

4. Jahrestagung von NOBIS Austria

2. - 3. Dezember 2010

Karl-Franzens-Universität Graz
SOWI-Zentrum

Programm und Abstracts



Berichte des Institutes für Erdwissenschaften
Karl-Franzens-Universität Graz

Band 15

Herausgeber: Harzhauser, M. & Piller, W.E.

GRAZ 2010



<ISSN 1608-816>

Impressum:

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Systematics – applied?

Donnerstag – 02. 12. 2010

*Institut für Erdwissenschaften, Bereich Geologie und Paläontologie
Heinrichstrasse 26 – Erdgeschoß – Seminarsaal SR 09.02*

17:00 – 18:00 **Generalversammlung von NOBIS Austria**

18:00 – 21:00 **Icebreaker**

Freitag – 03. 12. 2010

SOWI-Zentrum – Universitätsstraße 15 – 1. Stock/ HS 15.13

09:00 **Registrierung und Kaffee**

10:00 **Begrüßung** *W. E. Piller*, Leiter des Fachbereichs für Geologie und
Paläontologie der Karl-Franzens-Universität Graz

10:10 **Begrüßung** *U. Aspöck*, Präsidentin von NOBIS Austria

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

10:20 – 10:40 **G. Aubrecht**

“Do you know EDIT, CETAF, DEST, EJT, EoL and so on?”

Initiatives for the promotion of taxonomy on a European level.

10:40 – 11:00 **A. Kroh**

WoRMS and the World Echinoidea Database

11:00 – 11:20 **B. Berning, J.-G. Harmelin & B. Bader**

Long-distance travels with short-lived larvae – the peculiarities of seamount bryozoans

11:20 – 11:40 **M. Gross & W.E. Piller**

Linking high-resolution environmental analyses and taxonomy: a case study on ostracods in deep time

11:40 – 12:00 **A. Kern, M. Harzhauser, A. Soliman, W.E. Piller & M. Gross**

From taxonomy to deep time resolution: decadal scale Late Miocene vegetation dynamics deciphered from palynomorph assemblages

12:00 – 12:20 **T. Suttner**

What are conodonts?

12:20 – 13:30 **Mittagspause – Mensa, Sonnenfelsplatz 1**

13:30 – 15:10 **Vorträge 2** Chair: *E. Haring*

13:30 – 13:50 **H. Schuler**

The endosymbiont *Wolbachia* in fruit flies of the genus *Rhagoletis*: Horizontal transfer and impact in speciation

13:50 – 14:10 **J. Walochnik & H. Aspöck**

Is *Babesia* still *Babesia*?

14:10 – 14:30 **W. Foissner**

Boden-Protozoen als Indikatoren der Bodenqualität

14:30 – 14:50 **E. Lerceteau-Köhler, U. Schliewen, T. Kopun & S. Weiss**

Genetic variation in brown trout *Salmo trutta* across the Danube, Rhine, and Elbe headwaters: a failure of the phylogeographic paradigm?

14:50 – 15:50 Poster-Präsentation

15:50 – 16:10 Kaffeepause

16.10 – 17.30 Vorträge 3 Chair: *H. Aspöck*

16:10 – 16:30 **L. Muggia & M. Grube**

Systematics and cryptic species in lichenized fungi

16:30 – 16:50 **T. Spribille, S. Pérez-Ortega, T. Tønsberg & D. Schirokauer**

Mining lichen diversity: systematics as a framework for identifying 'known unknowns' in Alaska (U.S.A.)

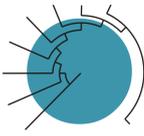
16.50 – 17.10 **L. Greimler**

Cryptic diversity in European *Gentianella* section *Gentianella* (Gentianaceae)

17.10 – 17.30 **D. Rakosy & H.F. Paulus**

Biology and phylogeny of the *Ophrys tenthredinifera* species group in Crete

GRAZ 2010

N  B I S AUSTRIA 4

Astonishing Diversity of Somatic Ciliary Patterns in Oligotrichid Ciliates (Protista, Ciliophora)

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Although the Oligotrichida (Ciliophora, Spirotricha) typically possess only two somatic ciliary rows, the diversity of ciliary patterns is tremendous, i.e., eleven, occasionally very complicated arrangements are distinguished. The evolution of these somatic ciliary patterns is reconstructed, using the orientation of the ciliary rows (which of the paired basal bodies bears the cilium) and the position of the oral primordium, the developing oral ciliature of the daughter cell. Even though molecular phylogenies are still in their infancies concerning the oligotrichids, the genealogy of the small subunit ribosomal RNA gene sequences is congruent with the current hypothesis. It is most parsimonious to assume a convergent pattern development in the tailless taxa and the tailed tontoniids, as the contractile tail is considered a strong synapomorphy due to its complex and unique ultrastructure. Indeed, ontogenetic data suggest that the Ω -shaped pattern evolved not only convergently in the tailed and tailless taxa, but also originated from different patterns. On the other hand, gene sequence data indicate that the sinistrally spiralled arrangement did not develop twice, but represents a synapomorphy of the tailed genus *Spirotontonia* Agatha, 2004 and the secondarily tailless monotypic genus *Laboea* Lohmann, 1908. The curious genera *Apostrombidium* Xu et al., 2009 and *Varistrombidium* Xu et al., 2009 were intuitively affiliated with the strombidiids. The present concept corroborates this assignment and proposes a position for the two genera within the family Strombidiidae. Furthermore, new ontogenetic data necessitate a split of the species-rich genus *Strombidium*. While the oral primordium forms posteriorly to the horizontal ciliary row in the type species of *Strombidium*, it develops anteriorly in three congeners, justifying the establishment of two new genera, which differ in the arrangement of their extrusomes (extrusive organelles): they insert along the anterior margin of the horizontal ciliary row and posteriorly to the oral primordium in one genus, while distinctly apart from the ciliary row and anteriorly to the oral primordium in the other; probably, both patterns evolved convergently (Agatha 2010).

This study was supported by the Austrian Science Foundation (FWF, Project P20461-B17).

Agatha, S. 2010. Updated hypothesis on the evolution of oligotrichid ciliates (Ciliophora, Spirotricha, Oligotrichida) based on somatic ciliary patterns and ontogenetic data. *Eur. J. Protistol.* (2010), doi:10.1016/j.ejop.2010.09.001.

“Do you know EDIT, CETAF, DEST, EJT, EoL and so on?” Initiatives for the promotion of taxonomy on a European level.

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The Darwin Declaration 1998 referring to the „taxonomic impediment“ started highlighting the global problems of taxonomic research. Calls for help and for improvement of this bad situation from museum and university taxonomists are already commonplace nationally and internationally.

Usually taxonomists are organized in their specific scientific societies, but it needs concerted communication and action on a much broader base to be heard politically. The recent improvement of communication and organization among taxonomists must not hide the fact that operative actions are needed in order to reverse the fatal situation.

The „Global Taxonomy Initiative – GTI“ is an intergovernmental project within the Biodiversity Convention and was ratified in 2002. Thus the problem was outlined and set into an institutional framework. But it did not yet bring a measureable improvement of the situation. New projects were initiated but especially the education of taxonomists at university and non-university level is still decreasing rapidly. This fact is really threatening and still unsolved. The foundation of NOBIS-Austria was an initiative on the national level with the aim of improving communication between Austrian taxonomists, of strengthening group dynamics and of offering a joint approach to the public.

Here some international projects are introduced concerning the wider frame of taxonomy. These might be of interest because project proposals often need a view on a broad scale. Recent projects are for example EDIT (European Distributed Institute of Taxonomy), CETAF (Consortium European Taxonomic Facilities), DEST (Distributed European School of Taxonomy), EJT (European Journal of Taxonomy), EoL (Encyclopedia of Life), etc.

Both national and international approaches will be necessary in the future in order to promote the legal concerns of taxonomists and to find political acceptance.

Long-distance travels with short-lived larvae – the peculiarities of seamount bryozoans

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In the intensified effort to study seamount biota during the last decade, the Bryozoa have almost completely been neglected, although they may form a major component of the sessile benthic community. A first screening of the sparse literature and some of the samples taken during several scientific cruises shows that cheilostome bryozoans are regularly found on NE Atlantic seamounts: 36 spp. on Gettysburg Smt, 27 on the Great Meteor Bank (GMB), 24 on Ampère Smt, 23 on Atlantis Smt, 21 on Hyères Smt, 14 on Irving Smt, and 13 on Conception Smt.

Due to the short-lived bryozoan larvae, dispersal is generally very restricted and long-distance transport of bryozoans to or between isolated offshore sites presumably only achieved by means of rafting of the colony. However, this mechanism is less likely for species adapted to bathyal habitats. Endemism, particularly on remote seamounts, is therefore expected to be comparatively high. Indeed, at least 18 of the 27 spp. (67%) found on the GMB are endemic to this seamount. Of the remaining species, one arrived on *Sargassum* from the W Atlantic, three species are known from the E Atlantic shelf, and another five are restricted to the Azores and other Atlantic seamounts. Moreover, at least 17 species, three genera and one family from the GMB are new to science.

Regarding the entire region, several higher taxa are endemic to seamounts, or are significantly more speciose there than on the continental shelf, indicating a long history of seamount faunas and, possibly, sporadic dispersal of founder species from seamounts to the shelf.

Given the number of scientific cruises to these and other NE Atlantic seamounts, and the great amount of unscreened samples that exist, a thorough taxonomic study of seamount bryozoans will certainly increase the number of taxa. With this knowledge it will then be possible to address more precise questions concerning the ecology, biogeographic patterns and processes, and the evolutionary history of seamount faunas.

