

Biodiversity Hotspots Evolution & Conservation

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Thanks...

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Welcome to Luxembourg

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

The evolution of diversity is not homogeneously distributed. Therefore, many scientists studied the reasons, which influence the evolution of ecosystems, species or genetic diversity. Many of these studies were performed on areas with exceptionally high biodiversity, so called “biodiversity hotspots”, for example on islands, in mountains ranges, in the tropics, or in regions acting as refugia during glacial periods. We selected these groups as headlines for our topic sections. Further, we added a section on aquatic ecosystems (freshwater and sea) and a closing section dealing with conservation priorities and the problems of an adequate protection of such areas with exceptionally high biodiversity.

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

Jan Christian Habel and Petra Dieker

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Programme Overview

Thursday, March 26, 2009

Time	Topic	Referent
19:00	Address of welcome	G. Bechet (MNHN) R. Bausch (FNR)
19.15– 20.00	Global biodiversity conservation: the critical role of hotspots	R. A. Mittermeier
20.00	Welcome party	

Friday, March 27, 2009

09:00	I S L A N D S	Diversity and diversification in the islands of the Macaronesian region	B. Emerson
09:30		Sulawesi, Island between the Realms: Biodiversity Research in Central Indonesia	A. Koch
09:50		Modelling the biodiversity of moths in the 'Heart of Borneo'	J. Beck
10:10		Amphibian hotspot Madagascar: species extinction risk through the chytrid fungus	S. Lötters
10:30		Coffee break	
11:00	T R O P I C S	Tropical forest biodiversity: threats and solutions	N. Stork
11:30		Responses of vertebrates to forest fragmentation in the Neotropics	D. Vetter, M. M. Hansbauer, Z. Végyvári, I. Storch
11:50		Herbivore hotspots in the Mara region of Kenya in relation to land use and vegetation	N. Bhola
12:10		Floristic diversity of wild coffee forests in SW Ethiopia and impli- cations for conservation	C. Schmitt

12:30		Lunch	
14:30	M O U N T A I N S	Global change effects on alpine plant diversity	G. Grabherr
15:00		Centres of endemism of Noctuidae in the Palearctic high mountains	Z. Varga
15:20		Multiscale evolution of species range under changing climate	C. Parisod
15:40		The Carpathian refugia in differentiation and speciation of aquatic Diptera: a case study	L. Ujvarosi, M. Balint, N. Meszaros
16:00		Coffee break	
16:30		Patterns of biodiversity in a Mediterranean landscape: Effects of land use and modeled effects of climate change	T. Dayan
17:00– 19:00		Poster session	

Saturday, March 28, 2009

09:00	A Q U I T A N E	New insights on explosive speciation and adaptive radiation of African cichlid fishes	C. Sturmbauer
09:30		Polychaeta associated with cold-water coral reefs in the Northeast Atlantic and the Mediterranean	D. Fiege, R. Barnich
09:50		Microendemism and environmental variability in the Malagasy biodiversity hotspot	B. Isambert
10:10		Phylogeography and conservation genetics of the Iberian three-spined stickleback (<i>Gasterosteus aculeatus</i>)	M. Vila, M. Hermida, C. Fernández, S. Perea, I. Doadrio, R. Amaro, E. San Miguel

10:30		Coffee break	
11:00		Mediterranean peninsulas – the evolution of hotspots	G. Hewitt
11:30	A	Species and genetic diversity in the Mediterranean: do the two levels of biodiversity correlate?	C. Conord
11:50	U	European hotspots as evidenced by the Palearctic distribution of songbirds	R. Sluys
12:10		Expansion of passerine bird taxa in the northern Palearctic in the holocene	C. S. Roselaar
12:30		Lunch	
14:30		Importance of biodiversity hotspot for species conservation: some examples in Europe and South East Asia	J. Michaux
15:00	CONSERVATION	Impacts of Biofuels on southeast Asian biodiversity hotspots	L. P. Koh
15:20		Biodiversity Action Plans in Portugal's Agroforestry Business	N. G. Oliveira
15:40		Using phylogenetic diversity to reveal conservation priorities	M. Monzel
16:00		Coffee break	
16:30		Deep-Sea Biodiversity Research	A. Brandt
17:30		Parting words	J. C. Habel, P. Dieker

**Oral Presentations
Abstracts**

Sulawesi, Island between the Realms: Biodiversity Research in Central Indonesia

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Keywords: Wallacea, speciation, endemism, reptiles, fish, butterflies

The majority of earth's biodiversity occurs in the tropics. Indonesia with its thousands of islands is one of the megadiversity countries of the world bridging Asia, Australia and the Malay Archipelago. Sulawesi (formerly known as Celebes) lies right in the centre of this vast archipelago. Due to its exceptional topographic position between these distinct faunal regions, Sulawesi together with the Lesser Sunda Islands in the south, and the Moluccas in the east represents a zoogeographic transitional region called Wallacea. Thus, Sulawesi's fauna comprises an assemblage of typical Oriental and Papu-Australian species. In addition, and because of long periods of isolation in its geological history Sulawesi is characterized by a high degree of endemism (e.g., >40% in butterflies) embedded in a complex biogeographic setting. Despite the investigations of numerous famous scientists of the 19th and 20th century such as P. Bleeker (fish, amphibians, reptiles), G. A. Boulenger (fish, amphibians, reptiles), L. Martin (butterflies), G. G. Musser (rodents), F. and P. Sarasin (fish, invertebrates), E. Stresemann (birds), and M. Weber (fish), recent fieldwork on Sulawesi reveals several new records for that island as well as many more undescribed species of fish, amphibians, reptiles, and butterflies. Thus, the peculiar fauna of Sulawesi is still far from being completely inventoried and further systematic investigations are urgently required to fill these gaps

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Modelling the biodiversity of moths in the “Heart of Borneo”

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Keywords: predictive modelling, Lepidoptera, conservation, GIS

We used a large data compilation of local diversity samples of geometrid moths from Borneo, fitted a statistical model explaining substantial data variance with just a few environmental parameters, and extrapolated this model to remote sensing grids of these environmental variables. We tested the predictive performance our model by an external validation procedure. As an output, we retrieved detailed, Borneo-wide predictive maps of various aspects of biodiversity, such as overall local diversity, diversity of Borneo-endemics, and uniqueness of local assemblages. With this approach, we (a) show how spatially scattered data on invertebrates can be treated to allow broader inclusion into macroecological as well as conservation-related research, and (b) we specifically provide data that may aid the implementation of WWF’s “Heart of Borneo” project, a plan for a tri-national, large reserve aiming to protect the remaining natural forests of the region.

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Amphibian hotspot Madagascar: species extinction risk through the chytrid fungus

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Keywords: Amphibia, chytrid fungus, Climate Envelope Model, extinction, Madagascar, risk assessment

Many amphibian species, at the global scale, are dramatically threatened with extinction. A major reason is chytridiomycosis, an emerging infectious disease elicited by the amphibian chytrid fungus, *Batrachochytrium dendrobatidis* (Bd). This pathogen is known to cause rapid drastic decline in naïve species, as observed in different regions of the world. Madagascar harbours remarkable amphibian species richness with more than 99 % of the at least 400 known species endemic to this island. Bd has not yet been detected in this amphibian hotspot and is apparently absent from it. The introduction of Bd in Madagascar is possible (e.g. via the international amphibian trade) and its arrival there is predicted to have a catastrophic effect. In order to assess the level of threat that the introduction of Bd poses to Madagascar's amphibian diversity, we ran a Bd risk assessment using a maximum entropy Climate Envelope Model. Our model shows that there is a high risk of Bd spreading post-introduction over a major portion of Madagascar. Areas most suitable for Bd largely overlap with those of highest amphibian species richness. As no meaningful in situ conservation action is available for the emergence of Bd, ex situ short-term conservation breeding (as devised in the IUCN Amphibian Conservation Action Plan) remains the best option for ensuring the survival of Madagascar's amphibian diversity. So far, merely a handful of species from this island has been incorporated in amphibian conservation breeding programs. Our risk assessment allows for an identification of species most threatened by Bd, which should be helpful when prioritizing species for ex situ conservation measures.

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Responses of vertebrate feeding guilds to forest fragmentation in the Neotropics – A Review

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Keywords: Neotropics, forest fragmentation, vertebrates, feeding guilds

Tropical forest ecosystems represent biodiversity hotspots that are threatened by deforestation and habitat fragmentation. However, fragmentation effects on tropical forest species still are poorly understood: Species' responses seem to be highly variable. In Neotropical birds, some feeding guilds seem to be especially vulnerable to forest fragmentation, whereas little is known about fragmentation sensitivity of mammals. We reviewed responses of terrestrial vertebrate groups to forest fragmentation in the Neotropics. We assumed that there is no difference in vulnerability across vertebrate groups but across feeding guilds. We conducted a literature search in the ISI Web of Science for international peer-reviewed articles on tropical forest fragmentation that use a spatial or temporal control. We extracted data on the studied vertebrate groups, feeding guilds, parameters, study designs and recorded fragmentation effects. We used Linear Mixed Models to assess the relationship between fragmentation effects on a species (response variable) and all other (random) variables. We obtained about 1000 species datasets of which more than 50% showed a negative response to fragmentation. The reported fragmentation effects were influenced by all variables. Those groups that were affected most (herpetofauna, insectivorous and carnivorous feeding guilds) might act as model species for conservation practice. Further, we recommend choosing study parameters and study design cautiously.

