, were surveyed and at each meadow three transect routes were fixed i.e. running (i) directly along hedgerows, (ii) at a distance of ca 10 m from hedgerows, and (iii) through the middle of the meadow. The studies were conducted between 2010 and 2018 in the flight period of the first brood of the butterfly (mid-April – early June). We found out that the density of imagines of both sexes was very uneven in the habitat i.e. the area covered by *B. officinalis*. The vast majority of individuals were counted at transects fixed just along hedgerows, and significantly less butterflies were observed at routes running just 10 m away. Very few individuals were recorded in the middle of the meadow, despite abundance of the larval food plant. The presence of shelters proved to be extremely important for Violet Copper, but we also found out that appropriate management is vital. A significant decrease in number of individuals was detected during our studies. Possible causes could be related to intensification of land use and the overgrowing of some parts of the site, as well as unfavourable weather conditions (especially droughts) in some seasons.

Seasonal variation in adult demography in the large population of the threatened Clouded Apollo *Parnassius mnemosyne* butterfly

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The Clouded Apollo, *Parnassius mnemosyne* is a charismatic West Palaearctic butterfly threatened in some European countries and listed in Appendix IV of the Habitats' Directive. We investigated a large lowland population of the species inhabiting the complex of irregularly coppiced light forest and adjacent wet meadows in the anthropogenic landscape in the valley of the Narew river in NE Poland. A mark-release-recapture (MRR) method was used for four seasons to estimate population size, adult catchability, daily survival and life span. The beginning and longevity of the flight period (which lasted 4-6 weeks) differed among years and was clearly related to weather conditions (temperature, sunshine) in April, i.e. the period most important for development. The forewings of butterflies in the season when emergence was later were longer compared to individuals measured in years with accelerated beginning of spring but these differences were significant only for males. The seasonal population size varied from 555 to 942 adults. Contrasting to some previous studies, the sex ratio turned out to be well-balanced although catchability of males was significantly higher than of females. Inter-seasonal variation in the life span (6.36-12.45 days) is more difficult to interpret but it is worth noting that individuals lived the longest in the coldest and the least shiny flight period. Temporal fragmentation index (i.e. the ratio of flight period length to adult life span) also varied (3.37-5.97) but was generally relatively low which suggests that there is no threat for the reduction of the effective population size at the moment. Nevertheless, the investigated population may be at risk of deterioration due to observed intensification of management of meadows. An even greater danger is associated with possible conversion of grasslands into corn fields observed in vicinity.

Forest management for endangered species: conservation of *Colias myrmidone* in the Knyszyn Forest (NE Poland)

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Colias myrmidone is one of the most endangered butterflies in Europe and has survived in only a few countries. In Poland, the last metapopulation inhabits the Knyszyn Forest, and in 2017 its size was estimated to be about 750 individuals in the summer generation (Sielezniew et al. 2019). The Knyszyn Forest is a large woodland complex covering an area of more than 1,000 km^2 but the occurrence of *C. myrmidone* is restricted to its eastern parts. Analysis has revealed that all the recently created habitats are on former agricultural lands, i.e., mostly extensive pastures that were afforested in the mid-20th century. The larval food plant (*Chamaecytisus ruthenicus*) has probably survived this process by being present in the forest stands for years. Logging enables its flourishing, and clearings are colonized by the butterfly. However, forestry-related practices that aim for rapid growth and compact replanting contribute to a more rapid disappearance of the habitat. In contrast, patches left for natural succession may be suitable for more than 10 years. In 2021, the consortium of the Forest Research Institute and University of Bialystok launched a project funded by the Polish State Forests aimed at ecological research, as well as elaboration and implementation of conservation measures for *C. myrmidone*. Knowledge of the detailed preferences and requirements of this butterfly and its larval food plant is vital to creating conditions for the functioning of a viable metapopulation that will mitigate the factors associated with climate change. As part of this project we will study, among others, factors that influence the mortality of *C. myrmidone*, at different stages of the life cycle. Genetic analyses to assess population fitness and comparative studies with specimens from museum and private collections are also planned.