Lichenized Fungi diversity of the Balkan Peninsula

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The present knowledge of lichenized fungi of the Balkan Peninsula is still rather incomplete and there are relatively few recent floristic papers. While numerous lichen collections from coastal parts revealed a lot of new species towards the end of Habsburg period and several important studies were published between World War I and World War II by the lichenologists F. Kušan, A. Popnikolov, M. Servít, J. Suza and Ö. Szatala, lichenological exploration of former Yugoslavia was interrupted almost completely in the period between World War II and the segregation of nations in the 1990s. In the 1970s first steps were undertaken to revitalize the lichenological investigation of the Dinaric region by J. Poelt and his students in Graz resulting in the description of several new species as well as by the Czech lichenologist A. Vežda and the Slovak lichenologist I. Pišút. In the late 1970s and early 1980s it was M. Murati, who published a series of floristic papers on the lichen flora of Macedonia. During the last twenty years H. Mayrhofer (Graz), his students and collaborators intensified lichenological activities on the Balkan Peninsula by establishing co-operations with local biologists, starting with floristic papers, followed by catalogues of lichens and lichenicolous fungi of Slovenia (2000), Bulgaria (2005), Montenegro (2009), Bosnia & Herzegovina (in press) and Macedonia (in prep.).

The area of the southern Dinaric mountains with its glacial refugia is highly attractive for biodiversity studies, because it represents one of the last remaining large virgin forest areas in Europe (e.g. Biogradska gora in Montenegro and Perućica in Bosnia & Herzegovina). These maintain a rich diversity of lichens, comprising many elsewhere rarely found oceanic species.

Actual investigations are focusing on population genetics of *Lobaria pulmonaria* in and around virgin forests, its fungi on large decaying thalli, on the general biodiversity of remote or otherwise interesting sites and ecological niches with special emphasis on Bosnia & Herzegovina, Bulgaria, Macedonia, Montenegro and Slovenia, and on the taxonomy and distribution of the family *Physciaceae*.

Today, Greece (incl. Crete) has a known diversity of c. 1200 lichen species, Slovenia, Croatia and Bulgaria c. 1000 each, Montenegro c. 700, Bosnia & Herzegovina, Serbia (incl. Kosova) and Macedonia c. 600 each and Albania c. 200(!).

How and why to achieve more objectivity in taxonomy, exemplified on a fossil ostracod from long-lived Lake Pannon

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Taxonomists are commonly confronted with poor descriptions. The situation is exacerbated for fossil taxa which display few homologue landmarks useful for defining morphological traits. These latter are either necessary for building a clear taxonomic diagnosis or for further phylogenetic analysis.

Amplocypris abscissa was briefly described by A. E. Reuss (1850) from several outcrops near Vienna and Sopron (Vienna Basin; Upper Miocene, Pannonian). Subsequently, it was mentioned all around the Pannonian Basin respectively the Palaeo-Lake Pannon, which covered this area at that time: from the western sites in Austria and Slovakia, to eastern and southern ones (Romania, Serbia and Croatia). This geographic distribution contrasts with the high number of fossil species belonging to this genus, which are considered to be endemic in Lake Pannon. Our project on fossil ostracods from Hengersdorf (Vienna Basin, Pannonian "D") document *A. abscissa* as a polymorphic taxon. Moreover the genus *Amplocypris* Zalani 1944, displays an elusive diagnosis and an unsecured phylogenetic position. We demonstrate, using a precise protocol, how the taxonomic status of both of the genus *Amplocypris* and of the species *A. abscissa* can be achieved in an accurate and reproducible way: (a) A comparative morphological study of the valves, for fossil *Amplocypris* species and Recent representatives of genera belonging to higher-rank taxa, using both TL- and SE-microscopy, is absolutely necessary for developing a clear differential diagnosis of this genus and its allocation to one of the Cyprididae subfamilies (i.e. the Eucypridinae). (b) *Amplocypris* displays few homologue landmarks. Geometric morphometrics for outlines, combined with an original algorithm, which resemble a semi-landmark approach, offers the possibility to create morphological traits: Linhart's B-spline Approach (cf. the web site "Methods in Ostracodology" at <http://palstrat.uni-graz.at>). (c) Data expressed as pair-wise resemblance matrix of Euclidean distances are further analysed using techniques specific to numerical taxonomy, like UPGMA-cluster analysis, Principal coordinate analysis and the SIMPER exploratory analysis (cf. the computer package PRIMER v6 and PERMANOVA+ for PRIMER). (d) A matrix of dissimilarity values of the traits, expressed as arithmetic means with their 99% CL, allow to produce a new diagnosis of *A. abscissa* and to separate it from two other unnamed taxa. Together they form a phylogenetic lineage.

Habitat requirements of the pulmonate land snails *Trochulus oreinos oreinos* and *Cylindrus obtusus* endemic to the Northern Calcareous Alps, Austria

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The Austrian endemic land snails *Trochulus oreinos oreinos* (Wagner 1915) and *Cylindrus obtusus* (Draparnaud 1805) have been in the focus of phylogenetic research in the course of our project about Austrian land snails. For *T. oreinos*, which was formerly regarded as a local subspecies of the widespread *T. hispidus*, a first phylogenetic analysis combined with more detailed morphological investigations was performed recently indicating that *T. oreinos* is an old phylogenetic lineage and presumably has a long independent history in the North-Eastern Calcareous Alps. *Cylindrus obtusus*, which is an old distinct lineage within the Helicidae, is – like *T. oreinos* - restricted to high elevations of the Eastern Alps. In its easternmost populations it shows some specific morphological traits, as a somewhat smaller size and irregular building of mucus glands.

In this study we wanted to know, if these findings are also reflected in the habitat preferences of these species. Four sites, which mark the easternmost distribution border of both species, were selected for further investigation: the mountains Hochschwab, Schneealpe, Rax and Schneeberg. From these areas we had an adequate sample and exact vegetation maps were available.

In *C. obtusus*, the morphological specialties of the easternmost populations are perhaps a result of the suboptimal climatic conditions on Rax and Schneeberg Mountain. Both massifs are under strong influence of the warm pannonic climate, which might afflict this cryophilic species. *C. obtusus* and *T. oreinos* prefer rocky habitats from the subalpine ecotone upwards. While *T. oreinos* is restricted to loose *Caricetum firmae* meadow and alpine boulder and scree societies, *C. obtusus* can inhabit several plant communities. Both species are restricted to primarily forest free sites on rocky ground or thin layer of rentsina soil. Therefore they are not afflicted by abandoning of man-made meadows, the most important recent change of alpine agriculture. As both taxa are restricted to the subalpine and alpine ecotone, at least populations at the lower altitudinal distribution are potentially afflicted by climatic changes

Protists as bioindicators for soil quality

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Several unique features favour the use of heterotrophic protozoa as bioindicators for soil quality:

1. Protozoa are an essential component of soil ecosystems, because of their large standing crop and production. Changes in their dynamics and community structure very probably influence the rate and kind of soil formation and soil fertility.
2. Protozoa, with their rapid growth and delicate external membranes, can react more quickly to environmental changes than any other eukaryotic organism and can thus serve as an early warning system.
3. The eukaryotic genome of the protozoa is similar to that of the metazoa. Their reactions to environmental changes can thus be related to higher organisms more convincingly than those of prokaryotes.
4. Protozoa inhabit and are particularly abundant in those soil ecosystems that almost or entirely lack higher organisms due to extreme environmental conditions, e.g. alpine regions above the timberline, Arctic and Antarctic biotopes.
5. Protozoa are not readily dislodged in soil (Kuikman et al., 1990). Many (but not all!) are ubiquitous and are useful in comparing results from different regions. Differences in patterns of distribution are almost entirely restricted to passive vertical displacement; thus, the difficult problem, especially with the epigaeon, of horizontal migration does not affect the investigations.

There are, however, several factors that have apparently restricted the use of soil protozoa and even metazoa as bioindicators (Aescht and Foissner, 1992):

1. The immense number of species; more than 1000 may occur in a square metre of forest soil. Many specialists are needed for identification and each species has specific requirements that are often incompletely known.
2. Enumeration of soil organisms is difficult and time-consuming.
3. Animals need other organisms for food. Thus, the constellation of factors is more complex than in plants and bioindication often remains un-specific, i.e. different factors induce similar reactions.
4. Most soil organisms are inconspicuous and invisible to the naked eye, making them unattractive to many potential investigators.

In the lecture, I show examples from comparisons of ecofarmed and conventionally farmed fields and grasslands.

Phylogeography and synchronous diversification of the *Corvus* corvids of the world

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The genus *Corvus* with its approximately 40 species is world wide distributed, except S America. Highest diversity is found in Australasia and SE Asian islands. Ten species (25%) are coloured black and white/grey, the rest are completely black.

We investigated the phylogeny of the genus *Corvus* employing DNA sequences of the mitochondrial control region. The study was based mainly on museum material allowing the analysis of more than 30 species. Inclusion of sequences of other corvid genera as available in GenBank confirmed the monophyly of the genus *Corvus*. Within the *Corvus* clade several distinct subclades can be distinguished. Some contain only single species or species pairs (e.g., *C. monedula* + *C. dauricus*; *C. frugilegus*; *C. palmarum*) while other clades are composed of many species (e.g., the Holarctic and African clade or the SE and E Asian clade). In general, the composition of the clades reflects geographic contiguousness. The basal relationships among clades remain unresolved with this marker sequence.

It is remarkable that each clade contains black as well as white/grey coloured representatives. None of the latter are found in N America, whereas almost all African species south of the Sahara show black-white pattern. The most parsimonious explanation for the distribution of plumage colour in the phylogenetic tree is that the pale markings evolved at least five times independently. The assumption that the white/grey colour pattern - which is found also in other genera of the family Corvidae, e.g., *Pica* - is the plesiomorphic state, is less likely.

