XVIIth European Congress of Lepidopterology

Luxembourg, 9-13 May 2011

Welcome to Luxembourg City

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- Luxembourg National Research Fund
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- Zoltan Varga, Debrecen University, Hungary

Introduction

Welcome to Luxembourg

We cordially welcome you at the National Museum of Natural History of Luxembourg and the Abbey de Neumünster, our conference location!

We are very pleased being the venue of the XVIIth European Congress of Lepidopterology. We hope to present you an interesting and manifold programme. We tried to combine classical aspects as with more recent, upcoming aspects as global change and evo-devo. Furthermore, one complete day is available for contributions of the field “DNA-barcoding”.

We wish you a nice time and a fruitful meeting! If you have any question or worries, we will always be at your disposal!

Thank you all for coming

Marc Meyer, Jan Christian Habel and Myriam Simon

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Programme

Date / Time	**Topic**	**Referent(s)**	Chair
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09.45-10.05	On the Polish population of *Polyommatus ripaertii* (Freyer, 1830) (Lepidoptera, Lycaenidae)	L. Przybylowicz	
10.05-10.25	Little known glands of lepidopteran larvae	F. Vegliante / I. Hasenfuss	
10.25-10.45	Coffee break		
10.45-11.30	Asymmetry of wing pattern in *Parnassius*	G. Nève	H. V. Dyck
11.30-11.50	Body temperature and territory selection by males of the speckled wood butterfly (*Pararge aegeria*)	L. Vande Velde	
11.50-12.10	Capital breeding and income breeding as life history strategies	T. Tammaru / J. Javoi / R. Davis / E. Õunap	
12.10-12.30	The Lepidoptera of *Acacia* domatia	D. Agassiz	
12.30-12.50	*Pseudophilotes bavius hungarica* (Diószeghy, 1913): ecological niche vulnerability due to habitat fragmentation and climate change	A. Crisan / C. Sitar / C. Craioveanu / L. Rákosy	
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15.30-15.50	Prediction of climate and land use change related range expansion in a butterfly of European conservation concern (*Lycaena dispar rutilus*)	Y. Martin / H. Van Dyck / N. Titeux	
15.50-16.10	First record of the homoneurous family Acanthopteroctetidae in Africa	W. Mey	
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12.00-12.15	DNA barcoding of European Gracillaridae leaf-mining moths	C. Lopez-Vaamonde	
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15.00-15.15	The role of DNA barcoding in the identification of wine pest: Antispila ampelopsifoliella	E. van Nieukerken / D. Wagner	
15.15-15.30	New records of European micromoths in North America detected through DNA barcoding	V. Nazari / J.-F. Laundry / P. Hebert	
15.30-15.40	Launch of the European campaign	R. Rougerie / A. Hausmann / E. Van Nieukerken / M. Mutanen	
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20.00-01.00	Light trapping (optional ltd. to 12 pax)		

TALKS

Key-note : Habitat-use in butterflies: how to move from structural to functional ecology?

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From a human observer's perspective, butterflies seem to be associated with certain vegetation types or biotopes; we refer, for example, to woodland or grassland butterflies, but what does that really mean? Behavioural ecological studies point at much more specific relationships between a butterfly in its different life cycle stages and the ecological resources and conditions in the environment. I will show examples focusing – amongst other aspects – on the functional significance of thermal variation. Structural habitats may no longer represent functional habitat if not all required ecological resources and conditions are available at the right spatial and temporal scale. This appears of particular significance in rapidly changing anthropogenic environments. Biogeography studies on presence/absence or abundance of species relative to general vegetation types are still useful, but there is a need in evolutionary ecology and conservation biology to shift from structural to functional relationships between an organism and the environment. Therefore, we need to combine the ecological niche concept with the ethological Umwelt-concept. Umwelt refers to the environmental factors, collectively, that are capable of affecting the behaviour of an animal or individual. The novel, behavioural approach to the understanding of habitats of butterflies (and other organisms) based on the recognition of specific resources and conditions has attracted much attention over the last few years or so. I will summarize our current insights and challenges, and I will advocate extending this rationale to vegetation types and structural landscape elements in the landscape matrix; the context of dispersal and functional landscape connectivity. A resource-based approach for analyzing condition-dependent functional connectivity is a matter of understanding organism x landscape matrix interaction effects. I will summarize the lessons and discuss perspectives for evolutionary ecology and conservation at the landscape scale.

On the Polish population of *Polyommatus ripartii* (FREYER, 1830) (Lepidoptera: Lycaenidae)

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The critically endangered population of Ripart's Anomalous Blue *Polyommatus* (*Agrodiaetus*) *ripartii* in Poland is studied. The species is recorded from only a few, small gypsum outcrops located in the Nida Valley (SE Poland). The confirmation of taxonomic status of this population was done by Vladimir Lukhtanov (S. Petersburg) after investigation of chromosome structure. The typical *A. ripartii* karyotype was established: n=90 including one large, one medium-sized and 88 small chromosomes. The molecular analysis conducted in the laboratory of ISEA did not reveal significant differences from the Bulgarian and Greek populations.

The food plants of caterpillars are two species of Sainfoins: *Onobrychis arenaria* and *O. viciifolia*. First of them is Polish native plant colonizing this area after Younger Dryas (about 10.000 B.P.). *O. viciifolia* has anthropogenic origin and came here probably in Neolith about 5000 B.P. The origin of the Nida population of *P. ripartii* remains unknown.

Biological observations show that females lay usually no more than 1-2 eggs on single shoot of Sainfoin. The egg is laid at the base of dry (or drying) bract. The bracts of the basal part of inflorescence are preferred.

Polish population is very small and can be estimated for no more than several hundred (200-500) specimens. Regular monitoring conducted from several years confirms that only in one place the butterflies are found yearly in a bigger number of specimens. At the remaining localities only single specimens are usually observed. The main factors responsible for declining of the Nida population are unfortunately unknown. It can be only assumed that the changing of the land management in this rural region can play the significant role in this process.

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Little known glands of lepidopteran larvae

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At least 28 pluricellular glands and 12 putative glandular structures have been recorded for lepidopteran larvae; some of them are still very little known from the functional or anatomical point of view.

The supposedly endocrine H-organ (eta-organ) was originally described as a perisympathetic neurohaemal organ connected to the suboesophageal and prothoracic ganglia, provided with intrinsic neurosecretory cells, and bearing a pair of neurohaemal organs (corpora prothoracalia) anatomically similar to the corpora cardiaca (Abou-Halawa 1987, Věst. čs. Společ. zool. 51: 161). These secretory components might have been overlooked in the single TEM investigation (Birkenbeil 1997, Eur. J. Entomol. 94: 425) which revealed the organ as almost entirely consisting of connective tissue.

An unpaired accessory gland opening in the common duct of the labial glands, recently discovered in a noctuid (Sorensen et al. 2006, Arthropod Struct. Dev. 35: 7), is not homologous with the Filippi's gland; both glands coexist in some caterpillars (e.g. Heterogynis penella (Hb., 1819), Scythropia crataegella (L., 1767), Plodia interpunctella (Hb., 1813)), and their function is unknown. We could ascertain the presence of a trilobed accessory mandibular gland of unknown function, recorded so far with certainty only from H. penella and Papilio demoleus L., 1758 (Vegliante 2005, Acta Zool. 86: 179, 189), also in Incurvaria pectinea Hw., 1828, S. crataegella, Yponomeuta evonymella (L., 1758), P. interpunctella, Operophtera brumata (L., 1758), and Pieris rapae (L., 1758). Pharyngeal glands opening in the hypopharynx or in the "pharynx" are recorded for some yponomeutids, cossids, and sesiids (Berlese 1909, Gli Insetti vol. 1: 730; Dauberschmidt 1934, Z. Angew. Entomol. 20: 233). Contrary to what the original description (Berlese 1909) may suggest, the pharyngeal glands of yponomeutids are paired structures. According to our observations on histological sections of Y. evonymella, they are cuticular thickenings of the latero-dorsal wall of the hypopharynx, the epidermis of which is not taller than the remaining hypopharyngeal epidermis. The cuticle filling the thickenings has a weary texture, giving the impression of a tubular structure with an inner lumen, but lacking an orifice. Histology of the larger, probably homologous "glands" of cossids and sesiids still needs investigation.

On the trunk, the Verson's glands, which in some species are believed to secrete a cement layer on the cuticle, show a great diversity in number, position and morphology, which has been so far sufficiently investigated only in the Lymantriidae (Klatt 1909, Zool. Jb. (Anat.) 27: 135). Here, one or more pairs of Verson's glands are specialized into defensive funnel warts. The "grooming glands" of some Nymphalidae Morphinae, of which only the external openings are known, might be modified Verson's glands as well. A midventral gland opening on the prothorax between the head and the first pair of legs has been recorded from some Yponomeutidae, Noctuoidea, Hesperiidae, and Papilionoidea (adenosma or jugular gland), as well as from some Trichoptera Integripalpia (Gilson's gland). However, even the homology of these glands between different lepidopteran families is doubtful. In fact, a nymphalid has been recently reported to have two jugular glands (de Oliveira Borges et al., Psyche 2010: 2), and further research is needed to check for their possible homology with the two main types of adenosma known so far (one in the Pieridae, and one in all other families). Caterpillars show a great diversity of eversible vesicles, many of which have been regarded as glands. Three glandular openings are reportedly borne on the paired, subdorsal eversible vesicle on the second abdominal segment of some Hypomecis Hübner, 1821 spp. (Heitzman 1982, Proc. Ent. Soc. Wash. 84: 111). The glandular nature of similar structures, such as the supracoxal vesicles of Drepanini (curiously recalling the non-glandular prothoracic subventral tubes of some Zygaenidae), the medio-ventral thoracic "glands" of Nolinae, and the small lobes located near to the abdominal spiracles of some Zygaenidae and Saturniidae, is more doubtful, since no observations on their histology and secretions are available. The best hidden exocrine glands of caterpillars are the midventral abdominal tracheal glands, recorded in some Noctuoidea, Saturniidae and Papilionidae. They consist of the modified, glandular epidermis of the tracheal nodes, which mark the junctions of right and left ventral tracheal trunks in some abdominal segments. The lipoid secretion, released by these glands into the tracheal lumen, might be functionally connected to the distastefulness of most of these larvae for predators (Byers & Hinks 1976, Can. J. Zool. 54: 1824).

Asymmetry of wing pattern in Parnassius

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Asymmetry has been suggested as a tool for individual and population health conditions. Examples from a range of populations of Parnassius mnemosyne show that the asymmetry index is difficult to use in the field. The isolated and declining population of Sainte Baume (Var, France) is not more asymmetric than populations from the Alps or the Carpathian Mountains.

In Parnassius apollo, wing asymmetry is clearly linked to some rare alleles which affect the wing pattern. Furthermore, individuals which are the result of sib-mating are more asymmetric than those from the mating of unrelated parents.

Asymmetry seem therefore a useful tool to detect extreme cases of inbreeding, but fails to end up as a general tool for the survey of population health.

Body temperature and territory selection by males of the speckled wood butterfly (Pararge aegeria): what makes a forest sunlit patch a rendezvous site?

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Insects locate mobile resources like prey items or mates using either sit-and-wait (‘perching’) or active (‘patrolling’) searching strategies. The sit-and-wait strategy can be accompanied by defending and monopolizing a site through territorial behaviour. We focus on the territorial perching behaviour in males of the speckled wood butterfly (Pararge aegeria L.). Recent studies suggested that the selection of territories (i.e. sunlit patches on the forest floor) is driven by structural characteristics of the site that affect male visual detection. However, given that adult butterflies are heliotherm organisms and that forests provide a diverse array of light environments, it seems likely that thermal aspects may also be used for territory selection. We tested whether used and unused sunlit patches differed in thermal profile under field conditions in a Belgian woodland. We also used dummy butterflies to quantify variation in operative thoracic temperature and to calculate heating rates within (i.e. different vegetation structures) and between patches. Sunlit patches occupied by a territorial male were larger, and were more frequently characterized by low vegetation structures compared to empty sunlit patches. It took longer to reach optimal thorax temperature (starting from a fixed suboptimal body temperature) in large patches compared to small patches. We suggest that aspects of visual detection need to be combined with thermal aspects to fully understand territory selection in the speckled wood butterfly, as synergetic and/or trade-off effects of ambient temperature, solar radiation, and canopy/vegetation structure may be involved.

