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Programm

09:00 **Begrüßung**

Gerhard Tarmann (Ferdinandeum Innsbruck)

Ulrike Aspöck (NHM Wien, Präsidentin NOBIS)

09:30 – 10:30 **Vorträge** Chair: *Erwin Meyer* (Uni Innsbruck)

Birgit Schlick-Steiner (Uni Innsbruck) Integrative Biodiversitätsforschung: Beispiele aus der Welt der Ameisen

Björn Berning, Mathias Harzhauser & Werner E Piller (OÖLM Linz, NHM Wien, Uni Graz)
The importance of deep time information for our understanding of modern ecosystems and biodiversity

10:30 – 11:00 **Postersession mit Kaffee**

11:00 – 12:00 **Vorträge** Chair: *Elisabeth Haring* (NHM Wien)

Julia Walochnik (Meduni Wien) Proteom-Phylogenie bei Akanthamöben

Nikola Szucsich (Uni Wien) Die Suche nach dem einen Baum im Wald der Arthropoden

12:00 – 13:00 **Mittagspause**

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13:00 – 14:00 **Vorträge** Chair: *Helmut Sattmann* (NHM Wien)

Anita Juen & Yasmin Klarica (Uni Innsbruck) DNA-barcodes in der Systematik am Beispiel der Regenwürmer - Fluch oder Segen

Gerald Timelthaler (Uni Wien) Visuelle Ökologie und Opsin-Evolution bei Kratersee-Cichliden aus Kamerun: Bedeutung für eine sympatrische Artbildung

14:00 – 14:30 **Postersession mit Kaffee**

14:30 – 16:30 **Vorträge und Diskussion** Chair: *Peter Comes* (Uni Salzburg)

Andreas Tribsch (Uni Salzburg) Biodiversität in den Alpen und Karpathen: Das Projekt IntraBioDiv.

Andreas Maletzky (Uni Salzburg) Neues zum schwierigen taxonomischen Status der Kammmolche in Österreich

Mathias Harzhauser & Oleg Mandic (NHM Wien) Mollusc Evolution in Neogene Lake Systems of Central and south-Eastern Europe

Ulrike Aspöck (NHM Wien) NOBIS Austria – Ausblick

16:30

Gerhard Tarmann: Führung durch die naturwissenschaftlichen Sammlungen des Ferdinandeum

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N B I S AUSTRIA 2

ABSTRACTS

Describing acoel flatworms in the new millennium

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Acoel flatworms are predominantly vermiform, marine, and microscopic animals, which are often difficult to recognize due to a paucity of characters and a high plasticity of these characters.

I show how a broad array of tools needs to be applied to properly establish relationships within the Acoela. Indispensable are the classical methods of natural history - observing appearance, behavior, life cycles, and ecological interactions - as well as histology and light microscopy. Where these techniques fall short, newer techniques of microscopy, including electron microscopy and confocal laser scanning microscopy, provide higher resolution and three-dimensional imaging capacity. For example, EM gives critical information on arrangement of organelles in spermatozoa, and CLSM yields images of 3D patterns of musculature among internal organs. Additionally, molecular techniques, especially sequencing of nucleic acids like the 18S rDNA, provide now-indispensable characters for phylogenetic reconstruction at various levels of relationships. Modern systematics of the Acoela, then, incorporates classical and new techniques that only together can support us with the amount of information and accuracy needed to decipher the evolutionary history of life.

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Conflicting mitochondrial and nuclear data in the six toothed spruce bark beetle *Pityogenes chalcographus*

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The six toothed bark beetle, *Pityogenes chalcographus* (Coleoptera, Scolytinae) is a major pest in European spruce stands. Analysis of about 10% of the mitochondrial DNA revealed a maximum sequence divergence of 2.3% and the sympatric coexistence of two genetically distinct groups, a pattern mostly observed in populations that initially evolved in allopatry and afterwards came in secondary contact. These findings are consistent with crossing barriers observed by E. Führer in the 1970ies and with the hypothesis that during Quaternary glaciations *P. chalcographus*, like its host tree, was restricted to at least three separated refugial areas.

To further elucidate the beetle's population structure we analyzed four highly polymorphic nuclear microsatellite loci, a 860 bp part of the 28S rDNA gene and a 1 kbp fragment of the Elongation Factor 1 α gene. Other than mitochondrial DNA all nuclear markers show low levels of genetic diversity across Europe. These results are indicative for unequal male and female genealogies. We discuss sex biased dispersal rates, repeated bottleneck effects due to outbreak associated fluctuations in population size and the presence of the reproductive manipulating endosymbiont *Wolbachia* as potential factors shaping the incongruent history of the beetle's nuclear and mitochondrial genome.

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The importance of deep time information for our understanding of modern ecosystems and biodiversity

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It is generally regarded that the present is the key to the past. While this is true for many aspects, such as the physiology of organisms, the opposite has certainly greater validity when it comes to addressing questions concerning larger scale patterns and processes, e.g. the history and evolution of higher taxa, modern ecosystems, or global biodiversity and biogeography. Considering the origin of modern floras and faunas during the Mesozoic, the constant restructuring of ocean basins and continental plates throughout the Mesozoic and Cenozoic, and the fact that the average lifespan of species is several million years, negligence of data from the fossil record (i.e. discarding the largest part of the history) may lead to erroneous conclusions. For instance, the prevalent assumption that the modern marine faunal composition and diversity of the tropical Indo-West Pacific were largely shaped by effects of the ice ages during the last 2 million years has recently been refuted and shown to have evolved considerably earlier during the Miocene (Renema et al., 2008). Other studies have demonstrated that the biogeographic histories of a number of taxa are much more complex than suggested by the present-day distribution of their species (e.g. Harzhauser et al., 2007), which is important to bear in mind when interpreting genetic data. Therefore, integrated studies, making use of both molecular phylogenetic data as well as biogeographic and palaeoclimatologic information from the fossil record, are the most promising ones for our understanding of the evolution of modern ecosystems, hotspots of biodiversity, and the possible response of biota to various effects of climate change.