Cryptic diversity in European *Gentianella* section *Gentianella* (Gentianaceae)

Greimler, J.

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Gentianella section *Gentianella* (Gentianeae, Swertiinae) includes ca. 20 taxa in Europe of which the majority is found in and around the Alps. Most taxa are highly variable due to ecological polymorphism among populations in different habitats and in part due to seasonal dimorphism. Investigations from reproductive biology, common garden experiments, morphology, nrDNA, cpDNA, and AFLP have revealed various patterns of divergence and in some cases disagreement between genetic and morphological data.

Genetic data (AFLP) in contrast to morphology indicate clear differentiation into two cryptic species within the widespread *G. germanica* agg. resulting in *G. rhaetica* in the Eastern Alps and *G. germanica* s.str. in northern Central Europe. These allopatric cryptic or sibling species appear to have been separated by Pleistocene climatic oscillations. Extensive patterns of haplotype sharing were observed in the cpDNA RFLP data. Both hybridization or introgression as well as incomplete lineage sorting can generate such patterns. It is, however, difficult to distinguish between these two processes. In the case of *Gentianella* reticulate evolution (introgression) may explain such patterns to a high degree as well as the often found morphological uncertainties or gradients on range margins of several taxa. AFLP data provided evidence for various scenarios of introgression and reticulate evolution among *G. rhaetica*, *G. obtusifolia*, and *G. austriaca* in the eastern Alps. Such reticulate patterns and/or ancient polymorphism towards southeastern Europe may be the reason for unclear relationships within *G. austriaca* agg. and its relation to other taxa especially in south-eastern Europe. The significance of those various cryptic patterns for conservation is discussed.

Linking high-resolution environmental analyses and taxonomy: A case study on ostracods in deep time

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Per se taxonomic investigations of fossils can neither include molecular biological approaches nor the study of soft parts. Environmental parameters cannot be measured directly. Consequently, the palaeontological approach is strictly morphologically-based and environmental factors must be deduced from abiotic and biotic proxies. However, the fossil record has one striking advantage over the study of extant organisms: time! If an appropriate time-model is on hand, long- as well as short-term changes (millions of years, down to years) can be extracted. Especially, micro-fossils are of prime importance in this case. Due to their small size, ten thousands of preserved remains provide a huge dataset for profound taxonomic analyses and phylogenetical reconstructions.

The examination of a limnic–deltaic sedimentary sequence, deposited on the western margin of Palaeo-Ancient Lake Pannon (~11.3 Ma), focused on the occurrence of the mussel shrimp genus *Cyprideis* (ostracoda) and its linkage to environmental shifts. Based on the timing of the section, we achieved by our high-resolution sampling (5 mm thick rock slices) a time-resolution of only a few years. Qualitative as well as linear and geometric morphometric valve analyses allowed differentiating three co-occurring *Cyprideis* species, which were probably adapted to different microhabitats. One of them is only recognized at the peak of a limnic transgression. In contrast, one other species seems to be more euryplastic because it appears well before this event and is recorded in the regressive prodelta sediments up section likewise. The remarkable low quantity of the third species clearly reflects its diverging paleoecological demands, since it mainly occurs in the littoral facies. Size, posteroventral spines, hinge structure, ornamentation and valve outline turned out to be appropriate diagnostic characters to define these sympatric species in the sense of a multidimensional species concept. These characters enable to delineate *Cyprideis* populations in Lake Pannon as segments of evolutionary lineages and thus phylogenetic species. This is essential for any well-founded biostratigraphic zonation and further palaeogeographic models.

This is a contribution to the FWF-project P 21748-N21.

Determination of the prevalence of *Fascioloides magna* (BASSI 1875) and other digenetic trematodes in *Galba truncatula* (O.F. MÜLLER 1774) in the area of Orth/Danube (Lower Austria)

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Digenetic trematodes comprise numerous species of great medical and veterinary importance. These parasites have complicated life cycles with multiple successive hosts. The introduced large American liver fluke *Fascioloides magna* was recorded in free-living red deer and roe deer in the wetlands of the Danube, east of Vienna since 2000. The aim of this study was to determine the current infection rate of the intermediate snail host *Galba truncatula* with *F. magna* and other digenetic trematodes in the area. A monitoring of *G. truncatula* from three locations near Orth/Danube was conducted during 2008. Single collections were taken from three locations from the opposed southern Danube banks (=other locations). A total of 3.871 *G. truncatula* were collected, measured and examined under the microscope for the presence of digenetic trematodes. Every tenth microscopically parasite-free snail was chosen as a random sample. Altogether 68 random samples and 30 microscopically detected isolated trematode stages were tested molecular biologically by PCR and sequencing. Two primer pairs were developed to enable both the detection of trematodes in general and the specific detection of *F. magna* in *G. truncatula*. In addition, a specific primer pair was chosen from literature for the detection of the common liver fluke *F. hepatica*, which is also a pathogen of humans.

Overall, 96 trematode infections (prevalence 2,48%) were detected in the 3.871 examined *G. truncatula*. Trematodes of Paramphistomoidea (prevalence 1,91%), Echinostomatoidea (0,46%) Strigeida (0,10%) and Plagiorchiida (0,05%) were found besides Fascioloidea. *F. magna* was found with an overall prevalence of 0,26% (n = 3.871), whereby the highest prevalence was found at the southern locations (0,47%, n = 427), but also at two northern locations (0,20%, n = 1.975 and 0,30%, n = 1.347). The common liver fluke *F. hepatica*, was found once in a snail collected at Orth. The infection peak of *F. magna* was in July (1,15%).

The comparison of microscopic and molecular biologic methods confirmed former studies, in which DNA-based methods have shown a higher sensitivity. It was possible to differentiate morphological similar trematode species by molecular genetic methods.

Phylogeography of the East-Alpine members of the landsnail species *Orcula dolium* (Gastropoda: Pulmonata: Orculidae)

Harl, J., Kruckenhauser, L., Sattmann, H., Duda, M. & Haring, E.

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Orcula dolium has the widest distribution among the species of the genus *Orcula* and inhabits the calcareous parts of the Alps and the Northern Carpathians. Since it had been described in 1801 by DRAPARNAUD, various authors added a minimum of 23 further subspecies. Most of these subspecies represent local forms that inhabit only small, partly isolated regions and differ from the nominate subspecies in their shell shape and the expression of their aperture's folds. Besides the common *O. dolium dolium*, six subspecies have been described from the Eastern Alps.

Two of them, *O. dolium edita* and *O. dolium raxae*, are restricted to different elevations of high mountain areas. According to the literature, the nominate subspecies is sporadically found in the same habitats as the high alpine forms, but no intermediate morphs have been detected. This observation raises the question if these taxa represent distinct species. To determine whether these taxa are differentiated genetically and to reveal their relationships, snails were collected from sites covering the main part of the East Alpine distribution range of the species. Two mitochondrial genes (*COI* and *16S rRNA*) as well as the nuclear *histone H3-H4*-spacer region were sequenced and genetic distances calculated. Additionally, morphometric landmark analyses were conducted to examine if the phylogeny is in accordance with shell morphological differentiation.

In the trees based on mitochondrial data several highly distinct clades were found, which are mostly not congruent with the described taxa. In particular, the high Alpine subspecies do not represent distinct lineages. In the *H3-H4*-spacer region almost no variation was found within the *O. dolium* group and the tree does not reflect the mitochondrial haplogroups.

The roots of sea-turtle fouling barnacles (Chelonibiidae, Cirripedia, Balanomorpha)

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The geological evidence for the phylogeny of sessile barnacles comes predominately from intertidal and shallow sublittoral records. Therefore, numerous balanoid species of genera such as *Acasta*, *Concavus*, *Perforatus* and *Balanus* are described. This wealth in data is contrasted by an extremely poor knowledge of open marine taxa which obligatorily cling to free swimming objects such as gars, cetaceans, sirenians, turtles and even sea snakes . This group is mainly represented by members of the coronuloid barnacles (chelonibiids, platylepadids & coronulids). The origin of the mainly sea-turtle fouling balanomorph family Chelonibiidae is still poorly documented. Aside from an erratic Eocene occurrence, assigned to an extinct subfamily, the extant subfamily Chelonobiinae did not appear in the fossil record before the Late Miocene. Now, a new lineage is recorded as an extinct sister-group of the Chelonobiinae. It is based on a 21-million-year-old fossil colony from Pucking (Ebelsberg Formation; Upper Austria). The new subfamily is known so far only from the proto-Mediterranean and the Paratethys seas and ranged from Early Miocene to Late Pliocene times. Members of the subfamily are characterised by large walls with tripartite rostra which display distinct sutures on the external surface. The tripartite rostrum, however, has evolved independently several times in the evolution of the balanomorphs and cannot be treated as synapomorphy. The subfamily comprises one new genus and two species.

The sculpture of the host substratum is preserved as imprints along the carino laterals of one specimen. Although the pattern of ridges and furrows cannot be identified with certainty, the similarities with the sculpture of the carapax of modern *Caretta* suggests the new genus as earliest record of sea-turtle fouling in balanids. The co-existence of members of both subfamilies during the Miocene and Pliocene documents a higher diversity of chelonibiids in pre-Pleistocene times and indicates that Chelonobiinae were able to outcompete their supposed sister-group with the onset of the glacial cycles.

