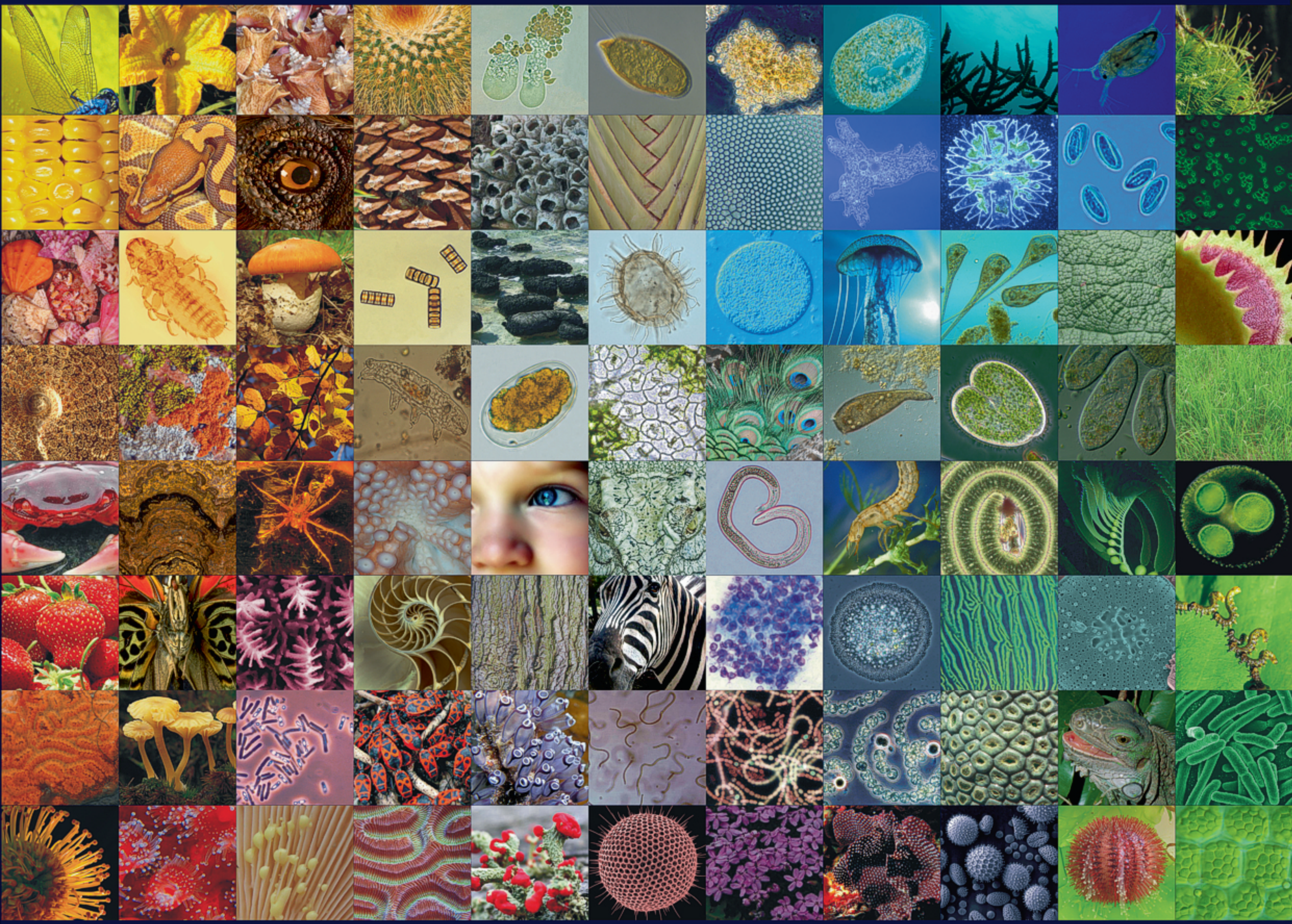
SYSTEMATICS OPEN

3. Jahrestagung von NOBIS Austria
4. Dezember 2009
Naturhistorisches Museum Wien



NETWORK OF BIOLOGICAL SYSTEMATICS AUSTRIA

WIEN 2009 NOBIS AUSTRIA 3

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Naturhistorisches Museum Wien
Vortragssaal
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1010 Wien

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Programm

09:00 **Registrierung und Kaffee**

10:00 **Begrüßung** *U. Aspöck*, Präsidentin von NOBISAustria

10:20 – 12:10 **Vorträge 1** Chair: *W. E. Piller*

10:20 – 10:50 *Ch. Sturmbauer*

Neues über die Entstehung der Arten aus dem Modellsystem der afrikanischen Buntbarsche

10:50 – 11:10 *R. Gemel*

Zur systematischen Stellung der Dreikiel-Erdschildkröte *Melanochelys tricarinata*

11:10 – 11:30 *A. Kroh & A. B. Smith*

Phylogeny of post-Palaeozoic Echinoids – Molecular vs. Morphological Data & the Fossil Record

11:30 – 11:50 *P. Grunert, F. Rögl, M. Harzhauser & W. E. Piller*

Taxonomy of microfossils as key to the past: foraminiferal communities of an ancient upwelling site

11:50 – 12:10 *A. Kern & M. Harzhauser*

Taxonomy as fundament of pollen-based paleoclimate analysis

12:10 – 12:30 **Poster I - Präsentation im Vortragssaal**

12:30 – 13:30 **Mittagspause**

13:30 – 15:20 **Vorträge 2** Chair: *N. Szucsich*

13:30 – 14:00 *H.P. Comes, Y.-X. Qiu & C.-X. Fu*

Molecular phylogeography of temperate plant endemics in East Asia – Population history in relation to Quaternary changes in climate and sea level

14:00 – 14:20 *A. Tribsch, K. Moosbrugger, J. Schistek, J. Suda & H.P.Comes*

Evolutionary patterns in the small, blue, and alpine gentians (*Gentiana* sect. Calathianae, Gentianaceae)

14:20 – 14:40 *M. Duda, H. Sattmann, D. Bartel, E. Haring, J. Harl, L. Kruckenhauser*

The genus *Trochulus* as an example for morphological, genetic, and ecological differentiation of Austrian Alpine Land snails

14:40 – 15:00 *E. Redl, T. Schwaha, S. Handschuh, L. Salvini-Plawen*

In search of phylogenetic signals in the soft body of Caudofoveata (Mollusca)

15:00 – 15:20 *P. Strutzenberger, F. Bodner, G. Brehm, K. Fiedler*

Molecular phylogeny of *Eois* moths – implications for the evolution of wing patterns and host plant use

15:20 – 15:40 **Poster II - Präsentation im Vortragssaal**

15:40 – 16:10 **Kaffeepause**

16.10 – 17.20 **Vorträge 3** Chair: *E. Christian*

16:10 – 16:40 *J. Boenigk*

Konzeptueller Fortschritt in der Systematik der Protisten

16:40 – 17:00 *S. Agatha*

Taxonomy and Evolution of Tintinnid Ciliates (Ciliophora, Spirotrichea, Tintinnina)

17.00 – 17.20 *W. Foissner*

Mimicry in a haptorian Ciliate?