Capital breeding and income breeding as life history strategies

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Adult lepidopterans may not feed at all (extreme capital breeders), or, as an opposite example, adult feeding may be critical for reproduction (extreme income breeders). The position of a species in the gradation from capital to income breeders appears to be a principal determinant of its ecological traits. We will illustrate this argument by various experimental data, and will present a phylogenetically explicit comparative analysis of life history traits of geometrid moths confirming our expectations. We will discuss how to experimentally quantify the degree of capital breeding.

The Lepidoptera of Acacia domatia

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Several species of Acacia produce swollen thorns (domatia) often known as pseudogalls or ant galls. Whistling thorn Acacia drepanolobium is a well known example. It is widely known that there is a mutualist relationship between ants and these Acacia trees, the trees produce domatia in which the ants can live and breed and the ants help deter herbivorous mammals.

These “galls” were found also to contain Lepidoptera larvae, even when ants were present. Instead of there being a mutualist relationship with ants, as in the case of Lyaenidae, moth species protect themselves from predation by ants. A total of 22 species from 11 families of moths have been bred. Some of these appear to be obligate domatium feeders, others facultative domatium feeders and others just inquilines. One Tortricoid genus is new to Africa, where there are 4 spp. but surprisingly this genus occurs in Western North America.

Pseudophilotes bavius hungarica (Diószeghy, 1913) ecological niche vulnerability due to habitat fragmentation and climate change

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Pseudophilotes bavius hungarica (Diószeghy, 1913) is an endemic subspecies with a high conservation value from Transylvania and Europe. We assessed a *P. b. hungarica* population from Suatu (Cluj, România), considered the largest known population in Transylvania (over 1000 individuals in 2010). As a consequence of the habitat degradation due to lack of any management within the botanical natural reserve, the size of the *P. b. hungarica* population decreased significantly over the last years, even in years with maximum population densities.

Our main aim is to assess how factors such as habitat fragmentation and climate can affect *P. bavius* populations from entire Romania.

First of all we developed a predictive modelling of *P. b. hungarica* distribution, based on environmental parameters (Climatic variables, Digital Elevation Model and Corine Land Cover). Due to the close relationship between species occurences and predicting variables, the potential habitat/distribution of species can be projected in a given area. Therefore we correlated these GIS layers (using ArcGIS 9.2) and we were able to fill the gaps and extrapolate potential habitat of the *P. b. hungarica* species onto geographical space of Romania.

Using land use maps from different years and different climate scenarios we are able to say that *P. b. hungarica* ecological niches decreased severely in the last decades and the forecast is not optimistic.

Another goal is to create a reproducible technique that can be applied to other rare or endangered species

Keywords: *Pseudophilotes bavius hungarica*, endemic taxon, ecological niche, habitat modelling

Glacial survival and postglacial dynamics of continental species in Europe

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The European fauna has been subdivided into a “holothermic” refugial and a “holopsychric” invasion type. Later, the faunal types have been characterised by "core areas" and interpreted as areas of survival (refugia) and, consequently, as "centres of dispersal". Recently, this view was re-formulated as repetitive patterns of generalised “paradigms” of core areas and tracks of post-glacial re-population. It was concluded that temperate species mainly derive from Mediterranean refugial populations that underwent range expansion in the late glacial and post-glacial periods. The other main group, the “holopsychric” type has been considered for a long time as result of a Siberian invasion, despite of evidence which revealed the taxonomical differentiation of north-eastern “boreal” and southern European montane populations. Several authors have suggested an additional mode of colonisation of central and northern Europe from one or more ‘continental’ refugia: central Europe, Carpathians, southern Ural, Caucasus and western Asia. Several species exhibit mixed patterns, where different parts of Europe have been colonised from Mediterranean and/or non-Mediterranean refugia. We can “dissect” and analyse the area stuctures by molecular phylogeographic methods. By these tools we can clearly disentangle the confusingly similar distribution patterns of widespread polycentric Euro-Siberian species from the expansive Boreo-Continental (“Siberian”) species without any phylogeographical structure at least in the western Palaearctic part of their range. The few “forest-dwelling” butterflies are connected either to some “parkland”-like light-penetrated forest structures or to woody-scrubby forest fringes. They do not show any close connection neither with the deciduous nemoral nor the coniferous forest vegetation, contrasting e.g. with the huge number of transpalaearctic Noctuidae, Geometridae, Tortricidae, etc. A large number of Noctuidae, typical for open zono- and orobiomes, are often connected with rupicolous or arid habitats with skeletic soil. Some highly diverse genera show peculiar larval adaptations (“cutworm” larvae) to these harsh environmental conditions. The majority of species of these genera is confined to the arid montane areas of Central or Inner Asia (called “xeromontane” species) but numerous representants of these genera could become expansive into the eremic or steppic belts. An other typical biogeographical phenomenon is the accumulation of stenochorous species in some parts of the Western Palaearctic (e.g. small Oncocnemidinae, or Leucochlaena, Polymixis, Stilbia, Luperina, Gortyna, the subgenus Paradrina, etc). Important core areas of endemism are some large Mediterranean islands as Creta, Corsica and Sardinia, but also some hilly areas of Iberia and Balkans (e.g. Agrochola, Catocala). We can observe some nested chorological structures (“refugia within refugia”) in the western Palaearctic, mostly in the Mediterranean region.

Two alpine burnet moth species in a changing environment and their future in the Pyrenees

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Global change influences most habitats on Earth, while the impact on high altitude ecosystems is exceptionally strong. As the impact of these changes on alpine species is poorly understood, a better knowledge is crucial to assess future trends. To study effects of global change, we selected the two related alpine burnet moth species *Zygaena anthyllidis* (endemic for the Pyrenees), and *Z. exulans* (distributed over major high mountain ranges of Europe), as model organisms. We compiled historical population records (1958–1986) from museum collections and Lepidopterists' field notes and re-investigated 14 sites for each species in 2008/09 in order to (1) examine if changes in altitudinal distribution ranges have taken place and (2) whether possible changes were attributed to climate and/or land-use. Climate (temperature, precipitation) and land-use data (livestock densities) were gathered for the study period and sites. The obtained data show that (i) during the last 49 years temperature has continuously increased, (ii) the controlled summer pastures received on average low livestock pressure, and (iii) both species showed a significant uphill shift. While uphill shifts of *Z. exulans* were related to changes in climate, those of *Z. anthyllidis* were attributed to changes in grazing intensities. The given examples show that even related species react differently on global change (climate and land-use). Moreover, the results emphasize the considerable role of land-use and that it can even overweight the impact of climate change. In such cases nature conservation becomes especially important as appropriate conservation actions can indeed help for the maintenance of populations.

Prediction of climate and land use change related range expansion in a butterfly of European conservation concern (Lycaena dispar rutilus)

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Recent climate change has altered distribution patterns of many species of different taxonomic groups, including butterflies. Together with habitat loss and fragmentation, climate change is recognised as a major factor of concern for conservation. Butterflies are suitable model organisms to analyse whether organisms will be able to track successfully climate change. Well-underpinned and accurate outcomes of predictive modelling approaches may provide a sound basis for climate-proof conservation strategies and future viable ecological networks.

Bioclimatic envelope models are often used in this purpose but most of the applications assume an unchanged land use in the future. However, increasingly available land use scenarios indicate that such an assumption may be subject to criticism. Pure climate-driven models are therefore likely to produce incomplete predictions. Hence, the joint inclusion of climate and land use change scenarios in the same analytical framework constitutes a challenging avenue of investigation.

We tested whether the integration of land use change scenarios improves the performance of classically applied bioclimatic modelling procedures across a range of spatial resolutions (50 km, 10km and 5 km) for a butterfly species of EU conservation-concern (Habitats Directive 92/43/EEC), the Large Copper (Lycaena dispar). Future species distributions were projected in North-West Europe for the years 2020, 2050 and 2080 under (1) climate change scenarios and current land use and (2) climate and land use change scenarios. Land use scenarios are based on the same storylines and socio-economic assumptions as those underpinning the climate change scenarios (ALARM scenarios).

The results illustrate to what extent the integration of land use change scenarios can provide contrasting predictions in comparison with the more commonly adopted approach of restricting the analysis to a changing climate and an unchanged land use.

First record of the homoneurous family Acanthopteroctetidae in Africa

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During field work on the Lepidoptera fauna of southwestern Africa, two specimens of Acanthopteroctetidae were collected in the Cederberg Mts., South Africa. The family was hitherto known from western North America and the Crimea, Ukraine. With South Africa another sub-range can be added to the widely disjunctive and enigmatic distribution of the family. The specimens represent a new species which belongs rather to Acanthopteroctetes than to a genus on its own. The morphology and habitat of the new species are described, and the distribution of the family is shortly discussed.

Key-note : "Bad species:" genetics and evolutionary importance of hybridization

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Although there are disagreements about species concepts, it is often said there are few cases where our ability to delimit species is severely challenged (e.g. Mayr). However, hybridization and bad species are rather more common than field guides tend to mention. Natural hybridization occurs between around 10% of all animal species, although there are many groups where hybridization rates are greater. Employing Henri Descimon's vast taxonomic knowledge, I helped to collate data on European butterfly species. Overall, around 16% of the 440 recognized European butterfly species are known to hybridize with at least one other species in the wild. In some rapidly radiating lineages, hybridization is much more extensive: for example, in *Heliconius* and *Eueides* butterflies of tropical America, 35% and 42% of species hybridize, respectively. In the Sphingidae, I believe that hybridization is also known to be prevalent. Bad species are relatively common!

Of the butterfly species that hybridize, perhaps 50% or more are fertile, and show evidence of backcrossing in nature. Recent genetic studies show that genomic introgression among hybridising species occurs, and this may lead to long-term hybrid lineages or hybrid speciation. Hybridization, as well as rapid radiation and "ancestral polymorphism" may lead to problems for simplistic mtDNA barcoding. Few good genetic studies have been done in Europe, although the *Papilio hospiton/machaon* studies in Corsica and Sardinia are an exception. Studies of gene flow and hybrid speciation could be especially fruitful in rapidly radiating groups like *Erebia* and the Polyommatini.

Hybridization may have important conservation implications for the effects of climate change and invasive species on endangered taxa. We have recently shown using nuclear as well as mitochondrial markers that the Brown Argus *Aricia agestis* used to hybridize in the past with the endangered Scotch form of *Aricia artaxerxes* in Northern England. Current projections of the rapid northward spread of *agestis* suggest that the two species will again meet in the near future as a result of climate warming, and this could lead to the extinction of the unique British population of *artaxerxes*.

Exploring the Northern Hemisphere: phylogeny, classification and evolution of Boloria (Lepidoptera: Nymphalidae)

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The nymphalid genus Boloria is a moderately species rich butterfly genus restricted to the Holarctic region. Many species are adapted to alpine and/or arctic environments, and the genus is very well suited for exploring recent evolutionary, diversity and biogeographical patterns in Holarctic butterflies. Here we infer the phylogeny of 37 potential Boloria species (81 specimens) based on characters from adult morphology and three genes. The results are used to address key questions about the genus’ evolution (larval foodplant associations) and zoogeography. We also revise the overall classification of the genus and propose informal species groups where appropriate. Based on the molecular results we address the taxonomic status of the problematic titania/chariclea, improba/acrocnema, and freija/natazhati species complexes.