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Species traits in the alpine stream fauna: promising tools to assess impacts from environmental change

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Alpine river systems are fed by glacial icemelt, snowmelt, and groundwater, share common features (e.g. steep gradients, high flow velocities and dynamics) but each source produces a characteristic discharge regime and a distinctive suite of physical and chemical characteristics. The distribution of snow, ice, and groundwater springs varies spatially from stream-reach to catchment scale, resulting in stream segments with characteristics, reflecting the different runoff sources. Recent investigations focused on the large variety of natural freshwater ecosystems in the Hohe Tauern Nationalpark, and based on hydromorphological conditions at catchment and reach scale specific river types were defined. Glaciation in the catchment turned out to be a major factor for defining the hydromorphological conditions. Subsequently, we tested the effect of glaciation on the bottom fauna in applying a preliminary set of species traits, indicating strategies and adaptations of resilience and resistance as well as to face environmental harshness (Füreder 2007). Our results demonstrated the high degree of adaptation of the bottom fauna in alpine streams but especially in glacial streams. As current climate change scenarios propose major impacts at both, high altitude and latitudes, considerable changes within the faunal assemblages including species number, densities and the distribution of species traits are to be expected. Moreover, the application of species-traits methodologies is recommended as an additional instrument in freshwater monitoring programs.

References

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Palaeo-Danube delta paradise: The vertebrate fauna of Atzelsdorf (Lower Austria, Late Miocene)

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The site of Atzelsdorf – an abandoned gravel pit about 30km north of Vienna – is situated at the western margin of the Vienna Basin at the borderland to the North Alpine Foreland Basin. The section represents Upper Miocene deposits of the paleo-Danube and its delta, pouring and discharging south-eastwards into the Lake Pannon. The sediments of this braided-delta system are united into the so-called Hollabrunn-Mistelbach Formation. However, the top of the Atzelsdorf section is formed by a bed, reflecting a transgression of Lake Pannon westwards into the delta wetlands (HARZHAUSER et al. 2004). Even if no absolute dating exists for the Atzelsdorf section, this flooding event is a well known marker, which falls within the Vienna Basin Pannonian Zone C and corresponds to an absolute age of c. 11.0-11.1 ma (HARZHAUSER et al. 2004). The underlying vertebrate fossil bearing layers at Atzelsdorf yielded the following vertebrate fauna: Quantitatively dominating are ruminants (*Miotragocerus*, *Dorcatherium*, *Micromeryx*, *Euprox*, *Palaeomeryx*). Somewhat rarer faunal elements are carnivores (*Sansanosmilus*, *Plesiogulo*, *Martes*, *Thalassictis*, *Semigenetta*), equids (*Anchitherium*, *Hippotherium*), rhinos (*Aceratherium*, *Brachypotherium*), chalicotheres (*Chalicotherium*), suoids (*Taucanamo*, *Parachleuastochoerus*, *Listriodon*), proboscideans (*Deinotherium*, *Tetralophodon*), beavers (*Trogotherium*, *Chalicomys*), lagomorphs („*Amphilagus*“), but also reptiles (*Pseudopus*, testudines indet.), birds (Anseriformes), and fishes. Due to sedimentary aspects of the Atzelsdorf section, to the position of the locality within the reconstructed delta system, and to the preservation of the vertebrate fossils it can be concluded that the fauna represents a relatively short-termed accumulation event of perhaps a few thousand years, that might range within about 11.2 -11.1 ma. Thus, the fauna represents a well dated snapshot assemblage of the early Lower Miocene which may serve as marker for comparisons and correlations of other Vallesian faunas in central Europe.

Harzhauser, M., Daxner-Höck, G. & Piller, W.E. (2004): An integrated stratigraphy of the Pannonian (Late Miocene) in the Vienna Basin. - *Austrian Journal of Earth Science*, 95/96: 6-19.

A giant among dwarfs – *Gyatermes styriensis*, a new termite from the Late Miocene of Styria

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Modern climates supporting “giant” insects are tropical or warm xeric environments, while such hotter conditions along with hyperoxic atmospheres were conducive to enormous arthropods in Paleozoic and other palaeofaunas. Among the ecologically pervasive and highly social termites, such giants are exceptionally rare. Recently, however, a giant termite, representing a new genus and species, which is primitive in overall features but shares some similarity with the dampwood termites (Termopsidae s.l.), was recovered in floodplain deposits of a meandering river system at Paldau (Late Miocene, Lower Pannonian, c. 11.3 mya). The associated insect fauna consists of beetle fragments (e.g. ground beetles) and wings of formicine ants, crane flies and brachyceran flies as well (Engel and Gross, in press a, b). Earlier palaeobotanical investigations indicate a warm-temperate, or even subtropical climate. *Gyatermes styriensis* gen. n. et sp. n. is represented by a relatively complete forewing, complete with basal scale. The presence of this species in the Late Miocene fauna of Europe indicates that climatic conditions were appropriate for the persistence of species and colonies requiring relatively stable, warm conditions. The largest extant reproductives being those of the genus *Syntermes* (Termitidae: Syntermitinae) from the tropics of South America, with individual wings up to 35 mm in length. Among more primitive termite families, several species of the family Termopsidae and the sole survivor of the Mastotermitidae, *Mastotermes darwiniensis*, are all robust and can have wing lengths up to 26 mm. The new discovery was certainly a giant among living and fossil termites and is the largest fossil termite on record.

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- Engel, M.S., Gross, M. (in press, b): The Pannonian Insect Fauna of Styria: A Preliminary Overview. *Austrian Journal of Earth Sciences*.