Sielezniew M., Deoniziak K., Dziekańska I. and Nowicki P. (2019). Dispersal in a metapopulation of the critically endangered Danube Clouded Yellow butterfly Colias myrmidone: implications for conservation. Journal of Insect Conservation, 23: 291-300.

Genetic diversity and population structure in Danish *Phengaris alcon* ([Schiffermüller], 1775): implications for biogeography and conservation

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Phengaris alcon (Denis & Schiffermüller 1775) is a rare and declining butterfly in western and northern Denmark where it occurs in heathland bogs where the larval host plant *Gentiana pneumonathe* Linneus is found. Previous studies based on wing patters (Kaaber 1964) and population genetics (Kelager 2015, Hauge 2016) have shown that there is clear distinction between populations in western Jutland and northern Jutland, perhaps with the seaway Limfjorden acting as a barrier. To explore this pattern further we analyse two different *P. alcon* micro satellite datasets. First we analyse a contemporary ’12 micro satellite’ dataset comprised by 184 specimens from 16 localities all collected between 2005 and 2021 to explore the current genetic structure in Danish populations. To explore historical population genetic structure and trends, we then sequence four of the 12 micro satellite loci for a further 272 specimens from natural history collections from a total of 30 localities (six localities included both current and historical specimens). Our results confirm that the populations found in mainland Jutland can be divided in two distinct populations. However, the division between the two is not the Limfjord, but instead a line that roughly corresponds to the maximum expansion of the Scandinavian Ice Sheet during the last Glacial Maximum. Furthermore, the specimens found on the oceanic island Læsø form a third, distinct cluster. This pattern is clearest in the contemporary, ’12 micro satellite’ dataset (likely due to the greater resolution power in that dataset), but can also be observed in the larger, historical ‘four micro satellite’ dataset. We interpret this pattern as potential evidence for two temporally distinct recolonizations events after the last glacial maximum. Interestingly, for the six localities from which we have both current and historical data, only one showed significant decline in genetic diversity over time.

Hauge, M. (2016). Change in genetic variation of *Maculinea alcon* populations over time [MSc. Thesis]. Department of Biology, University of Copenhagen. 55 pp.

Kaaber, S. (1964). Studies on *Maculinea alcon* (Schiff.)—*rebeli* (Hir.) (Lep. Lycaenidae) with Reference to the Taxonomy, Distribution, and Phylogeny of the Group. Entomologiske Meddelelser, 32, 277–318.

Kelager, A. (2015). Biotic interaction in space and time: The social parasitic butterfly *Maculinea alcon* and its hosts as model system [PhD Thesis]. Department of Biology, University of Copenhagen. 189 pp.

Diversity of the Acrocercopinae (Lepidoptera: Gracillariidae) of the Afrotropics

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The subfamily Acrocercopinae Kawahara & Ohshima with the type genus *Acrocercops* currently comprises 29 genera and 13 of these are recorded from the Afrotropics (De Prins & De Prins, 2012–2022). Apomorphies of Acrocercopinae include: a long intersegmental membrane between the eight abdominal segment and the external genital organs in males; a curved forewing anal vein; and a completely red final larval instar (Kawahara *et al*. 2017). In total, 72 species currently assigned to Acrocercopinae are known to occur in the Afrotropics. The species of *Acrocercops* are strongly predominant, comprising over 54% of all Acrocercopinae species. Remaining genera contain from 1 to 9 species only. The majority of species (96%) are geographically restricted to an area of tropical Africa or a single Afrotropical country (72%). Only 2 species (*Cryptolectica bifasciata* and *Phodoryctis caerulea*) are known from 10 and 7 countries respectively. Three species are also reported to occur outside Africa: *Acrocercops coffeifoliella* from Sri Lanka; *Eteoryctis gemoniella* from India and *Telamoptilia cathedraea* from India, Japan and Taiwan. The Acrocercopinae specimens were collected by Jurate and Willy De Prins during the expeditions 2001–2014 lasting from March until June, in October, and December in various habitats in Kenya, Cameroon and the Democratic Republic of the Congo. All traditional sampling methods were used, although most specimens of the specimens were collected using mercury vapour light traps. Among thousands of collected moths of Gracillariidae we discovered 191 specimens of Acrocercopinae, belonging to 17 species and 6 genera (*Acrocercops*; *Cryptolectica*; *Dialectica*; *Amblyptila*; *Spulerina; Telamoptilia*). Our forthcoming investigation predicts describing about 12 new species and new data of distribution of other 5 species. Despite the efforts that are already made, sub-saharan Africa still remains as one of the major sources for new species discoveries especially in fragmented and restricted microhabitats suitable for the Acrocercopinae fauna.