17.30 Möglichkeit der Teilnahme an einer der beiden Führungen:
Darwin-Ausstellung oder *NHM inkl. Blick vom Dach*.

ABSTRACTS

Scanning Electron Microscopic Study of Mediterranean Tintinnid Loricae (Ciliophora, Spirotrichea, Tintinnina)

Agatha, S.

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Usually, tintinnid loricae were investigated only by means of a light microscope. Therefore, a scanning electron microscopic study was preformed on the loricae of four species from the families Codonellidae, Codonellopsidae, and Rhabdonellidae collected in the Mediterranean Sea near Villefranche-sur-mer (France). This site is the type locality of *Codonella aspera* Kofoid & Campbell, 1929. The ultrastructure of its lorica and the peculiar closing apparatus is demonstrated for the first time. The agglomerated lorica is about 94 µm long and urceolate, viz., it comprises a globular bowl and an obconical collar. The agglutinated particles are apparently incrustrated by a successive accretion of distinct homogenous matrix layers. *Stenosemella ventricosa* (Claparède & Lachmann, 1858) Jörgensen, 1924 is the type of the genus. Its lorica is about 87 µm long and consists of an agglomerated obovate bowl and a short hyaline collar with some minute ellipsoidal windows. Thus, the genus *Luminella* Kofoid & Campbell, 1939 established for *Stenosemella*-like tintinnids with collar windows is considered a synonym. The lorica of *Codonellopsis schabi* Brandt, 1906 is about 85 µm long and lageniform, viz., it is composed of an agglomerated globular bowl and a hyaline cylindroidal collar with several spirals and some small windows. Based on the material from the type locality, the lorica of *Rhabdonella spiralis* (Fol, 1881) Brandt, 1906, the type of the genus, was ultrastructurally studied for the first time. The lorica is about 315 µm long and elongate obconical. Minute circular windows are scattered between the sinistrally spiralled and anastomosing ribs of the outer lorica surface; the alveoli of the wall are, however, only recognizable in the light microscope. The present findings contribute together with cytological studies to the establishment of a natural tintinnid classification.

Supported by the Austrian Science Foundation (FWF; Project P20461-B17).

Taxonomy and Evolution of Tintinnid Ciliates (Ciliophora, Spirotrichea, Tintinnina)

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The taxonomy and classification of the about 1,200 tintinnid species are mostly based on features of the lorica, which, however, is subject to a considerable phenotypic plasticity. Therefore, characters of the cell and the resting cysts, the ultrastructure and chemical composition of the lorica, and gene sequence analyses are also necessary to (i) define the species, (ii) reconstruct the evolution, and (iii) establish a natural tintinnid classification. The phylogeny of the small subunit ribosomal RNA gene roughly matches the cladistic analysis, indicating that the complexity of the somatic ciliary pattern increased and that the hyaline and agglutinated loricae do not characterize distinct lineages, i.e., the hyaline loricae apparently evolved several times independently. Accordingly, the hyaline as well as the agglutinated loricae can be associated with the most highly developed ciliary pattern.

Supported by the Austrian Science Foundation (FWF; Project P20461-B17).

Conceptual progress in protist systematics

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Protist systematic is currently under dramatic change both, regarding the megasystemastics and phylogeny of eukaryotes as well as the species concept and species richness of protists. Both aspects were prestressed by the historical division of protists into animals, i.e. protozoa (zoology), and plants, i.e. algae (botany). With currently less than 10% described species the basic concepts are still unsettled. Protist megasystematics stays problematic even in the molecular era as the multifold endocytobioses of cell organelles, specifically the secondary and tertiary endocytobiosis of plastids, blurs the phylogenetic reconstruction. Similarly, the perception of species and the species concept are controversial. On the one hand closely related organisms are partly described following the botanical code and partly following the zoological code. On the other hand the traditionally most widely applied morphospecies concept is in many cases too rough. I will outline the current view of protist megasystematics and the trends in describing and classifying the diversity of protists.

Molecular phylogeography of temperate plant endemics in East Asia – Population history in relation to Quaternary changes in climate and sea level

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The warm temperate climate zones of E China, S Japan and S Korea (the 'CJK region') show remarkably greater species richness of vascular plants when compared with their counterparts in other regions of the world, such as eastern N America. This might relate to Quaternary (< 2 Ma) changes in climate and sea-level, providing greater opportunities for repeated cycles of habitat fragmentation and allopatric speciation within a physiographically heterogeneous region (Qian & Ricklefs, 2000). In fact, simulated palaeo-forest reconstructions (Harrison *et al*. 2001) indicate that during the Last Glacial Maximum temperate deciduous forests of E Asia were mostly restricted in distribution, despite the possibility for migration and expansion on the glacially exposed East China Sea (ECS) land-bridge. However, the modelling of entire palaeo-forest biomes cannot provide a detailed picture of past range fragmentation, expansion and/or contraction of their constituent species populations.