Discriminating *Legionella*, atypical mycobacteria and *Acanthamoeba* using a MALDI biotyper

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The genus *Mycobacterium* including more than 100 described species is divided into three subgroups: the *M. tuberculosis* complex, *M. leprae* and NTM – non-tuberculosis mycobacteria. The latter have been isolated from hospitals, water, humid rooms, soil and from the mucosa of humans and animals. NTM can provoke potentially lethal lung infections in children or immunocompromised persons.

Legionella spp. an anaerobic, gram-negative, rod-shaped, non-spore forming bacterium is the causative agent of legionellosis (Legionnaires' disease). Legionellosis, which represents 4% of community-acquired pneumonia cases worldwide, can have a lethal outcome in 18-20% of cases if untreated. *Legionella* spp. has been isolated from air condition units, swimming pools, ground- and surface water. Legionnaires' disease is acquired by the inhalation of infectious aerosols.

Acanthamoeba spp., single-celled eukaryotic organisms, can provoke severe infections, including *Acanthamoeba* keratitis, GAE (granulomatous amoebic encephalitis) and infections of the lung and the skin. *Acanthamoebae* have two life cycle stages – a trophozoite and a cyst – and play a significant role as vectors for bacteria (particularly also *Legionella* spp. and MOTT).

The aim of the present study is the establishment of a reference database for protein mass spectra of *Legionella* spp., NTM and *Acanthamoeba* spp. using MALDI TOF MS (Matrix Assisted Laser Desorption Ionisation Time of Flight Mass Spectrometry) and the MALDI Biotyper software. This reference database is aimed to serve as an essential tool for the identification of *Legionella* spp., NTM and *Acanthamoeba* spp. and furthermore for the detection of *Legionella* spp. and NTM in *Acanthamoeba* spp.

Integrative taxonomy: Combining chemical, morphological and molecular data for delineation of the parthenogenetic *Trhypochthonius tectorum* complex (Acari, Oribatida, Trhypochthoniidae)

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There is a long-standing controversial about how parthenogenetic species can be defined in absence of a generally accepted species concept for this reproductive mode. An integrative approach was suggested, combining molecular and morphological data to identify distinct entities, and propose them as distinct taxa. Using this approach, speciation of parthenogenetic lineages was recently demonstrated for groups of bdelloid rotifers and oribatid mites. We investigated Austrian populations of the parthenogenetic oribatid mite *Trhypochthonius tectorum*. Besides morphological and molecular data, we included the chemical composition of complex exocrine gland secretions in our analyses. This is the first attempt to combine these three types of data for a delineation of parthenogenetic oribatid mites.

We show that Austrian *T. tectorum* underwent a parthenogenetic radiation and now consists of three distinct lineages, each separated by morphology including morphometry, gland secretion profiles and mitochondrial *cox1* sequences. This diversification happened in the last ten million years.

From taxonomy to deep time resolution: decadal scale Late Miocene vegetation dynamics deciphered from palynomorph assemblages

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Lake systems are fast responding to environmental changes, which makes their detection in the geological record challenging. However, fine sediments from lakes provide ideal preconditions to analyse different environmental proxy data in high resolution sampling method including pollen as in indicator for terrestrial adaptation.

To demonstrate such high frequent vegetation changes far back in the Late Miocene (Pannonian, 11.4 Ma), a continuous 98-cm core from the locality Mataschen in the Styrian Basin was studied each centimeter corresponding to approximately a decade in time. The vegetation at the beginning of the sequence was mainly characterized by a far distributed brackish marsh around Lake Pannon merging into forested swampy Taxidoideae wetlands. A moderate drop of the mean annual precipitation caused a change in the structure of the marsh as the formally dominating Poaceae were replaced by the more dry adapted Cyperaceae grasses within a few decades.

The subsequent increase in annual rainfall is reflected by a rise of the lake level with a lag of 5 decades. This led to an almost complete dieback of the marsh vegetation due drowning, but coincides with the expansion of the open-water dinoflagellate cyst *Impaginium* sp. As soon as the rainfall switched back to moderate levels of ~1100–1200 mm/yr, the rise of the lake level slowed down, the marsh plants could keep up again and the former vegetation belts became re-established. During the whole period of less than 1400 years, the other climatic parameters did not vary much, resulting in a constant composition of the zonal hinterland forests.

For the first time, high-frequency interactions between climate and plants can be documented on a decadal scale in Late Miocene.

This study is financially supported by FWF-project no. P 21414-B16 and P 21746-N21.

Morphological distinctness despite large-scale phenotypic plasticity – analysis of wild and pond-bred juveniles of allopatric populations of *Tropheus moorii*

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Cichlids are an excellent model to study explosive speciation and adaptive radiation. Their evolutionary success has been attributed to their ability to undergo rapid morphological changes related to diet, and their particular breeding biology. Relatively minor changes in morphology allow for exploitation of novel food resources. The importance of phenotypic plasticity and genetically based differences for diversification was long recognized, but their relationship and relative magnitude remained unclear. We compared morphology of individuals of four wild populations of the Lake Tanganyika cichlid *Tropheus moorii* with their pond raised F1 offspring. The magnitude of morphological change via phenotypic plasticity between wild and pond-bred F1-fish exceeds pairwise population differences by a factor of 2.4 (mean Mahalanobis distances).

The genetic and environmental effects responsible for among population differentiation in the wild could still be recognized in the pond-bred F1-fish. All four pond populations showed the same trends in morphological change, mainly in mouth orientation, size and orientation of fins and thickness of the caudal peduncle. As between population differentiation was lower in the wild than differentiation between pond-raised versus wild fish, we suggest the narrow ecological niche and intense interspecific competition in rock habitats is responsible for consistent shape-similarity, even among long-term isolated populations.

Increase of the corallum in the Silurian rugose coral *Idiophyllum* (Arachnophyllidae) from the Ningqiang Formation, China

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Rugose corals are a fossil marine group which appeared in the middle Ordovician and became extinct end of Permian. Rugosa are identified based on the morphological features of their skeletal elements such as septa, tabulae, dissepiments, and wall, which are observed from serial transverse and longitudinal thin sections. The Silurian rugose coral *Idiophyllum* Cao occurs in the Ningqiang Formation (Upper Llandovery), Ningqiang-Guangyuan area near the border of Shaanxi and Sichuan, China. This coral occurs as both compound and solitary forms. Its corallum is characterized by possessing carinate septa displaying pinnate arrangement, convex tabularium which consists of incomplete tabulae, wide dissepimentarium, and distinct cardinal fossula. *Idiophyllum* has major, minor and tertiary septa. Tertiary septa are inserted irregularly and partly. The total number of septa in this coral reaches up to more than two hundred. Seven species have been assigned to *Idiophyllum* (He and Chen, 1986; Kido and Sugiyama, 2005); *Idiophyllum dabashanense*, *I. multifurcatum*, *I. ningqiangense*, *I. tenuiseptatum*, *I. major*, *I. shaanxiense* and *I. massulatum*. One of them, *I. massulatum* has a compound thamnasterioid corallum. He and Chen (1986) indicated that in the compound corallum of *I. massulatum* generally 2 to 5 offsets arise in the axial or peripheral region of the corallum of the parent. Lin *et al.* (1995) mentioned that the increase in the solitary corallum of *Idiophyllum* is parricidal. However, characteristics of the increase in corallum of *Idiophyllum* and septal insertion which is observed in the offsets have not been described in detail. Additional specimens of *Idiophyllum massulatum* and the species of *Idiophyllum* with solitary form were collected in the Ningqiang Formation of Yanzishi, Guangyuan, Sichuan. In these species peripheral and parricidal increase were observed, respectively. Modes of increase in *Idiophyllum*, together with the septal insertion observed in the offsets, are presented.

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The eastern wolf: truths and myths – a molecular perspective

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There has been an extensive debate on origin and taxonomic status of wolf-like canids in the North American Great Lakes region and the consequences for conservation politics regarding these enigmatic predators. Many different hypothesis have been put forward, but in recent years the hypothesis that the eastern wolf represents a distinct species *Canis lycaon* that evolved in North America as sister species of the coyote *C. latrans* and not a sub-species of the old world evolved gray wolf *C. lupus* received an increasing number of followers despite questionable evidence for this particular hypothesis, which largely rests on the presence of exclusively coyote-like mtDNA in (present and historic) samples from the Great Lakes region.

Many recent studies have focused on elucidating the evolutionary history of this enigmatic canid taxon, but have used a restricted geographic and taxonomic sampling and/or applied insufficient amount of molecular markers. Using a broad geographic and taxonomic sampling (including historic samples) and applying maternally, paternally and biparentally inherited molecular markers, we demonstrate that the wolves of the Great Lakes regions do not represent a native North American wolf species but rather are a population of gray wolves that has repeatedly experienced introgression from the coyote. Increased genetic drift as a consequence of reduced population size during Pleistocene glaciations likely resulted in fixation of coyote-like haplotypes in this geographic region.

Thus, we demonstrate that both broad taxonomic and geographic sampling and large amounts of molecular markers with different modes of inheritance are required to elucidate the complex evolutionary history and hybridization dynamics of North American wolf-like canids.

Biodiversität – Wer soll sie in Zukunft erforschen?

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Das österreichische Nationalkomitee für das UNESCO-Programm „Man and the Biosphere“ (MAB) an der Österreichischen Akademie der Wissenschaften (ÖAW) will die Öffentlichkeit und die Politik mit einer Deklaration, die bislang von über 230 Wissenschaftler(innen) und Institutionen (darunter der Präsident der ÖAW, der Bürgermeister der Stadt Wien, WWF-Österreich u.v.m.) unterschrieben wurde, auf den eklatanten Mangel an Fachleuten mit fundierter Artenkenntnis hinweisen.