Distinct phylogeographic patterns in widespread corvid birds revealed by mitochondrial sequences

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We used the mitochondrial control region as a molecular marker to analyse widespread Palearctic corvid taxa with respect to phylogeographic patterns. In five cases the DNA-based trees showed a deep split into two lineages: Within *Corvus corone* (carrion crow), *Corvus frugilegus* (rook), and *Pica pica* (magpie) and between the species pairs *Corvus monedula* - *Corvus dauuricus* (jack dows) and *Cyanopica cyanus* - *Cy. cooki* (azure-winged magpies). Interestingly, in these five examples the genetic pattern and level of divergence between clades are rather similar, although the respective taxa display a variety of distribution patterns from disjunct to para/allopatric and continuous. Especially interesting is the finding that in *C. corone* the mitochondrial clades do not correspond to subspecific division or plumage morph.

In contrast to the taxa with west-east pattern, no differentiation into clearly divergent lineages was detected in three corvid taxa: *Corvus corax* (common raven), *Perisoreus infaustus* (Siberian jay), and *Nucifraga caryocatactes* (Eurasian nutcracker). To explain these two types of phylogeographic pattern (west-east pattern and single group pattern) one has to take into account ecological conditions which may have accompanied the climatic changes during the Pleistocene. A prominent factor influencing the pattern of genetic differentiation seems to be the preference for either open to semi-open habitats (west-east pattern) vs. forest dominated habitats (single group pattern).

Diploma Thesis:

A Study on the Ants of the National Park Thayatal

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The aim of this diploma thesis was to provide an insight into the diversity of ants (Hymenoptera, Formicidae) of some forest sites and dry meadows of the National Park Thayatal. The National Park is located in the North of Lower Austria and is with 1330 ha Austria's smallest National Park. Over a length of 25 km the river Thaya forms the international boundary to the Czech Republic. It separates the Austrian National Park Thayatal from the Czech Národní Park Podyjí, which is nearly five times as big as the Austrian part. Together they represent the International Park Thayatal/Podyjí.

From 2005 to 2007 several studies were carried out to examine the diversity of some selected orders of insects, spiders and gastropods. During 2005 and 2006, altogether 22 forest sites were investigated by using pitfall traps. The classification of the collected ants was the first part of the diploma thesis. In a second study 2007 twelve areas of dry grass meadows on open rocky sites of the upper slopes of the Thaya and the Fugnitz valleys were sampled also with pitfall traps as well as hand collecting and tree traps. The ants were preserved in 70 percent alcohol. The specimens were determined with a 40x magnifying Wild M3 binocular using the Identification Key for Central European Ants of SEIFERT (2007) and classified according to the Red List of Ants of Lower Austria (STEINER *et al.*, 2003). Finally photos (head, lateral view and dorsal view) of one or more specimens of every ant species were taken.

In the forest habitats 25 ant species were found, among those eight were red list species. On the dry meadows 40 species could be found, 24 of them registered on the red list. Seven species were found on the meadow near the Fugnitz River. Including three further species records offside the official investigation sites, a number of 57 ant species was found altogether in the National Park Thayatal. For the Czech Národní Park Podyjí BEZDĚČKA (1999) indicated 67 ant species until 1999. The combined species list of both parts north and south of the Thaya contains a total number of 76 ant species for the International Park Thayatal/Podyjí.

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SEIFERT, B., 2007: Die Ameisen Mittel- und Nordeuropas. Lutra Verlags- und Vertriebsgesellschaft, Görlitz/Tauer, 368 pp.

A giant early Miocene sunfish from the North Alpine Foreland Basin and its implication for molid phylogeny

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The Molidae Ranzani, 1839 comprise a family of ocean sunfishes and represent the largest extant bony fishes, reaching lengths of over 3 m. All known Molidae are characterized by a stout, truncated shape, with a body that ends rather abruptly just behind the dorsal and anal fins. They are epipelagic and are distributed worldwide in tropical to temperate seas. Due to their largely cartilaginous, weakly ossified and spongy skeleton, the fossil record of the Molidae is very poor. Representatives of the family Molidae are mostly represented by isolated jaws and dermal scale plates. Complete skeletons even of modern sunfishes are rare in museum collections and, unsurprisingly, no complete Molidae skeletons have been reported so far in the fossil record. Consequently, the record of three fossil Molidae skeletons, found by private collectors during construction work for a hydroelectric power plant near Pucking in spring 1980, is extremely outstanding. The specimens were associated with a complete dolphin skeleton, numerous small teleost fishes and scattered lucinid bivalves along with a diverse algal- and leaf flora. The pelitic deposits are part of the Ebelsberg Formation and are dated as Aquitanian (lower part of nannoplankton Zone NN2) based on the presence of *Helicosphaera scissura* and *Helicosphaera sellii* and the absence of *Helicosphaera ampliaperta*. In terms of regional stages, the deposits are part of the upper Egerian stage and are c. 22 Ma old. During that time, the area was part of the Central Paratethys Sea, and the North Alpine Foreland Basin was covered by a deep sea. The section was situated on the northern shelf of that sea within the outer neritic zone.

The skeletons represent the the oldest known modern-type sunfish, which will be described as the new genus *Austromola*. A giant size of more than 320 cm body length and 400 cm maximum diameter can be calculated based on linear extrapolation of morphometric parameters of recent *Mola mola*. Thus, this early Miocene Molidae was the largest sunfish known so far. Phylogenetic analysis shows that it forms a sister-clade of *Ranzania* together with *Mola* and *Masturus*. Therefore, its Aquitanian age suggests an Oligocene age for the origin of *Ranzania* and an at least early Oligocene age for the last common ancestor of the extant Molidae. The radiation of the (*Austromola*(*Mola*+*Masturus*)) clade occurred soon thereafter during the Early Miocene and, consequently, oldest *Mola* fossils turn up in Middle Miocene deposits.