De Prins, J. and De Prins, W. (2012–2022). Afromoths, online database of Afrotropical moth species (Lepidoptera). World Wide Web electronic publication (http://www.afromoths.net).

Kawahara, A. Y., et al. (2017). A molecular phylogeny and revised higher-level classification for the leaf-mining moth family Gracillariidae and its implications for larval host-use evolution. Systematic Entomology, 42: 60–81.

Weather sensitivity of automatic bait traps

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The efficiency of automatic sugar bait traps for nocturnal moths is highly variable with the reasons of the variability being poorly understood. To shed light on the dependence of bait trap catches on weather parameters we performed a study in which 5 bait traps were operated on 32 nights (July to September 2021) on forest clearcuts in southern Estonia. Weather parameters were recorded using portable meteorological stations which were set up next to each of the traps. Trapped moths, 864 in total, were identified and counted on a daily basis. GLM models were constructed to study the dependence of the total number of moths caught and Shannon diversity index on weather parameters. The number of moths caught showed a strong positive dependence on temperature, and a weaker positive dependence on air humidity. Shannon index showed a similar dependence on temperature and humidity but was also negatively affected by air pressure and positively by air pressure change, i.e. the difference between the values of air pressure from sunset to midnight. We also showed that the values of the weather parameters which were averaged over the entire scotophase usually had better predictive power than various alternative measures like minimal and maximal values of the variables, and values recorded for the first half of the night only.

Some examples of Lepidoptera species identification in Plant Health and Microbiology Laboratory of Agricultural Research Centre

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The Agricultural Research Centre is an institution administrated by the Estonian Ministry of Rural Affairs. The Centre involves different laboratories, field testing centres and departments which are dealing with agri-environmental monitoring, analysis of rural economy and rural networking. *Dendrolimus sibiricus* Tschetverikov and *Spodoptera frugiperda* Smith have been suggested for regulation as quarantine pests for European and Mediterranean Plant Protection Organisation member countries. These quarantine pests in EU are not spread to Estonia for now. In Plant Health and Microbiology Laboratory (Plant Health National Reference Laboratory) of the Agricultural Research Centre, Lepidoptera species are analysed among other entomological samples. In purpose to find *Dendrolimus sibiricus* and *Spodoptera frugiperda,* the Estonian Agricultural and Food Board is collecting material by setting the traps. In the Plant Health National Reference Laboratory species are analysed and identified. During morphological analyses preparers of genitals are made according EPPO protocol. Slides are documented with microscopy software and camera photos. Species identification is done according to morphological keys and if necessary, with molecular analyses like COI (cytochrome c oxidase subunit I) sequencing. Additionally, we have analysed and identified different samples sent by private clients, for example *Nemapogon granella* Linnaeus, *Hofmannophila pseudospretella* Stainton, *Plodia interpunctella* Hübner, *Cadra cautella* Walker, *Corcyra cephalonica* Stainton and *Acronicta psi* Linnaeus.