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Herbivore hotspots in the Mara region of Kenya in relation to land use and vegetation

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Keywords: herbivore hotspots, climate, land use, NDVI, Mara-Serengeti

Aggregation of ungulates in savannas is constrained by land use and forage. To understand how forage biomass and quality as indexed by the Normalized Difference Vegetation Index (NDVI) constrains herbivore aggregation, we examined hotspots or locations of persistently high concentrations of 11 ungulate species. We used 44 aerial surveys of wildlife conducted in the Mara region of Kenya to characterize 5x5 km² grid cells as hotspots during 1977-1987 and 1988-2002. The probability that a grid cell was a hotspot was significantly related to NDVI according to the humped, exponentially increasing or decreasing patterns depending on period and land use type. The humped relationship suggests that herbivores concentrate in areas of intermediate plant biomass and quality to balance the low digestibility and nutritional quality of high plant biomass against the high nutritional quality of low vegetation biomass with low ingestion rates, consistent with the intermediate biomass hypothesis. Overall, the relationships suggest that herbivore species segregated along the NDVI gradient presumably to minimize interspecific competition through resource partitioning and satisfy their energy requirements. Hotspots of buffalo (*Syncerus caffer*), topi (*Damaliscus korrigum*) and hartebeest (*Alcelaphus busephalus cokii*) were concentrated in the protected reserve, rare in the pastoral ranches but absent from the cultivated areas. In contrast, hotspots of giraffe (*Giraffa camelopardalis*), impala (*Aepyceros melampus*), Grant's (*Gazella granti*) and Thompson's gazelle (*G. thomsoni*) were concentrated in the pastoral ranches and near cultivated areas but were virtually absent from the reserve. Thus, protection of reserves alone is insufficient to guarantee the future viability of large herbivore aggregations without co-coordinated management of reserves and their buffer zones.

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Floristic diversity of wild coffee forests in SW Ethiopia and implications for conservation

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Keywords: conservation planning, Eastern Afromontane Biodiversity Hotspot, forest management, ordination techniques, rainforest, reserve network

The Ethiopian montane rainforests form part of the Eastern Afromontane Biodiversity Hotspot. They are the centre of genetic diversity for Arabica coffee (*Coffea arabica*), which grows wild in the forest understorey between 1,000 and 2,000 m asl. The unique plant diversity of the Ethiopian Afromontane rainforests is threatened by increasing habitat destruction. 40% of the forest cover in southwestern Ethiopia has been destroyed or degraded since the 1970ies. In the study region Bonga, the rainforest is fragmented, and wild coffee populations in the remaining forest areas are strongly used by the local population, e.g., by simple coffee collection or by management in semi-forest coffee systems. This study aimed to assess the floristic diversity of managed and unmanaged forest parts in the Bonga region as a basis for conservation planning. Vegetation surveys were conducted in four forest fragments that vary in altitude and encompass managed and unmanaged forest parts. In 85 study plots (20 m x 20 m), all vascular plant species were identified. Plant height > 0.5 m and diameter at breast height (dbh) > 2 cm were measured. The vegetation survey recorded 309 vascular plant species, and revealed that the altitudinal gradient had a strong impact on plant species composition: The study identified “upper montane forest” (1,830 - 2,280 m asl), characterized by Afromontane endemics and near endemics and high pterophyte diversity, and “lower montane forest” (1,600 - 1,830 m asl), which also included Guineo-Congolian-East African linking species and had high tree diversity. Species of the understory had dense populations throughout the forest, while tree species had a more scattered distribution. Wild coffee was observed throughout the forest with high variations in population density. The study also showed that simple wild coffee collection did not have a large impact forest structure and species composition, while wild coffee management in semi-forest coffee systems jeopardized the original plant species diversity of the Afromontane rainforest. Recommendations are given for location, size and management of protected forest areas in the Bonga region.

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Centres of endemism of Noctuidae (Lepidoptera) in the Palearctic high mountains

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Keywords: oreol fauna, xeromontane fauna, Noctuidae, areas of endemism, monophyletic species groups

In the Palearctic two types of oreol fauna co-exist. The alpine type of the humid orobiomes shows strong connections to the tundraI zonobiome. Oppositely, the xeromontane faunal type of arid orobiomes shows connections to deserts and grasslands of the eremic zonobiome. The alpine type is influenced by the Quaternary glaciations, resulting in long-distance area disjunctions (arctic-alpine species). The xeromontane faunal type typifies the summer-dry Mediterranean mountains and the arid mountains of Central Asia. High potential of speciation was observed in taxonomic groups adapted to cold-arid conditions (e.g. rodents, cutworm Noctuidae, Orthoptera). The members of the xeromontane fauna often have endemic/disjunct areas. Basic faunal structures were recognised by accumulated occurrence of endemic species and by high species-diversity of some typical genera. The restricted areas of allopatric sister-species fulfill the criteria of the "areas of endemism". Core areas indicated by the accumulation of endemic species can be supported by the allopatric subspecies of polytypic species and by allopatric sibling species of superspecies. Noctuinae genera with "cutworm" larvae originated in the continental orobiomes (e.g. *Euxoa*, *Dichagyris*, *Chersotis*, *Rhyacia*). Other genera are connected with xerophytic scrub formations (*Auchmis*, *Lophoterges*, *Copiphana*). Their Mediterranean-Anatolian taxa often show Western and Central Asiatic connections. Other genera evolved under the influence of the young Tertiary aridisation of the Mediterranean basin. The south-eastern Palearctic orobiomes are the most important core areas of many relict genera (*Erebophasma*, *Palaeamathes*, *Hoeneidia*, *Hadulipolia*, *Niaboma*, etc.) and ancestral species from widely distributed genera. They have connections to the high-mountains of Central Asia and Southern Siberia and also to the continental steppe areas. The stenochorous, ancestral taxa are regularly connected to the monsoonic forested biomes, while the derived species or species groups are inhabitants of the at least seasonally dry orobiomes, or they are zonally distributed in the boreal coniferous forests of the Palearctic/Holarctic).

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Multiscale evolution of species range under changing climate

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Keywords: Alpine biodiversity, historical constraints, marginal processes

The extreme climate changes of the Quaternary have had a major influence on species distribution and evolution, including the diverse alpine species. This study addresses evolutionary processes at different spatiotemporal scales. A regional phylogeographic survey tackles distal factors (history), while local, landscape genetics studies explore proximal factors (mechanisms) underlying patterns of biodiversity. The results at the regional scale show that the external Alps, but also central Nunataks, have played a major role in the persistence of populations during the glacials and presently show outstanding levels of diversity, at the genetic level, but also at the species level. In addition, the central Alps are viewed as an important crossroad where lineages with different evolutionary histories are meeting, certainly enhancing levels of diversity. The comparison of local populations growing in contrasted historical situations indicate that populations persisting in the external Alps present restricted gene dispersal and are in equilibrium with their environment, presenting patterns of local adaptation. At the contrary, founder effects together with great gene dispersal influence populations at the altitudinal margin, and the genotypes have a nearly random distribution. This study thus highlights the importance of the historical component in shaping the distribution of genetic variation across the species range. Accordingly, refugial areas of the external Alps and, to a lesser extent, in the central Alps seem to play a dual role of “museum” and “cradle” for biodiversity, arguably providing rational for future conservation strategies.

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The Carpathian refugia in differentiation and speciation of aquatic Diptera: a case study

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Keywords: South-eastern Carpathians, glacial refugia, speciation, aquatic insects, Diptera, Pediciidae

The Carpathians are considered to be one of the most important “hot spots” of biodiversity in Central Europe, due to their historical, biogeographical and ecological features. Prominent among this is their role in differentiation and speciation of aquatic insects during the Pleistocene, with evidence on a number of refugia and periglacial survival. Despite their major role in the cold spring ecosystems, very little is known about the pattern of speciation of various diptera species from here. To analyze the importance of the Carpathian refugia in divergence of aquatic diptera we select as model organism *Pedicia (Amalopsis) occulta* (Meigen, 1830). This species has a major Mediterranean presence, but not pass the permafrost line in north. Mitochondrial sequence data (COI) of 69 individuals from well known Carpathian and Balkan refugia completed with morphological data on additionally 275 individuals from the entire species range revealed a highly structured pattern in the south-eastern Carpathian area. Our data suggest that species survived glaciations in suitable cold springs during the Quaternary period, in multiple mountainous Mediterranean refugia, colonized from here its present area, having several range expansions and regressions. Quite contrary, a very few isolated populations in the north-east periphery underwent a peripatric speciation, surviving as refugial populations in the south-eastern Carpathian area. Based on our results we can conclude that *Pedicia (Amalopsis) occulta* has a rather complicated biogeography with two major lineages with overlapping geographic distribution, which are now in contact in the south-eastern Carpathians, but remain separated because of their different genetic settings, particular morphology and shift in flying period. No intermediate forms were identified during our study, which date the peripatric divergence early in the Pleistocene. Secondary allopatric events occurred between the resident Carpathian populations, with divergent genetic structures, but without conspicuous morphological evidences.