Bucculatricidae revisited from a southern vantage point

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Position and rank of the Bucculatricidae have long been contentious. Larval morphology first suggested a separate family for Bucculatrix Zeller and several immature characters later helped confirm a position within the Gracillarioidea. The overall plesiomorphic, monotypic South African Leucoedemia Scoble & Scholtz was included in the Bucculatricidae on the basis of its ribbed cocoon, one larval character and two life history traits. A revision of the Australian Ogmograptis Meyrick has now revealed a plesiomorphic southern bucculatricid clade including Leucoedemia, Ogmograptis and Tritymba Meyrick, as the sister group of Bucculatrix. Apomorphies for the family are so far restricted to characters of the immatures: a longitudinally ribbed cocoon and a larva with strongly modified tarsal setae and an internal skeleton in the last abdominal segment, with remnants of the latter apparently present in the penultimate larva of some Bucculatrix species. Ogmograptis and Tritymba are both miners in Eucalyptus, emphasising their Gondwanan connection.

Online dissemination of taxonomic information on family-, genus- and species-group names of global Gracillariidae and all moths of the entire Afrotropical region

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Currently, many studies on taxonomic revisions and molecular phylogenies are hampered by the fact that the world fauna of Lepidoptera is still not inventoried. Therefore, we are convinced that the scientific society badly needs a reliable and well structured packet of information containing the essential items: taxonomy and type specimens, host plants, distribution and parasitoids.

The searchable website "Global Taxonomic Database of Gracillariidae" got a new, modern layout and its own URL: www.gracillariidae.net. Furthermore, this website became much more user-friendly because of the possibility to search on any taxonomic or geographical name, retaining the advanced search possibilities as well. Differently from many other websites with only a simple search possibility, a user of the website Global Gracillariidae has obtained the search possibility of creating any combination of taxonomic, biological, distribution and ecological (parasitoid) keywords he/she needs. This website provides an online database of Gracillariidae (Lepidoptera) on a worldwide basis, updated with the latest information obtained from published sources and from our own studies. It currently holds information on
family-group names: 17
genus-group names: 142 (recognized genera: 99)
species-group names: 2,579 (recognized species: 1,855)
The current list is continuously updated and information on the original description, type locality, types and their depository, distribution, host plants, and parasitoids is added at a regular basis. We added the information on the unplaced species, fossil species, and taxa transferred to other families. In a later stage also pictures will be added. We have checked the information on the primary types deposited in 57 museums all over the world.

The website AfroMoths, available at http://www.afromoths.net/, provides an online database of ALL the Afrotropical moth species (Lepidoptera), updated with the latest information obtained from published sources and from our own studies. It currently holds information on
family-group names: 573
genus-group names: 7,140 (recognized genera: 4,042)
species-group names: 32,248 (recognized species: 24,029)
The current list is continuously updated and information on the original description, type locality, types and their depository, distribution and foodplants is added at a regular basis. It covers the species information from the zoogeographic area which can be defined as the Africa continent south of the Sahara (i.e. excl. Morocco, Algeria, Tunisia, Libya and Egypt), the islands in the Atlantic Ocean: Amsterdam Island, Ascension, Cape Verde Archipelago, Inaccessible Island, St. Helena, São Tomé and Principe, Tristan da Cunha, and the islands in the Indian Ocean: Comores (Anjouan, Grande Comore, Mayotte, Mohéli), Madagascar, Mascarene Islands (La Réunion, Mauritius, Rodrigues), Seychelles (Félicité, Mahé, Praslin, Silhouette, a.o.). Furthermore, also those moth species occurring in the transition zone to the Palaearctic fauna have been included, namely most of the Arabia Peninsula (Kuwait, Oman, Saudi Arabia, United Arab Emirates, Yemen with Socotra) but not Iraq, Jordan and further north.

Both websites are cited as the reference source in Wikispecies, which indicates the reliability and quality of the websites. Both websites were composed by a very small team – the authors – of this presentation.

Key-note : Getting a sense of time for massive radiations in Lepidoptera

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The diversity of life on Earth is enormous and our task of documenting it is still underway. One important part of this documentation is understanding the generation and maintenance of biodiversity over evolutionary time frames. When have major divergences happened? How have these divergences happened? I will be investigating these questions using the megadiverse clade of Lepidoptera (butterflies and moths) as my model group. In this talk, I will review what we know about the evolutionary history of Lepidoptera and point to the directions we are going in the future to understand why there are at least 150,000 extant species in all the world's habitats.

Key-note: Lepidoptera systematics 2011: state and challenges

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During the past decade, when phylogenies of living organisms have come to be increasingly based on analyses of molecular markers, the role of comparative morphology is changing, but remains crucially important role in evolutionary biology: mapping the distribution of structural character states – and hence of 'enabling mechanisms' – and thereby tracing underlying evolutionary pathways, are among the most rewarding uses that can be made of robust cladograms, irrespective of whether these were in the first place generated from molecules, morphology or both.

Large-scale molecule-based Lepidoptera phylogenies published during the last few years importantly converge on a number of clade arrangements which are at variance with previous suggestions. In most cases the latter have had so weak support, that the innovations are little surprising, but exceptions do occur and obviously present special challenges. Also, sizable sectors of the lepidopteran phylogeny still comes in the form of a 'lawn' rather than a 'tree', i.e., with internodes between high-rank-taxa being very short/weakly supported. Remedying this state of affairs remains another major challenge.

Keywords: Lepidoptera, phylogeny, genomics, morphology

Developments on Ditrysian phylogeny

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Ditrysian i.e. the ‘advanced’ Lepidoptera comprise the vast majority of all Lepidoptera. Its phylogeny has always been a challenge due to paucity of strong morphological evidence. We review the recent developments that have been, and are being, achieved by extensive use of molecular data, and analytical interpretation of morphological data. The established division into “basal superfamilies”, Apoditrysia, Obtectomera and Macrolepidoptera is with some modification supported with recent evidence. Tineoid familes appear the most basally arising ones, then Yponomeutoidea and most of Gracillarioidea form together a monophylum. Cossoid-Sesioid-Zygaenoid families need closer scrutiny. Many other areas of Ditrysia are also still unclear, but significant and well supported changes appear to be expected regarding the position of Gelechioidea which is an apoditrysian, if not even obtectomeran group, butterflies that are not among traditional Macrolepidoptera and Pyraloidea that appear to belong to ‘macros’. The data suggest that the generally short diverging nodes between major groupings in basal non-tineoid Ditrysia are due to their rapid radiation, presumably in correlation with the radiation of flowering plants.

The female postabdomen and genitalia of eriocraniid moths (Lepidoptera: Eriocraniidae) and its phylogenetic significance

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Eriocraniidae are currently believed to be the sister group of all other extant Lepidoptera-Glossata and it is an intriguing question whether their female postabdominal configuration with a piercing oviscapt suited for endophytic oviposition represents the glossatan ground plan; it has counterparts in the families arising in the two following splitting events, Acanthopteroctetidae and Lophocoronidae. Eriocraniid females like those of most lepidopterans and many trichopterans have two pairs of long rod-like apophyses, arising from segment VIII and IX (+X); females of the non-glossatan moth family Agathiphagidae are unique in having two anterior pairs, a dorsal and a ventral. Evidence for homologizing either the dorsal or the ventral pair of Agathiphaga with the glossatan single pair is ambiguous; possibly the latter is a composite formation that includes both dorsal and ventral elements. Six eriocraniid postabdominal mucle pairs (including three inserting on the complex genital chamber sclerotization, the “vaginal sclerite”) seem to have no counterparts in other Lepidoptera, while an otherwise widespread ventral intersegmental VIII-IX muscle is lacking. More detailed information about conditions in acanthopteroctetids and lophocoronids are needed to assess which, if any, of the peculiarities of the “Eriocrania type” piercing oviscapt (such as the vaginal sclerite and its associated muscles) are family autapomorphies.

Redefining butterflies

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A comprehensive phylogenetic analysis of the superfamilies Papilionoidea, Hesperioidea and Hedyloidea is presented. The study is based on revised morphological data, including extensive data derived from larvae and pupae, as well as on eight protein coding gene regions (one from the mitochondrial genome and seven from the nuclear genome). The data are used to estimate divergence times of lineages leading to extant papilionoid families.

The analyses of combined molecular and morphological data suggest that Papilionidae are the sister-group to all the other families including Hedylidae and Hesperiidae. A sister-group relationship between Hedylidae and Hesperiidae is also found in all analyses of combined data as is a sister-group relationship between Riodinidae and Lycaenidae. The position of Pieridae is unstable. In the consensus tree Pieridae is the sister-group of the branch including Nymphalidae and its sister-group of Lycaenidae and Riodinidae.

The divergence time analyses suggest that the three lineages leading to Papilionidae, to Hesperiidae and Hedylidae and to the rest of the butterflies diverged rapidly from each other in the early Cretaceous, some 110 million years ago. Lineages leading to the other extant families had diverged from each other by 90 million years ago. Most within family divergences leading to present subfamily lineages have happened circa 65 million years ago, after the Cretaceous-Paleogene extinction event.

A molecular phylogeny of European Coleophora

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With more than 1,300 described species, Coleophora is one of the largest lepidopteran genera. The majority of the described species is distributed in the Holarctic Region. There have been different attempts to classify this species-rich genus either by defining species groups or by splitting it into many genera. A more recent study focussing on characters of the larval case architecture and ecology of North American species is the only so far available cladistic analysis for the group.

For the first time, we used molecular data for a phylogenetic analysis of Coleophora. Baysian statistics was applied to a data set of COI and wingless sequences for 104 European species. The analysis of the concatenated data set yielded a hypothetical tree with eight well supported species groups (alticolella, albella, lutipennella, frischella, saturatella, serpylletorum, vacciniella and vibicella species groups) and five monophyletic species pairs. Mapping the 'multigeneric' concept on the tree, our results clearly support formerly defined species groups than the splitting into many genera. Only for some groups, synapomorphies in larval ecology and behaviour could have been revealed. Nevertheless, all species groups are characterised by a certain set of traits by which they could be distinguished from each other. Analysis of host plant association in Coleophora revealed that some clades radiated on certain plant taxa along with a specialisation on certain plant tissues, e.g., the clade containing the saturatella (leaf miners) and frischella (blossom/seed miners) species groups is associated with Fabaceae, the albella species group (seed/blossom miners) with Caryophyllales and the serpylletorum species group (leaf miners) with Lamiaceae. Our data suggest that primary host plant exploitation in Coleophora is associated with herbaceous plants and an unspecified feeding on various plant tissues (seeds/blossoms/leaves). Both occupation of woody plants and seed feeding evolved several times independently. We checked the formerly established synthetic model of host fidelity and confirm that host fidelity tends to be highest in seed feeders on herbaceous plants, moderate in leaf feeders on herbaceous plants and lowest in leaf feeders on woody plants. However, differences in host fidelity are only significant between woody and seed feeders and between seed and leaf (woody and herbaceous) feeders.

Integrative taxonomic of the genus Gnopharmia Staudinger, 1892 (Geometridae, Ennominae)

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Abstract. The genus Gnopharmia (Macariini, Ennominae) includes traditionally thirteen recognised species; however, these species are very difficult to distinguish. Due to its difficult taxonomy, former authors could not achieve satisfying results since they used just the external morphology of the adults. In an integrative taxonomic revision of Gnopharmia we applied three different methods to achieve a better insight on the morphological and molecular variation within this group of species.

Over 850 genitalia preparations were made and analysed by traditional genitalia examination of both sexes. A comparison of this huge number of slides allowed us to recognise some new and formerly undiscovered characters of the sclerotised parts of the genitalia. As a result of the simultaneously executed comparison of all type specimens, we synonymised 6 taxa, producing a new preliminary checklist of Gnopharmia.