On this backdrop, we have performed molecular phylogeographic tests of explicit refugial isolation vs. expansion in three flowering plant species confined to temperate-deciduous forested habitats in the CJK region [*Dysosma versipellis* (Berberidaceae); *Kirengeshoma palmata*, *Platycrater arguta* (Hydrangeaceae)]. Overall, our data support the importance of population fragmentation in driving (incipient) allopatric species formation of temperate plant endemics in E Asia over multiple glacial/interglacial cycles (> 0.45 Ma). Accordingly, the origin of presently disjunct distributions across the ECS pre-dates the most recent land-bridge submergence in this region (c. 16,000 BP). Moreover, several phylogroups identified match previously uncertain taxonomic entities, while others qualify as 'cryptic taxa' without detectable morphological divergence. Together, these phylogroups should be viewed as separate 'evolutionarily significant units' with major ramifications for population conservation and management. This especially could be of relevance for *D. versipellis* with regard to the species' potential variation in podophyllotoxin-type lignans of chemotherapeutic relevance.

Qian, H., Ricklefs, R.E., 2000. Large-scale processes and the Asian bias in species diversity of temperate plants. Nature 407, 180-182.
Harrison, S.P., Yu, G., Takahara, H., Prentice, I.C., 2001. Palaeovegetation: diversity of temperate plants in East Asia. Nature 413, 129-130.

The genus *Trochulus* as an example for morphological, genetic, and ecological differentiation of Alpine Land snails

Duda, M. [1], Sattmann, H. [1], Bartel, D. [1], Haring, E. [1], Harl, J. [1], Kruckenhauser, L. [1]

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In the course of our project "Phylogeography of Alpine land snails" three genera (*Trochulus*, *Orcula* and *Cylindrus*) are investigated, which comprise Austrian Alpine endemic species including high elevation forms. One major question is whether highland forms are genetically and morphologically differentiated from lowland forms.

In the present contribution we focus on members of the genus *Trochulus*. *Trochulus oreinos oreinos* (Wagner 1915) and *T. o. scheerpeltzi* (Mikula 1957), both endemics of the north-eastern Austrian Alps, have originally been regarded as regional subspecies of *Trochulus hispidus* (Linné 1785), but later *T. oreinos* has been raised to species status.

We analysed these taxa morphologically and genetically to resolve their phylogenetic relationships and their systematics. Shell measurements indicated that the *T. oreinos* subspecies tend to be smaller than *T. hispidus*, but measures of shell size showed overlapping ranges. In contrast, the length of hairs at the last whorl turned out as a suitable trait to discriminate both *T. oreinos* subspecies from *T. hispidus*. Furthermore, the groove beneath the keel turned out to be a constant character of *T. o. scheerpeltzi*. Analyses of the mitochondrial COI and 16S rRNA genes showed very high sequence divergence between the three taxa. Also, the two *T. oreinos* subspecies differ from *T. hispidus* in habitat preference. They are restricted to rocky habitats above 1400 m asl, while *T. hispidus* is distributed over a wider altitudinal range occurring in moist areas and scrubby vegetation near water bodies. In summary, morphological and genetic results indicate that the three taxa represent very old lineages. Whether *T. o. oreinos* and *T. o. scheerpeltzi* should be considered as independent species shall not be decided at the current state of knowledge.

Mimicry in a haptorian Ciliate?

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Typically, haptorids have toxicysts for killing other ciliates, their preferred prey. Further, they have so-called cortical granules which are usually less than 2 µm in size and colourless. Possibly, these granules are mucocyst-like extrusomes with a defensive function. In African and North American soils, we discovered a red haptorian ciliate, possibly belonging to the genus *Enchelyodon*. The colour is due to cortical granules which have a similar absorption spectrum as those of the red heterotrich ciliate *Blepharisma,* whose pigment granules have a defensive function against predators. The new *Enchelyodon*, an about 200 µm long, cylindroidal ciliate, is the first coloured haptorid that ever has been found. Among 30 food items offered (various ciliates, flagellates, micrometazoans …), *Enchelyodon* fed only on *Blepharisma* spp. When this prey is lacking, it makes red resting cysts. However, some become smaller and colourless, indicating that the colour depends on the specific prey. Based on some preliminary experiments, I suggest that *Enchelyodon* mimics the toxic *Blepharisma* to escape predators, for instance, the large *Bursaria* and *Dileptus*.

Supported by FWF, project P-19699-B17.

On the systematic status of the Tricarinate Hill turtle *Melanochelys tricarinata* (BLYTH, 1856) (Reptilia: Testudines: Geoemydidae)

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Recent revisions of both phylogeny and taxonomy of Geoemydid turtles resulted in differing phylogenies and the establishment of various ‘new’ generic names.

However, some poorly known species left aside by building up these revised and more detailed phylogenies might provide helpful insights into the phylogeny of the Familiy Geoemydidae. One of these species was *Melanochelys tricarinata*, described by British scientists in a late period of exploration of the Indian subcontinent. Since that time only scanty material was available for investigations and most publications upon *Melanochelys tricarinata* were anecdotal. Consequently, during a revision of the geoemydid turtles in 1964, the systematic position of *Melanochelys tricarinata* was allocated to this genus not by examination but in consensus with a historical concept by earlier authors. Based on six voucher specimens at the Natural History Museum in Vienna, we studied the systematic position of this turtle species both by applying molecular biological (mt-DNA sequence data) as well as comparative morphological methods. In addition, we verified the specific allocation of the holotype (stored in the collection of the Zoological Society of India in Kolkata) and provided an updated type description.

Our studies revealed that (1) the two species of *Melanochelys*, *M. trijuga* and *M. tricarinata* are phylogenetically closer to each other than to the remaining genera of the Family Geoemydidae. (2) *M. tricarinata* represents the sister taxon of *Melanochelys trijuga* and (3) *Melanochelys* is a monophyletic group within the geoemydine turtles. Moreover, we demonstrated that most diagnostic features used in earlier studies of *Melanochelys* referred to highly variable structures and, thus, not suited for phylogenetic-systematic purposes. A revised diagnosis based on morphological characters is provided for both species.

Taxonomy of microfossils as key to the past: foraminiferal communities of an ancient upwelling site

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Actualism is the fundamental principle of modern paleobiology. Understanding the composition and distribution of recent faunal and floral communities enables us to reasonably reconstruct past environments. The basis of any actualistic approach is a thorough taxonomic groundwork.

Recently, foraminiferal assemblages from an Early Miocene (c. 22 Ma) *Konservat-Lagerstätte* in the North Alpine Foreland Basin (NAFB) of Upper Austria have been studied. In order to understand the depositional environment and the origin of the fossil-rich sediments, benthic and planktic foraminifers have been determined on the species level and compared to similar assemblages in the present-day oceans. The herein presented results will exemplary show the key-role of taxonomic actualism in paleobiology.