Identifying municipalities with high conservation value using macrolepidopteran records reported by expert hobbyists

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For an efficient mitigation of biodiversity loss, the conservation priorities such as high biodiversity, large number of endangered species and unique communities should be identified and communicated to local decision makers. We assessed the conservation priorities for 97 municipalities based on the 3,023,681 records of 878 native macrolepidoptera reported in the Finnish Biodiversity Information Facility in 2001-2020 (Schulman et al. 2021). Species richness estimated with a rarefaction technique (Hiesh et al. 2016) was highest in southern coastal municipalities and decreased towards North. The species richness was highest in the municipalities of Kotka, Hamina and Pyhtää when estimated with rarefaction, not in the extensively examined Kemiönsaari, Vironlahti and Raasepori, which had the largest reported species richness. The number of endangered species correlated with the overall species richness but was higher than expected in the North. The uniqueness of communities was identified by the species replacement component of beta diversity (Legendre 2014). Most unique communities were often in the municipalities located between the biomes (Hemiboreal vs. Boreal and Boreal vs. Alpine tundra). Our study demonstrates that a careful selection and analysis of records reported by expert hobbyists into biodiversity information facilities can identify municipalities with conservation priorities.

Hsieh, T. C., Ma, K. H. and Chao, A. (2016). iNEXT: an R package for rarefaction and extrapolation of species diversity (Hill numbers). Methods in Ecology and Evolution, 7(12), 1451–1456.

Legendre, P. (2014). Interpreting the replacement and richness difference components of beta diversity. Global Ecology and Biogeography, 23: 1324-1334

Schulman, L., Lahti, K., Piirainen, E., Heikkinen, M., Raitio, O. and Juslén, A. (2021). The Finnish Biodiversity Information Facility as a best-practice model for biodiversity data infrastructures. Scientific Data, 8(1), 137.

An expansive species, *Cosmopterix sibirica* (Sinev, 1985): description of female and some features of biology

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Cosmopterix sibirica (Sinev, 1985) is a moth described near Lake Baikal (Russia). The moth has expanded its range across Russia, to Finland, Estonia and Latvia (Koster and Sinev 2003, Aarvik et. al. 2017; Sinev 2019). The female and biology of the species have been unknown (Koster and Sinev 2003). We compiled the 35 records reported into the Finnish Biodiversity Information Facility since 2016 when the species was found new to Finnish fauna. Based on those observations, the distribution range is currently limited to South-East Finland. The main flight period of *C. sibirica* is in June. The moth is active at dusk and attracted by light. We found numerous copulating pairs of *C. sibirica* at 22:45 on 17 June 2020 from a half-hectare *Elytrigia repens* (L., *Poaceae*) stand on an old landfill, where the average density of moths was ca. 10 moth m^{-2}. In July at the same site, the leaves of *Elytrigia repens* contained large blotch mines occupied by yellow larvae, similar to those of *Cosmopterix orichalcea* (Stainton, 1861). The *C. sibirica* female and male are externally similar like the other monomorphic *Cosmopterix* (Hübner, 1825) species. The shape and inner sclerotization of sterigma separates the female genitalia of *C. sibirica* from other European *Cosmopterix* (Hübner, 1825) species.

Aarvik, L., Bengtsson, B.Å., Elven, H., Ivinskis, P., Jürivete, U., Karsholt, O., Mutanen, M. and Savenkov, N. 2017. Nordic-Baltic Checklist of Lepidoptera. Norwegian Journal of Entomology. Supplement 3. 1–236

Koster, S. J. C. and Sinev, S. Yu. 2003. *Momphidae*, *Batrachedridae*, *Stathmopodidae*, *Agonoxenidae*, *Cosmopterigidae*, *Chrysopeleiidae*. — In: Huemer, P., Karsholt, O. & L. Lyneborg [ed.]: Microlepidoptera of Europe 5: 1-387. Stenstrup (Apollo Books)

Sinev, S. Yu. (ed.). 2019. Catalogue of the Lepidoptera of Russia. Edition 2. St. Petersburg: Zoological Institute RAS, p. 448.