Subsequently geometric morphometric methods (procrustes analyses) were used to analyse two character complexes: the morphological variation of the aedeagus and of left forewings´ venation.

Finally, we sequenced a 658 bp fragment of cytochrome oxidase 1 (CO1). The resulting Maximum Likelihood tree showed a good congruency towards the previously defined morphospecies: seven species were confirmed by the three different methods explained above.

Millieriidae, a polyphyletic familly : can this four-taxon mess be sorted out ?

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Millieriidae, which were recently elevated to the family status from Millieriinae, a subfamily in Choreutidae, consist of four species classified in three genera. *Millieria* Ragonot is monotypic and its only species is found in Europe; *Phormoestes* Heppner, also monotypic, is found in Florida; and both species of *Nyx* Heppner are found in Chile. In 1982 Heppner described Millieriinae as a subfamily within Choreutidae to accommodate these three genera as he considered them related. However, our current understanding of their morphology and the published studies based on molecular data strongly suggest that these taxa are not close relatives of each other and that Millieriidae is a polyphyletic family. Analyses of molecular data from eight protein-coding genes (one mitochondrial and seven nuclear) provide new evidence for the phylogenetic placement of these groups.

A rediscovered butterfly-species in Mauritius

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On an excursion to the Afrotropical Island Mauritius in 2007 a very rare butterfly-species not recorded since 1953 was rediscovered.

Some pictures from the Island including the species are shown.

Nocturnal lepidoptera inventory of atlantic islands national park (cíes, ons, sálvora y cortegada) (galicia, spain)

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The first entomological inventory of Atlantic Island National Park (Galicia, Spain) was conducted between 2007 and 2008. The main objectives were to study the specific entomofauna in the park, the specificity of each one of the existing systems considering their geographic isolation, evaluate their biodiversity richness and settle the first steps for a study about their potential as early indicators of global warming disorders.

The National Park is formed by four archipelagos (Cíes, Ons, Sálvora y Cortegada) located in the "Rias Baixas" area. The climate there is really different from the seaboard zone due to their small altitude, which makes the clouds pass over those islands.

The Nocturnal Lepidoptera results were concluded with a total amount of 194 species, in 26 different families, distributed as follows: Cíes, 73 species; Ons, 90 species; Sálvora, 90 species; and Cortegada, 82 species.

The most remarkable families are Noctuidae and Geometridae, found in all the archipelagos and representing more than a half of the identified species. On the other hand Depressaridae, Phsychidae and Ethmiidae are the less represented. The first ones were only found in Salvora and the last one in Cortegada.

The Biodiversity indices were applied in order to obtain further information, showing that Cíes and Ons are the most similar archipelagos (0.503 in Sørensen index), followed by Ons and Salvora (0.486). These results are completely logical due to the proximity between the two pairs of archipelagos.

This is the first complete catalogue of moths of the Atlantic Island National Park.

Key words: National Park, Nocturnal Lepidoptera, First Inventory.

The Mysterious Systematics and Conservation of Hawaii’s Endemic Omiodes (Crambidae)

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The crambid moth genus Omiodes contains 23 species endemic to Hawaii. We have studied both the evolutionary biology and ecology of Hawaii’s Omiodes with some surprising results. While some species have been the target of biological control efforts, others are now extinct, and the decline of some species poses challenges for their conservation. Over the past 6 years we have conducted controlled exposure trials and field surveys to assess the non-target impacts of introduced biological control parasitoids on several species. Biological control impacts are more complicated than expected, with some areas acting as apparent refugia. We have also constructed the first molecular phylogeny for the Hawaiian members of the genus, and examined population-level genetic structure. Speculation about explosive Omiodes speciation on banana in the past 1,000 years prompted an evolutionary analysis. The phylogenetics of Omiodes does not suggest recent speciation, but the revelation of several cryptic species, and complex population structure across the islands that differs among different species, defies a general paradigm for cladogenesis.

The digital project "Geometridae mundi" of the Bavarian State Collection of Zoology Munich (ZSM)

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The project Geometridae mundi aims to construct an illustrated html-data bank of the global biodiversity of Geometridae basing on the updated checklist of the world's Geometridae (SCOBLE & HAUSMANN 2007, http://www.lepbarcoding.org/geometridae/species_checklists.php). Because of the large amount of data the project was split in three parts:
Part I: Subfamilies Archiearinae, Oenochrominae, Desmobathrinae, Geometrinae, Sterrhinae (ca 7,900 taxa).
Part II: Subfamily Larentiinae (ca 7,970 taxa).
Part III: Subfamily Ennominae (ca 13,300 taxa).
We will provide digital photographs for all taxa (both sexes, underside) at three functional levels: Overview pages (100 species each in systematic order), genus pages (one genus only with larger images) and species pages, including all photographs at high resolution. We plan to include also images of genitalia. Distribution maps may be added later on such as short texts with additional information on each species. Overview pages, genus pages and species pages are linked with each other, but genera and species can also be browsed directly through an alphabetical index. The structure of the database is ready for the first two parts and most of part III, and includes about 20,000 images, currently.
The following steps are planned
(1) Providing photographs for all species available in German collections and museums, subdivision to the faunas of the main zoogeographical regions, electronic publication.
(2) Providing photographs of genitalia.
(3) Organising photographs of missing species through co-operations, with appropriate accreditation of the partners.
(4) Providing text information for each species, compiling a related literature data bank.
Steps (2) – (4) can partly be performed in parallel and will not be finished quickly. After the first data release publication the users of the offline-version should receive regular updates in intervals of 2-3 years. The data bank is planned to be published online later on.

Updating the Phylogeny of the Superfamily Gelechioidea: An Integrated Approach

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The superfamily Gelechioidea is one of the biggest groups in Lepidoptera. It includes more than 18.000 described species and that might only be a fraction of the total amount. In spite of – or because of – the size of the superfamily, there have been only a few published phylogenies.

Kaila published 2004 a morphology-based phylogeny on Gelechioidea. He found a basal split that separated the superfamily into two main lineages: the ‘gelechiid’ and ‘oecophorid’ lineages. Kaila, Mutanen and Nyman submitted a manuscript in 2011 with a molecular phylogeny. The main difference between these phylogenies is the place and composition of the ‘gelechiid’ lineage which is intermingled with Elachistidae s.l. In molecular phylogeny, Elachistidae break up into three pieces: Elachistidae s.s. (including Elachistinae), Elachistidae s.l. (Stathmopodidae and Parametriotinae) and Elachistid s.l. assemblage (e.g. Depressariinae, Hypertrophinae, Stenomatiinae, Ethmiinae and also Oditinae of Lecithoceridae). Surprisingly, only the Elachistid s.l. assemblage was located together with groups of the Oecophorid lineage.

I will present a new, unpublished phylogeny of Gelechioidea based on a combined data set of revised morphological and molecular characters and compare this phylogeny with previous suggested phylogenies of Gelechioidea.

A new genus and species of Spilomelinae (Lepidoptera, Pyralidae) from the Galapagos Islands, Ecuador

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The morphology of a new genus and species of Spilomelinae endemic to the Galapagos Islands, Ecuador, is presented. Hypotheses of relationships based on analyses of morphological and molecular characters will be discussed. The caterpillar is a borer in stems of the endemic Tournefortia pubescens Hook. f. (Boraginaceae).

Attraction of modern illuminations on night active insects

Peter Huemer, Hannes Kuehtreiber & Gerhard M. Tarmann (presentation)

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Artificial light sources are a long underestimated environmental problem. The Austrian project 'The plight with the light' ("Die Helle Not") contributed to a solution of this problem by giving convincing arguments to change from white and energy consuming mercury vapour lamps to yellow and less energy consuming sodium vapour lamps. Improvements in public and private illumination have minimised the problem within the last 10 years significantly. However, in the EU new types of lamps are on the market and the producers are claiming that their new lamps are even less attractive for night active insects than the older sodium vapour lamps combined with a higher variety in light colour and less use of energy.

Parallel tests to evaluate the attraction of these lamps for insects were necessary to receive profound data. Therefore five types of these new lamps were tested against the yellow sodium vapour lamp in a sophisticated test near Innsbruck in Austria. The results of 18 nights are compared and the attraction of the tested lamps on night active insects in general and Lepidoptera in particular are presented. Based on 22.000 specimens (3,877 Lepidoptera) a clear result can be seen. The tested LED lamps are less attractive to night active insects as the tested metal halogen lamps even if the latter have UV filters. They also use less energy.

DNA Barcoding symposium

1/2 million DNA barcodes for Lepidoptera: Where are we now and where are we going?

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DNA barcodes are small DNA fragments used across all Life as diagnostic markers for species identification and discrimination. With more than half a million records in BOLD, the Barcode of Life Datasystems, Lepidoptera are the most heavily sampled organisms, both taxonomically (54K species) and geographically (samples from 197 countries).

In this presentation, we dissect the fundamentals of the campaign, emphasizing the strategic and methodological elements that underpin its success. We give examples of immediate taxonomic implications as well as recent applications based on the DNA barcode reference library.
We also point at the largely unexplored parts of the barcode library, where no taxonomy is available, or where DNA barcodes occasionally diverge from the existing taxonomy.

Through the continuation of existing campaigns and the development of emerging ones such as the European campaign, the reference library for Lepidoptera keeps progressing at a rapid pace. In fact, thanks to the growing participation by the community of lepidopterists worldwide, we expect to surpass the target of gaining barcode coverage for half of known Lepidoptera species (165K species) by 2015.

Barcoding Fauna Bavarica: The first genetic all-species survey of a whole country

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Though being situated in the centre of Europe, Germany still lacks a comprehensive faunistic monograph for its more than 3,600 Lepidoptera species, including a number of yet unresolved taxonomic problems. As DNA barcoding is a rapid, cost-effective alternative strategy for both the identification of described species, challenging existing species concepts, and discovery of new species, the Zoological Collection of the State of Bavaria (ZSM) activated the project 'Barcoding Fauna Bavarica (BFB)' in the year 2009, representing the first program to create a DNA barcode library for all animal species in a whole country. The project is in close cooperation with the Biodiversity Institute of Ontario under the framework of the International Barcode of Life Project (iBOL) and supported by a 5-year grant from Bavarian State Government. Research activities involve an active network of private collectors and entomological associations, Nature Reserve authorities and other cooperating institutions. The DNA Bank facility at the ZSM holds extracts for spin-off research projects.

As of March 2011, barcode records were available for ~2,250 lepidopteran species (~70% of the Bavarian fauna). Coverage is close to be complete for the known Rhopalocera and Macroheterocera species, at ~80% for Pyraloidea and ~52% for the non-obtectomeran Lepidoptera. Preliminary results show that barcoding is capable of unambiguously discriminating ~99% of the species investigated so far, including some of the highly similar species traditionally known to cause significant identification problems. The method led to the discovery of unexpected new faunal elements, but pointed out also interesting cases of barcode similarity, barcode sharing, and deep intraspecific splits. First tests revealed that many more divergences result when extending the study area to the whole continent of Europe, indicating that international collaboration, data-sharing and democratization of biodiversity information may significantly increase the taxonomic impact of data from DNA barcoding.

Barcoding 2500 lepidopteran species of Finland – experiences and taxonomic observations

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Finnish lepidopteran fauna with about 2500 species was subjected to a comprehensive DNA barcoding. Basically three-four specimens per each species were barcoded, while in taxonomically problematic groups more specimens were often sequenced. The results indicate that barcodes alone allow safe identification of over 95% of species. Several species pairs with shared barcode haplotypes were detected, but only in a few cases more than two species were mixed. The results provide evidence for validity of several species of uncertain status. Some problematic species are shown to share the same barcodes. The data has revealed several new species to Finland, and several dozens of species with deep intraspecific divergences were detected, calling attention for closer taxonomic scrutiny. Overall, comprehensive DNA barcode library makes taxonomy more accurate, identification more straightforward, and enable large-scale inventories of life histories.