Amongst benthic foraminifers, calcareous taxa of bolivinids (mainly *Bolivina crenulata*, *B. korynoides* and *B. trunensis*), buliminids (mainly *Caucasina coprolithoides* and *C. schischkinskayae*), discorbids (*Eoeponidella ampliportata*) and stilostomellids (*Myllostomella advena*) are the dominating faunal elements. They depend on a high downward flux of nutrients and capable of tolerating very low oxygen levels. A comparison to recent foraminiferal communities points to an upwelling setting. One of the most intensively studied upwelling sites is situated in the Arabian Sea where communities along the Oman and Pakistan shelves show striking similarities to the herein studied assemblages. The dominance of bolivinids and the lack of agglutinated species allows a determination of the *Konservat-Lagerstätte* as deposits of an oxygen minimum zone of an upwelling site along the northern shelf of the NAFB.

The evaluation of planktic assemblages agrees very well with the upwelling scenario. They are mainly composed of opportunistic species like *Globigerina praebulloides* and peculiar mass-occurrences of microperforate tenuitellids (mainly *Tenuitella brevispira* and *Tenuitellinata spp.*). The latter are usually restricted to subpolar waters and contrast the warm, subtropical paleoclimate of the region documented by the terrestrial record.

Geographical and temporal variation in mating behaviour and its impact on sexual selection pressure in a mouthbrooding cichlid fish from Lake Tanganyika

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Disparities between findings based on observations of mating systems and on genetic parentage analysis need not always be for methodological reasons. If the contrasting data were collected from different populations or at different times, these disparities can also represent intraspecific variation in mating behaviour.

In cichlid fishes (Teleostei: Cichlidae) of the East African Great Lakes, the strength of sexual selection was proposed to influence the evolution of male nuptial colour. The use of mating system parameters as proxy of long-term sexual selection pressure enhances the need for mating system information. Most genetic studies on the mating behaviour of cichlids have been conducted without temporal or geographical replication, such that the prevalence of intraspecific variability remains largely unknown despite its fundamental importance for inferences regarding behaviour, speciation and evolution.

In 1993 a behavioural study was carried out on a population of the endemic maternally mouthbrooding cichlid fish *Ctenochromis horei* (tribe Tropheini) in the north of Lake Tanganyika. The results suggested mate monopolization by the most dominant male. However, polyandrous spawning and attempts of sneaking were also observed, but whether sneakers succeeded in fertilization could not be determined. In our recent study we conducted parentage analyses on a population of *Ctenochromis horei* in the south of the lake, with samples collected in the dry season as well as in the rainy season. Genetic reconstructions of paternity provided no evidence for male mate monopolization, as none of the inferred sires had offspring in more than one brood. Furthermore, multiple paternity occurred in several broods and was significantly more frequent in the sample taken in the rainy season than in the dry season. The data suggest geographical and temporal variation in the mating behaviour of *C. horei* despite its continuous year-round reproduction, invariable brood care behaviour and habitat-specific distribution in the relatively constant and confined environment of a tropical lake. Moreover, our data show that inferences on the distribution of male reproductive success, if based on each geographical or temporal data set alone, would fail to describe the potential for sexual selection in this species.

Taxonomy as fundament of pollen-based paleoclimate analysis

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Paleobotany has always been a useful science to reconstruct terrestrial environments in addition to the marine and freshwater habitats, where information derives mainly from fossil animals. Due to wider distribution abilities of pollen grains, palynological studies give a detailed insight into different vegetation systems including even drier areas and mountainous vegetation, where macrofossils are often missing. Based on a fossil plant assemblage, an explicit picture of the paleo-environment can be reconstructed, considering all major criterions, which also limit recent plants' distribution. One of the main determining factors is climate, thus the use of paleobotany, is a powerful tool in climate analysis, especially genus level pollen-based taxonomy.

Neogene pollen have the advantage to be present in high numbers in suitable samples and to allow a precise identification by comparison with extant relatives, which is the basement of a modern analysis method called the Co-existence Approach.

In this presentation the results of own high resolution studies will be shown. These provide information on long term trends and high-frequency environmental shifts based on a huge amount of quantitative data. Different examples over time and environment conditions will be demonstrated; 1. Early Miocene records from India, which give information on the onset of the Indo-Pacific monsoon system, 2. The Early Miocene of Austria, to evaluate precipitation and seasonal temperature range at the onset of the Miocene Climate Optimum, and 3. Late Miocene records from a huge fossil European Lake to emphasize the tempo and mode of lake level change and coupled vegetational shifts.

Interestingly, many taxa co-occur in all records and a taxon-based ecological interpretation of these samples seems to be little promising on first sight. Nevertheless, the analysis of each dataset by the Co-Existence Approach method allows defining the boundary conditions for each assemblage and provides clues about the past climate.

The studies are supported by FWF-Project P-21414-B16

Patterns of morphological variation among allopatric and sympatric populations in the Lake Tanganyika cichlid genus *Tropheus*

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Lake Tanganyika contains the oldest and most complex flock of cichlid fishes. They are excellent subjects for the study of explosive speciation and adaptive radiation. Many species are subdivided into arrays of geographic morphs, each colonizing particular sections of the shore line. Their present distribution was shaped by a series of lake level fluctuations. One of the best examples of this phenomenon is the genus *Tropheus*, counting about 120 distinctly colored populations and sister species, some living in sympatry. There is strong evidence from ecological and genetic studies that *Tropheus* is not capable of covering large distances across unsuitable habitats or open water, as a consequence of its pronounced habitat specificity, site fidelity, and territorial behavior.

Our study analyzes phenotypic variation in three *Tropheus moorii* populations living in sympatry with its sister species *Tropheus polli* compared to three allopatric *Tropheus moorii* populations. We use geometric morphometrics based on Procrustes superimposition of 19 morphological landmarks to quantify overall body shape. Canonical variate analysis and principal component analysis are used for data description. In addition to comparisons of overall shape we apply discrete measurements in form of interlandmark-distances (ILD).