Mollusc Evolution in Neogene Lake Systems of Central and South-Eastern Europe

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The gastropod γ -diversity of 12 Neogene lake systems is evaluated. In total, 1184 gastropod taxa from 119 localities are recorded deriving from the Early Miocene *Rzehakia* Lake System, the Early to Middle Miocene Dinarid Lake System, Lake Skopje, the Paratethyan Sarmatian lakes and the South German lakes, the Late Miocene Lake Pannon, the Pliocene lakes Dacia, Transylvania, Slavonia, Kosovo and Šoštanj as well as the Holocene Lake Petea. Each lake system is characterised according to its faunistic inventory and endemism.

Many papers dealing with extant mollusc faunas of Eurasian aquatic systems refer to Lake Pannon when explaining extant biogeographic distributions and phylogenetic relations. Our dataset, however, points to a much more complex history of the faunas reaching back at least to the Early Miocene. High endemisms and low inter-lake relations of the Early and early Middle Miocene lake systems suggest that these experienced the first autochthonous evolutionary pulses. Many genera display their FADs in these systems (e.g. *Marticia*, *Kosovia*, *Orygoceras*, *Pyrgula*, *Dianella*, *Emmericia*). This pattern changed at the Middle/Late Miocene boundary when Lake Pannon inherited numerous species which evolved prior in the Sarmatian Paratethyan lakes. On the generic level, parts of the Lake Pannon fauna can be traced back even to the Early Miocene faunas of the Dinarid Lake System. The combined effect of heritage and new radiations in a geochemically unique aquatic system allowed Lake Pannon to accumulate an enormous diversity of 497 gastropod species. Lake Pannon itself acted as a stepping stone for species and genera which settled the descendant freshwater systems such as Lake Slavonia, Lake Dacia and Lake Transylvania. Generic endemism thus decreased during the Pliocene.

The Neogene lake systems represent a unique laboratory of evolution. Examples of parallel evolution and the phenomenon of iterative morphologies make the analysis of ancient lake faunas a tantalizing endeavour. Repetitive morphologies of related lineages have been documented to occur in Lake Pannon melanopsids. Even more interesting are such iterative developments of unrelated taxa as shown for DLS and LP dreissenids.

*Evolutionary processes in continental island systems:
molecular phylogeography of the Aegean *Nigella arvensis*
complex (Ranunculaceae) by means of AFLP markers

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The complex paleogeographic history of the Aegean Archipelago makes this mostly continental island system a unique biogeographic setting for the study of plant evolution and speciation. In this area, *Nigella* has radiated during the (Late) Quaternary into six species (12 taxa) of mainly allo- or parapatric distribution (*N. arvensis* complex). While most taxa are outcrossing and interfertile, two species are predominantly selfing and reproductively isolated from each other and the former. Phylogeographic evidence based on chloroplast (cp) DNA (Bittkau & Comes, 2005; Comes *et al.* 2008) indicated that geographic isolation, limited seed flow, and genetic drift had a major role in the evolution of the complex, but failed to resolve inter-species relationships. Here, we will re-address these issues based on a survey of amplified fragment length polymorphisms (AFLPs) across all species of the complex (48 populations/565 individuals). Results and conclusions drawn from genetic distance, population structure and diversity analyses are: (1) Most nominal species of the complex are genetically distinct entities, suggesting that erratic instances of cpDNA haplotype sharing across species boundaries are due to incomplete lineage sorting rather than ongoing hybridization. (2) In line with the cpDNA data, AFLPs are supportive of the existence of a major phylogeographic break in the eastern Aegean in place of "Rechinger's line", though with the difference of providing a finer phylogeographic/taxonomic resolution throughout the study area. (2) The enigmatic disjunct distribution of *N. arvensis* ssp. *brevifolia* in Crete and Rhodes likely reflects the existence of two separate species. (3) Although the spatial-temporal origin of the two selfing island taxa (*N. doerfleri*, *N. stricta*) is not yet fully understood, they clearly do form separate genetic entities rather than being nested within the outcrossing alliance. (4) Given the genetic distinctness of *N. doerfleri*, its present co-occurrence with the outcrosser *N. degenii* in the Cyclades is best interpreted as secondary contact. (5) As expected from theory, in both selfing species, genetic diversity is markedly reduced and between-population differentiation increased compared to the outcrossers, most likely as a result of reductions in effective population size due to selfing.

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* Dieser Abstract wurde nachträglich in der PDF-Version des Abstractbands ergänzt.

DNA-barcodes and biological systematics exemplified on earthworms – boon or bane?

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Nucleotide sequence variation has been used to investigate evolutionary relationships for some years, when Hebert et al. (2003) proposed to use “DNA barcodes” as a taxonomic tool. He favoured the cytochrome c oxidase I (COI) gene that appears to possess a greater range of phylogenetic signal than any other mitochondrial gene as the core of a new molecular identification system. This concept provoked controversial discussions. In five years of research DNA barcodes allowed to identify a wide range of species and have been used in numerous scientific domains (e.g. ecology, biomedicine, evolutionary biology, biogeography). Moreover, it became possible to identify specimens which miss morphological characteristics for accurate identification (e.g. juvenile stages, stomach extracts, food). Beside such successes, numerous limitations arose due to incomplete coverage of the existing diversity, intra-specific variations, differences in evolutionary rates of the investigated genes and anomalies in mitochondrial inheritance. Based on sequences of earthworms, we will illustrate some of the risks inherent to molecular identification systems and discuss the consequences for taxonomy and applications in evolutionary biology and ecology.