Das rasante Aussterben von Pflanzen, Tieren und Lebensräumen bedeutet nicht nur einen Kultur- und Erkenntnisverlust für uns und unsere Nachkommen. Die Abnahme der „Dienstleistungen“ von natürlichen und naturnahen Ökosystemen („*ecosystem services*“) bewirkt auch einen enormen wirtschaftlichen Schaden und eine Verringerung von Zukunftschancen. Aber um den Verlust überhaupt bemerken zu können, bedarf es einer genauen Dokumentation der noch existierenden Lebensformen. Leider hat die Faszination von Molekularbiologie und Genetik die Fachbereiche Taxonomie, Systematik, Pflanzen- und Tierökologie eine Zeitlang vergleichsweise unattraktiv erscheinen lassen. Die Zahl der Lehrstühle und Professuren wurde verringert, immer weniger Studierende wurden umfassend ausgebildet. Jetzt aber fehlen weltweit Expertinnen und Experten mit fundierter Artenkenntnis an Universitäten, naturkundlichen Museen, Schulen, in der Feldforschung und in der Naturschutzpraxis. So auch in Österreich.

Die Erhaltung der biologischen Vielfalt setzt aber fundierte Artenkenntnis voraus. Top ausgebildete Fachleute der Taxonomie und Systematik sind also unerlässlich, damit Österreich auch weiterhin seinen internationalen Verpflichtungen zur Erhaltung der biologischen Vielfalt nachkommen kann.

Das österreichische MAB-Nationalkomitee fordert daher gemeinsam mit zahlreichen WissenschaftlerInnen und Institutionen, dass der Ausbildung in Taxonomie und Systematik an den Universitäten und den naturkundlichen Museen höchste Priorität eingeräumt und darüber hinaus die beruflichen Perspektiven junger TaxonomInnen verbessert werden.

WoRMS and the World Echinoidea Database

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The aim of the World Register of Marine Species (WoRMS) is to provide an authoritative and comprehensive list of names of marine organisms, including information on their synonymy. While highest priority goes to valid names, other combinations in use are included to facilitate linking data from various sources, both online and offline. Echinoids (sea urchins) are covered by the World Echinoid Database (part of WoRMS). Taxonomic coverage of the database includes all currently known extant echinoid genera and species, as well as most of the valid fossil echinoid genera. Extinct species, which surpass modern echinoid diversity by a factor of 10, are at present included only when they have erroneously been reported from modern faunas or are type species of extant genera.

The information contained in the World Echinoidea Database (WED) derives largely from Mortensen's epochal Monograph of the Echinoidea (1928-1951), updated by the data contained in the Index of Living and Fossil Echinoids by Kier & Lawson (1978) covering the years 1925-70 and Kroh (2010) covering the years 1971-2008. Information on distribution, ecology, and physiology are still largely missing from database, but are included progressively as the database is complemented with data from additional, detailed studies. The classification used in the WoRMS and the World Echinoid Database is that of Kroh & Smith (2010).

With about 1,070 valid extant echinoid species known from the world oceans, sea urchins constitute a relatively small group compared to other echinoderms. Only extant crinoids are less diverse than echinoids. However, in the fossil record things look different, with echinoids and crinoids dominating while asteroids, ophiuroids, and holothuroids are less diverse. This shift in diversity patterns is due to differing lifestyles, skeletal construction, and concomitant biostratigraphic and taphonomic pathways.

The diversity of fossil Echinoidea vastly surpasses present sea urchin biodiversity. More than 10,000 nominal species and 1,000 genera have been described. Although large numbers of these turn out to be junior synonyms, new species continue to be discovered.

Endoparasitic bivalves in Philippine palaeopneustid sea urchins (Echinoidea: Spatangoida)

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Recently, a large number of Philippine upper shelf sea urchins (Echinodermata: Echinoidea) became available, presumably due to shifting of local fishing activity from over-exploited shallow water habitats to deeper areas. The use of tangle nets and bottom fishing accounts for a huge number of by-catch, including echinoids. The faunal spectrum recovered from these fishing nets is rather selective, consisting mainly of large and epifaunal species, while burrowing or small species are underrepresented. Among the echinoids recovered, members of the genus *Plesiozonus* (Irregularia: Spatangoida) are especially large, often exceeding 120 mm test length and are thus commonly collected by the fishermen. Previously, *Plesiozonus* species were known by very few specimens only. Consequently, little is known on their biology, ecology, and physiology. While cleaning specimens of *Plesiozonus hirsutus*, we discovered double-valved bivalves in their rectum. Our first assumption, namely that these animals were simply swallowed by the deposit-feeding sea urchins proved to be unlikely: in every specimen with preserved intestine, a single articulated bivalve was located close to the periproct and contained mummified tissue. This strongly suggested that the bivalves were actually living inside the intestine of the sea urchins, rather than having been accidentally swallowed during feeding. Considering the size of the bivalves, which approaches or exceeds that of the respective echinoid peristome, the latter possibility seems even less likely. The bivalves are characterized by an extremely thin shell as well as a reduced hinge region and represent yet unknown galeomatid or montacutid species. Both taxa are known to live in association with echinoderm hosts, mainly holothurians. From sea cucumbers, the minute endoparasite *Entovalva mirabilis* has been reported. In echinoids, endoparasitic bivalves have not yet been described, although three galeomatid species are known to live externally attached to the periproct of the spatangoid *Brissus latecarinatus*. We hypothesize that it is probably only a small evolutionary step from such a life style to an endoparasitic one. Especially so, as *Entovalva* has been observed to actively force its way back into the intestine of its holothurian host when artificially removed.

Population genetics and phylogeography of *Cylindrus obtusus* (Gastropoda: Pulmonata: Helicidae) an endemic of the Austrian Alps

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Cylindrus obtusus (Helicidae) is a hermaphroditic land snail, endemic in the Austrian Alps, which is restricted to high elevations (1600 to 2500 m asl) and limestone. As a specialist of high alpine rocky habitats, *C. obtusus* has a quite patchy distribution area which may become even further reduced in the future due to global warming. Previous investigations revealed geographic differences in the genital apparatus: All specimens from the more western populations had one stylophore and two equally developed mucus glands more than twice the length of the stylophore. In contrast, in individuals from the eastern margin of the species distribution one or two mucus glands were found and the size ratio between stylophore and mucus gland(s) was highly variable. To find out whether these anatomical differences reflect a genetic differentiation, which might be an indication for distinct glacial refugia, we investigated a 650 bp fragment of the COI sequence (200 individuals) and 9 microsatellite loci (500 individuals from 29 populations) from samples covering the whole distribution range of the species. The COI sequences showed a geographic differentiation between eastern, central and western populations. However, genetic distances are small (max. 1.7 %). The microsatellite analysis reveals a high differentiation between the populations implying restriction of gene flow. The highest genetic variability was found in the central populations. Remarkable nearly all individuals from the eastern populations, which are variable in their genital morphology, are homozygous in all microsatellite loci (although different alleles were found within populations). The most plausible explanation for this finding is an altered mode of reproduction. Further investigations shall elucidate whether this lack of heterozygotes is caused by selfing and if so, why it occurs at such a high frequency.

Genetic variation in brown trout *Salmo trutta* across the Danube, Rhine, and Elbe headwaters: a failure of the phylogeographic paradigm?

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Population genetic screening ($N = 97$) of brown trout *Salmo trutta* across the Danube/Rhine/Elbe catchments of Austria and Bavaria revealed a counter-intuitive phylogeographic structure with near fixation of the Atlantic lineage in the Bavarian Danube. Along the Austrian Danube, phylogeographic markers (mtDNA and LDH-C1) revealed increasing percentages of Danube-specific alleles with downstream distance. Pure Danube lineage populations in Austria were rare, occurring as isolate relicts either within or on the edge of previously glaciated regions north, south, and east of the Alps, whereby unglaciated regions revealed high percentages of Atlantic lineage genotypes. Both empirical data and simulated hybrid comparisons support that trout in non-glaciated regions of Austria have an admixed origin largely based on natural colonization from Atlantic basin watersheds. In contrast, most trout populations in glaciated regions of Austria south of the Alps revealed admixture based primarily on human-mediated release of hatchery strains. Despite the extensive use of Atlantic lineage hatchery strains in management, little evidence of first generation stocked fish or F_1 hybrids between stocked and wild fish was found.

The distribution pattern of the Atlantic and Danube lineages, as well as the clear signal of natural admixture is difficult to explain without invoking strong biological mechanisms in combination with a not-yet-visualized complex paleo-hydrological scenario. We conclude that the Atlantic lineage of brown trout is native to regions of the upper Danube and has been a very successful invader into unglaciated regions of the Austrian Danube north and east of the Alps, but there is no sign of its natural occurrence on the previously glaciated south slopes of the Alps.

Microscopic and molecular analyses on digenean trematodes in red deer (*Cervus elaphus*).

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Digenean trematodes are a large group of internal metazoan parasites that are characterized by a complex life cycle including mollusc and vertebrate hosts. This study focuses on trematodes of the red deer (*Cervus elaphus*) in the Danube backwater forests southeast of Vienna. Particular emphasis was given to the naturally occurring liver fluke *Fasciola hepatica* and the introduced American liver fluke *Fascioloides magna* and the species specific differentiation between these two species. The former is a pathogen of medical and veterinarian, the latter only of veterinarian relevance.