Although overall morphology appeared similar, we found significant shape differences and patterns of morphological variation in allopatric populations in comparison to sympatric populations. All three sympatric *Tropheus moorii* populations showed larger fins but smaller head and smaller eyes compared to the allopatric populations. Results showed consistent patterns of morphological distinctness of all *Tropheus moorii* populations which co-occur with *Tropheus polli* compared to *Tropheus moorii* populations living without a potential competitor.

Phylogeny of post-Palaeozoic Echinoids – Molecular vs. Morphological Data & the Fossil Record

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To test ideas about major relationships amongst post-Palaeozoic echinoids we have carried out a cladistic analysis in which all named Post-Palaeozoic echinoid families have been included. Analysis at this taxonomic level provides a compromise between capturing the diversity of form that exists, and number of taxa. We scored 169 taxa for 306 skeletal characters. Here we present a framework for the classification of the group based on extant taxa into which fossil taxa have then be incorporated. The reasons for adopting this approach are straightforward. Extant taxa are not only more completely documented in terms of their morphology, but are also more completely known. Furthermore, we are not reliant on just one source of data for constructing phylogenies: all phylogenetic hypotheses are open to independent testing using both morphological and molecular data.

Our phylogeny compares favourably with previous morphology and gene-based estimates. The most comprehensive study of echinoid phylogenetic relationships prior to this is that of Smith et al. (2006). In that study 49 extant species covering 13 of the 14 extant orders were sampled for morphological and genetic characters. Sequences from three nuclear genes totalling almost 4,000 base pairs were assembled. The comparison with our morphological data throws up two major differences. Firstly molecular data (with low support) suggests that echinothurioids lie in a clade with diadematids, aspidodiadematids and pedinoids. This arrangement contrasts with the relatively strong morphological support we find for placing echinothurioids as sister group to all other acroechinoids. More worryingly, however, is the very strong support from molecular data for a paraphyletic Clypeasteroida, with extant cassiduloids forming a clade that is sister group to just the scutelline clypeasteroids, and with clypeasterine clypeasteroids as sister group to a combined scutellines plus cassiduloids. There is absolutely no morphological support for this, and morphological analyses consistently identify cassiduloids as a grade taxon comprising a series of branches leading up to a monophyletic clypeasteroid clade. At present, however, this mismatch remains inexplicable.

Overall the fit of cladogram to stratigraphy was extremely good and significantly better than random. Echinoids show a much better correspondence than do the majority of dinosaur phylogenies. Among the echinoids correspondence between inferred phylogeny and the fossil record is best in the atelostomates while Echinacea+Calycina have the lowest fit, supporting the idea that Echinacea+Calycina have a relatively poor fossil record because they have adapted for life in hard bottoms where preservation potential is considerably reduced.

Taxon boundaries in the early stages of divergence: Behavioral and genetic studies in the Lake Tanganyika Cichlid *Tropheus moorii*

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A stunning diversity of geographic color morphs makes the Lake Tanganyika endemic cichlid genus *Tropheus* (Teleostei, Cichlidae) a model system for studies of evolution. Being stenotopic and philopatric shallow-water rock dwellers, populations are separated by unsuitable habitat and display strong genetic structure. However, there is evidence for introgression between morphs, probably due to incomplete reproductive isolation in times of secondary contact when lake level fluctuations force migration, and perhaps also due to current gene flow between populations.

Our population genetic and behavioral studies focus on two *T. moorii* color morphs in the south of Lake Tanganyika. There, a blue and a yellow-blotched morph are separated by a sandy bay. The two morphs belong to two highly divergent mitochondrial lineages, but in one population immediately west of the bay, 30 % of the individuals carry “eastern” haplotypes, and all individuals display a somewhat eastern-type color pattern. By contrast, the population immediately east of the bay shows no evidence for introgression, neither in terms of genetics nor in terms of color pattern. At face value, these data suggest unidirectional migration from the eastern into the western population.

Mate choice experiments with the two morphs revealed asymmetric reproductive isolation: while females of the western (blue) morph discriminated against the eastern males and mated assortatively, females of the eastern (yellow-blotched) morph showed no preference for males of their own type, but rather a propensity to mate preferentially with blue males.

If this mating behavior is retained in the wild, unidirectional mitochondrial introgression may occur despite bidirectional migration. When eastern (yellow-blotched) individuals migrate west, females would mate with the resident blue males and introduce their mitochondrial DNA, along with nuclear genes, into the western population. In contrast, when western (blue) individuals migrate east, the blue females would abstain from mating with resident yellow-blotched males and not pass on their mtDNA into the eastern population. However, immigrant blue males would be accepted by the resident yellow-blotched females and procure nuclear introgression.

Presently, we test whether nuclear gene flow occurs in both directions between the two color morphs. Moreover, we aim to reconstruct whether introgression is due to ongoing gene flow or dates back to a single period in the past, perhaps associable with some known hydro-geographic or geologic event.

The geographical origin of peripheral populations in the *Gentiana verna* group (Gentianaceae) evidenced by phylogeographical analyses using AFLP fingerprinting

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Gentiana sect. *Calathianae* Froehlich, comprising ca. 20 taxa, is one of the most interesting alpine plant groups that has mainly diversified within the Alps. The most widespread taxon is the *G. verna* group with several subspecies and closely related species. Many of these are mainly found geographically isolated in the periphery of the *G. verna* distribution (*G. verna* ssp. *arctica* in N-Ural, *G. uniflora* in Central Asia, *G. verna* s.str. in Ireland and England, *G. sierrae* in the Sierra Nevada and *G. penetii* in the Atlas Mountains). Here we present the phylogeography based on AFLP fingerprints of the group with special emphasis on the geographical origin of the isolated populations and taxa. 68 populations with 404 individuals in total were analysed. 442 AFLP markers from three selective primer combinations were scored with the software DAx. Distance-based analyses (Neighbor Joining, NeighborNet) of AFLP phenotypes and Bayesian clustering analyses (Structure) support a recent origin of the Ural populations from Alps/NW-Carpathians and of *G. sierrae* and *G. penetii* from Pyrenean *G. verna*. *Gentiana uniflora* is derived from Turkish-Caucasian *G. pontica* & *G. angulosa* which in turn connects to SE European *G. verna* ssp. *tergestina*. The latter result represents one of few instances of a taxon endemic to Central Asia with a European origin.