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Closing a gap – Discovery of a rare fossil leather sea urchin

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The echinothurioids or "leather sea urchins" are a group of echinoids characterised by their delicate skeleton with imbricate plates. Unlike most other echinoids, which have a relatively strong corona and are often preserved as fossils, the echinothurioids have an extremely poor fossil record. Apart from *Echinothuria floris* WOODWARD from the Santonian of England of which eight specimens are known. The present record is the only other fossil echinothurioid known from "complete" tests. Disarticulated material, mainly spines, have been reported from the Santonian to Pliocene of Europe and New Zealand.

The present specimens were recovered from the Lower Badenian (Langhian, Middle Miocene) marls overlying the corallinacean limestone of the Weissenegg Formation, outcropping in the quarries of the Lafarge cement company in Retznei, Styria.

Extant echinothurioids are almost exclusively confined to deep sea habitats, although some species of *Asthenosoma* are also found in shallow depth. The echinothuriids are epibenthic scavengers, which seem to ingest mainly macroplant debris, but may also feed on invertebrate prey. The spines and pedicellariae of some species contain strong toxins protecting the animals from predators.

Despite their poor fossil record the echinothurioids are a considerably old group. The earliest representatives known (*Pelanechinus*) come from Middle to Upper Jurassic sediments of England. In contrast to later members of this group they have a relatively strong skeleton and occur in shallow water environments. *Echinothuria* from the Late Cretaceous of England is the first and only well known fossil crown-group member of the echinothurioids.

A cladistic analysis was carried out to map the new taxon from the Middle Miocene of Austria on published trees for the echinothurioids. An extended set of characters, yielded a single most parsimonious tree that places the new taxon (*Retzneiosoma jaseneki*) as sister-group to all living echinothuriinids and *Echinothuria* as sister-group of all living echinothuriinids plus the new taxon. This result is supported by the stratigraphic distribution of the taxa in question.

Hemipatagus & *Maretia* – a sea urchin tale of confusion

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The sea-urchin genus *Hemipatagus* is a poorly understood fossil spatangoid taxon that usually has been treated as subjective synonym of the extant genus *Maretia* but was subject to considerable dispute within the scientific community. Restudy of the type species of *Hemipatagus*, and a range of presumably related spatangoids including *Lovenia* and *Maretia* has been carried out to solve this problem. Cladistic analysis shows that *Hemipatagus* is not close to *Maretia*. In contrast, it is closely related to *Lovenia* and should be placed in the Loveniidae, which is here confirmed to represent a monophyletic group. Characters of the adapical tuberculation suggest that in *Hemipatagus* an internal fasciole is present in early ontogeny, but lost in the adults

These results explain the disjunct spatial and temporal distribution pattern observed in these sea urchins. *Hemipatagus* first appeared in the Eocene, c. 50 million years ago together with *Lovenia* and vanished at the end of the Middle Miocene (~ 12 million years ago). Up till now it never was recovered from fossil deposits of the Indo-Pacific region. *Maretia*, in contrast, appeared much later in the Pliocene (~ 5 million years ago) of the Red Sea and occurs all over the Indo-West-Pacific region today.

When do cave fish get blind? Genetic analysis of the cyprinid fish *Garra barreimiae* from cave and surface populations in Oman

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The cyprinid fish *Garra barreimiae* is an endemic of the Hajar Mountains in southeast Arabia, inhabiting caves and surface waters. Individuals from cave waters display characteristic features connected with their subterranean habitat, lacking eyes and pigmentation. In contrast, *G. barreimiae* from surface waters have functional eyes and well-developed pigmentation. It is unknown to which degree the development of functional eyes in *G. barreimiae* is genetically determined or induced by environmental factors. As a first approach we wanted to test whether there is a genetic differentiation of the two morphotypes, which would indicate that the developmental differences are based on genetic traits. We investigated 126 samples of *G. barreimiae* from three different parts of the Al Hoota cave system as well as six more distant populations of the Hajar Mountains in Oman. As a genetic marker we used sequences of a 438 bp section of the mitochondrial control region. Between the populations from the Al Hoota cave system with non-functional eyes and the adjacent surface population with functional eyes there is no clear genetic separation, indicating either gene flow or very recent divergence. In contrast, some surface populations from geographically separated localities possess quite distinct haplotypes.

Genetic differentiation of selected Alpine land snails in Austria

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The widely accepted opinion about locations of Pleistocene refugia in the Mediterranean and southeastern Europe has been challenged by recent studies postulating more northerly or even Alpine refugia. The focus of our project is to establish a more detailed view on differentiation processes in the Alpine region, colonization routes, and finally on the evolution of species. The results will be the basis for evaluating current systematics and taxonomy of the selected taxa. In the centre of our interest are three Eastern Alpine land snail species: *Cylindrus obtusus*, *Orcula dolium*, and *Trochulus hispidus*. Like many Alpine snail species, *O. dolium* as well as *T. hispidus* have been subdivided into several subspecies based on minor morphological differences and/or geographic and altitudinal distribution. Here we present first results on the basis of a 660 bp fragment of the mitochondrial *cytochrome oxidase* subunit I (*COI*) gene.

So far, 69 individuals of *Orcula dolium* were analysed which revealed four mitochondrial lineages. The most common haplogroup covers a wide geographic range and various altitudes. The other three haplogroups are restricted to small geographic areas with p-distances from the main type as high as 7 to 16%.

Trochulus hispidus, from which so far 39 individuals were analysed is paraphyletic because of the internal positions of *T. striolatus* and *T. sericeus*. The *T. hispidus* individuals are divided into two main haplogroups with average p-distances of 18%. One group again covers a wide geographic range and has a high diversity compared to the other two species. All individuals collected at high elevations are found in the second clade. These results confirm the proposed species status for the high Alpine form *T. h. oreinos* (*Trochulus oreinos*).