Three-dimensional reconstruction of the genitalia of *Tortrix viridana* L. during copulation (Tortricidae)

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The fine mechanisms of copulation and functional morphology of the internal copulatory organs in Lepidoptera are poorly studied. Since the internal genitalia of both sexes are in tight contact, their role in sexual selection seems obvious but its mechanism is only tentative. The present study is focused on the internal genitalia of *T. viridana*, a species with relatively simple copulatory structures. The study aims to reveal the mechanisms of copulation and functional morphology of the internal copulatory organs of a model Lepidoptera species. Various techniques were used in the current study, such as: micro-CT scanning and histology of couples fixed at different stages of copulation ("serial morphology"), Scanning Electron Microscopy and video recording of males poisoned with dichlorvos. The preliminary results reveal a relatively long copulation (90 min) that can be divided into certain phases, in which different substances of the ejaculate are ejected and the vesica (endophallus) achieves different stages of eversion. During the second half of the copulation most of the ejaculate is already transferred to the female bursa, the endophallus is maximally extended and the sclerotized cornuti on its tip perform pulsating movements in a certain area of the ductus bursae of the female, the insertion of ductus seminalis.

New biological data on the rare Geometrid *Boudinotiana touranginii* (Berce, 1870) (Geometridae: Archiearinae) in Madrid (Central Spain)

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Hausmann (2001) cites *Boudinotiana touranginii* (Berce, 1870) as being endemic to central France with subsequent French data much more to the west. It was discovered in Spain at the beginning of the century with data from the northern Castillian meseta which includes Madrid, but as far east as Daroca in Zaragoza province (Aragón). Pino Pérez et al. (2021) cite an example taken in Orense west of Castilla-León. Its biology and early stages are described from France. It was cited also from the extreme SW of Germany (Lörrach) quite recently (Trusch et al., 2016).

B. tourangiini is a diurnal species, which flies in Madrid from mid-February till early March with larvae taken as early as late March not long after poplar bud burst (*Populus nigra* L.); five larvae were collected and reared on *Populus nigra* L. leaves. A parasitoid wasp, *Macrocentrus* (Macrocentrinae: Braconidae), emerged ex-prepupa. Pictures of larva, pupa, adult and parasitoid are also provided.

Hausmann, A. (ed.) (2001). Introduction; Archiearinae, Orthostixinae, Desmobathrinae, Alsophilinae, Geometrinae. The Geometrid Moths of Europe. Vol. 1. Brill.

Pino Pérez, J.J., Silva-Pando, F.J., Baladrón, J. and Pino Pérez, R. (2021) *Boudinotiana touranginii* (Berce, 1870) (Lepidoptera, Geometridae, Archiearinae), en Orense (Galicia, NO España). Burbug*,* 63: 1-13.

Trusch, R., Asal, J., Falkenberg, M., Leipnitz, M., Reusch, M., Widder, C. and J.-U. Meineke (2016): Entdeckung des Purpurweiden-Jungfernkindes *Boudinotiana touranginii* (Berce, 1870) in Deutschland (Lepidoptera: Geometridae, Archiearinae). — Entomologische Zeitschrift 126 (2): 67-76. Schwanfeld.

Interesting biological and faunistic data on the Geometrid (Lepidoptera) fauna of Castilla-La Mancha and Teruel (Aragón) (Central Spain) with information on the early stages

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We supply the data from the collection of 259 specimens of 79 taxa belonging to the family Geometridae in the four main subfamilies: Ennominae, Geometridae, Sterrhinae and Larentiinae. The last of these subfamilies is the most represented faunistically: 29 taxa (=36.6%). Some taxa are interesting corologically, being as they are Euro-Siberian or Euro-Asiatic elements, with representation in the Supra-Mediterranean region e. g. *Ourapteryx sambucaria* (L., 1758), *Selenia dentaria* (F., 1775), *Angerona prunaria* (L., 1758), *Alcis repandata* (L., 1758), *Ascotis selenaria* (D & S, 1775), *Idaea straminata* (Borkhausen, 1794), *Thera britannica* (Turner, 1925), *Thera obeliscata tristrigaria* Donovan, 1808, *Ecliptopera silaceata* ([D & S], 1775), *Dysstroma citrata* (L., 1758), *Philereme vetulata* (D & S), *Eupithecia pyreneata* Mabille, 1871, *Eupithecia venosata* (F., 1787), *Eupithecia intricata* (Zetterstedt, 1839) and *Eupithecia vulgata* (Haworth, [1809]). For this reason, their range extends much more towards the south than was originally thought. Other taxa are endemic to the Iberian-Balear-Mahgreb realm, e.g.: *Thetidia smaragdaria gigantea* (Millière, 1874), *Idaea korbi* (Püngeler, 1917), *Idaea consanguiberica* Rezbanyai-Reser & Expósito, 1992, *Idaea figuraria* (Bang-Haas, 1907), *Idaea incisaria* (Staudinger, 1892), *Idaea bigladiata* Herbulot, 1975, *Idaea joannisiata ibericata* (Wehrli, 1927), *Rhodostrophia pudorata perezaria* (Oberthür, 1875) and *Hydria montivagata andalusica* (Ribbe, 1912). Some data are also provided on the early stages of those species whose females oviposited in captivity.