Diploid and polyploid cytotypes distribution in the white-rayed complex of *Melampodium* (Heliantheae, Asteraceae)

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The genus *Melampodium* (Heliantheae, Asteraceae) comprises 39 recognized species distributed throughout Mexico, Central America and the southwestern U.S.A, All species have yellow rays except for three shrubby, xerophytic taxa, *M. leucanthum*, *M. cinereum and M. argophyllum*, which form the so-called white-rayed complex and mark the northern limits of the distribution range. Based on morphological characters, *M. cinereum* has been further divided into three varieties: *var. cinereum*, *var. hirtellum*, and *var. ramosissimum*. The three *Melampodium* species are clearly separated by their distributions and ecology. They also are well supported in molecular analyses.

Previous studies revealed the presence of three different ploidy levels within the white-rayed complex: diploids and tetraploids (plus occasional triploids) in *M. cinereum* and M. *leucanthum*, and exclusively hexaploids in *M. argophyllum*. In both *M. cinereum* and *M. leucanthum* diploid cytotypes prevail in the western part of their distribution area, while tetraploids are dominating in the east.

It is hypothesized that *M. cinereum* evolved out of peripheral populations of *M. leucanthum* in low mountains of northeastern Mexico. Further dispersal northeastward led to divergence now recognized as taxonomic varieties. Tetraploidy developed within the easternmost populations of *M. cinereum var. cinereum*. *M. argophyllum* was hypothesised to be of allopolyploid origin, involving *M. leucanthum* and *M. cinereum* as parents.

The current study concentrates on ploidy distribution in *M. leucanthum, M. argophyllum* and *M. cinereum.* It presents the data on the ploidy levels estimations for 148 populations (2094 individuals) of *M. leucanthum*, for 2 populations (36 individuals) of *M. argophyllum*, and for 30 populations (450 individuals) of *M. cinereum* covering the varieties: M. *cinereum var. cinereum* (21 populations, 274 individuals), *M. cinereum var. hirtellum* (6 populations, 139 individuals) and *M. cinereum var. ramosissimum* (3 populations, 37 individuals).

The data obtained in this study agree well with the reports on ploidy level distribution (on the smaller scale) in the white rayed complex performed 40 years ago, suggesting that the polyploid establishment and maintenance is connected to ecological and perhaps historical biogeographical factors.

For ploidy determination, flow cytometry of DAPI stained silica gel-dried material has been applied, using *Glycine max* 'Merlin' as the internal standard.

Morphometric differentiation among haplochromine cichlid fish species of a satellite lake of Lake Victoria

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Lake Victoria holds a young but species-rich assemblage of cichlid fishes which form a monophyletic assemblage with additional species from surrounding water bodies, termed as the Lake Victoria super-flock. Lake Victoria is surrounded by smaller lakes that are somewhat disconnected from the main lake. Lake Kanyaboli is such a small lake, having a markedly reduced species diversity, in part comprised of Lake Victoria species and endemics. Here we studied the modern haplochromine component of the cichlid fauna, represented by *Lipochromis maxillaris*, *Astatotilapia nubila*, *Xystichromis phytophagus* and *Astatotilapia sp. nov. “Bigeye”,* plus a number of unidentified haplochromine specimens. We used landmark-based geometric morphometrics to study the degree of morphological divergence among those young entities. Twenty landmarks and 14 interlandmark distances were used for shape analysis. MANOVA revealed significant differences between all four species, but, principal component analysis and canonical variate analysis did not clearly discriminate between *A. nubila* and *X. phytophagus*, demonstrating great overall morphological similarity despite clear dietary differences. In all the species, thin plate splines and Goodall’s F-test revealed that sexual dimorphism was slight but significant and that it did not inflate the distinction among species. In all four species the observed similarities and differences in body shape conform to ecological specialisation of the fish. Most unidentified specimens scattered within the range of one of the four described species, but some specimens turned out to be distinct. To test their reproductive distinctness and to test for potential hybridisation, microsatellite data are needed.

Evolution in peripheral isolates: population genetic history of *Tephroseris helenitis* (L.) B. Nord. (Asteraceae) at the northern edge of the Alps

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Tephroseris helenitis (L.) B.Nord. ssp. *helenitis,* a hexaploid perennial herb (2n=48), is distributed in wet meadows and fens throughout Western and Central Europe, i.e. from the Normandy eastwards to the foothills of the notrthen Alps. Here, ssp. *helenitis* co-occurs with ssp. *salisburgensis* (Cuf.) B.Nord., which is a local endemic of the Salzburg city and adjacent areas in Upper Austria and Bavaria. Both subspecies form mixed stands in the region around Rosenheim in the West and Salzburg in the east. Subspecies *helenitis* is distributed mainly in areas that remained unglaciated throughout the Pleistocene, whereas ssp. *salisburgensis* is restricted to areas that have been glaciated. This pattern allows for hypothesizing incipient speciation in *Tephroseris* at the northern edge of the Alps: After melting of the Inn and Salzach glaciers, the expansion of populations might have resulted in peripherally isolated populations that finally differentiated into another subspecies. We use AFLP-markers to quantify levels of genetic differentiation and diversity among 27 populations of both subspecies from in the area between SW Bavaria and Salzburg. Moreover, ecological data (e.g. vegetation data, soil samples) and morphological variables were assessed for selected populations. The following questions will be addressed: (1) is there significant genetical and morphological differentiation between the two subspecies? (2) Is the genetic differentiation among populations or taxa related to climatic and edaphic factors or simply to geographical distance? (3) Does within-population genetic diversity decline from the western, formerly ice-free habitats to the eastern, formerly glaciated habitats, as would be expected under a scenario of post-glacial range expansion?