From the Austrian endemic *C. obtusus* we analysed 73 individuals. There is a weak east-west differentiation, but the differentiation between the two groups is very low (<1.3% p-distances). Moreover, there is very low genetic variation over the whole distribution range.

Neues zum schwierigen taxonomischen Status der Kammolche in Österreich

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In the area between south-eastern Bavaria (Germany) and Upper Austria the distribution ranges of northern (*Triturus cristatus*) and Italian crested newts (*T. carnifex*) are narrowly sympatric and a hybrid zone has been suggested on the basis of morphological data. In our study of 35 autochthonous populations in this region, we compared distribution patterns and hybridization on the basis of one morphological (Wolterstorff index, WI) and two molecular (cytochrome b, microsatellites) markers. Tissue samples from Bavarian populations (preserved phalanges) were already available from a previous study. Austrian samples were gained non-destructively, by collecting buccal cells with sterile cotton buds. Results showed good concordance for all markers in most populations. Average WI values per population were within the range of the species *T. cristatus* and *T. carnifex*. Six populations from Salzburg and Upper Austria showed intermediate index values in males and females. Applying standard measures of genetic diversity within populations as well as Bayesian analysis of population structure, we detected admixed populations and individuals in three regions of Salzburg and Upper Austria. No autochthonous population of *T. carnifex* could be detected in Bavaria. The hybrid zone is probably unimodal, with hybrid individuals predominating in the centre. As the present-day distribution ranges of both species in the surveyed area are fragmented and populations are heavily reduced in numbers, we only can observe their remains. The analysis of molecular markers revealed considerable genetic uniformity. The studied area has been colonized by a limited number of individuals and probably less often than areas with slightly higher diversity. Hybrid zones in the study region were most probably formed by one genetically different *T. carnifex* population and two different *T. cristatus* populations.

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Phylogeography and Evolution of *Gentiana verna* s.l. (Gentianaceae)

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The Spring Gentian (*Gentiana verna*) is a perennial herb frequently occurring in montane and alpine grasslands throughout the European mountain ranges. Geographically disjunct are populations located in Ireland, Scotland and in the Northern Ural region. From Turkey eastwards *G. verna* is replaced by *G. angulosa* in the Caucasus and by *G. uniflora* from the Tianshan over the Altai to the Baikal region.

The present study aims to elucidate the evolutionary history and phylogeographical patterns of *Gentiana verna* by applying AFLP fingerprinting (amplified fragment length polymorphism). Of special interest is the biogeographical origin of the isolated British and Ural populations and the degree of their genetic divergence from populations of the Central Europe. The sampling covers the entire distributional range of the species group (including Asian populations of *G. angulosa* and *G. uniflora*). A number of 380 samples originating from 54 populations are examined in a preliminary analysis.

As hybridization and introgression might blur phylogeographic patterns, further investigations are addressing potential gene flow between *G. verna* and the closely related and sympatrically distributed taxa *G. brachyphylla* and *G. orbicularis*. Being morphologically similar these species differ regarding their edaphical requirements. *Gentiana orbicularis* requires calcareous substrate whereas *G. brachyphylla* is confined to siliceous soils. At three mixed stands within the Austrian Alps (Eastern & Central Hohe Tauern, Stubai Alpen) leaf material of 10 individuals per species was collected. First AFLP analyses proved the presence of hybrid individuals (*G. verna* x *G. brachyphylla*, *G. verna* x *G. orbicularis*) evidencing the potential of gene flow among these species.

East European lowland rivers as refugial areas for aquatic biodiversity

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The Volga – Europe's largest river (3531 km) – arises in the Valdai Hills. Its uppermost course is located in Tver Region: an area that stretches over 84,586 km² of gently undulating landscape (sea level less than 300 m), with temperate deciduous and mixed forests. Volga and many of its tributaries (in Tver Region) arise from fens or lakes, which affects hydrochemistry: low mineralization and a high degree of organic components, as well as high chromaticity and chemical oxygen demand are the main characteristics of the Upper Volga Basin (Kosov et al. 2003, Kuzovlev & Schletterer 2006).

Up to now 265 benthic macroinvertebrates were identified: The most remarkable mayfly is *Prosopistoma pennigerum*, which was recorded for the first time in the Russian Federation (Schletterer & Kuzovlev, 2007). Pristine sites on the Upper Volga River are still inhabited by typical potamal species (e.g. *Ephoron virgo*, *Heptagenia sulphurea*, *Potamanthus luteus* and *Prosopistoma pennigerum*) that became nowadays rare in European rivers. This underlines the importance of East European running waters as refugial habitats for rare and endangered species (Schletterer & Füreder, in press). It was shown that also other species that became extinct in the large rivers (e.g. *Isoperla obscura*, *Xanthoperla apicalis*) are still present. Within the Bivalvia especially the findings of *Anodonta cygnea*, *Unio crassus* (FFH Annex II species) and *Unio tumidus*, as well as the other molluscs, are remarkable, because in European Rivers the mollusc fauna decreased significantly within the last century. Evidently, the headwaters of East European rivers like the Upper Volga River, still have large sections in natural conditions with an unaltered type-specific flora and fauna. The study of these intact structures build a basis for future management issues in aquatic conservation and the test of general ecological theories for large European rivers.