Between May and November 2008, a *F. magna*-monitoring within the area of the "Nationalpark Donau-Auen" has been performed. Altogether, 158 deer faeces samples were collected from 13 sites. All samples were processed for microscopy with a modified Benedek sedimentation method and subsequently screened for trematode eggs. A collection of samples was chosen for molecular biology. 109 samples were homogenized, the DNA was extracted by two different types of DNA-extraction kits and subjected to three different kinds of PCR (trematodes, *F. magna*, *F. hepatica*). Species-specific differentiation was achieved by sequencing. In 49 of 158 samples (31%) trematode eggs were found by microscopical means. Additionally, there were eggs found in six samples which could not be specified. With molecular methods, 35 of 109 samples (32%) showed positive results during PCRs. The most frequent trematode species were members of the family Fasciolidae (29 samples), followed by Paramphistomidae (eleven samples). One sample contained eggs of Dicrocoeliidae and eleven samples showed eggs/DNA of more than one trematode species.

The overall trematode burden in the investigated area was 37%. This was not surprising concerning a naturally parasite load of wild living ruminants. However, the remarkably high percentage of positive *F. magna* samples points out the dangerous potential of an introduced parasite. No one sample was positive with *F. hepatica*.

Echinoids from the Late Miocene-Early Pliocene & Pleistocene of Santa Maria Island, Azores

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The Azores is an archipelago composed of nine volcanic islands, located almost midway between the North American and European continents. In this relatively young island system, fossiliferous deposits are only found on the oldest island, Santa Maria. These strata are mainly Late Miocene to Early Pliocene in age. A second set of outcrops is associated with Pleistocene wave-cut platforms and presumably of Eemian age (Pleistocene). These deposits are relatively small, outcropping mostly in the coastal areas, and consist of lithic sandstones and carbonates intercalated by volcanic material, testifying periods of relative calm between intensive volcanic activity, during the formation of the island. During the international workshops 'Palaeontology in the Atlantic islands' (2002, 2006–2009), new echinoid material was collected, mainly composed of disarticulated fragmented skeletal material. The echinoid fauna found in the Mio-Pliocene outcrops of Santa Maria island, is dominated by tropical shallow waters taxa (*Eucidaris tribuloides*, *Echinoneus* cf. *cyclostomus*, *Clypeaster altus*, *Meoma* ? sp.), all locally disappeared with the exception of the temperate species *Echinocyamus pusillus*. Additionally, remains of two undetermined species of *Echinocardium* were also found. The Pleistocene material, in contrast, represents a fauna more typical of temperate waters: *Arbacia lixula*, *Paracentrotus lividus* and *Sphaerechinus granularis*. All three species are common present day inhabitants of Azorean rocky shores. In spite of the facies restriction and thus the palaeoenvironments preserved, it is clear that the fossiliferous deposits of the Santa Maria can aid in the understanding of how the fauna in this oceanic island system was shaped through time.

Lichen diversity of Armenia

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The lichen mycota of Armenia has been poorly studied to date, especially when compared to the mycota of the other Caucasian countries Georgia and Azerbaijan. Only very few studies have been undertaken by Armenians like V. Nikogosyan in the Sixties and A. Abrahamyan in the Eighties but Sh. Barchalov from Azerbaijan has mentioned 195 species from Armenia in a series of papers dedicated to the Caucasus region in the Sixties of last century. The Czech lichenologist A. Vězda has visited the country and distributed some species in his famous exsiccate. The Czech naturalist V. Vašák and the Viennese botanist E. Vitek have collected specimens and deposited in the lichen herbaria GZU (Graz) and W (Vienna). In order to obtain more representative data about the lichen biodiversity a large range of habitats from low to high elevations and from dry to humid sites have been sampled. More than 900 specimens have been collected in 2005 and 2006 containing 246 taxa, of which 114 have been new for Armenia (Harutyunyan & Mayrhofer 2009). In addition a phylogenetic study of black fungi inhabiting lichens from seasonally arid habitats in Armenia has been carried out (Harutyunyan et al. 2009). Based on a comprehensive evaluation of the literature (more than 50 publications), herbarium and field studies, Armenia has an actually known diversity of c. 400 species. Crustose saxicolous taxa dominate, which is in accordance with the dry climate and mountainous nature of the country.

A catalogue is in preparation which includes information regarding references, localities placed under provinces, ecology and herbarium specimens as a solid basis for further inventories or taxonomic projects in this country.

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Systematics and cryptic species in lichenized fungi

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In lichen systematics the naming of species results from their accurate delimitation based on morphological and, increasingly, on phylogenetic data. During the last years several studies have presented multilocus phylogenetic analyses that elucidated the identity of many sterile lichen species, or conclusively placed morphologically well known taxa to well defined phylogenetic groups. The microfilamentous lichens *Cystocoleus ebeneus* and *Racodium rupestre* were confirmed to be ascomycetes belonging to the Dothideomycetidae but not close to lichenized members within the subclass. Similarly, the genus *Normandina* turned out to be a monophyletic group within the Verrucariaceae. Morphological and phylogenetic species concepts complement each other. In-depth molecular studies focusing on critical lichen groups often reveal the presence of cryptic species forming well defined phylogenetic clades and result in the description of new taxa. However, the phylogenetic species concept should also be carefully considered when applied to cosmopolitan lichens which exhibit a high degree of morphological diversity, such as species constituting the *Tephromela atra* complex. In such cases what might appear to be clear genetic differentiation at a small scale may dissolve when the sampling is extended to wider geographic areas, owing to ongoing genetic differentiation and/or incomplete lineage sorting.

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Species evolution in lichen symbiosis: *Tephromela atra* species-complex as a model study

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Lichens constitute one of the most wide-spread fungal symbioses. However, the contribution of symbiotic relationships to species diversification is still under-investigated among this group of fungi. Lichenized fungi (mycobionts) depend on their association with an algal partner to form the symbiotic structure. These fungi are found only in the lichenized stage, and therefore represent interesting models to address questions of evolution under symbiotic conditions. The classification of lichens relies largely on morphology, but many species are heterogeneous and represent unresolved species complexes. In these cases the morphological classification fails to resolve species complexes and identify uniform species. Furthermore, species complexes prevent the understanding to what extent mycobiont genotypes correlate with photobiont selectivity. We investigate the genetic aspects of the symbiotic speciation of lichens using taxa belonging to the cosmopolitan *Tephromela atra* species complex as models. *Tephromela atra* has been considered as a phenotypically and ecologically plastic, cosmopolitan species occurring on diverse substrata. It is an example *par excellence* for a lichen species complex in Europe with taxa that were controversially considered as varieties or species. Further, the association of *Tephromela atra* with different photobiont species could indicate a certain degree of selectivity or specificity for the algal partners in diverse habitats, and can play a determinant role in speciation processes.

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Photobiont association and genetic diversity of the optionally lichenized fungus *Schizoxylon albescens*

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The fungus *Schizoxylon albescens* occurs both as lichen and as saprobe. Lichenized colonies grow on bark of *Populus tremula*, saprotrophic morphs grow on dead *Populus* branches. We wanted to (i) test if lichenized and saprotrophic *Schizoxylon albescens* are genetically distinct, (ii) investigate photobiont association and diversity, (iii) investigate interactions between fungi and algae that occur during co-cultivation, (iiii) test if *Schizoxylon* shows algal selectivity during the lichenization. Fungal and algal genetic diversity were investigated for three markers. Algae from lichenized thalli were isolated in axenic cultures, and the isolate sequence diversity was compared with the algae amplified directly from thallus fragments. Co-culture experiments of fungi and algae were performed to study morphological interaction patterns. Two distinct phylogenetic units are revealed in *S. albescens*, which are interpreted as phenotypically cryptic species.

The algae are related to *Coccomyxa* and *Pseudococcomyxa*, and form two distinct sister-clades separating samples isolated in cultures from those amplified directly from thallus fragments, indicating that more easily cultured strains of algae are not necessarily major components of the lichens. *Schizoxylon albescens* interacts with isolated algal strains, similarly to fungal-*Coccomyxa*-symbioses in nature. As the system is maintained without difficulty in culture, it can potentially be an easily controlled lichen symbiosis study system under lab conditions.

Quantifying evolution – paleolake mollusks from the Dinaride Lake System (Middle Miocene, Sinj Basin, SE Croatia)

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The present investigation deals with the mollusk evolutionary patterns and environmental change in a lower Middle Miocene succession in the Sinj Basin (Dalmatia, SE Croatia) reflecting the depositional history of a long-lived freshwater lake. Despite its mature investigation stage, an analysis of a quantified mollusk record, providing insight into species contributions, taxonomic relationships and the nature of the morphologic changes, is completely missing up to now.

The taxonomic diversification of freshwater gastropods and its connection with morphologic disparity events are documented for a ca. 100-m-thick section representing the topmost infill of the Sinj Basin. Based on the available age model, these alterations occur extremely fast on a millennial scale, re-proving the significance of long-lived lakes for evolutionary research. Furthermore, the simultaneity of morphologic shifts in systematically independent taxa suggests them to be tightly linked to environmental changes. Most probably, climatic fluctuations leading to variations in lake-level and habitat types are the driving factors for these radiation events.

The study provides statistical treatment of quantified samples accompanied by a taxonomic revision of the taxa. Additionally, based on the mollusk distribution a paleoenvironmental interpretation is given, supported by sedimentological data and previous palynological analysis. Actually, it supports previous results of the section's division into two limestone-coal cycles, grading from shallow intermediate-energy settings with high freshwater input via fossil-poor transgressive limestones to shallow low-energy conditions, resulting finally in a total lake drought at the section top.

The discussion will focus on the evolutionary lines of four species, two of *Melanopsis* and two of *Prososthenia*. All four species appear almost continuously and can be divided into several morphotypes based on different sculpture features; in some cases also size plays a role. It will be demonstrated that the morphs occur sequentially, each more or less limited to a special interval. Moreover, the changes in morphology appear at the same time in different taxa.