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Polychaeta associated with cold-water coral reefs in the Northeast Atlantic and the Mediterranean

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Keywords: Cold-water coral reefs, Polychaeta

Cold-water coral reefs have long been known to local fishermen as productive fishing grounds especially in the NE Atlantic. Increasing exploitation of deep-water resources in recent years has raised awareness and subsequently shown that the extent and distribution of these reefs is apparently much wider than anticipated. They occur in all oceans mainly in areas of enhanced primary productivity and water flow on the continental shelf edge, the continental slopes, and on seamounts. Although the ecology of these reefs is still poorly understood they are known to support a diverse invertebrate fauna. Cold-water coral species, e.g., *Lophelia pertusa* a key structural species in the NE Atlantic, form a three-dimensional skeletal framework simultaneously providing hard substrate for the settlement of a wide variety of suspension feeding invertebrates and potentially acting as nursery areas, e.g. for commercial fish species. With about 1300 species reported from *Lophelia* reefs in the NE Atlantic, they are considered biodiversity hotspots similar to shallow tropical warm-water coral reefs. Polychaeta as a key marine taxon, also play a dominant role in diversity and abundance on cold-water coral reefs in the NE Atlantic. For example the scale worms (Polynoidae), a highly diverse and ubiquitous group of polychaetes, are important as motile predators and/or scavengers in this peculiar habitat. Some polynoid species might even be restricted to cold-water coral reefs, since they have only been found associated with the respective coral species to date. In comparison to cold-water coral reefs of the NE Atlantic those of the Mediterranean are impoverished in terms of coral species and associated fauna. This can be explained by the same factors as already discussed for the paucity of the deep benthic Mediterranean fauna in general, and some polychaete taxa, e.g. Serpulidae and Aphroditoidea, in particular.

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Microendemism and environmental variability in the Malagasy biodiversity hotspot

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Figuring at the top of the list of the biodiversity hotspots, Madagascar shows outstanding levels of endemism as well as a strong imbalance across the different taxonomic levels of its fauna and flora. The island's history of isolation and contacts with other landmasses together with dispersal events have been put forth to explain present biodiversity patterns, but for many groups, the causes of endemism remain poorly understood. This study aims at understanding species diversification and endemism patterns within the highly endemic fauna of aquatic beetles. Mitochondrial DNA sequencing was used to quantify the species diversity, and a geographic and ecological approach was employed to investigate species turnover on the island. The results suggest an underestimation of endemic species diversity, and that both climatic variations and geographic distance are responsible for present beta diversity patterns within the island.

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Phylogeography and conservation genetics of the Iberian three-spined stickleback (*Gasterosteus aculeatus*)

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Keywords: phylogeography, stickleback, fish, mtDNA, microsatellite, *Gasterosteus*, Iberia

The three-spined stickleback *Gasterosteus aculeatus* Linnaeus, 1758 (Teleostei, Gasterosteidae) is a species included in several Red Lists in Portugal and Spain. Its distribution is quite localized in the Iberian Peninsula. We examined the genetic diversity and differentiation showed by *G. aculeatus* in 15 Iberian and one German population (external reference). For this, we genotyped 448 individuals using 18 nuclear microsatellite loci. There was significant differentiation between all surveyed populations, with F_{st} values ranging from 0.107 (rivers Asma-Rato, same hydrographic basin, Galicia, NW Spain) to 0.559 (Txingudi-Sado, Basque Country-Portugal). Principal component analysis showed two highly differentiated populations: Majorca and Mira (southernmost Portuguese locality), and the following clusters: Peñíscola (Valencia region, E Spain, extinct population), Tagus river (Portugal), Basques ($n = 3$)/nothern Portuguese ($n = 2$)/German populations, and Galician ($n = 5$)/Sado (southern part of Portugal, between Tagus and Mira rivers). The most genetically diverse population was Vouga (N Portugal: unbiased $H_e = 0.6627$, 8.82 alleles/locus), whereas the Basque Txingudi and the Portuguese Sado were the localities with lowest variability values (unbiased $H_e = 0.3997$, 0.3548 and 2.78, 3.72 alleles/locus, respectively). We also sequenced 1,400 bp of mtDNA comprising part of the control region and the cytochrome b in up to 20 individuals per population. Undergoing analyses with the mtDNA haplotypes will complement the pattern provided by nuclear microsatellite loci.

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Species and genetic diversity in the Mediterranean: do the two levels of biodiversity correlate?

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Keywords: Biodiversity, heterozygosity, allelic richness, species richness, paleo-climate, spatial structure

Do species diversity and genetic diversity in the Mediterranean have a similar geographic organization and correlate as a result of similar factors, concurrently affecting micro- and macro-evolutionary processes? We used the Med-Checklist taxonomic database and published geo-referenced within-population genetic data for tree species having populations in the Mediterranean. We normalized vascular plant species richness estimates per country as well as heterozygosity and haplotypic richness for each population across species. Linear regression analysis was used to correlate genetic data with population longitudinal position. We then compared the populations' geographic and bioclimatic trends for genetic diversity with Late Glacial Maximum paleo-climate data and the species current ecological requirements. The eastern Mediterranean and the coast of former Yugoslavia had higher species richness than other regions. There was no overall spatial structure of species diversity in the Mediterranean although there was a decreasing west-east genetic diversity trend. This trend co-varied with an east-west warm/cold trend detected during the Late Glacial Maximum (LGM). Low elevation xerothermic pine species displayed significantly less within-population genetic diversity than higher elevation mesothermic or mountain pine species. Lack of co-variation between vascular plant richness and within-population genetic diversity (in trees) across the Mediterranean Basin indicates that dissimilar past processes influenced species diversity (macro-evolution) and genetic diversity (micro-evolution) at this scale. As a phylogeographic signal alone seemed improbable, we suggest that LGM climate was a powerful driver for shaping the current tree genetic diversity patterns. Because neutral genetic diversity may co-vary with adaptive genetic diversity, we also suggest that Western Mediterranean taxa may be at higher evolutionary risk than their Eastern Mediterranean counterparts. Species diversity and genetic diversity may thus not be used as surrogates of one another in the Mediterranean, except for hotspots of species endemism that may also be hotspots of evolutionary risks.

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European hotspots as evidenced by the Palearctic distribution of songbirds

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Keywords: Passeriforms, Palearctic, Europe, hotspots, species richness, endemism

Previously, a database was created of digitized equal area distribution maps of 3,036 phylogenetic species of Palearctic passeriforms. Geographic distribution of species richness suggested several hotspot regions in the Palearctic, mostly located in mountainous areas. For the analysis of hotspots of endemism or range-size rarity, partly extra-limital species were excluded, thus resulting in a dataset of 2,401 taxa. The index of range-size rarity generally identified similar hotspot regions as that for species richness, although it de-emphasized the large central-Siberian hotspot. Europe does not represent a natural biogeographic region, housing a coherent fauna, but merely represents a political entity. Therefore, it is to be expected that databases restricted to merely European organisms will identify a different set of hotspots, as compared with a spatial analysis of a more natural biogeographic region such as the Palearctic. In the present study we test this hypothesis. For this purpose we have selected from our dataset of 2,401 phylogenetic species only those taxa that occur in the geographic region delimited by the map used in the EBCC atlas and the Climatic Atlas of European Breeding Birds. This map excludes regions such as Turkey, North Africa, and areas east of approximately 60 degrees longitude. We will compare hotspots suggested by our restricted, European dataset of Palearctic songbirds with European hotspots identified by (1) our full database of Palearctic songbirds, (2) our dataset on endemic Palearctic passeriforms, (3) the EBCC atlas data, and (4) the EBCC atlas data for only songbirds.

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Expansion of passerine bird taxa in the northern Palearctic in the holocene

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Keywords: hotspots, glacial refugia, Palearctic, passerine birds, breeding range expansion

With help of ca 3000 literature references on bird distribution and after examining specimens in over 15 bird collections detailed breeding distribution maps of 3016 Palearctic passerine bird-taxa have been constructed. These have been implanted in the WorldMap program (Paul Williams, NNM London), using a map of equal-area gridcells of ca 4000km² each. All maps combined show that two rows of hotspots of bird diversity exist in the Palearctic (see *J.Orn.*: 147: 24-30): a northern one of six hotspots (of which three in Europe) and a southern one of ca 12 hotspots ranging from Morocco through the Himalayas to the Beijing mountains in China. Species with small range sizes are virtually all confined to these hotspots. The three western (European) hotspots of the northern row agree with glacial refugia of summer-green trees (*J Biogeogr* 34:2115-2128), and preliminary data on vegetation for the three eastern hotspots also indicate that no trees occurred north of these during the last ice-age. When comparing present-day distributions of passerine taxa breeding north of the tree-limit of the last glacial period it appears that many of these taxa still have a foothold on one of the refugia, making reconstruction of breeding range expansion possible. Relatively few taxa have footholds in 2 or more refugia of the northern row. These may include taxa in which morphological differentiation is present but has not yet been detected, or are birds which showed a rapid east-west expansion after the last ice-age.