Data on the bio-ecology of the moth species *Amata kruegeri* (Ragusa, 1904) and the first female record of *Penthophera morio* (Linnaeus, 1767) in northern Albania (Lepidoptera: Noctuoidea: Erebidae)

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Moths of Albania are less studied, represented by only some sporadic papers so far. This faunistic survey gives significant data on the occurrence and distribution of two new country record moth species of the family Erebidae, *Penthophera morio* (Linnaeus, 1767) and *Amata kruegeri* (Ragusa, 1904) (Lepidoptera: Noctuoidea). The field expeditions were carried out during June 2019 in northern Albania. A total of 50 specimens were randomly collected; nevertheless, many more individuals were observed flying.

Amata kruegeri is documented for the second time in northern Albania after Rebel & Zerny, 1931 have identified it under *Syntomis marjana* (Stauder, 1913), which in fact represents the subspecies *A. kruegeri marjana* (Stauder, 1913). Here, a description of the specimens showing morphological dimorphism of the wing dot patterns and sizes is given. The similarities and differences in morphological features between the species identified so far in Albania, *Amata kruegeri* (Ragusa, 1904) and *Amata phegea* (Linnaeus, 1758), are analysed.

The males of *Penthophera morio* are previously reported in northern (Rebel & Zerny 1931) and southern Albania (Beshkov et al, 2020). In our study, several active males and the motionless female are both found in the same natural habitat in northern Albania, making thus the male the second report for the area and the female the first country record.

Although this is a faunistic study, it gives some important data on the bio-ecology of the new country records, raising awareness to protect their habitats. Detailed bio-ecological data on both species are given.

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Rebel, H. and Zerny, H. 1931. Die Lepidopterenfauna Albaniens. Denkschriften der Akademie der Wissenschaften, Math. Nat. Kl. Wien 103: 37-161.

The northern distribution limits of the vine bud moth *Theresimima ampellophaga* (Bayle-Barelle, 1808) (Lepidoptera: Zygaenidae, Procridinae) in Albania: evidence by sex pheromone traps

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The vine bud moth, *Theresimima ampellophaga* (Bayle-Barelle, 1808) (Lepidoptera: Zygaenidae, Procridinae), occurs as partly harmful species in vineyards in the Mediterranean region, where it has the proper conditions for larval development, including the host plants and hilly relief. In 2017, the vine bud moth has been identified as a new country record in the vineyards of the western lowland in Albania on the base of a large-scale study using traps baited with the synthetic sex pheromone of *Th. ampellophaga* females, (2*R*)-butyl (7*Z*)-tetradecenoate or the sex attractant containing the racemic mixture of (2*R*)-butyl 2-dodecenoate and (2*S*)-butyl 2-dodecenoate (Vrenozi et al., 2019). The following field work in 2018 and 2019 using sex pheromone traps aimed to establish the vine bud moth in new localities in Albania and to determine the northern distribution limit of *Th. ampellophaga* in this country. The research field work in June – September 2018 in the central to northern Albania resulted in negative results. In 2019, low numbers of vine bud moth males were captured in three vineyards at the districts of Fier (Apolloni, Radostinë) and Vlorë (Dukat i Ri), southern Albania, all from the first generation. As a preliminary result, the northern distribution limits of vine bud moth will be described. Future field work will be focused on the western lowland to check the occurrence of *Th. ampellophaga* in the vineyards and further determine the status of the vine bud moth in Albania.

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