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Integrative biodiversity research: examples from the ant world

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Integrating data from multiple sources promises to improve the success of biodiversity research to an unparalleled degree. Ant examples from my research collaborations illustrate the integrative approach. **Intra- and interspecific diversity:** We uncovered cryptic diversity of unexpected extent in Central Europe (1). The profits to systematic biology from integrating molecular and other methods include firmer species delimitations than ever before and new determination routines. Morphology is essential to link molecular research to zoological nomenclature. The multi-source approach also is a potent interface between alpha taxonomy and evolutionary research: evolutionary scenarios are discovered when resolving disagreement across disciplines, and disagreement becomes increasingly understandable with increasing knowledge of the evolutionary scenarios. **Social diversity:** The case studies presented reveal alternative social strategies in ants (2) and that the evolution of social diversity may be triggered by the ecological framework (3). **Diversity of symbiotic interactions:** Collating phylogenetic inferences and ecological data for all partners allowed us to discover an extraordinary mosaic of evolutionary and ecological interrelations between fungi and ants as a new modelsystem for mutualism research (4, 5). **Biodiversity crisis:** Biological invasions threaten diversity. The complementary use of DNA methods and ecological niche modelling can strengthen the identification of origin populations of invasive species (6, 7), crucial for preventive measures.

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Genetic and morphological investigations indicate vicariant speciation in the genus *Plecotus* (Chiroptera, Vespertilionidae)

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Recent molecular analyses of populations of long-eared bats had revealed that the Palearctic genus *Plecotus* contained phenetically similar but genetically highly distinct species. The existence of cryptic species explained why the taxonomy of this genus was notoriously confused. Our aim was to produce a taxonomic revision of the genus *Plecotus* by combining genetic and morphological methods.

We analysed morphological characters of 697 individuals including 10 holotypes and one lectotype and performed genetic analyses of 151 individuals from throughout the range. As marker sequences we employed a highly variable section of the mitochondrial control region (CR) and a partial sequence of the more conserved *16S rRNA* gene.

Phylogenetic and phenetic analyses resulted in similar but not completely concordant arrangements of the species. The molecular data identified nine clades representing 11 species which were grouped in the *16S* tree in two major lineages, one consisting of only one primary clade restricted to the Mediterranean, the other consisting of eight primary clades representing Eurasian taxa. The morphological analysis revealed five additional species. Together with three recently described species which were not included in our analysis, the genus *Plecotus* comprises at least 19 more or less cryptic species.

We assume vicariant speciation through a multitude of disruption and isolation events within a formerly continuous range of the broad-leaved Arcto-Tertiary forest in which *Plecotus* probably originated. The Early Oligocene age of the presumed ancestor of the Plecotini and a correlation of the molecular diversifications with palaeo-geographic reconstructions suggest that the divergence of the two major lineages may have occurred already during the Middle Miocene, 14.5 mya.

DNA-based identification of *Agriotes* wireworms

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This study focuses on larvae of European *Agriotes* species (Coleoptera: Elateridae), which are abundant below-ground living herbivores and cause considerable damage to field crops. There are up to 20 species occurring in arable land, which differ in regard to ecology, abundance and pest status. The basis of any wireworm risk assessment is the correct identification of the larvae; however, this is considerably hampered when morphological features are being used: current identification keys do allow identifying just eight of the 20 species in larval stage (Klausnitzer 1994). Moreover, some morphological characters used for identification are hard to discriminate among some of the described species and their intraspecific variability has yet not been assessed.

Here we used a DNA-based approach to identify the different *Agriotes* species in larval stage. Within each species adult beetles, which are readily identifiable, were collected from different locations all over Europe. From these beetles, part of the mitochondrial cytochrome oxidase subunit I gene was sequenced to estimate the genetic variation within and between species. A non-destructive DNA-extraction method was used to gain DNA of rare specimens from insect collections. For the main *Agriotes* species in terms of distribution, abundance and pest status (*A. obscurus*, *A. ustulatus*, *A. litigiosus*, *A. sordidus*, *A. rufipalpis* respectively 'groups' due to low interspecific variation: *A. brevis/sputator* and *A. lineatus/proximus*) species-specific markers were designed. Their application in a multiplex-PCR approach allowed discriminating between these species/groups within a single-step reaction. Identification of the remaining 11 European *Agriotes* species can be done by comparing sequences we will provide for all 20 species at NCBI's public database GenBank (Benson et al. 2000). Once the feasibility of this molecular identification system has been evaluated, it can easily be used by other researchers to routinely and securely differentiate between *Agriotes* wireworms, which will improve our ability to determine subtle differences in their specific ecology.

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Searching for the one true tree in the "forest of arthropods"

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Every taxonomist, especially when dealing with ancient phylogenetic splits, is nowadays confronted with an ever growing number of conflicting trees. Among the four major arthropod groups, for example, nearly each possible sister group was considered valid by at least one author. Moreover for each of the groups monophyly was challenged by at least one analysis. Many proposed relationships, however, are only weakly supported, and the respective nodes only occur if a special data set is used, often even depending on the choice of a special method of tree reconstruction. One possible approach to this high number of incongruent trees is to test whether the phylogenetic hypothesis is possibly a result of a misleading effect. In this contribution I want to address three possible kinds of sources for misleading effects in phylogenetic reconstruction; (i) erroneous input hypotheses, introduced during the reconstruction of the character matrix, (ii) violations of method-specific demands on the data set, and (iii) violations of general assumptions of tree reconstruction.

For all three sources of error an example will be given, from studies performed in the FWF-project "*Are the Hexapoda monophyletic? Conflicting hypotheses regarding their relationships to myriapods and crustaceans.*"

ad (i) erroneous input hypotheses: When constructing a character matrix for a parsimony analysis, homology hypotheses have to be proposed for each single character state. A character-specific example from a putative apomorphy of Diplura, will point out problems, which may occur, when information is extracted from literature without re-analyses.

ad (ii) violations of method-specific demands: Nearly all model-based methods of tree reconstruction demand the evolutionary rate to be homogeneous among all lineages of the tree. The misleading effect of this method-specific demand will be exemplified on a study on arthropod relationships.

ad (iii) violations of general assumptions of tree reconstruction: The misleading effect of violations of character independence will be discussed in a molecular data set based on the 28S rRNA-gene.