Biology and phylogeny of the *Ophrys tenthredinifera* species group in Crete

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The species of the genus *Ophrys* rely on sexual deception for pollinator attraction, imitating the complex olfactory, visual and tactile cues of their pollinator's females in order to attract males. This plant – pollinator relationship is highly specific, allowing for strong prezygotic isolation of *Ophrys* species, coupled with comparatively weak postzygotic isolation mechanisms. The occurrence of hybrids and the high morphological variability of most species, have led to a confusing classification system of the genus. This is also the case of the newly described species complex *Ophrys tenthredinifera*. Till recently there was only one species (*Op. villosa* DESFONTAINES 1807) or subspecies (*Op. tenthredinifera* subsp. *villosa* WILLDENOW 1805) described from the eastern Mediterranean basin. Delforge (2005) describes, based mainly on phenological and morphological criteria, 3 new species for the region: *Op. Ulyssea* (Ionian Islands), *Op. leochroma* (Egean Islands) and *Op. dyctinnae* (Crete). A fourth new species *Op. dimidiata* has been recently discovered in Crete. Due to the absence of evident morphological differences, because of high interspecific variability the taxonomic status of these taxa has been questioned.

The present study employs genetic fingerprinting, biotests and morphometry to investigate the strength of prezygotic reproductive isolation (based on pollinator specificity) and genetic separateness of the four taxa occurring in Crete: *Op. dyctinnae*, *Op. leochroma*, *Op. dimidiata* and *Op. villosa*. Using classic morphometric analysis we attempt to identify reliable traits for species delimitation. At this moment only partial results are available, these being mainly the results from pollinator experiments and partial results from morphometrics. From the four occurring species, only three could be analyzed, as *Op. villosa* seems to be extremely rare in Crete. Pollinator experiments indicate that these three species are indeed reproductively isolated from each other, with only few cases where one *Ophrys* species attracted two different pollinators. Additionally, it became apparent that in several locations two or all three species occurred sympatrically. The molecular analysis will have to confirm the species delimitation drawn by pollinator experiments, thus certifying the species status of these taxa.

Oil gland chemistry as a source of novel taxonomic characters in glandulate Oribatida (Acari)

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Oil glands (syn. opisthonotal glands) constitute *the* major exocrine system in oribatid and astigmatid mites. These glands are present in many different character states in more than 15.000 species. According to current ideas, oil glands evolved only once in ancient oribatids several hundred million years ago and represent an important synapomorphic character of the “glandulate” Oribatida (= the four more derivative cohorts of Oribatida [Parhyposomata, Mixonomata, Desmonomata, Brachypylina] and the Astigmata). Moreover, oil glands produce multicomponent secretions that have been proven valuable complex data for phylogenetic studies on different taxonomic levels. 1) With respect to oribatid gross taxonomy, major evolutionary traits are reflected by oil gland chemistry: The (primitive) Parhyposomata are characterized by phenols and naphthols while distinct sets of terpenes and aromatics (so-called “Astigmata-compounds”) are considered to have evolved stepwise within ancient mixonomatans, now characterizing all rectant taxa above middle-derivative Mixonomata (i.e., higher Mixonomata, Desmononata, Brachypylina and the Astigmata). In these terms, the evolutionary origin of Astigmata within Oribatida is strongly supported by chemical data. In some of the groups mentioned above, the “Astigmata-compounds” have again been reduced and replaced by novel components such as iridoid monoterpenes in some Euphthiracaroidea (Mixonomata) or by alkaloids in some groups of Brachypylina. 2) In addition, regarding oribatid alpha-taxonomy, species- or even population-specific secretion patterns have already successfully been applied to the delineation of phyletic lines within species complexes or even led to the discovery of cryptic species.

In all, about 100 different oil gland secretion components have already been identified. Another 200 - so far unknown - components await their structural elucidation. I here summarize the importance of oil gland secretions profiles as independent character sets for modern integrative taxonomic studies in the Oribatida.

Middle Miocene holothurians (Echinodermata) from the Vienna Basin (Austria)

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Compared to other modern echinoderm groups, the evolutionary history of holothurians is poorly understood, owing to their preservation almost exclusively as microfossils. In comparison to older strata, the Cenozoic fossil record of sea cucumbers is particularly scarce. This is in stark contrast to most other invertebrate groups, in which the fossil record tends to improve with declining age.

The Central Paratethys (Europe) is one of the most intensely studied Neogene basins and has yielded a rich echinoderm fauna including representatives of all modern echinoderm classes. Unfortunately, most of the holothurian sclerites reported from that area by previous authors have been lost. Here we present new data based on a survey of old micropalaeontological samples (second half of the 19th century), deposited in the Natural History Museum of Vienna, as well as new samples collected from deposits rich in echinoderm remains. The samples studied derive from silty clays and marls from the Austrian part of the Vienna Basin and are Badenian (= Langhian to Early Serravallian) in age. The samples were processed to preserve the fine fractions needed for the successful recovery of holothurian sclerites. Out of more than twenty-five samples, only two yielded well preserved holothurian echinoderms.

At least ten biological species of the Molpadiida (Molpadiidae), Dendrochirotida, Aspidochirotida (Holothuriidae), Apodida (Synaptidae, Chiridotidae, and Myriotrochidae) could be documented in form of sclerites from the body wall, as well as calcareous ring elements. Especially the classic 'Badener Tegel'-samples of Baden near Wien (former brickyards between Baden and Sooss) yielded exceptionally well-preserved material. Infaunal molpadiid representatives dominate the faunal holothurian association of the 'Badener Tegel'. This includes the first fossil record of small amorphous ferric phosphatic dermal granules, which are typical for members of the Molpadiidae and a unique biomineralogical phenomenon for the Echinodermata as a whole.

The endosymbiont *Wolbachia* in fruit flies of the genus *Rhagoletis*: Horizontal transfer and impact in speciation

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Wolbachia is an endosymbiotic bacteria present in up to 65% of all insects. *Wolbachia* infections are described in all major insect orders. This bacterium manipulates the reproduction and causes male-killing, parthenogenesis, feminization and cytoplasmic incompatibility (CI). The most common effect is CI, an incompatibility between sperm and egg caused by crossing of infected males with uninfected females. This incompatibility can lead to a reduction of gene flow in a population and hence lead to reproductive isolation.

The Apple Maggot *R. pomonella* has been the focus of sympatric speciation over more than a century. In the middle of the 19th century a population shifted from the native host hawthorn to the newly introduced apple. These populations are ecologically and genetically different. Different *Wolbachia*-infections were found in the two host species and potential impact in speciation will be discussed.

The Eastern Cherry Fruit Fly, *R. cingulata*, infests different *Prunus* species. Native to North America, this species was introduced to Europe in the 1980ies where it coexists with the European Cherry Fruit Fly *Rhagoletis cerasi*. *R. cerasi*, is an established field model species for multiple *Wolbachia* infections and CI. Two strains of *R. cerasi* were detected in *R. cingulata* and a potential horizontal *Wolbachia* transfer will be discussed.

Miocene dinoflagellate cysts as links between taxonomy and oil industry

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At about 11.6 Ma a glacioeustatic sea-level drop caused the final disintegration of the Paratethys Sea, and Lake Pannon arose in the Pannonian basin system. The benthic ecosystem collapsed at that point and marine life completely vanished. The lake was initially brackish, slowly freshening and slightly alkaline. Lake Pannon attained a maximum length of 860 km (from the Karlovac Basin close to Zagreb in the west to the Transylvanian Basin in Romania in the east) and a width of 550 km (from the Vienna Basin in the north to Belgrade in the south). It covered an area of c. 290,000 km². The lake was highly structured by numerous islands and mountain ranges. Its maximum water depth may have reached 800 m in its central part but less than 200 m elsewhere. The aberrant water chemistry and the decline of marine taxa gave rise to the evolution of an impressive assemblage of dinoflagellate cysts. Whilst the dinoflagellate cyst assemblages are fairly similar to assemblages recorded from adjacent areas during the Middle Miocene, the assemblage is nearly fully endemic thereafter in Lake Pannon. Simultaneously, the high diversity of 126 taxa declines strongly to about 40 taxa. The paleoecological interpretation of the dinoflagellate assemblages in Lake Pannon is complex. Most taxa have roots in marine ancestors, which became adapted to brackish water conditions of Lake Pannon with the onset of the Late Miocene. Therefore, a straightforward comparison with congeneric open marine taxa is difficult. A more promising source for comparison are the marine-derived assemblages from the Black Sea, the Marmara Sea, the Caspian Sea, the Aral Sea and some adjacent lakes.

This endemism is reflected by the absence of cosmopolitan taxa and the appearance and dominance of new morphotypes. Well studied examples are *Spiniferites bentorii* and *Impagidinium sphaericum* and their allies. Both taxa exhibit, an enormous morphological variability within Lake Pannon. This variability has been used to introduce several endemic species/subspecies. These taxa are probably mere eco-morphotypes and are difficult to define as systematic units. Nevertheless, they are valuable tools for Pannonian stratigraphy. A typical application is their use in biostratigraphic correlations of well cores in the Pannonian Basin by oil companies. Thus, despite the problematic taxonomic status of many of these morphotypes, their applicability in industry is obvious.

This study is financially supported by FWF-project no. P 21414-B16 and the Austrian Academy of Sciences / Commission for the Paleontological and Stratigraphical Research of Austria.

Clypeasteroid echinoids of the Indian Subcontinent

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Clypeasteroid echinoids are common members of shallow benthic habitats in late Eocene to modern echinoid faunas of the tropical and warm temperate zones. Due to their high fossilization potential, they have an exceptionally good fossil record and have been intensely studied in the past. From the Indian subcontinent, clypeasteroids have been recorded by Grant (1837), Duncan & Sladen (1882-86) and a number of subsequent authors. Many of these records, however, lack proper stratigraphical information and data on associated taxa.