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Impacts of Biofuels on Southeast Asian biodiversity hotspots

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Keywords: biofuels, biodiesel, palm oil

The finitude of fossil fuels, concerns for energy security and the need to respond to climate change have led to growing worldwide interests in biofuels. However, political and public support for biofuels has recently been undermined due to environmental and food security concerns, and by reports questioning the greenhouse gas emissions benefits of biofuels. In particular, oil palm agriculture (for food and biodiesel production) has been blamed for the loss of tropical forests and for threatening the survival of many native species in Southeast Asia. In this talk, I address the following questions: Is oil palm agriculture really destroying tropical biodiversity? Can we make oil palm plantations more hospitable for forest-dwelling species? Using land-use data compiled by the Food and Agriculture Organization of the United Nations, I show that between 1990 and 2005, 55-59% of oil palm expansion in Malaysia and at least 56% of that in Indonesia had occurred at the expense of forests. Furthermore, the conversion of either old-growth or secondary (logged) forests to oil palm results in substantial declines in the diversity of forest-dwelling butterflies and birds, whereas the conversion of degraded habitats such as rubber plantations to oil palm is very much less damaging. In Bornean oil palm plantations, I find that oil palm growers could marginally increase the species richness of butterflies and birds in oil palms by changing management practices such as encouraging epiphytes, flowering plants, or weed cover in their plantations; or by preserving remnant forest patches in the landscape. However, the magnitudes of these biodiversity enhancements are low relative to the biodiversity of undisturbed tropical forests, which suggests that little can be done to make oil palm plantations more hospitable for biodiversity.

Unless future expansion of oil palm is restricted to degraded habitats, such as pre-existing croplands or anthropogenic grasslands, rising global biodiesel demand is likely to exacerbate the high rates of forest conversion and threats of extinction to species in major oil palm-producing countries.

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Biodiversity Action Plans in Portugal's Agroforestry Business

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Keywords: Biodiversity Action Plans, agroforestry; Monitorinig Natural Value, Biodiversity Baseline, Portugal, Business & Biodiversity

In Portugal, the Natura 2000 network and the protected areas network cover about 25% of the overall territory. Most of these areas are largely covered by managed forests, crops, ecosystems like “Montado”, pastures, grasslands, among other forestry or agricultural related use. Even the hydrographical basins were adapted and transformed to serve the purpose of food, fiber, fodder and fuel production, by innumerable dams, artificial lakes and canals. All this human intervention as largely affected the structure and diversity of habitats and the respective fauna and flora associated with each ecosystem assemblage. Nevertheless, in some cases, the existence of agroforestry activities seem to benefit the Biodiversity, such is the case of oak “Montados” (*Quercus suber* and *Q. rotundifolia*), used for cork (from *Q. suber*), fiber and cattle production, where Biodiversity values are high, especially regarding endangered birds and mammals, such as the black vulture (*Aegypius monachus*) and the European wildcat (*Felis sylvestris*). Since 2005, AmBioDiv has been working to develop and adapt the concept of Biodiversity Action Plans (BAPs) to the Portuguese agribusiness and forestry reality, with special focus to the development of „Business and Biodiversity“ inspired strategies, in order to get Biodiversity into the businesses balance sheet and report on the conservation values and good practices. The main goal of the BAPs is to evaluate and monitor the natural value, i.e., habitats, flora and fauna of a particular area, establish a Biodiversity baseline and define/implement adequate conservation measures in order either to maintain or improve that baseline. By the end of 2008, AmBioDiv had design and aid the implementation of over 12 BAPs, covering more than 130.000 hectares, mostly inside Natura 2000 and protected areas, with promising results regarding conservation of rare, endemic and regionally threatened habitats and species. In most cases, the BAPs were used to define and protect High Conservation Value Forests and Farmlands regarding certification processes such as Forest Stewardship Council or GlobalGAP standards.

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Phylogenetic diversity to reveal conservation priorities: a case study in the Southeastern Neotropics

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Keywords: phylogenetic diversity, organismal diversity, cryptic diversity, conservation priorities, Mata Atlantica, Southeastern Neotropics

The presence of major biodiversity hotspots all over the world has drawn the attention of taxonomists, evolutionary biologists, biogeographers and scientists concerned with the conservation of landscape entities of all scales. They are confronted to a problem raising from WILSON'S definition of biodiversity as encompassing the variety of all living forms from genes to species to ecosystems: this multiscale consideration may enhance the scientific discussion about the systematic status of the taxa involved but makes it difficult to decide which level of biodiversity should be the focus of protection activities. One such biodiversity hotspot in the Neotropics is the Atlantic rainforest of Brazil (Mata Atlantica) with many endemic species even though only a narrow stripe along the Eastern coast of Brazil has remained from its original extension. Besides this very popular forest hotspot there is one almost neglected area in the Southeastern part of the Neotropical realm, the Southern Brazilian Highlands (partly connected to the Southernmost Atlantic forest) displaying an enormous variety of species diversity that has only become evident in recent years by sampling efforts and molecular approaches. A thorough knowledge of the evolutionary history of a hotspot is crucial to infer effective conservation strategies for such species-rich localities, but robust phylogenies do only exist for a few well known taxa. Molecular markers and DNA-based methodologies developed in the past decades are an important yet not unbiased tool to increase the information content of the genetic level of biodiversity but it is controversial whether this molecular heterogeneity does in fact represent organismal diversity. Some studies based on genetic data have attempted to quantify the biodiversity value of localities as its phylogenetic diversity to obtain a more objective measure for the management of hotspots. The aim of the present study is 1. to discuss the expression "biodiversity (hotspot)" by comparing the taxonomical, morphological and molecular approaches used to describe it for amphibian and reptile species in Southeastern Brazil and 2. to discuss if the cryptic diversity revealed in some model species is worth considering in the scope of defining conservation priorities.

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**Poster Presentations
Abstracts**

Biodiversity of land planarians (Platyhelminthes) from the Atlantic Forest (Brazil)

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Keywords: phylogeography, coalescence, population genetics

The Brazilian Atlantic Forest boasts one of the highest diversity of animal and plant species in the world. Yet, less than 10 percent of the forest remains. For its protection and recovery, the Brazilian government is introducing biological corridors sketched based on fauna and flora inventories. In this project, using morphological data and molecular techniques with phylogeography and coalescence-based methods, we analyse the function of one of these corridors with a new model taxon, land planarians. This is an optimum group for biogeographic and phylogeographic studies, and especially to those for conservation biology, due to their physiological and dispersal limitations. We have conducted a comprehensive sampling of terricolan planarians in different parks distributed along the biological corridor, and also in some regions located south and north of the corridor. The preliminary analysis at the morphological level identified a number of species in the area higher than previously thought. Even more, the levels of molecular variation among animals identified morphologically as the same species, are in some cases extraordinarily high; these values are in the range of that found for congeneric species in other groups of animals including freshwater planarians. All these data point to the existence of a high diversity of land planarians in this bioma. In this communication we report preliminary estimates of the diversity of species at the morphological and molecular level, and some analyses on the genetic variability within and among populations for a pair of selected species.

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History of the *Rhyacophila aquitanica* complex (Insecta: Trichoptera) in European mountain systems

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Keywords: allopatric speciation, mountain aquatic species

A study was carried out to investigate genetic relationships among populations of a mountain Trichoptera species. While the European mountains harbor an important amount of the European biodiversity, mountain aquatic and semi-aquatic species are still not sufficiently investigated. We chose *Rhyacophila aquitanica* as model organism: the populations of this species are known from several European mountains, but the distribution of the species is very fragmented, raising a number of questions about the origin and identity of different populations. Previous works describing taxonomic structures within *R. aquitanica* also facilitated our choice. Specimens were obtained from almost all major distributional areas of the species. A number of morphometric and genetic analyzes were carried out on collected and museum specimens. The study revealed important aspects of speciation events among the investigated species and thus presented evidence for allopatric differentiation in the European mountain systems. The study proves that many of the observed present-day structures of the European mountain diversity may be much older, than the last Pleistocene glaciation. In the case of the *R. aquitanica* complex the differentiation events probably happened several hundreds of thousand years earlier than the last glacial maxima among the Carpathian, western and Southern Alps clades. The study also points on the importance of mountain aquatic habitats as biodiversity hotspots and emphasizes their role in the preservation of the European mountain diversity.

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Scale worms associated with cold-water corals in the Northeast Atlantic and Mediterranean Sea

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Keywords: cold-water coral reefs, Polychaeta, Polynoidae, diversity

Among polychaete worms, the family Polynoidae Kinberg, 1856 is one of the richest in terms of species and generic diversity. Members of this scale worm family are highly motile predators/scavengers and are encountered in all known habitats from the littoral to abyssal depths. According to Martín & Britayev (1998) about 23 % of the polynoids are commensal and many of them are found on cnidarian hosts. But, due to the high number of species involved and the lack of taxonomic experts, the systematics of polynoids is rather confused. This explains why, in studies assessing the biodiversity of the fauna associated with cold-water corals, polynoids are rarely identified to species level, except for *Harmothoe oculinarum* (Storm, 1879) and *Neopolynoe paradoxa* (Storm, 1888), which occur on *Lophelia* reefs along the Norwegian coast. In the course of our revisions of several polynoid genera in the NE Atlantic and Mediterranean Sea, we found six additional species associated with cold-water corals: *Acanthicolepis asperrima* (M. Sars, 1861); *Harmothoe vesiculosa* Ditlevsen, 1917; *H. viridis* Loshamn, 1981; *Leucia nivea* (M. Sars, 1863); *L. violacea* (Storm, 1879); and *Neolagisca jeffreysi* (McIntosh, 1876). Judging from extant records *Harmothoe oculinarum* and *H. vesiculosa* seem to occur exclusively on cold-water coral reefs. The scale worms considered here are mainly differentiated by the number and ornamentation of their scales (elytra), but also by their prostomial and chaetal characters. One of the most important generic characters is the number of elytra (*Acanthicolepis* 18 pairs, *Leucia* 16 pairs, and *Harmothoe*, *Neolagisca* and *Neopolynoe* respectively 15 pairs), whereas the elytral ornamentation is used for species distinction. Unfortunately polynoids are rather fragile and thus easily fragmented, which makes identification difficult for non-specialists.