Character divergence in pharyngeal structures in sympatric species pairs and allopatric populations of the rock-dwelling cichlid genus *Tropheus*

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Lake Tanganyika harbors the oldest and most diverse species flock of cichlid fishes, well known for studies of explosive speciation and adaptive radiation. The study species *Tropheus* consists of six nominal species all of which live in the upper littoral zone in various kinds of rocky habitats. Over 120 distinctly colored populations are known. In some regions more than one sister species lives in sympatry with another *Tropheus*. This study addresses character divergence of particular viscerocranial bones with known relevance for trophic specialization in allopatric populations and in sympatric populations coexisting with a sister species. Three sympatric populations of *T. moorii* and *T. polli* were analyzed in comparison to two allopatric *Tropheus* populations and one outgroup. Preparation of the selected bones (dentary, angular, premaxillary, quadrate, preopercle and pharyngeal teeth) includes enzymatic disarticulation of the heads, staining of the bones with alizarine red, and applying a landmark system for geometric morphometric analysis on the images taken. A principle component analysis (PCA) is carried out based on partial warp and uniform component scores. To state possible variations between the three populations a canonical variate analysis (CVA) is performed. Finally, pairwise comparisons based on the CVA-results, are obtained. While previous studies of allopatric *T. moorii* populations found a significant difference in both views of the dentary, none of the allopatric populations in this study showed any difference. It has also been shown that sympatric and allopatric populations of *T. moorii* are distinguishable via proportions of the eyeregion. To demonstrate potential differences among populations of *T. moorii,* this study focuses on the underlying bones of the eyeregion. Another objective of this work, which is still in progress, is to exemplify possible disparities between the males' and the mouthbrooding females' digestive part of the viscerocranium.

In search of phylogenetic signals in the soft body of Caudofoveata (Mollusca)

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The Caudofoveata constitute a group of exclusively marine molluscs characterised by a worm-shaped body, an anterior oral or pedal shield, a terminal mantle cavity and a mantle cuticle with embedded aragonitic sclerites covering almost the whole body surface. They show a worldwide distribution in euhaline conditions, predominantly inhabiting muddy bottoms from shallow waters to the deep sea. Their phylogenetic position with respect to the other higher-ranked molluscan taxa is still under debate, as is the definition of genera and families within the group. Since the current taxonomy and systematics of caudofoveates are almost exclusively based on the morphology of hard parts, i.e. the radula and the sclerites, these structures are very well investigated. Data on soft-body anatomy, in contrast, is often not very detailed or completely lacking, especially in recent publications. Such data, however, could contribute significantly to the above-mentioned discussions. Promising character complexes are for example the various muscle systems (e.g. the pedal shield and ctenidial retractors or the radula musculature) and the nervous system.

In this study we compare the anatomy of the nervous system and the muscular system in several species taken from all three presently distinguished families (Limifossoridae, Prochaetodermatidae, Chaetodermatidae) using computer-based 3D-reconstructions of serial sections. The results so far, combined with data from the literature, point to a general usefulness of the two character complexes at different hierarchical levels and also support some of the traditional groupings, but taxon sampling needs to be considerably expanded in order to strengthen the hypotheses presented. In some cases this proves to be a challenging task because material is often difficult to obtain, especially in a well preserved state.

Geographical variation in chloroplast sequences and genome size in *Gentiana* Section *Calathianae*

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Gentiana sect. *Calathianae* is a small section within the 15 sections of the genus. It comprises about 20 taxa which have their main occurrences in the European mountain ranges in subalpine to montane and high alpine habitats. The section includes mostly perennial taxa and is mainly diversified within the Alps where several species are endemic (*G. pumila, G. terglouensis, G. schleicheri, G. brentae*) or subendemic (*G. brachyphylla, G. bavarica*). *Gentiana verna*, the spring gentian, is the most widespread perennial species. Its distribution covers nearly the entire European Alpine System and the Pontic Mountains in Turkey. Several closely related (sub)species are found in geographically isolated areas at the periphery of *G. verna*'s distribution. Common morphological characters are the flowering stems which arise singly from often shortly creeping stolons as well as the solitary and terminal, mostly intensive blue coloured flowers. The corolla with its five spreading lobes is salverform, the slender calyx tube often possesses wings which are amongst others (e.g. basal leaf shape) criteria for distinguishing species or subspecies. There are some interesting aspects regarding the section *Calathianae* in general and the *G. verna* group in special. The taxonomy of the section is still under debate and different classifications are in use today we try to shed light on the phylogenetic relationships within sect. *Calathianae* in general with special emphasis on the diverse *G. verna* group. Apart from AFLP fingerprinting data including almost all taxa, this will be realized by comparison of chloroplast DNA sequences from two regions: trnL-ndhJ (1,000 bp) and rpL32-trnL (600 bp). In total 130 individuals (62 samples from the *G. verna* group, 68 samples from 14 other species) from 47 populations were examined. Preliminary results will be shown in a haplotype network and a neighbour-joining tree. Beside remarkable ecological variation there is a reported high variation in chromosome numbers between the species (and subspecies). We, moreover, carried out genome size measurements from 15 species comprising 54 populations with 158 individuals (including 25 populations with 77 individuals from the *G. verna* group). Astoningishly a high variation and a geographical pattern was found within the *G. verna* group with absolute genome sizes (measured by Flow Cytometry) from 4.73 to 7.12 pg (2.66 to 7.12 pg in the entire sect. *Calathianae*).

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Exploring population differentiation in *Altolamprologus compressiceps* using microsatellite markers and geometric morphometrics

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Lake Tanganyika is well known for its extraordinary diverse cichlid fish fauna and represents an often studied system for different speciation processes. The Lamprologini represent the most species-rich tribe in Lake Tanganyika comprising 90 species in 7 genera. Most of the lamprologine species are endemic to Lake Tanganyika and represent a monophyletic group.

Altolamprologus compressiceps is a substrate spawning, highly specialized philopatric species in rocky habitats. Here, it prefers living between boulders and seems to avoid crossing large sandy areas. Those stretches of unsuitable habitat can increase population differentiation if gene flow is interrupted.

In this study we want to investigate population differentiation in *Altolamprologus compressiceps*. We are analyzing geographically separated populations from three bays at the southern tip of Lake Tanganyika (Zambia). We will assess population differentiation and levels of gene flow among populations using nuclear DNA markers in terms of highly polymorphic microsatellite loci. In addition to the genetic markersystem, differences in the overall body shape are analyzed using geometric morphometrics.

Results will shed light on genetic and morphological population differentiation and levels of gene flow in this rather philopatric species.

Molecular phylogeny of *Eois* moths – implications for the evolution of wing patterns and host plant use.