Testing the own results for possible misleading effects, increases the heuristic value of analyses for two reasons. Firstly tests are performed by the scientists, who best know the weaknesses of the own data. Secondly, and more important, tested results do not only provide phylogenetic hypotheses, but likewise give insights into the evolutionary history of characters and character complexes.

Visual Ecology of Cameroon's Crater Lake Cichlids

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The tiny Crater lakes Barombi-Mbo and Bermin in Western Cameroon, Africa, harbour an astonishing number of morphologically and ecologically different cichlid species (12 and 9 respectively). The monophyly and sympatric origin of these species flocks has previously been established (Schliewen et al., 1994). However, the underlying mechanisms and genes involved in the process of speciation are yet to be elucidated.

For cichlids the importance of vision in the context of natural as well as sexual selection has long been known. Moreover, visual sensory drive has recently been shown to facilitate speciation in various cichlid species flocks (Seehausen et al., 2008).

We therefore sequenced the rhodopsin and UV-sensitive opsin genes in most of the endemic species of both lakes. In addition we measured UV-chroma from the fishes' body, which probably plays an important role in visual communication. This part of the light spectrum is visible to cichlids but not to humans.

We found two amino acid substitutions at known spectral tuning sites in the UV opsin of all the Bermin species. These presumably shift the maximum absorbance of the visual pigment by more than 3 nm to longer wavelengths. In addition, we found several variable AA sites in species of both lakes and determined their position relative to the chromophore binding pocket by 3D visualisation of the receptor molecule in order to assess their potential function for spectral tuning.

Substitution-rate-tests identified the UV opsin to be under strong purifying selection. The phylogenetic gene tree we constructed from the UV opsin data is congruent with traditional topologies of the species phylogeny.

UV photography and quantitative reflectivity measurements revealed considerable variation of UV reflection in species from both lakes. The species we investigated are likely to use UV markings for inter- and/or intraspecific communication that may have been facilitated the radiation of these flocks.

This study therefore presents molecular opsin data and UV reflectance measurements for sympatrically evolved cichlids from Western Africa for the first time.

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Biodiversity in the Alps and the Carpathians: The Project

IntraBioDiv

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Biodiversity has three components: genetic, species and ecosystem diversity, and there are complex ecological and historical factors shaping biodiversity patterns. Disentangling these factors is important for our understanding of biodiversity. Moreover it is important to understand the relationships among the biodiversity levels. The goal of this chapter is to introduce the aims, methods and outcomes from the project IntraBioDiv, "Tracking surrogates for intraspecific biodiversity: towards efficient selection strategies for the conservation of natural genetic resources using comparative mapping and modelling approaches". We used electronic databases and newly generated data of the rich vascular plant flora of the high-mountain regions of the Alps and the Carpathians, well suited as model regions for assessing general aspects of regional species diversity and genetic diversity and link these with habitat diversity.

Database entries of 2030 high-mountain taxa (species and subspecies) with an altitudinal abundance peak at or above timberline are present, 542 taxa are endemic. The database contains joint distribution data of these taxa obtained from a series of regional and national inventories. Moreover, georeferenced genetic diversity data for 40 species were obtained by genetic fingerprinting (AFLP; Amplified Fragment Length Polymorphisms), and a broad range of environmental variables were collected to describe potential habitat diversity as a proxy for ecosystems diversity.

Biodiversity is not randomly distributed in the Alps and the Carpathians. Species diversity is clearly correlated with habitat diversity and higher in the Southern and the Western Alps than in other areas. Although genetic diversity in single species datasets does, overall genetic diversity does not show any clear pattern. Diversity of rare (endemic) species, however, tends to be higher in or close to the peripheral refugia than in the once heavily glaciated Central Alps, although present habitat diversity is lower in refugia than in other areas. In conclusion, genetic/species diversity might be more correlated with present ecological factors like population density and habitat diversity, whereas genetic/species rarity (endemism) is rather a result of historical factors.

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Proteome phylogeny in *Acanthamoeba* spp.

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Acanthamoebae are ubiquitously occurring potentially pathogenic protozoa. Not all representatives of the genus can act as pathogens, but obviously pathogenicity is not a species-specific character and the validity of the *Acanthamoeba* species generally has been challenged.

In 1977 Pussard and Pons divided the genus into three gross groups on the basis of the sizes and overall shapes of the cysts (stellate, polygonal or round). Further classification within these groups has resulted in currently 22 described species altogether, differentiated mainly by the number of cyst arms and trophozoite temperature tolerance. However, polymorphisms can be observed even within one clone and the *Acanthamoeba* species system is not supported by molecular data. A new system dividing the genus into 15 genotypes has been established in the past years on the basis of 18S rDNA sequence data and it has been shown that sequence dissimilarities are extremely high, reaching values of over 30% between groups. Most clinical isolates exhibit genotype T4, but not all representatives of T4 are pathogenic, and pathogenic strains have also been described in almost all other genotypes. Thus, genotyping alone does not provide any information on the virulence of an isolate.

At the Department of Parasitology we are currently working on the discrimination and classification of *Acanthamoeba* strains by genomic and proteomic data within the framework of several research projects, including a project on the genetic diversity of *Acanthamoeba* group I, a project on the encystment in *Acanthamoeba*, a project on the identification of pathogenicity-related proteins in *Acanthamoeba* and a project on the glycosylation of *Acanthamoeba*.

In these studies it was shown that on one hand most characters traditionally used for *Acanthamoeba* taxonomy vary dramatically depending on growth conditions and that several traits are lost during long term culture, most probably epigenetically regulated. On the other hand, however, it was shown that the genomes and proteomes of different *Acanthamoeba* strains are so divergent that new approaches might well enable a reliable classification – and even pathogenicity typing – for these organisms, for which the biological species concept is not applicable.

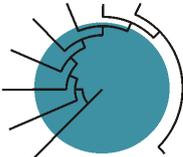
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