Barcoding complete Lepidopteran fauna's – challenges and opportunities

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Lepidoptera collected at light can be used for biodiversity assessments, but identifying all the material can be a hurdle. All Lepidoptera collected during a three weeks expedition at Gunung Lumut, Kalimantan, Indonesia have been sorted and identified (partly to morphospecies). A total of 2197 specimens belonging to 917 species was offered for DNA barcoding at the CCDB. This resulted in 1626 DNA barcodes, covering 85% of the species. The DNA barcodes aided with species recognition and the identification of various difficult taxa. One example even showed that two species previously placed in separate genera actually represent a sexual dimorphism. Initial biodiversity analyses suggest that only about half of the fauna was recovered, the total of singletons being 64%. Recent material of light collecting trips in the United Arabic Emirates, the Netherlands (both of which the complete Lepidoptera fauna is described) and Vietnam (where specialists will verify the results) will be used for further optimizing this biodiversity assessment method.

Rapid inventory via DNA barcoding: cross-lepidopteran diversity survey of Nouragues inselberg, French Guiana

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DNA barcoding has great potential for profiling relatively unknown tropical faunas, but even at high taxonomic level among relatively well-known insect orders such as Lepidoptera, barcodes may be lacking. In cases where there is no close hit in a DNA database, strong potential exists to examine species richness/identities and thus spatial and phenological turnover between surveys. We twice visited Nouragues inselberg in French Guiana in two seasons (January and September) of 2010, attempting to barcode representatives of all moths attracted to light. A sample of 2247 moths in the first visit contained approximately1383 species, at least 71% of which were singleton species and 15% which were doubletons. This indicates that our survey was very incomplete: estimates of total faunal site richness from light trapping methods alone varied from ~150-300%. We use these data to estimate phenological turnover. We used a character-based system to order sequences and thus improve identification efficiency prior to database querying/voucher examination, and used a similar approach to develop a pragmatic unique species-numbering system for such a single site inventory. This procedure also worked well on groups that could be reliably identified morphologically. Many species thus could be identified to higher taxon from barcode information alone, even when there was no prior representative of its genus or species in the DNA database. A striking example is a single character (phenylalanine,178th codon) that reliably flags (at >99% efficiency) the most important clade of larger moths (Macroheterocera). Use of such higher taxon character information would be a powerful feature in the BOLD identification procedure, because some so-called “microlepidoptera” have quite similar barcodes to some traditionally termed “macros”. The curve of nearest "non-site" hits (using automatic querying on the entire BOLD database), indicates that the vast majority of "microlepidopteran" sequences from Nouragues were novel, including unrepresented lineages at up to 16% K2P-distance.

On the use of DNA barcodes as a proxy for lepidopteran species richness in hyperdiverse regions

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In this study, we assessed the potential of DNA barcoding as a tool to accelerate the inventory and analysis of biodiversity for complex species assemblages of tropical Lepidoptera. The study was carried out in the National Parks of La Lopé and Ivindo in Gabon, a recognized hotspot of biodiversity. Moths were collected by light trapping during three successive nights in each site, and a selection of 2803 morphologically sorted specimens was DNA barcoded. We obtained sequences for 2730 specimens belonging to 1100 distinct barcode clusters. Rarefaction curves and richness indices were further calculated using the number of clusters as a proxy for species richness, while species lists were obtained for some families by identifying the sequences against reference libraries in BOLD. Although saturation points were never reached in rarefaction curves, richness estimates suggest higher species diversity in the forests of Ivindo compared to the savanna/forest patchwork of La Lopé. This study provides evidence for the enormous potential of DNA barcoding as a standardized tool permitting the rapid assessment of lepidopteran biodiversity in hyperdiverse ecosystems

Rapid biodiversity assessment: 50% of the world's geometrid moth species are DNA barcoded

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Lepidoptera have served as a model group to test the effectiveness and utility of DNA barcoding. The campaign to barcode all species of Geometridae represents one of the most ambitious components of the overall barcode effort on Lepidoptera. Reflecting work carried out since 2006, Geometridae are now the most heavily sampled family worldwide, both numerically (>90K barcodes in BOLD), taxonomically (>12K species sampled), and geographically (samples from 139 different countries). Because of its status as a core compent of the International Barcode of Life Project, the geometrid campaign is progressing at a rapid pace and we expect barcode coverage to reach at least 80% (18.4K species) of all known geometrid species by 2015.

In this presentation, we emphasize the crucial role of DNA barcoding for the rapid assessment of global biodiversity and show results and patterns from sequence analyses of Geometridae. We highlight the importance of data release publications with examples drawn from our work on "Barcoding Fauna Bavarica", "Geometrids of Europe" and "Geometrids of Africa". The application of barcode data in identification, taxonomy, ecology and other disciplines of biodiversity science, such as in applied entomology and industry, are shown based on case studies drawn from the geometrid campaign.

The value of COI in the identification of Afrotropical Lymantriidae

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From a sample of 167 DNA extracts of Lymantriidae caught in tree different African localities, each about 2300 km away from each other (Ghana : Bia Forest Reserve, DRC : Lukolela and Tanzania : Uluguru Mountains) a COI tree was produced. The vast majority of the COI branches matched the classical morphological identifications, 73 in total. Only in three cases the molecular analysis did not match, but it concerns three *Euproctis* species. At this stage of the research it can be considered that in Lymantriidae COI can be considered perfectly safe for identifications on species level except for *Euproctis* taxa. None the less, a strange phenomenon also appeared in the tree. In a number of species the difference in COI between males and females can be much greater than what is accepted as species level. Sometimes it is negligible, but in one case it can reach up to 2.5 times the species scale.

DNA barcoding of European Gracillariidae leaf-mining moths

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Moths in the family Gracillariidae constitute one of the primary groups of plant-mining Lepidoptera. Gracillariids include 1855 described species of which 256 have been recorded in Europe. Here we present barcode data for more than 1000 specimens of 180 European species. Morphology and DNA barcodes were carefully studied and compared. Our results indicate that most species form barcode clusters allowing their reliable identification. We detected a few cases for which there is a mismatch between morphology and barcodes. DNA barcoding revealed divergent clusters within several described species and careful re-inspection revealed morphologic diagnostic characters associated with several of those genetic clusters.

Zygaenidae taxonomy and a DNA study: status quo

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The taxonomy of the Zygaenidae is based on profound morphological, biological, ecological and biochemical characters. However, there are still unresolved problems. Great progress has been expected from nucleic acids study that has been ongoing during the last few years.

Here we present DNA results of the Zygaenidae based on investigations of a 658-bp region of the cytochrome *c* oxidase I (COI) gene. 380 sequences of 104 species belonging to 16 genera of the subfamilies Procridinae (76 species), Zygaeninae (27 species) and Chalcosiinae (1 species) have been examined so far. The specimens originated from all over the world.

Our results demonstrate specificity of sequences of COI gene at species level in most of the studied Zygaenidae (in 94.2% of examined species). The mean intraspecific distance (within species) is 1.48%, interspecific (within genus) – 6.41%, intergeneric (within family) – 12.61%. We also have examples when the study of COI gene sequence revealed misidentifications. Re-examination of these specimens based on genitalia structure confirmed the barcoding result. However, we found some exceptions in which the sequence data of the COI gene do not reflect the interspecific differences, viz. in the subgenus *Jordanita* of the genus *Jordanita*.

Our study also shows that geographical factors have to be taken into account. A good example demonstrates the study of different populations of *Jordanita subsolana*. When comparing specimens from the Crimea, Turkey and Armenia, we found barcode similarity between Crimean and Turkish populations, while the Armenian population forms an isolated group. This may reflect migration into different geographical regions at different times. Another example is more complicated. The *Adscita geryon* population from the Crimea shows a smaller distance to Crimean *A. albanica* (a species that is morphologically and biologically well separated) than it does to *A. geryon* from the Balkans.

Based only on the DNA data, it is not possible to decide whether we have subspecies or species because the distance between populations of one species is sometimes greater than the interspecific one.

Disjunct mountain populations of obviously the same species can show remarkably large differences in COI gene sequences. This may be connected with long isolation. An example is *A. subdolosa* from different mountain ranges in Central Asia.

Long isolation (e.g. on different continents) can cause such large differences in COI sequence that the sole African *Adscita* species (*A. mauretanica*) is placed separately on the tree (created using the Kimura 2 parameter model) and is isolated from all the other species of the genus *Adscita* (inhabiting Europe and Asia) with which it shares all important morphological and biological characters.

These results not only confirm the value of DNA investigation for species determination but also show interesting new data that, when compared with other observations, can be used for taxonomic and biogeographical decisions.

Taxonomy of European Scopariinae revisited using DNA barcoding

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Based on morphological characters, European Scopariinae are taxonomically well investigated between 1984 and 2005. Though identification literature is available for the 52 species occurring in Europe, many lepidopterists still feel difficulties identifying at least some of the species due to their very uniform appearance. Against this background, it is tested whether DNA barcoding can help to identify scopariines more confidently.

Using a fragment of the mitochondrial cytochrome c oxidase subunit I (COI), we are able to reliably identify most of the species. Even in the Palaearctic Region widely distributed species generally show very low levels of infraspecific variation, if at all, and can be well discriminated against other species. For example, European *Gesneria centuriella* is clustering close to *G. centuriella caecalis* from North America, but other North American individuals of this species are significantly discriminated (data of North American specimens from UBC).

In contrast, species of two species complexes of European Scopariinae can not be confidently identified using the COI-DNA barcode. These are (1) *Scoparia manifestella* and *S. italica* as well as (2) *S. ambigualis* and *S. basistrigalis*. The first complex is widely distributed in the Alps and more southerly situated mountain systems in Europe. Species discrimination remained difficult based on morphological characters and interspecific variation could not be assigned to taxonomic units. In contrast, *S. ambigualis* and *S. basistrigalis* can be identified based on wing pattern elements, male and female genitalia. In typological concepts, they were even placed in different species groups.

Though we basically selected specimens which typically represent known species, we discovered a case of cryptic diversity in an *Eudonia* species, which points to the necessity of barcoding more individuals from different parts of the range of ‘known’ species in order to clarify genetic variation and in consequence taxonomic status of isolated populations.

The data have been compiled within the International Barcode of Life project (iBOL).

The role of DNA barcoding in the identification of a wine pest: Antispila ampelopsifoliella

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The North American grapevine leafminer Antispila ampelopsifoliella is a new important invader in North Italian vineyards since 2006. The species could be identified by comparison morphology (including genitalia) and DNA barcodes with North American representatives, despite the lack of previous taxonomic treatments. Final proof was obtained by comparing DNA barcodes from various North American specimens. European ones differ only from 0-0.91% from American barcodes, showing that the Italian population very recently spread from eastern North America. DNA barcodes of the three European grapevine leafminers are highly diagnostic. For quickly identifying potential new grapevine pests, taxonomic and DNA work on this group should be prioritised.

New records of European micromoths in North America detected through DNA barcoding

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DNA barcoding is increasingly gaining popularity among microlepidopterists mainly for its powers in discriminating between otherwise poorly characterized species, association of sexes, and discovery of new taxa. Here we present the first records of 20 Palaearctic species of microlepidoptera in North America, detected through a DNA barcode match with their European counterparts, and confirmed via post-facto genitalia dissection.

Launch of the European Lepidoptera campaign

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The authors jointly announce the official launch of a new DNA barcoding campaign targeting all European Lepidoptera. The current progress will be presented and a quick tour of the dedicated web-platform (currently under construction) will be given, featuring some key resources (e.g. live-progress reports based on the Fauna Europaea checklist, national/regional points of contact, etc.) as well as a few case-studies emphasizing the valuable input of DNA barcoding to address unsolved taxonomic questions.