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The Patagonian Fjord Region: A hotspot that should not leave us cold

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Thousands of islands and inlets with more than 80,000 km of coastline in a region with 1500 km north-south extension; channels and fjords that can reach 1200 m depth and coastal mountains with more than 2000 m altitude – these are some basic parameters that help to describe the morphological complexity of the Patagonian fjord region of southern Chile. Steep slopes and high precipitation provoke a regime of natural erosion that adds dynamics to the morphological heterogeneity and create torrential rivers that cut the landscape. In higher altitudes and higher latitudes glaciers are still the dominant molding factors. These elements and processes form a multitude of gradients, successions and particular conditions which produce a dense pattern of different habitats leading to the expectation of high diversity and local endemism. Despite all this the Chilean fjord region belongs to one of the least studied areas in the world. This may also seem surprising and gains importance when taking into account the region's impressive economic boom which includes many high impact activities such as fisheries and aquiculture, dams and industrialization projects, and urbanization and infrastructure development. First data from studies of the Huinay Scientific Field Station indicate unique biocenoses and exceptionally high biodiversity, distributed in highly complex biogeographic patterns. Especially in the marine environment there are still a high number of completely un-described species, demonstrating a large gap between the level of economic exploitation and the level of knowledge regarding the affected ecosystems. We present terrestrial and marine examples as evidence that Chilean Patagonia should be considered a biodiversity hotspot, and we discuss in which way the fast growing activities and dramatic lack of knowledge of the ecosystems could spell serious threats for the biodiversity and ecosystem functioning. We also discuss in how far taxonomic and biogeographic inventories, as the base for spatial planning, should have priority for science aimed toward conservation and sustainable resource management.

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Distribution Modelling of Sphingid Moths

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Keywords: Species distribution, predictive maps, statistical modelling

The prediction of species distributions is a topic with manifold applications in ecology, evolution and conservation biology. Models that make accurate predictions are important keys to landscape planning, management and reserve development. We present our plan to apply environmental niche modelling to all the Old World members of the Lepidoptera family Sphingidae in order to predict each species' distributional range. Due to their variability in life history strategies and their worldwide occurrence, sphingid moths are an excellent model taxon for macroecological research. Combining presence-only records collected from literature, museum collections and own fieldwork we will compare various range modeling approaches, such as GLM's, MARS and MAXENT, among others. Based on objective evaluations as well as "expert opinion" we will assess which approach provides the most satisfying predictions. Distribution models will give account of the environmental factors and dispersal events relevant to shaping the range of each species. Resulting distribution maps will represent, to the best of our knowledge the first comprehensive data set at global spatial scale for any insect taxon. This will help reducing the current "vertebrate-bias" in macroecological research and large-scale conservation biology.

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Non-invasive population genetics of wolves (*Canis lupus*) in the Lazio, Abruzzo and Molise National Park, Italy - Preliminary results

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Keywords: non invasive genetics, conservation, wolves, microsatellites

Non-invasive molecular techniques have become an essential tool in the study and conservation of endangered wildlife. The possibility to derive genetic data from hairs, scat, urine or blood spots has revolutionised our ability to study species and populations which could not be sampled through conventional capturing and handling methods. Endangered species, species with particular low population densities, and elusive or trap-shy species are all ideal candidates for non-invasive sampling. A wide spectrum of genetic analyses can help to describe numerous aspects of demography, behaviour and conservation status, supplementing and, in many cases replacing, data collected through traditional field methodology. We report results of non-invasive analysis of scat samples collected from wolves (*Canis lupus*) in the Abruzzo National Park, Italy. Despite being large charismatic species, very little is currently known about the status of these populations and directed studies have not been carried out to accurately determine their size and trends. Demographic and behavioural data are being interpreted in conjunction with multilocus genotyping results to eventually assess population size, sex ratio, distribution of groups, degree of relatedness and levels of inbreeding and incidence of hybridization with feral dogs. Preliminary data are presented describing risk of misinterpreting microsatellite data associated with non-invasive genetic sampling due, for instance, to low copy numbers and degradation of DNA, false alleles and allelic dropouts. Optimization of individual identification is achieved through multiple-tube approaches and estimation of the number of polymorphic loci needed to optimize results between probability of genotyping error and resolution.

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The importance of headwater streams as resilience areas for freshwater benthic invertebrates

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Keywords : Biodiversity, streams, benthic invertebrates, climate change, resilience

Springing from upland and flowing overland, 1st order streams join together to form discernable channels called 2nd order streams and so forth. Estimates indicate that 1st to 3rd order streams (headwater streams) account for about 70% of total stream-channel length in Luxembourg. In the face of an increasing anthropogenic pressure brought on freshwater ecosystems and of the ensuing decline of many benthic species, there is growing evidence that the ecological health of these ecosystems depends on the manifold functions provided by headwater streams.

In order to show the relevance of headwater watersheds in Luxembourg, benthic invertebrate assemblages from 90 headwater streams (1st to 3rd order - catchment area $<10 \text{ km}^2$) are compared to the assemblages from 118 larger streams (4th to 6th order - catchment area $>10 \text{ km}^2$). Overall species richness and diversity measures are found to be significantly higher in larger streams in comparison with headwater streams. This result is in agreement with the river continuum theory and the gradually increasing availability of nutrient downstream. Some taxa (i.e. Plecoptera, Coleoptera) clearly exhibit a contrasting pattern of richness and diversity, therefore indicating the importance of headwater streams for these groups. The proportions of rare and weakly abundant species are non-significantly different in headwater and larger streams. However, species with a narrow ecological niche – in terms of habitat requirement, substrate preferences or behavioural features – are significantly associated with headwater streams.

Accordingly, these findings draw attention to the importance of headwater stream ecosystems to preserve a significant part of freshwater invertebrate diversity. Strongly marked variations in microhabitat conditions among and within headwater streams create a variety of ecological niches for a number of species, including strictly headwater-related invertebrate species. Preserving the long-term functional integrity of freshwater ecosystems cannot succeed without a statutory protection of headwater streams in line with the Water Framework Directive currently applied to larger rivers with catchment area above 10 km^2 .

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The Strait of Gibraltar and the adjacent Alboran Sea as MPAs

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Keywords: Strait of Gibraltar, collision, cetacean, human impact, conservation, MPA

The Strait of Gibraltar is the only connection between the Atlantic Ocean and the Mediterranean Sea. Deep cold water from the Mediterranean flows outwards below warmer Atlantic water, which flows into the westernmost part of the Mediterranean Sea, the Alboran Sea. Upwellings in the Strait of Gibraltar make it a high productivity area, attracting in return a high number of cetacean species. Up to 7 species of cetaceans can be found here, including the bottlenose dolphin (*Tursiops truncatus*), the striped dolphin (*Stenella coeruleoalba*), the common dolphin (*Delphinus delphis*), the long-finned pilot whale (*Globicephala melas*), the killer whale (*Orcinus orca*), the fin whale (*Balaenoptera physalus*) and the sperm whale (*Physeter macrocephalus*). The Strait of Gibraltar is nevertheless the second busiest shipping lane in the world, with over 90,000 large vessels crossing it every year. This represents an important collision risk, and several cetacean deaths have been reported as resulting from ship strikes. Shipping is drastically increasing in the area, with the opening of the new commercial mega-port of Tangiers-Med and the development of the mega-port of the town of Tarifa. Actions have been taking to redirect shipping lanes, but the main routes still go through main sperm whale feeding grounds. Furthermore, the area is an intense fishing ground, and bycatch represents the most important source of cetacean fatalities (with an estimated 6000 dolphins bycaught in the area). This is far more than the viable limit for resident populations. Moreover, competition between fishermen and cetaceans is becoming increasingly problematic. Pollution is another problem, as most large cities in the Strait of Gibraltar do not possess water treatment plants. The bottlenose dolphin is one of the species protected by the EU habitats directive; whereas the killer whale populations present in the area have been proposed to be listed as critically endangered by the IUCN. It is therefore of utmost importance that the proposal for the creation of the MPA of the Strait of Gibraltar and the Alboran Sea be ratified by the relevant authorities and governmental bodies.

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La Réunion- THE perfect island in the EU to study island biology in insects and nematodes

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Keywords: biogeography, phylogeography, insects, nematodes

The whole department for Evolutionary Biology at the Max Planck Institute for Developmental Biology works on the nematode *Pristionchus pacificus* which was established as a satellite organism for comparison with the best studied metazoan the nematode *Caenorhabditis elegans*. We discovered that *P. pacificus* -like all members of the genus- has an insect association (living necromenic on scarab beetles) and by collecting insects from different places of the world we could isolate many new *P. pacificus* strains. One topic of interest is the origin and dispersal of the nematodes. La Réunion turned out to be a perfect addition to our past sampling sites. The island between Madagascar and Mauritius is relatively young (2-3-mya), easy to cover (50x60km), with an excellent infrastructure and as an oversea department of France part of the European Union, which makes all the paperwork much easier. In addition the island has a high rate of endemic AND imported insects (plus associated nematodes). Many of the insects species on La Réunion are new to science and have not been described to date. As the directions of insect-introductions are in most cases well known we can as well trace back the origin of the associated nematodes to get the whole nematode-biogeography-picture of ancient distribution, dispersal (with insects) over a long period of time and recent anthropogenic introductions to different parts of the world.