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Eois is a pantropical genus of Geometridae moths with 247 described species, the majority of which occur in the Neotropics. The real species count is likely to be at least twice that number. *Eois* is a prominent component of Andean moth communities accounting for up to 10% of geometrid individuals in certain regions. A dataset of partial COI and Ef1α sequences (~2200 bp altogether) was used for phylogenetic reconstruction in maximum parsimony, maximum likelihood and Bayesian analyses. With 142 taxa our dataset is the largest taxon set of Geometridae analyzed in a molecular phylogenetic study so far. Monophyly of *Eois* was always strongly supported. Ten monophyletic clades were found with consistently high support. Seven of these clades have characteristic wing pattern phenotypes, while only one wing pattern type occurs in two clades. The species richness of Neotropical *Eois* is most likely the result of a single radiation as Central American species cluster with morphologically similar Andean species. Old World *Eois* were recovered as the basal clade within *Eois,* and African *Eois* are nested within Asian species. This pattern suggests that *Eois* originated in Asia with later colonization of Africa and the Neotropics. The affiliations of *Eois* within the subfamily Larentiinae where the genus has been placed close to the tribe Eupitheciini remained unresolved in our analyses.

Eois larvae are commonly feeding on *Piper* plants; a smaller number of species feeds on two other genera of Piperaceae (*Peperomia* and *Manekia*). At least two species live on *Hedyosmum* (Chloranthaceae) and single instances of feeding on Gesneriaceae and Monimiaceae are known. These host plant affiliations were analyzed against the phylogenetic hypothesis derived from sequence data. The trophic association with representatives of the family Piperaceae occurs in all 8 (of 9) Neotropical clades for which host information is available. Species feeding on *Peperomia, Manekia* and *Hedyosmum* are usually nested in *Piper*-associated clades. Species associated with Gesneriaceae and Monimiaceae are scattered in otherwise Piperaceae-associated clades. These patterns suggest multiple parallel host shifts away from *Piper* as ancestral food plant. Close co-evolution with *Piper*, as proposed for Neotropical *Eois* by other workers, is therefore likely confined to certain clades within *Eois*. Old World *Eois* are known to feed on Euphorbiaceae. Records of *Eois* larvae from invasive *Piper* species in New Guinea suggest that some Old World species may have been preadapted to feeding on Piperaceae.

New insights on explosive speciation and adaptive radiation from East African cichlid fishes

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The species flocks of cichlid fishes in the three Great East African Lakes, Victoria, Malawi and Tanganyika, provide excellent model systems to study speciation and adaptive radiation. Due to their different age, species flocks evolved to different levels of eco-morphological and genetic divergence. While the connection of speciation and eco-morphological divergence is a central feature of the theory of adaptive radiation, evidence in nature is scarce. Our goal was to elucidate pathways, common patterns and differences in the three radiations, and the role of natural selection in driving the process. We analyzed DNA sequences, AFLP and microsatellites of several lineages and studied populations by combining population genetics and comparative morphometrics. Phylogenetic analyses not only suggested similar patterns of diversification, they also linked the three radiations by placing the origin and spread of the haplochromine cichlids, the most species-rich group of cichlids, right within the primary radiation of Lake Tanganyika. Concerning pace and timing, radiations were most likely catalyzed by the interplay of geological and biological processes, indicating a truly “explosive” pace at the beginning, as evidenced by the tree shape of the molecular phylogenies of Lake Malawi Mbuna and the Tanganyikan tribe Tropheini. Concerning the connection of speciation and eco-morphological divergence, our experimental study of closely related allopatric populations and sympatric sister species of the genus *Tropheus* demonstrated small but clear differences in morphology among sym- and allopatric entities. Divergent selection on particular morphological characters is likely to act in sympatry, while allopatric populations seem to be under stabilizing selection. Patterns observed in populations of sympatric species pairs are consistent with character displacement driving morphological divergence.

Evolutionary patterns in the small, blue, and alpine gentians (*Gentiana* sect. *Calathianae*, Gentianaceae)

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Phylogeographical methods, in both molecular and data analyses, have brought new possibilities for the study of origin and diversification of biota. Based on molecular data the evaluation of the mode of speciation and the biogeographical history of species and species groups has become possible in detail. Species of the Alps are of particular interest for research as these cold adapted taxa have diversified rather recently, i.e., during the end of Tertiary and the Pleistocene. Moreover alpine plants did not get affected to such an extent by the Ice Ages as other ones. By studying cpDNA sequences, genome sizes, and AFLP fingerprints of the *Gentiana* sect. *Calathianae* (Gentianaceae; with ca. 17 species and 22 subspecies, more than 100 population samples) in combination with statistical phylogeographic methods we aim for analyzing origin, mode and timing of diversification and speciation. We selected variable cpDNA regions that allowed for certain phylogeographical analyses. Moreover we analyzed AFLP fingerprints as a second source for obtaining phylogenetic and phylogeographic hypotheses. Genome size data showed that substantial variation is found in sympatric species probably reducing gene flow among closely related species. Our study is of particular interest in terms of the understanding of speciation in alpine habitats and the establishment of species barriers enabling sympatry.

The tentorium in Neuropterans (Insecta) – an evolutionary approach

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The tentorium is a cuticular invagination of the arthropod head capsule that serves as a muscle attachment structure. It has been studied in adults and larvae of various arthropod taxa and has provided informative characters for reconstructing phylogenies. This inspired us to study the tentorial structures in Neuroptera.

Head capsules of representative neuropteran families were imaged using X-ray microtomography (microCT) and volumetric images of the tentoria were reconstructed and compared.

Dorsal tentorial arms are present in *Nevrorthus*, *Sisyra*, *Osmylus* and *Chrysopa*, as well as in the outgroup orders Raphidioptera and Megaloptera (Achtelig 1967). They certainly represent a plesiomorphic feature that has been reduced in all other families studied. *Nemoptera* and *Libelloides* – both belonging to the well-established clade Myrmeleontiformia – have strongly differing tentoria. Apparently this is due to highly diverse and specialized feeding habits. Shovel-like extensions of the anterior tentorial arms serve as attachment areas for maxillary muscles in many neuropteran families, and in *Nemoptera* for antennal muscles as well. The “shovels” might be a synapomorphy of all Neuroptera except Nevrorthidae and Sisyridae, thus corroborating the hypothesis that these two families branched off independently (Aspöck & Aspöck 2008).

All things considered, the tentorial structures of Neuroptera seem to be phylogenetically significant in the “average“ polyphagous Neuropterans, but their phylogenetic signal may be obscured in specialized feeders due to adaptive modifications.

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