Attendees to the SEL congress are invited to join this campaign already involving a community of institutional and "amateur" lepidopterists. Considering the richness of Lepidoptera collections and the broad expertise of lepidopterists in Europe, we expect quick progress of the campaign toward assembling a comprehensive reference library of DNA barcodes for the ca. 10K species of European Lepidoptera.

Posters

Pupation of some Acronicta species (Lepidoptera, Noctuidae)

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Observations of the pupation of three Acronicta species - A. alni (12 larvae), A. rumicis (19) and A. aceris (6) - were carried out during three years (2008-2010) in July-August. All larvae were found in 17 km to the north of Moscow and were kept in the same conditions (T 22-24°C, sufficient humidity, foodplants, oak and birch wood, pieces of bark).

Most of A. alni larvae (83.3%) pupated in dry wood (burrowing into oak and birch branches and forming a cradle); 66.7% of A. aceris larvae pupated in a bark crevice (forming a cradle and a double-layered cocoon). Other specimen, including all A. rumicis larvae (100%), pupated in foodplant leaves. The loss of larvae was low and only one A. alni specimen died during diapause.

A proposal for the taxonomy and classification of the Olethreutini genera *Hedya* Hübner and *Metendothenia* Diakonoff (Tortricidae, Olethreutinae)

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During a study of olethreutine material collected in North and North-West Iran in the summer of 2007 we detected a male species superficially similar to some species of *Metendothenia* Diakonoff but whose genitalia differ from those of other related species in the distribution of spine clusters in the neck of the valva of the male genitalia. Moreover the wing pattern revealed some similarities with species of the genus *Hedya* Hübner. Additional material –males and females- was found as result of field work and curation in the Hayk Mirzayans Insects Museum of Iranian Research Institute of Plant Protection (IRIPP). The tribe Olethreutini, with about 1400 species in over 144 genera, occurs in all parts of the world but chiefly in the Oriental and Holarctic regions (Horak & Brown, 1991). The taxa examined are relevant from a faunistic point of view because previous records from Iran included only nine species of Olethreutini (Barou, 1967; Razowski, 1963, 2003). Moreover *Hedya* Hübner (1825) and *Metendothenia* Diakonoff (1973) are related Olethreutini genera in a poorly defined taxonomic area. Recent insights into the knowledge of Olethreutini (Aarvik, 2004; Horak, 2006) and the study of this new material revealed some inconsistencies in the assignations of species to *Metendothenia* and *Hedya*. The authors propose a more natural distribution of taxa according to morphological characters: wing pattern, male and female genitalia.

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Phylogeny of Cyclidiinae (Lepidoptera: Drepanoidea, Drepanidae), a drepanid group endemic to Oriental region

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The Cyclidiinae is a small macrolepidopteran group endemic to the Oriental region, comprising few species in 2 genera, Cyclidia Guenée, 1857 and Mimozethes Warren, 1901. The larvae of the entire subfamily are specialists on Alangium (Cornaceae) and exhibit conspicuous colouration that possibly functions as a warning signal. Historically this subfamily was inconsistently treated as either a separate family from Drepanidae, or lumped as a subordination of Drepanidae with Thyatirinae and Hypsidia, a bizarre genus endemic to Australia. The presence of a paired tympanal organ in the 2nd abdominal sternite is the only putative synapomorphic character supporting the monophyly of Drepanidae. In the present study, we investigated the phylogenetic relationships of Cyclidiinae based on morphological characters obtained from all the cyclidine species and using representatives of Drepaninae, Thyatirinae, Doidae, Mimallonoidea and Cimelioidea as the outgroup taxa. Our analysis shows that: (1) the genera Cyclidia and Mimozethes constitute a monophyletic clade, which is the sistergroup of (Drepaninae + Thyatirinae); (2) this phylogenetic pattern suggests an evolutionary trend that the territorial sound-production behaviour of cryptic solitary larvae of Drepaninae and Thyatirinae evolved from no sound production of aposematic gregarious larvae; and (3) the monophyly of Drepanoidea, Drepanidae and Cyclidiinae are supported in this study.

Keywords: Cyclidiinae, Drepanoidea, larval gregariousness, aposematism, brush organ

DNA Barcoding at the NCB Naturalis

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The Netherlands Centre for Biodiversity Naturalis started a DNA Barcoding pipe-line. The aim is to produce 12.000 DNA Barcodes annually, covering the entire biodiversity. This will include several thousand DNA barcodes of Lepidoptera, under the LepBOL initiative. The first groups of focus include Pterophoridae, Momphidae and Nepticulidae and other leaf-mining Lepidoptera. All of this material has been identified by specialists and will be photographed. The data standards we hold are compliant with the IBOL requirements, and all data will be added to BOLD. Recently collected expedition material that has only been tentatively identified will also be barcoded. Specialists will then be invited to examine this material, also using the barcoding knowledge. The barcoding program is open to possibilities for new projects and international collaboration.

The Wind of Change-Butterfly diversity and Global Change

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During the last century, invertebrate diversity has rapidly declined throughout many parts of Europe (e.g. Warren 1993). Various reasons for this decrease have been discussed including man-made factors like habitat destruction and fragmentation or anthropogenic climate change. These effects are thought to alter distributions and abundances of animals on a global as well as on a local scale. Butterflies belong to the best studied groups of invertebrates. Researchers largely agree that they are useful indicators of habitat quality as many of them have certain habitat requirements and quickly respond to alterations (Warren et al. 2001). Long-term data now allow comparisons of species compositions within a remarkable time frame.

We have evaluated changes in butterfly abundance and species composition of eight fallow grounds in south-western Germany since 1973 with Pollard’s transect technique (Pollard & Yates 1993). We observed a severe decline in the number of individuals and the species richness as well as a striking change in community composition. This trend was even more pronounced if only specialists and Red Data Book species were considered.

Our study suggests that the observed trends might derive from a combination of anthropogenic landscape changes and global warming. In course of structural land-use changes during the last century, landscape heterogeneity declined, affecting especially species with poor dispersal abilities, high larval food plant specialisation and specific habitat requirements. Increasing temperatures and stronger temperature variability due to global warming caused a remarkable decrease of hydrophilic and cold-adapted species in the region of Trier. On the other hand temperature increases have favoured the emergence of thermophilic taxa and the range expansion of Mediterranean species northward. However, the negative responses to the dramatic habitat losses for many species might have outweighed the positive effects of global warming (Warren et al. 2001).

An Ongoing Project: Phylogeny and Taxonomy of Hypertrophinae (Gelechioidea: Elachistidae s.l.)

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The taxonomy and position of subfamily Hypertrophinae has been debated for many decades. Nevertheless, several recent studies have reached the same conclusion that Hypertrophinae belongs to the enlarged concept of Elachistidae (Gelechioidea). No phylogeny has ever been published from the subfamily and the latest treatment is from 1950`s.

Hypertrophinae includes ca. 50 described, mainly Australian species from 11 genera, but many undescribed species are known. Their larvae feed on green leaves of trees mainly belonging to Eucalyptus. The adults are brightly colored and the pupae are erect without a cocoon.

My PhD project aims are (1) to reconstruct a phylogeny of Hypertrophinae based on combined data including morphological and molecular characters and (2) to make a revision of at least one hypertrophine genus. DNA barcoding of hypertrophine species will also be conducted.

List of members and collaborators of the project: Lauri KAILA University of Helsinki, Finland; Marko MUTANEN, University of Oulu, Finland

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Deep sympatric mtDNA divergence in the autumnal moth (Epirrita autumnata, Lepidoptera, Geometridae)

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Deep intraspecific divergence in mtDNA may reflect cryptic species or formerly distinct lineages in the process of remerging. Preliminary results from DNA-barcoding of Scandinavian butterflies and moths show high intraspecific sequence differences in the Autumnal moth, Epirrita autumnata. In this study, Epirrita-samples from different locations in Norway, and some samples from Finland and Scotland were investigated to resolve the discrepancy found between mtDNA divergence and present division to species. Sequencing of the cytochrome c oxidase I unit (COI) -, the nuclear ribosomal internal transcribed spacer 2 (ITS2) - and the Wingless (wg) region was performed. We found five COI sub clades within the E. autumnata complex, without any obvious geographical pattern. Sequencing of the nuclear markers showed little variation, and gives no indications of E. autumnata comprising more than one species. As endoparasitic symbionts like Wolbachia are common in arthropods, all samples were sequenced with primers for Wolbachia outer surface gene (wsp). 12 % of the samples examined in this study tested positive for Wolbachia, with two different strains associated with two of the mtDNA haplotypes found within E. autumnata which suggests indirect selection/selective sweeps on haplotypes. These findings indicate that E. autumnata does not consist of several cryptic species and that its high mtDNA variation is maintained by selective sweeps from multiple Wolbachia infections.

How many genera of Nygmiini (Erebidae: Lymantriinae) do we need? A phylogenetic analysis of Nygmiini based on morphological characters and global taxon-sampling

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The Nygmiini is a tussock moth tribe which is predominantly distributed in most regions of the Old World. It was established in order to accommodate several genera that were previously associated with the polyphyletic genus Euproctis Hübner, 1819, which was erected upon the western European Euproctis chrysorrhoea (Linnaeus, 1758)(=Phalaena chrysorrhoea) and has included 682 valid specific names since the early 19th century. Some of the caterpillars of Nygmiini are fairly polyphagous on various woody plant families, and thus many species are considered as pests with significant importance. They are also known for having importance in public health due to the strong allergic reaction caused by the urticating setae. Although the tribe Nygmiini as well as the "core genus" Euproctis has such importance in various aspects, it's monophyletic status and phylogenetic relationships have never been tested using modern phylogenetic methods. We therefore sampled 175 lymantriid species representing most of the potential members of Nygmiini plus one arctiid species as the functional outgroup taxon to reconstruct the phylogeny of this tribe based on morphological characters from all development stages. The results suggest that the tribe Orgyiini forms a monophyletic clade with the Nygmiini, while neither the Nygmiini sensu Holloway nor the genus Euproctis sensu auctorum is monophyletic, and thus the taxonomic boundary of the tribe should be redefined in accordance to the hypothesis proposed by the present study. On the other hand, larval characters become the major source of the synapomorphies of the Nygmiini. The adult wing patterns which are used to taxonomic identification, however, are highly convergent among genera possibly due to mimicry and thus these characters are not supposed to be informative in systematic research.

Keywords: Noctuoidea, Lymantriinae, Nygmiini, phylogenetics, larval morphology

COI sequence data reveals a remarkable case of intraspecific variation and asymmetry in male genitalia of Syntomini (Erebidae: Arctiinae)

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The Synotomini represents a small and unattended group among the arctiine tribes. This tribe is characteristic with the reduction of wing venation of both fore- and hindwings as well as the putative and doubtful wasp-mimicking morphology. Previously the genitalic asymmetry and variability of this group were already addressed by several authors, but the biological implication of this phenomenon was not studied using modern methods. In the present study, we investigated the phylogenetic relationships and genetic divergence of Amata wilemani Rothschild, 1914, a nocturnal species endemic to the subalpine region of Taiwan, and its congeners in Taiwan and the surrounding areas. This study is aimed to address if the highly variable and asymmetric male genitalia, which is fairly unusual among the lepidopteran insects, suggests a case of morphological plasticity in reproductive organ, which is often considered to be responsible for mechanic isolating mechanism, or a case of misidentifying cryptic species due to undetectable and unjustifiable characters. We used sequence data of COI gene to investigate this question and found that all the samples of A. wilemani, no matter how significant the genitalia and wing pattern were, constituted to form a monophyletic species. The result suggests that the morphological plasticity of the species is unlikely to be linked to geographical or elevational differentiation, but possibly due to sexual selection relevant to copulatory behavior. We also wish to address the importance of using both molecular and morphological evidence from multiple samples when describing a new species to avoid over-splitting of species that are actually polymorphic in wing pattern and genitalia.