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Least cost path analyses for determining effects of habitat structures on landscape permeability

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Keywords: barriers, *Canis lupus*, ecological corridors, GIS, habitat suitability, migration

Białowieża primeval forest (BPF), extending over 1500 sqkm at the Polish-Belorussian border, is a hotspot for temperate woodland species. It is particularly well known for its large ungulate community (including European elk and bison) and its large predators, wolf and lynx. The Polish wolf population is not restricted to BPF and the Carpathians, but there are some small populations in the West that also serve as sources for migrants into neighbouring countries, particularly Germany. The determination of ecological corridors connecting suitable habitat patches is crucial for any broad scale conservation efforts on in fragmented habitats. Large carnivores may act as flagships to maintain connectivity between forest habitats even if the general use of carnivores as flagships species might be debatable. Commonly employed least-cost path (LCP) analysis relies on the underlying cost matrix. The Ecological Niche Factor Analysis (ENFA) minimises the problems connected with subjective cost assessment or the use of presence/absence data. We propose that apart from supplying the basis for direct conservation efforts, LCPs can be used for more detailed analyses that offer valuable insights into factors that facilitate or hinder migration by statistically comparing different subsets of LCPs. Using data on wolves we do not only provide a habitat suitability map as calculated by ENFA and LCPs, but also point out factors that contribute to distinguishing populated and unpopulated patches, and LCPs between different subpopulations. We were able to show that the most densely populated patches in the East are surrounded by a significantly lower proportion of cities and roads than patches elsewhere in Poland. LCPs between areas where little migration takes place (i.e., leading to unpopulated patches or between different genetic subpopulations) ran through significantly higher proportion of roads, and through lower proportions of meadows and wetlands, features that seem to be of additional importance to those that distinguish LCPs in general from random routes. The methods employed should be widely applicable to gain more in-depths information on potential migration barriers.

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Lepidoptera of Dhofar (South Oman) and possibilities of their protection

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Keywords: Lepidoptera, Dhofar, endemic Lepidoptera, protection

The Dhofar region, the southernmost province of Oman, is world away from the industrialised north and is geographically separated by an interminable rock desert. This region is the only place in the Arabian Peninsula with constant annual precipitation. From mid-June to mid-September, southwestern monsoon winds bring moisture that usually occurs as very dense fog. At that time, region looks like a green oasis surrounded by a desert. This is the reason for a great variety of endemic flora and fauna species in the region. The Dhofar region is dominated by two types of habitats dry river valleys in the lowlands, which are rich in grass species and various Acacia species (*Acacia tortilis*, *A. ebrenergiana*, *A. senegal*, *Acridocarpus orientalis* etc.), and narrow deep valleys in the mountains, which abound in different bush and tree species (*Maytenus dhoariensis*, *Croton confertus*, *Blepharis pernum*, *Euphorbia larica*, *Physoleucas arabica*, *Ficus salicifolia* etc.). Despite its unique fauna, this region of Oman has been poorly studied so far. Only one solid work dealing with Lepidoptera of the Dhofar region has been published: study by Wiltshire, E.P. (1980) in which he describes fewer than twenty new to science species of lepidopterans, most of which are endemic to the Dhofar region. The group of Macrolepidopterans alone is known to contain over 30 endemic species. The number of endemic species recorded in various families is as follows: Noctuidae - 18, Arctiidae - 4, Lasiocampidae - 2, Lymantriidae - 2, Thaumetopoeidae - 1, Thyretidae - 1, Geometridae - 3 and Cossidae 1. Two Lithuanian-German entomological expeditions were organized to Dhofar in 2006-2007, as a result of which abundant lepidopteran material was collected. At present the collected lepidopterans are being investigated by various European scientists. Among the most significant findings is the revelation of new to science lepidopteran species that are endemic to the Dhofar region. The main attractions of the area - unique nature and picturesque coastal scenery account for the ever expanding utilization of its recreational potential, which can prove hazardous for unique fauna.

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Long-term changes of genetic composition in trout *Salmo letnica* populations, endemic to the Balkan Lake Ohrid: human impact?

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Keywords: Lake Ohrid, *Salmo letnica*, microsatellite DNA, conservation, endemism

Lake Ohrid is well-known for its outstanding biodiversity and endemism. The relict nature and taxonomic value of the endemic, an endangered trout species *Salmo letnica* has been a disputed issue and is still uncertain. It has been previously shown, that this species in fact comprises three distinct populations, probably different intra-lacustrine forms inhabiting the lake: *Salmo letnica* typicus Stefanovic, *S. l. aestivalis* Stefan. and *S. l. balcanicus* (Karaman). These populations differ in their intralacustrine distribution, ecology and the season of spawning. One more stock occurring in Lake Ohrid has been described: *Salmo letnica lumi* Poljakov, Filipi & Basho, 1958, a river form, inhabiting the tributaries of the western shore of the lake. The genetic structure of trout populations was studied. We compared polymorphism at seven microsatellite DNA loci in contemporary and past samples collected from 1951 to 2003. A principal component analysis and assignment tests showed that the genetic composition of populations was not temporally stable. Our results reveal a decrease in population structuring within Lake Ohrid, ascribed to human impact. Overfishing seems to be the major cause of the decline of the trout population whereas erroneous management and stocking practices are seen as a threat to the genetic integrity of indigenous populations.

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Biodiversity in Lake Ohrid: a diverse endemic Proasellus species flock from a molecular perspective

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Keywords: species flock, isopods, morphological diversification, mitochondrial DNA, Proasellus, Lake Ohrid

Biodiversity in Lake Ohrid: a diverse endemic Proasellus species flock from a molecular perspective. The Balkan Lake Ohrid is the oldest one in Europe and one of the oldest in the world and has been designated as a UNESCO World Heritage Area. Like other ancient lakes, Lake Ohrid harbours a wealth of endemic species diversity. The degree of endemism in Lake Ohrid ranges from 47% to 86% for various animal taxa. It was proved that crustaceans tend to display higher degree of endemism in long-lived habitats, such as ancient lakes, than in other habitats. Indeed, members of Ostracoda, Amphipoda and Isopoda form the most numerous part of radiation in Lake Ohrid. On the basis of morphological and karyological analysis, the Proasellus asellids from Lake Ohrid may be considered as an example of autochthonous species flock consisted of three species divided into several morphological forms or subspecies connected with different bathymetric zone of the lake. The observed morphological richness of Proasellus species was also proved by cellulose acetate electrophoresis and direct sequencing of two fragments of mitochondrial DNA: coding for the cytochrome oxidase c subunit I (COI) and 16S ribosomal DNA. The results suggest that endemic isopods from lake Ochrid constitute a species flock created by means of intralacustrine speciation based on the mechanism of ecological isolation by habitat. However, relationships within the Proasellus species group support the conclusion that morphological and molecular evolution seem to have been uncoupled during the diversification of Ohrid's isopods. Different levels of correlation between morphological and genetical similarity were observed. Moreover, the results indicate that in some cases gene flow between populations considered presently as one species is limited and none of the nominal species appear to be monophyletic. It suggest that present taxonomic status of the ochridian asselids should be revised. According to the molecular clock analysis the last common ancestor of the whole lineage existed 7,5 mln years ago, but the proper radiations of ochridian asselids started about 3-2 mln.

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Biodiversity hotspots and endangered specialists: A case study on the Mollusca of Northrhine- Westphalia, Germany

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Biodiversity hotspots have risen special attention, as the conservation of hotspot regions seems to be the most parsimonious way of conserving rare species. Here, we show the example of hotspots of mollusc diversity in a recently well-studied region (federal state of Northrhine-Westphalia, Germany). There are several hotspots of terrestrial snail diversity, that as in other regions- coincide with hilled or mountainous landscape surfaces that are additionally characterized by calcium-rich soils. Some of the hotspots are indeed worth to focus on, as they are rather small, contain relict species and are threatened by limestone quarries and expanding suburbs. However, many populations of rare and endangered terrestrial species (some of which are even listed in the FFH-directive of the European Union) would not be sufficiently included in hotspot-based conservation measures, as they live in different, more specialized habitats such as wetlands. Even in the complementary approach with biodiversity hotspots of freshwater molluscs, or a combination of freshwater and terrestrial species, the main range of species such as *Oxyloma sarsii* and *Vertigo moulinsiana* are not included. Thus, conservation policies should use an integrated strategy of the two approaches, i.e. focusing on biodiversity hotspots and on special habitats.

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Evolutionary History of the Eastern Afro-Montane Biodiversity Hotspot

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Keywords: hotspot, Eastern Arc Mountains, biogeography, Amphibians

The Eastern Arc Mountains (EAM) of Tanzania and Kenya are a biodiversity hotspot with remarkable patterns of endemism. Many taxa are restricted to single blocks of the chain, a pattern thought to reflect a history of persistent but fluctuating forest cover so that the mountains are analogous to an island chain. Using amphibians, a group considered especially sensitive to environmental change, this study investigates the phylogenetic relationships of independently derived amphibian groups to understand biogeographic patterns in the EAM. Temporal and Spatial analysis of the biogeography of the EAM amphibians reveal important insights into the biogeographic patterns in this region.