We are currently revising the clypeasteroid taxa documented from the Indian Subcontinent based on the type material housed at the Geological Survey of India, as well as new material collected from the field by one of us (DKS). Clypeasteroid diversity is low in the Eocene, rises in the Oligocene and reaches a peak in the Early Miocene of the Indian subcontinent. From the Early Miocene onwards, clypeasteroid and echinoid diversity as a whole drops to comparatively low levels in the Pliocene. Many of the taxa reported previously from the Eocene, actually derive from Oligocene deposits records. The genus *Clypeaster*, for example, does not occur in the Indian Eocene at all, despite several previous records stating the contrary. The Eocene deposits, so far, yielded only representatives of *Echinocyamus* and the enigmatic fibulariid *Tridium*. *Clypeaster* is the most diverse of the Indian clypeasteroid genera, being represented by almost 20 species in the Indian Cenozoic. In the Miocene a second group becomes important – the astriclypeids, with forms that share characteristics of the two astriclypeid genera *Amphiope* and *Echinodiscus*.

Mining lichen diversity: systematics as a framework for identifying ‘known unknowns’ in Alaska (U.S.A.)

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Lichens are a species-rich group of symbiotic organisms found in every ecosystem on the planet. Relatively few areas of the globe have had the benefit of comprehensive lichen inventories and many species remain to be discovered. In a recent project in southeast Alaska (U.S.A.) we inventoried lichens and lichen-dwelling parasitic fungi in the 53 km² Klondike Gold Rush National Historic Park, largely without the benefit of a written flora and consolidated identification keys. We documented a total of 766 species, the largest ever found for a comparable study area in the New World (Spribile et al. 2010). More remarkably, fully 10% of the documented species were either new to science or in a category we called ‘known unknowns’ – species with an identity but currently without a name, for a variety of reasons. Lichen inventory in poorly known regions is an exercise in observational feedback that requires an organic interaction with applied systematics and a deep knowledge of the global literature dataset. It is critical that the nuances of the systematic decision-making process are explained to conservationists and land managers with an eye to fully accounting for biodiversity and adequately protecting species of unresolved taxonomic status.

Spribile, T., Pérez-Ortega, S., Tønsberg, T., Schirokauer, D. 2010. Lichens and lichenicolous fungi of the Klondike Gold Rush National Historic Park, Alaska, in a global biodiversity context. *The Bryologist*, 113, 439-515.

What are conodonts?

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Conodonts are a group of extinct marine organisms that are divided into Proto-, Para- and Euconodonts. Commonly fossil remains are represented by 0.5-4-mm sized discrete elements consisting of apatite. These elements were in use as biostratigraphic tool for Palaeozoic to low Mesozoic strata long before the first “conodont-animal” was discovered (Briggs et al., 1983). As soon as fused conodont clusters, bedding plane or natural assemblages were known, it became obvious that several element types (S, M and P elements) belong to distinctive apparatuses. Since its discovery by Pander in 1856 about 284 genera are described, which result in more than 3000 species. Until now the phylogeny of conodonts is still controversial.

Szaniawski (2002) discussed the chemical composition and anatomical similarity of simple cone elements of protoconodonts in comparison with spines of the grasping apparatus of chaetognaths. On the basis of molecular investigations he concluded that chaetognaths should have originated at about the same time as protoconodonts, and that protoconodonts of the lineage of *Phakelodus* probably formed a stem group of chaetognaths. In contrast, Euconodonts are considered as early vertebrates probably being more derived than hagfish or lamprey (Donoghue and Purnell, 2005). This is based on about 13 natural assemblages of Euconodonts from Scotland, South Africa and Canada. Specimens are about 4-10-cm large, elongate, possessing a head with eyes, extrinsic eye muscles, a notochord, chevron-shaped muscle blocks, a caudal fin, features that they share with jawless vertebrates. But they also possess a mineralized dermal skeleton, which is considered as gnathostome apomorphy.

That shows that within the Conodonts fossil groups of different origin might be lumped and that Euconodonts may be more closely related to living jawed vertebrates rather than to lampreys. The only way to learn more about the true nature of conodonts is the discovery of additional natural assemblages and the examination of diagenetic processes affecting hard and soft tissue during fossilization (e.g. solution of calcium carbonate, emplacement of phosphate).

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Donoghue, P.C.J., Purnell, M.A. 2005. Genome duplication, extinction and vertebrate evolution. *TRENDS in Ecology and Evolution*, 20, 312-319.

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Morphological and genetic analysis of moss-dwelling tardigrades

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Tardigrades, or water bears, are a diverse phylum of microscopic invertebrates that have existed since the Cambrian. They are especially noted for being polyextremophilic existing both in hot springs as well as in solid ice. They are among the few organisms capable of suspending metabolism and entering a state of cryptobiosis. To date there are approximately 1000 described species although it is widely recognized that the group has attracted little research attention and their diversity is thus vastly underestimated. The armored tardigrades, or Heterotardigrades, have morphological characteristics such as cephalic appendages, cuticular extensions, claws and the pattern of dorsal cuticular plates, whereas the main characteristics of the naked tardigrades (Eutardigrade) are claws, the buccopharyngeal apparatus and a cuticle structure, which can be smooth, granulated or bearing tubercles. The phrase "naked" refers to the absence of cuticular dorsal plates, which are present in Heterotardigrada. We investigated a total of 192 moss samples from both man-made (botanical gardens) and natural habitats (Graz vicinity) for the presence of tardigrades. From a total of 88 moss samples with tardigrades, 104 individual slide preparations were made for morphological evaluation. Nearly all preparations ($N = 103$) could be assigned to the genus level, whereby 59 individuals were assigned to one of six species. An additional four species were determined with the aid of an mtDNA sequence (COI gene). Eutardigrades dominated the collected moss samples with *Macrobotus* as the most frequent genus and *Macrobotus cf. hufelandi* ($N = 47$) as the most common species. *Macrobotus cf. hufelandi* was found at different altitudinal levels in Styria, whereas other species were only found in specific locations. There was no apparent species-specific relationship between moss and tardigrade taxa and there was no apparent relationship between the colonization of tardigrades and various man-made substrates within the botanical gardens. Further molecular genetic analysis was hindered by the extreme divergence of the group, and thus lack of universal primers for species-level identification. Based on our own phylogenetic reconstruction of available GenBank sequences it is clear that the current systematic and taxonomic assignment of tardigrades requires substantial revision.

Is *Babesia* still *Babesia*?

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The babesias belong to the Apicomplexa (Alveolata; Eukaryota), as do the causative agents of malaria. Likewise they also parasitize red blood cells of vertebrates. Human babesiosis is a zoonosis transmitted by ixodid ticks, in which the relevant hosts are bovines, other mammals, and also birds. Most human cases are caused either by *Babesia divergens*, which occurs exclusively in Europe, or *B. microti*, which mainly occurs in the northeastern eastern parts of the USA.

In 1888 the Romanian pathologist Victor Babes described *Haematococcus bovis*, a blood parasite of cattle. Later he found a similar parasite in the blood of sheep and named it *H. ovis*. One year after Babes' first description, Smith and Kilbourne, described *Pyrosoma bigeminum* (later re-described as *Piroplasma bigeminum*) isolated from blood specimens of cattle suffering from Texas fever. Finally, the genus *Babesia* was established by Starcovici in 1893, uniting *B. bovis* and *B. ovis*, and later also including *B. bigemina*.

Meanwhile, more than 100 species have been described, mainly according to their respective vertebrate hosts. In the past years, however, the validity of many species has been questioned and also new species have been described, including *B. venatorum*, Herwaldt et al. 2003 and *B. duncani* Conrad et al. 2006, both isolated from humans. Moreover, it has been shown that *B. microti* is more closely related to the genus *Theileria* than to other *Babesia* species. According to molecular data, five distinct groups can be discriminated within the Piroplasmidae: *Babesia* sensu stricto I, *Babesia* sensu stricto II, *Babesia microti* group, *Theileria*-like group and *Theileria* sensu stricto.

Three cases of human babesiosis have been described in Austria, two caused by to the newly described species *B. venatorum* (Herwaldt et al. 2003, Gattringer et al. in preparation) and one by *B. microti* (Ramharter et al. 2010).

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Is there independent anatomical support for the Odontophora (Echinoidea: Echinoida)?

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The taxon Odontophora has recently been established and comprises camarodont sea urchins with a distinct skeletal protrusion on the epiphysis. This process, termed tooth support, lies on the adaxial edge of the wing of the epiphysis and flanks the proximal part of the sea urchin tooth at the point where the plumula merges with the solid tooth shaft. Although the function of the tooth support is still unknown, it constitutes a skeletal feature that can be easily observed both in fossil as well as extant material and could therefore be useful for classification purposes. Originally, three taxa are included in the Odontophora: the Echinometridae, the Strongylocentrotidae, and the Toxopneustidae. Although closely related to the former taxa, the Parasaleniiidae, the Parechinidae, and the Echinidae were excluded based on the absence of a tooth support as well as other characters. Here, we try to show whether the hypothetical grouping based on a cladistic analysis on the family level also holds true on the genus level. We combined classical dissection and SEM imaging of skeletal structures with μ CT imaging of whole specimens, thereby improving our understanding of the position and potential function of the tooth support. Representatives of almost all extant genera of the Odontophora were examined. Further results, acquired using magnetic resonance imaging (MRI), strongly indicate that there is indeed independent anatomical support for the taxon Odontophora, as exemplified by the presence of highly specialised protractor muscles present in the Echinometridae, the Strongylocentrotidae, and the Toxopneustidae.

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