Keywords: morphological plasticity, cryptic species, species concept, Barcode of Life

Skipper butterflies (Lepidoptera: Hesperiidae) of the Caldera de Lubá (Bioko Island, Equatorial Guinea)

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The Hesperioidea (Skipper butterflies) belong to a group that has not been deeply researched, specially those afrotropical species (Douglass, 2003), its organization in subfamilies and tribes is currently under revision (Warren et. al. 2008, 2009). In the present work, the species shown are those found in the Caldera de Lubá (only sample of the monsoon forests in Equatorial Guinea), being the first records of these families in the already mentioned south area of Bioko island (Martín and Cobos, 2010). The information given in this paper contributes to the knowledge of the geographical diversity and distribution of skipper butterflies.

The first records about the flora and fauna diversity of the Caldera, were obtained during the scientific expeditions carried out by the Polytechnic University of Madrid in the years 2005 and 2007 (Prieto and Martín, 2008; Martín and Cobos, 2010, 2011). Both expeditions were done with correspondence to the Spanish Investigation, Development and Innovation (I+d+i) National Plan, CGL2005-23762-E and CGL2006-27110-E/BOS

Of a total of 546 Lepidoptera collected on both expeditions, 7 correspond to skipper. Out of seven species belonging to this family and referred for the first time to the interior of the Caldera de Lubá, three of them mean the first quotes in the Island of Bioko: Coeliades forestan forestan (Coeliadinae), Semalea pulvina and Ceratrichia phocion camerona (Hesperiinae). Another one was registered in Equatorial Guinea for the first time: Celaenorrhinus plagiatus (Pyrginae). Finally, about Celaenorrhinus galenus (Pyrginae) no records within the previous 100 years. The other two skippers founded were Pyrrhochalcia iphis (Coeliadinae) and Ceratrichia clara medea (Hesperiinae).

Keywords: Hesperiidae, Skipper, Bioko Island, Caldera de Lubá.

Invasive Lepidopterans in France

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The Plant Health Laboratory (Laboratoire de la Santé des Végétaux) looking after plants' health is a national reference laboratory and the located in Montpellier, specialised in entomology and the study of invasive plants.
In France, bio monitoring is implemented by the NPPO throughout the country using monitoring guidelines which allows early detection of organisms harmful to plants and management measures to eradicate or to maintain the population involved under an acceptable level.

Land monitoring is the backbone of the European plant passport's process, a system put in place throughout the European Union to guarantee the health of plants and plant products circulated.

The cartographic study of some invasive Lepidopteran species observed in France, shows here a summary of analyses carried out at the Plant Health Laboratory on samples sent by the NPPO as recommended by the monitoring program.
The aim of this study is to evaluate our knowledge regarding the dispersion in our country of the invasive species of Lepidopteran.

The following species had been studied :

Bucculatrix chrysanthemalla (Rebel, 1896), *Bucculatrix chrysanthemalla* (Rebel, 1896), *Cameraria ohridella* Deschka & Dimic 1986, *Diaphania perspectalis* (Walker, 1859), *Opogona sacchari* (Bojer, 1856), *Paysandisia archon* (Busmeister, 1880), *Spodoptera littoralis* (Boisduval, 1833), *Tuta absoluta* (Meyrick, 1917).

For each of these species, a map of France is displayed, along with a picture of the habitus, the genitalia and the last larval instar.
The geographical origin of the moth is represented by a map.

The hourly distribution of moths caught by light-trap in a tipical mediterranean ecosystem (the dehesa): a posibility to detect the climate change

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In Sylviculture, dehesa is a wooded hill with low tree density and well developed herbaceous layer whose primary use is livestock (Forest Dictionary, 2005).

During 2010 an entomological inventory was developed in Quintos de Mora, (Toledo, Spain), a dehesa ecosystem. One of the studied groups was the nocturnal Lepidoptera by using a light trap.

Light trapping is a method to collecting insect which manifest positive phototaxis which had an important development over the past decades (Nowinszky, 2008).

The variation of the catches with light-trap during the course of a night has been research for years. Williams (1935) used a fractionating light trap to examine flight activity and how it changes during the night. The hourly distribution of catches could be an important method to measure the possible effect of the climate change.

The majority of entomologists do not record the arrival of insects. They make only a qualitative or quantitative analysis of the catches, missing out on valuable information.

The hourly results obtained from May to October 2010, show the distribution of catches ordered by families for the eight fractions of time in which is divided the light trap. These results could be a first step to compare this distribution with other ecosystems, changes in land use in the dehesa and a possible indicator of global warming disorders.

Keywords: light-trap, hourly, dehesa.

Slowing down the loss of biodiversity of moths in vineyards

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Recently biodiversity research in the agrarian landscape, which occupies about 60% of the area here, has been very topical in the Czech Republic. In order to slow down the decline of biodiversity in nature-like areas of small size, for rare populations of some species it is necessary to seek alternative habitats in the agrarian landscape allowing communication between the island populations which may be doomed to extinction. Research on biodiversity of moths was conducted in South Moravia (Czech Republic) in 2010. Four experimental sites were at two locations near the protected landscape area of Pálava, three of them included methodically different managements in vineyards (conventional, integrated and organic) and the comparative closest forest-steppe habitat. Biodiversity of moths was studied using portable light traps with an 8 W ultraviolet lamp. A spectrum of moths called Macrolepidoptera was studied. The results demonstrate that biodiversity in vineyards is increasing with vineyards ecologization even at relatively large distance from natural habitats (up to several kilometers). The broad diversity and equitability indicators (Simpson's and Shannon-Wiener diversity index) show that organic vineyards have more distributed equitability and species balance is lower. The cluster analysis (Euclidean graph) indicates that conventional vineyard forms a cluster of similarities of these vineyards. It is therefore clear that the conventional vineyards are the most similar to each other by poor species spectrum and a low number of specimens. The most interesting findings resulted from Spearman's correlation coefficient. The most demonstrable (probability of 99%) is the influence of vegetation succession in alleyways on the number of specimens in the vineyards. Highly demonstrable (95%) are also influences of vegetation succession (on the number of species, number of specimens, Simpson's equitability index and Shannon's diversity index), duration of pheromones application in order to confuse male pests (the Simpson's diversity index and Shannon's equitability index), vineyard age on abundance of specimens and the use of insecticides on the number of species and specimens.

Preliminary results of the butterfly mapping in the Őrség Special Protection Area (Western Hungary) (Papilioniodea and Hesperioidea)

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As part of the EU co-financed Interreg Project „Harmóniában a Tájjal” (In Harmony with Landscape) we started landscape scale butterfly mapping of the Őrség SPA in Western Hungary in 2010. The SPA covers approximately 46 000 hectares including the entire Őrség National Park. The scale of mapping was the 2,5x2,5 km UTM grid network (114 grid covers the Őrség SPA); we basically recorded all butterfly species from each grid during 3 sampling periods. Besides grid-mapping, we selected butterfly species of regional, national and community conservation concern. Each butterfly record of the selected species received geo-referenced accurate data (dot-mapping), allowing better implementation of management and protection plans of conservation authorities in the future. We chose non-quantitative methods for mapping, because it proved impossible to implement regular recording in each survey plot, especially for species with restricted distribution or special habitats. The majority of butterflies were recorded by hand-held netting or field observations, while search for early stages for Alcon Blue – *Maculinea alcon* (eggs on *Gentiana pneumonanthe*) and Marsh Fritillary – *Euphydryas aurinia* (larval web) revealed important additional information. In 2010 we collected over 12 000 grid records and 3 000 dot records of 101 butterfly species. During the mapping we recorded 3 species new to the Őrség (*Psudophilotes vicrama*, *Everes alcetas* and *Lopinga achine*) and we documented important populations of threatened species such as *Lycaena hippothoe*, *Maculinea arion*, *Euphydryas aurinia*, *E. maturna* and *Erebia aethiops*.

Butterflies of Croatia: status, threats and conservation

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The checklist of butterflies of Croatia is a result of our recent attempts to document the butterfly diversity and create a national database. The overall picture showed a total of 194 species. The history of studying butterflies in Croatia begun in 19th century and the level of knowledge has raised considerably from that time. Still, information on distribution and trend of species are poor because the majority of studies are focused on fauna on a small region. Problems of categorizing a poorly-documented fauna will be pointed. Some examples of recent changes in range and species diversity will be linked with the causes of change: habitat decline, loss and fragmentation. Recently we assessed the status of butterfly fauna of Croatia. In the absence of substantial historical information on abundance changes, we used the distribution change criteria of IUCN to create a list of threatened butterflies of Croatia and the Red book of threatened butterflies of Croatia which is under preparation. About 25% of Croatia's butterfly fauna is of conservation concern including species of national and European concern. All threatened species are legally protected. The main causes for the declines are thought to be changes in rural land use, especially land abandonment or agricultural intensification.

Correlation between ovipositor length and habitat type of Paracymoriza, an "amphibious" genus of Acentropinae (Pyraloidea: Crambidae)

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The genus Paracymoriza Warren, 1890, is a moderate-sized acentropine genus comprising about 30 species ranging throughout southeast and east Asia. Historically the genus was often confused with many unrelated crambid genera due to the superficial resemblance in wing maculation, which is termed the “nymphuliform wing pattern”. The genus is currently divided into 8 species-groups, and 4 of them are known having completely aquatic larvae feedings feed on aquatic vascular plants or mosses under water, while the others having terrestrial habit feed on terrestrial mosses. We were interested if any morphological trait was phylogenetically informative and linked to larval habitat. We first reconstructed a phylogenetic relationship of Paracymoriza using morphological characters obtained from all the known Paracymoriza species plus 33 outgroup species representing 25 genera of Acentropinae and Schoenobiinae. We then used the phylogenetic hypothesis to investigate the correlation between ovipositor length and habitat type. The results show that Paracymoriza is a monophyletic genus and composed of two clades: the terrestrial and aquatic ones. The ovipositor length of terrestrial Paracymoriza is relatively longer than that of aquatic one. This is correlated with the different egg-laying behaviours; ovipositor of the terrestrial clade needs penetrating the moss layer, while that of aquatic clade only needs deposit eggs on leaf surface.

Keywords: aquatic insects, phylogenetics, adaptive evolution, egg-laying preference

Would female oviposition preference affect larval anti-predator defenses? A case study using a polyphagous aquatic lepidopteran species

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Host plant selection could be determined by two stages, adult oviposition preference and larval acceptance. The factors determining host selection include olfactory (e.g. chemical extracts and secondary metabolites), visual (e.g. leaf shape and plant growing form), tactile cues (e.g. texture and toughness) and other ecological criteria (e.g. prior feeding experience, competition and predation pressure). For those species whose neonates are considered less mobile, the ability of adult female to accurately locate and choose oviposition site is considered to affect the initial survival and development rate of newly hatched larvae. Here we reported a case based on a polyphagous moth, Parapoynx crisonalis, whose purely aquatic caterpillars build portable case with host plant leaves in order to reduce predation risk. It is expected that females lay more eggs on the plant which is suitable for larval development and case making instead of investing her eggs by chance. We firstly analyzed the growing types of aquatic plants utilized by P. crisonalis through literature review and field observations. Second, we carried out a choice experiment to assess whether adult female oviposition is biased on different host plants. Meanwhile, survival rate, development time of each instar, and average shelter building time of 10 larvae on each host species were recorded to evaluate whether adult's host plant choice corresponds with larval feeding and case-making performances. Our preliminary results show that although P. crisonalis were recorded feeding on a wide variety of aquatic plants, they were actually confined to only some floating plant species possibly due to the constraint of its stereotypical building behavior. In addition, differences in thickness and shapes of leaves would affect shelter building efficiency, which is remarkably important for larval survival.