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Amphibian Diversity, Distribution and Conservation in the Ethiopian Highlands

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Keywords: Amphibians, Bale Mountains, biodiversity hotspots, conservation, Ethiopia, highland forests

The Ethiopian Highlands comprise about 70% of altitudes exceeding 1500 m asl in Africa, and about ten of the peaks extend to over 4000 m asl. The Bale Mountains and the highlands at the southwest of the country lie on opposite, east and west, sides of the Great African Rift Valley. These highlands harbor ecosystems such as Afroalpine forests, broad-leaved deciduous forests, riverine forests, and highland grasslands and are part of the wider ranging Eastern Afromontane biodiversity hotspot. These ecosystems are in turn home to some of the most threatened amphibian taxa in Africa. About 40% of the 65-70 described species of Ethiopian amphibians are endemic to the country, and specifically to the Afroalpine highland forests about 45% of the endemics are threatened at different levels. Despite the importance of these areas in conserving unique biodiversity, human activities such as agriculture and building of new settlements are rapidly threatening amphibian habitats. The main aim of this research is to generate knowledge and data on the diversity and distribution of these highly fragile organisms. Ultimately, the outcome will be vital as an input into prospective conservation prioritization. The methodology followed in this study is to use a combination of molecular and morphological approaches as tools to refine the existing taxonomy of Ethiopian amphibians, as well as potentially reveal new species. The molecular work will focus on nucleotide sequences of DNA purified from tissues of sampled amphibians across the highlands. Diversity will also be combined with biogeographic information to show the distribution patterns of the different species. This includes generation of reliable geographic data and the respective analysis using GIS software. We expect with a refinement of taxonomy and species distributions, appropriate conservation measures can then be best evaluated. In addition, this project will compile available information on Ethiopian amphibian specimens kept at various natural history museums in the world. This will aid in developing a centralized database of amphibians of Ethiopia, an important biodiversity hotspot that needs urgent attention.

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Biodiversity of the brown lemur group: Taxonomy and phylogeography of *Eulemur fulvus* ssp.

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Keywords: Eulemur, taxonomy, phylogeography, speciation

Madagascar is one of the hottest global biodiversity hotspots because of its high rate of endemism. Lemurs are among the best-known endemic Malagasy animals, but their diversity is still not completely assessed. The diverse brown lemurs (*Eulemur* spp.) were traditionally considered as one species, *Eulemur fulvus* with six to eight subspecies, most of which are distributed in allopatric populations across Madagascar. Although all subspecies were recently elevated to full species level, comprehensive genetic and morphological data are still missing. In this study we will characterize the phylogenetic relationships among brown lemurs, using a non-invasive molecular approach by extracting mitochondrial and nuclear DNA from faecal samples obtained from wild populations. Because vocalizations of non-human primates are predominately innate, we also recorded loud calls of brown lemurs to characterize acoustic differences. Morphological data will be obtained from museum specimens and additionally from photos of wild animals will be evaluated. By combining genetic, acoustic and morphological analyses, we hope to contribute to a clarification of brown lemur taxonomy and to reconstruct their historical biogeography.

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Vertical distribution and diversity of epiphytic macrolichens in Central French Guiana – hints for the occurrence of a new forest type

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Recent studies on bryophyte diversity in lowland forests of northern South America suggest the existence of a new type of cloud forest, the "Tropical Lowland Cloud Forest" (TLCF). We have tested the occurrence of TLCF near Säul, central French Guiana, using lichens as indicator taxa. Macrolichen diversity was analysed in two one hectare plots, one situated in putative TLCF in a river valley and one in rain forest on the upper end of a slope. Total macrolichen diversity was higher in putative TLCF than in the slope forest. This difference in diversity seemed to be due to the greater heterogeneity of the TLCF canopy and the preference of hygrophilous blue-algae lichens for the TLCF. We also found that the forest canopy was much richer in species that trunks in the forest understory. The vertical distributions of some macrolichen species shifted to lower heights in rain forest as compared to TLCF. We hypothesize that the detected diversity patterns are mainly determined by microclimate factors, especially humidity, and competition with other epiphytic organisms (bryophytes, ferns).

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Genetic variability in *Dugesia sicula* (Platyhelminthes, Tricladida) asexual and sexual populations from Tunisia and the West Mediterranean

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Keywords: flatworms, phylogeography, gene flow

The genus *Dugesia* is composed of free-living Platyhelminthes that live in freshwater, it includes 70 species, 20 of them in the Mediterranean basin. Of these species *D. sicula* is the most abundant and more widely distributed, populations have been described in North Africa and in the European coast, from Spain to Greece. In the Mediterranean region most species of *Dugesia* present simultaneously diploid populations with sexual reproduction and triploid populations with asexual reproduction by fissiparity. For *D. sicula* however, although it was described in Sicily from a sexual population, at present only triploid populations with asexual reproduction are found despite the abundant number of populations analyzed. Moreover, in a recent molecular study on the phylogeny of the *Dugesia* species in the Mediterranean, it has been found that the genetic variability among *D. sicula* populations geographically distant is very low compared to that found for other species of the genus. This situation could be explained as a consequence of a recent colonization of the area after triploidization, specially favoured by their mode of reproduction, however this hypothesis contradicts all ideas about their low dispersal capability. In this study a thorough sampling for *D. sicula* have been done in Tunisia, resulting in 13 new populations found, two of them being diploid. In order to try to understand the success of the fissiparous forms of this species in the Mediterranean area and its present distribution we have analyzed the genetic variability of all the Tunisian populations and also of 9 populations coming from Sicily, Sardinia, Minorca, Ibiza and Morocco, representing a total of 200 individuals analysed. The variability of the COI gene have been compared for sexual versus asexual populations from Tunisia and with the asexual populations from other localities and a nested clade analysis of the haplotypes found done. The results show a slightly higher diversity within sexual populations vs. asexual ones, and the existence of two main haplotypes, highly differentiated among them, and with the rest of haplotypes presenting a star distribution around one or the other.

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Perspectives for population viability analysis (PVA) in conservation biology

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Keywords: Population Viability Analysis, structured population models, Individual-Based Models

Population Viability Analysis is one of the scientific tools used in conservation biology for decision-making on biodiversity preservation. PVA can be defined as a quantitative modeling of the risk of species extinction. A PVA model uses species and landscape data to simulate population dynamics and extract conservation guidelines; many model runs are integrated to take into account stochastic effects. My research project aims at assessing the relative interest for conservation biology of two features of PVA models:

- Type of model. Two categories of models can be clearly distinguished on the basis of the way individuals are represented in the model: structured population models (SPM) and Individual-Based Models (IBM). SPMs treat all the individuals in the population as being similar and exploit matrices of equations describing population dynamics. IBM simulate the fate of every single individual by using a set of the rules describing the behavior of individuals at each time step under certain circumstances. The question asked is to assess whether the superior level of detail of IBM is worth to improve predictions or not.
- Landscape description. Models can also differ by the representation of resources available to individuals. The simplest approach is modeling habitat patches vs. hostile matrix, but it is also possible to include both the spatial and temporal dynamics of the resources into the model. Here the question is whether the simplification made in the patch vs. matrix approach is adequate.

To answer these two questions, a series of models of different complexity levels will be developed for two butterfly species – *P. ennomia* and *B. acqulionaris*. Comparison to the results produced by different approaches is expected to reveal the population processes, which are better depicted by either of them. Additionally, studying two species will permit the check of the transferability level of submodels between species. As a result, suggestions are to be made regarding which modeling approach has to be used in a certain case, in order to efficiently and timely suggest the measures needed for effective species preservation

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On bryophyte diversity hotspots in Serbia

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Keywords: bryophyte, diversity, hotspots, Serbia

The knowledge on bryophyte flora of Serbia (SE Europe) increased significantly during last decade. However, comparing to vascular plants where highlands of Serbia represent one of the European diversity centers, it can not be assumed that the same areas are diversity hotspots for bryophytes. Also, bryophyte express many peculiarities due to their specific biology. Bryophytes have overlapping with vascular plant diversity hot spots only to some extent, mainly when species diversity in huge space is taken into account. In smaller space studied, bryophyte species diversity often overtop vascular plant species diversity. Genetic diversity among bryophyte species remain almost underexplored in Serbia. Refugial and protected area are not always the hotspots of bryophyte species genetic diversity and so with aim to make good action plans for protection and conservation, it should be taken into consideration also the spots where bryophyte species express higher genetic diversity within popullations presented. The case studies on different species showed the regions that have no high bryophyte species diversity can have high genetic diversity within same species and so such regions should be protected as well. On the other hand, in some cases genetic structure of selected bryophyte species (expressed by different genotypes inferred by isozymes and/or selected DNA marker(s)), in some protected and well conserved areas remains generally uniform.