Keywords: host selection, anti-predation, polyphagy, herbivore, Lepidoptera

DNA barcoding of the leaf-mining moth subgenus Ectoedemia s. str. (Lepidoptera: Nepticulidae): are cryptic species recognised?

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We sequenced 665bp of the Cytochrome C Oxidase I (COI) barcoding marker for 258 specimens belonging to the leaf-mining subgenus Ectoedemia (Ectoedemia). Next to that we tested a 482bp section of the nuclear Elongation Factor 1-alpha (EF1-alpha) for 240 specimens. The dataset includes 46 out of 48 European Ectoedemia s. str. species and several species from Africa, North America and Asia. Both COI and EF1-alpha proved reliable as an alternative to conventional species identification for the majority of species and the combination can aid in species validation. Cryptic species in the E. rubivora complex could only be distinguished by EF1-alpha. In the common species Ectoedemia albifasciella we discovered two haplotypes of 2.17% divergence in COI in sympatric populations. These haplotypes are not found with EF1-alpha, and not supported by other characters.

How to determine the boundary of a mimicry complex when there are multiple models, sexual dimorphism and cross-oceanic distributions?

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Defensive mimicry refers to an interspecific relationship that a profitable or less profitable prey, viz. mimic, benefits from possessing a warning signal displayed by an unprofitable prey, viz. model, when encountering the same predator. Conventionally determination of a mimicry complex relies on three scenarios, geographical sympatry and phenological synchrony between model and mimic species, and accurate matching between shared warning signals. The best examples are the three well-known cases based on Nearctic (Limenitis vs. Danaus and Battus), Neotropical (Heliconius spp.), and Ethiopian (Papilio dardanus vs various models) butterflies. However, the "taxonomic boundaries" of many more putative mimicry relationships involving polymorphism, sexual dimorphism, intermediate forms, allopatric distribution, and multiple models with incomparable unprofitabilities are usually assumed by subjective assignment. In the present study, we reassessed the wing pattern matching and distributions of several lepidopteran groups resembling selected Euploea species in South-East Asia. We extracted collection information of around 2,600 specimens of the relevant species from several museum collections. These data were then plotted onto a South-East Asian map generated using Google Map service and analyzed by the aid of GIS techniques. The results show that two geographical regions, e.g. northern India and Sundaland (Sumatra, Java, and Boneo) harbor the highest richness of the species sharing the same wing patterns. Meanwhile, we found that switches of wing pattern among co-mimicking groups with sexual dimorphism and polymorphism were remarkably common in these two regions. This result suggests that the "Euploea dominant mimicry" in South-East Asia does not only provide an opportunity for investigation of multi-model mimicry, but also a window that sheds light on exploring the origin of sexually dimorphic mimicry occurring in these regions.

Keywords: mimicry, warning signal, Euploea, spatial distribution

The preliminary phylogenetic study of the Papilio memnon complex and the evolutionary origin of mimetic characters

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Papilio memnon is a swallowtail butterfly widely distributed in south-east Asia. The females are highly polymorphic and many of them were considered as mimics of Troidini swallowtail butterflies. Previous studies reported that in total seventeen female forms are inheritable and the variations are controlled by what appears to be a series of at least eleven autosomal alleles at three loci, sex-controlled to the female in effect. The polymorphism restricted to the female of P. memnon has been regarded as classical textbook example of Batesian mimicry. However, having examined a long series of the museum material and observed field populations from different geographical areas, we strongly doubt if some of the putative mimicry of P. memnon really exist. Meanwhile, most females forms of P. memnon do not seem to involve in any mimicry ring, and this implies a peculiar and very unique case of female-limited polymorphism which is not necessarily correlated with mimicry. In order to investigate these questions, we first need to reconstruct a phylogeny to infer the evolutionary trend of putative mimetic characters, and the origin of accurate or imperfect mimicry within the species complex. In the present study, we reconstructed the phylogeny using sequence data of COI-COII and EF1a genes from 6 subspecies of P. memnon, 6 species of the memnon complex and 5 other species of the subgenus Melelaides as outgroups. The result shows that: (1) Papilio memnon seems to be a monophyletic species, while there is significant differentiation between the subspecies of Himalaya-China-Taiwan-Japan and those of Sundaland; (2) no directional evolutionary trend from imperfect to accurate mimicry is observed; and (3) the red basal patch on forewing underside represents a synapomorphic character of P. memnon + P. thaiwanus groups. The final product of this study will be used to address if the “mimetic locus(loci)” of P. memnon is homologous with that of P. polytes and P. dardanus, or an unexplored locus(loci) which has promoted the enormous diversity of female polymorphism.

Keywords: imperfect mimicry, sexual dimorphism, polymorphism

Phylogenetic relationships of Agaristinae (Lepidoptera: Noctuidae) based on adult morphology, with special reference to the phylogeography of "sound-producing clades" and the evolution of diurnality

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The Agaristinae represents a large subfamily of Noctuidae, consisting of 127 genera and about 500 species ranging throughout all the major continents except Antarctica and Greenland. The adults of this subfamily could be diurnal, crepuscular, or nocturnal, and are often characteristic with bright and contrasted colouration that is considered relevant to aposematism or mimicry, which are unusual in Noctuidae. The larvae of Agaristinae are also bright-coloured and feed on several plant families that contain alkaloid secondary compounds. The male of several genera possess an exaggerated forewing tymbal structure which is used for sound production, and distribution of these sound-producing genera seems to imply a Gondawanan origin. In contrast with its high diversity, the studies on Agaristinae systematics and biology are fairly rare compared with other noctuid groups due to the rarity of them both in the field and museum collections. In the present study, we present the first phylogenetic study of Agaristinae to address several questions: (1) is Agaristinae a monophyletic group? (2) is the classification system proposed by Kiriakoff (1976) approved by modern method? (3) if the taxa having swollen forewing costal margin are closely related and suggest any biogeographical significance? We first reconstructed a phylogeny using 69 adult characters obtained from 85 agaristine species representing 73 genera plus Oncocnemis confusa (Oncocnemidinae) and Condica illecta (Condicinae) as outgroups. The phylogenetic pattern shows that Agaristinae of the current concept is monophyletic, but adult morphology may have little help in resolving the relationship because both the male and female genitalia are relatively conservative across genera. The "chorotaxa" system proposed by Kiriakoff, therefore, cannot be rejected due to the poor resolution of the phylogeny. Meanwhile, the taxa having protruded forewing do not constitute a monophyletic clade, so this character might have evolved independently in different continents.

Keywords: diurnality, aposematism, Noctuidae, phylogenetics, sound production

Molecular phylogenetics of Erebidae (Lepidoptera, Noctuoidea)

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Abstract. As a step toward understanding the higher-level phylogeny and evolutionary affinities of quadrifid noctuoid moths, we have undertaken the first large-scale molecular phylogenetic analysis of the moth family Erebidae, including almost all subfamilies, as well as most tribes and subtribes. DNA sequence data for one mitochondrial gene (COI) and seven nuclear genes (EF-1α, wingless, RpS5, IDH, MDH, GAPDH, CAD) were analyzed for a total of 237 taxa, principally type genera of higher taxa. Data matrices (6407 bp total) were analyzed by parsimony with equal weighting and model-based evolutionary methods (Maximum Likelihood), which revealed a well-resolved skeleton phylogenetic hypothesis with 18 major lineages, which we treat here as subfamilies of Erebidae. We thus present a new phylogeny for Erebidae consisting of 18 moderate to strongly supported subfamilies: Scoliopteryginae, Rivulinae, Anobinae, Hypeninae, Lymantriinae, Pangraptinae, Herminiinae, Aganainae, Arctiinae, Calpinae, Hypocalinae, Eulepidotinae, Toxocampinae, Tinoliinae, Scolecocampinae, Hypenodinae, Boletobiinae and Erebinae. Where possible, each monophyletic lineage is diagnosed by autapomorphic morphological character states, and within each subfamily, monophyletic tribes and subtribes can be circumscribed, most of which can also be diagnosed by morphological apomorphies. All additional taxa sampled fell within one of the four previously recognized quadrifid families, mostly into Erebidae, which was now found to include two unusual monobasic taxa from New Guinea: Cocytiinae (now in Erebidae: Erebinae) and Eucocytiinae (now in Noctuidae: Pantheinae).

Key words: Lepidoptera, Noctuoidea, Erebidae, Molecular phylogeny, Mitochondrial and nuclear genes

Drastic loss of Large Blues' habitat (*Phengaris teleius* and *P. nausithous*) in Northeast Slovenia

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Up until the end of the last decade, very little was known about distribution of *Phengaris teleius* and *P. nausithous* in the northeastern Slovenia. In last decade, two centers of their distribution have been recognized: the rural hilly countryside of Slovenske gorice and Goričko. Goričko and the neighboring part of Hungary represent one of the largest contiguous distribution of both *Phengaris* species in this part of Europe. To get further insight into the dynamics of the habitat availability and occupancy in this region a survey spanning from 2003 to 2010 with irregular intervals was carried out.

During the extensive field work in 2003 and 2004 in the central region of Slovenske gorice (240 km^2) 124 patches (altogether 84.3 hectares) of suitable habitat for both *Phengaris* species (with the larval host plant *Sanguisorba officinalis*) were observed. In 2010, the survey was repeated to check for the changes in the distribution of both species. Surprisingly, in 2010, on 26 % (23.5 hectares) of the habitat recorded as suitable in 2003, no larval host plant was found. The main reason for this decline is the intensification of the agricultural use. In 2003 *P. teleius* was present on 69 % of all patches, in 2010 only 16 % of the suitable patches were occupied. In 2003 *P. nausithous* was present on 51 % of all patches, and in 2010 44 % of patches were occupied. Evidently, the decline of the Large Blues in this region is much faster than the habitat loss, possibly due to low population sizes and isolation of remote habitat patches.

Goričko has a formal status of a landscape park and most of it was also designated as Natura 2000 site in 2004. It is a large rural countryside (460 km^2), where almost half of its surface is covered by a forest and one fourth is fields. Only 15 % of the area is meadows. In 2002 and 2003: 4678 hectares of *Lowland hay meadows* and 146 hectares of *Molinia meadows on calcareous, peaty or clayey-silt-laden soils* were mapped. Usually, these habitat types are indicative for the presence of *S. officinalis*. In 2006, one third of the known sites with potentially suitable habitat were visited and checked for the presence of both *Phengaris* species. Again, more than 8 % of the previously suitable habitat was permanently lost by agriculture use (converted to fields). From that it is clearly evident that Slovenian nature conservation policy is still not playing the same role in the development of modern society as other policies are, although appropriate legislation has been adopted.

Comparison of lepidoptera diversity of different ecosystems in the iberic peninsula

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The first step to approach to a natural system is the inventory. The use of the information obtained from this inventory continues with the identification and the data analysis. Usually these analyses are independent among ecosystems or environments.

The comparison among ecosystems, not only between different species but also among phenology and statistic balances, shows notable differences and greats similarities.

Two butterflies' inventories were conducted by the team of the Zoology Department of the University in the Atlantic Island National Park (Galicia) and in Quintos de Mora (Toledo). The contrast between those two different environments is highlighted by comparing both inventories.

In this case, the main reasons to choose these two inventories were the differences between the two well-known ecosystems, the sampling time of the inventories (three years in both cases) and knowledge of sampling effort.

First of all, the total amount of identified species was not significant –around 40 species in the Atlantic Islands National Park and more than 50 in Quintos de Mora. Doing an initial comparison, 24 species from Quintos de Mora were not present in the National Park, while only 15 species from the Atlantic Islands were not found in Quintos de Mora.

Keywords: differences, Atlantic Islands, Quintos de Mora, Spain.

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