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Distribution of two sympatric mouse lemurs in Western Madagascar: the world's smallest primate, *Microcebus berthae*, and its sister species *M. murinus*"

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Keywords: population ecology, interspecific competition, coexistence, habitat selection, Cheirogaleidae

Menabe Central was identified as one of the two areas of highest conservation priority in Madagascar by Conservation International and declared a protected area in March 2006. However, still little is known about the distribution of the eight lemur species inhabiting the major remaining tract of dry deciduous forest in Western Madagascar (ca. 400.000ha). Menabe Central is the exclusive global range of the smallest primate of the world, *Microcebus berthae*, where the species occurs in low population densities. In spite of its peculiar status population parameters are widely unknown, and the species is presently not evaluated in the red list of IUCN (2007). Aside of this flagship species, four other nocturnal cheirogaleid species inhabit the forest, all together representing a taxonomic assemblage: the congener *M. murinus*, *Mirza coquereli*, *Cheirogaleus medius*, and *Phaner pallescens*. Our main aim was to identify determinants for the mouse lemurs' inhomogeneous distribution and for their coexistence despite ecological similarity. Distributions and abundances of the five cheirogaleids were assessed by distance sampling and line trapping on different spatial scales. Interspecific effects, differential habitat selection, and anthropogenic disturbances were considered potential determinants of the mouse lemurs population structure. Lemur diversity and abundance were highest in well protected areas where anthropogenic influences are comparatively low. On a large scale, *M. berthae* was found in highest density in the northern part of the forest part, whereas *M. murinus* mainly inhabited the south. *M. murinus* appears to have a continuous medium-scale distribution, even occurring in heavily degraded habitats, while the other species show a patchy distribution on the same scale, with populations being largely restricted to pristine habitats. The two mouse lemurs show a negative spatial association on both, medium and small spatial scales, pointing to interspecific competition. Results will provide essential data to accurately estimate the conservation status in *M. berthae*, and will likely indicate the mechanisms that allow for the coexistence of *M. berthae* and *M. murinus*.

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Comparative phylogeography and genetic diversity of two montane aquatic insects in Europe

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Keywords: Refugia, Postglacial dispersal, mtCO1 sequences, climate change

In central Europe the legacy of the Pleistocene ice ages and their effects on the European biota have been subject to much study over the last few decades. Repeated climatic oscillations in the Pleistocene led to numerous range expansions and regressions in much of the world's biota. Recent studies have shown that aquatic species often exhibit different phylogeographic patterns than terrestrial species, reflecting their very different life histories and varied responses to past climate change. The main aim of the project is to test hypotheses on differences in phylogeographic history of two montane aquatic species across Europe: the stonefly *Arcynopteryx compacta* and the mayfly *Ameletus inopinatus*. The species have similar geographical distributions, restricted to mountain ranges with peaks of higher elevations, but vary in life-history pattern and dispersal capabilities. By studying mtCOI and microsatellite variation across each of these species entire European distribution ranges, we investigate the phylogeography to make inferences about their population history and discuss these in a comparative framework. By revealing consistent or different patterns between species with similar distributions the results from this comparative study will improve our understanding how historical climate changes directly influenced the evolution of populations and species. Identifying common threads in the history of taxa is also important for conservation biology. Both selected species of this study are listed as endangered by the World Conservation Union (IUCN). Through determining and comparing levels of genetic diversity within and between populations we will be able to say how aquatic insects, particularly those exhibiting cold tolerance, have dealt with global change and climatic shifts in the past, which habitats need to be preserved or restored to maintain the highest possible levels of genetic diversity, and which areas could play a role as refugia in the context of future climate change.

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Hotspots of diversity and cross-taxon congruence of a hyperdiverse insect taxon, vertebrates and plants across the Palaearctic

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Keywords: carabid beetles, cross-taxon congruence, diversity, hotspots, endemism

Macroecological studies on diversity distributions are often used in regional or global conservation planning, e.g., to identify biodiversity hotspots. However, previous studies are biased towards specific taxa (plants, vertebrates). Invertebrates, comprising the bulk of global biodiversity and being important in ecosystem functioning, are largely ignored. Yet, understanding general patterns of biodiversity and developing adequate conservation strategies requires integration of invertebrates. We studied spatial patterns of carabid beetle diversity and cross-taxon congruence with vascular plants and vertebrates across the Palaearctic, trying to reassess the generality of results from studies on the latter taxa. As a hyperdiverse insect taxon, carabids offer an excellent opportunity to analyze macroecological patterns which might be representative of many other species-rich invertebrate groups. We compiled a database of carabid, plant, amphibian and reptile diversity for 107 Palaearctic countries/regions. Based on decreasing completeness of carabid data, we subdivided our dataset into the western and eastern Palaearctic and Chinese provinces. Species richness and endemism of carabids was highly congruent with patterns of plants and vertebrates across the Palaearctic. Collective centers of diversity were identified for the well-sampled western Palaearctic, showing highest diversity in Southern Europe. Weak relationships involving carabids were only found for badly sampled Chinese provinces. China still shows a strong increase in species numbers of carabids, with more than 50% of recent new descriptions in the Palaearctic being from China. But even with this incomplete data, China harbors 25% of all Palaearctic carabid species. Our study extends the limited knowledge on broad-scale invertebrate distribution. It shows that diversity patterns of a hyperdiverse insect taxon are similar to those of well-studied plants and vertebrates and that diversity hotspots based on data of the latter are likely to include high diversity of invertebrates. China qualifies as an outstanding multi-taxon hotspot, requiring intense biodiversity research and conservation effort.

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Population Genetics and Phylogeography of the rare Mayfly *Ameletus inopinatus* in Europe

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Keywords: Microsatellites, refugia, migration routes

The rare mayfly *Ameletus inopinatus* inhabits mountain ranges of higher elevation on the British Isles and in Central Europe. In northern Eurasia, it is known from Scandinavia to western Siberia, where it occurs also at lower altitudes. It is considered a representative of the Eurasian, boreo-montane biome-type. Its absence in the Alps and the Pyrenees indicates that *A. inopinatus* was not distributed in Europe during the last ice age (Haybach 2003), and is a recent colonizer of Central Europe with postglacial retreat to higher elevations (Malicky 1988, Haybach 2003). Under this scenario we would expect to observe little historic population differentiation measured by mtCOI sequence variation between isolated montane populations. As the zoogeographic origin of the species lies in northern Central Eurasia (Haybach 2003) we would expect to trace the colonization from north-eastern and eastern Europe towards the northern and central European mountain ranges. However, because the species is limited to higher mountain ranges in Central Europe we expect that it is presently not dispersing between mountain ranges and expect to see stronger, recent population differentiation as measured with microsatellite variation. The microsatellite loci that we developed primers for in this study are sufficiently variable to help detect population differentiation. Together with mitochondrial sequence data, we analyse nine microsatellite loci to detect patterns of population structure and use coalescent estimates of migration rates to examine the phylogeography of the rare mayfly *A. inopinatus* across its European range.

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Positive correlation between genetic diversity and fitness in a large, well-connected metapopulation

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Background

Theory predicts that lower dispersal, and associated gene flow, leads to decreased genetic diversity in small isolated populations, which generates adverse consequences for fitness, and subsequently for demography. Here we report for the first time this effect in a well-connected natural butterfly metapopulation with high population densities at the edge of its distribution range.

Results

We demonstrate that: (1) lower genetic diversity was coupled to a sharp decrease in adult lifetime expectancy, a key component of individual fitness; (2) genetic diversity was positively correlated to the number of dispersing individuals (indicative of landscape functional connectivity) and adult population size; (3) parameters inferred from capture-recapture procedures (population size and dispersal events between patches) correlated much better with genetic diversity than estimates usually used as surrogates for population size (patch area and descriptors of habitat quality) and dispersal (structural connectivity index).

Conclusion

Our results suggest that dispersal is a very important factor maintaining genetic diversity. Even at a very local spatial scale in a metapopulation consisting of large high-density populations interconnected by considerable dispersal rates, genetic diversity can be decreased and directly affect the fitness of individuals. From a biodiversity conservation perspective, this study clearly shows the benefits of both in-depth demographic and genetic analyses. Accordingly, to ensure the long-term survival of populations, conservation actions should not be blindly based on patch area and structural isolation. This result may be especially pertinent for species at their range margins, particularly in this era of rapid environmental change.

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Decoupling of molecular and morphological evolution in endemic amphipods from Ochridagammarus complex of species (Lake Ohrid, Macedonia).

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Keywords: Lake Ohrid, ancient lake, Gammaridae, mitochondrial DNA, molecular evolution

The Balkan Lake Ohrid, similarly to others from the set of "ancient lakes", preserves numerous endemic species and genera of various freshwater animals, including amphipods. The strongly marked endemism and diversity have been most likely caused by its continuity of existence, exceptional geological age and the long isolation of the lake from outside water systems. In Lake Ohrid seven of the amphipod species from genus *Gammarus* Fabr. are endemic and belong to the *Ochridagammarus* complex of species. All these species are difficult to distinguish from each other on morphological basis even though they settled various ecological niches of the lake. Karyologically, these species are more variable than any other examined European *Gammarus* species. These observations are especially interesting taking into account that amphipods of the superfamily Gammaroidea are known from the high morphological diversity, apparent morphological convergence of unrelated lineages in similar environments and evolutionary plasticity of many characters. The amphipods from other ancient lake Baikal in particular are by far the most morphologically diverse gammaroideans. This study aimed to show the decoupling of morphological and molecular evolution within the *Ochridagammarus* complex of species based on genetic variation of partial sequence of the cytochrome c oxidase subunit I (COI) gene. The problems of origin and taxonomic status of the different mtDNA genotypes within the complex are discussed.

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