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Program & Abstracts



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Austrian Biosystematics

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Vorträge Redezeit: 15 Minuten + 5 Minuten Diskussion
Sprache Deutsch oder Englisch
Poster Format: A0
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**Für Interessierte besteht im Anschluss an die Tagung noch die Möglichkeit an einer Führung
durch die Sammlungen des Landesmuseums teilzunehmen.**

Treffpunkt 17:15 im Festsaal

Dauer: ca. 1 Stunde

09:10 – 10:30

NOBIS-Preis Beiträge 1 Chair: A. Tribsch

(in alphabetischer Reihung)

09:10 – 09:30

Dejaco, T., Gassner, M., Arthofer, W., Schlick-Steiner, B.C, Steiner, F.M

Integrative Artabgrenzung in der Felsenspringergattung *Machilis* (Microcoryphia: Machilidae)

09:30 – 09:50

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

Trochulus oreinos and *T. hispidus* (Gastropoda: Pulmonata: Hygromiidae) in the Eastern Alps and adjacent areas: Morphology, ecology and their context to phylogeography

09:50 – 10:10

Engelbrecht, A.

Eocene lamniform sharks from Antarctica with special reference to sandtiger sharks (Odontaspidae)

10:10 – 10:30

Gaub, L., Feix, A.S., Hörweg, Ch., Sattmann, H. & Walochnik, J.

A molecular approach to resolve the biodiversity of the Digenea of selected freshwater snails in Eastern Austria

10:30 – 10:50

Pause

10:50 – 11:50

NOBIS-Preis Beiträge 2 Chair: J. Kriwet

10:50 – 11:10

Grunert, P.

Application of taxonomic actualism to fossil benthic foraminiferal communities reveals the history of the Burdigalian Seaway

11:10 – 11:30

Hametner, C. & Stocker-Wörgötter, E.

Systematic positions and evolution within trentepohlialean algae living in symbiosis with lichen-forming ascomycetous fungi

11:30 – 11:50

Weissensteiner, M., Koblmüller, S. & Sefc, K.

Morphologische und genetische Unterschiede zweier Unterarten der Maskenammer *Emberiza spodocephala*. (Aves, Emberizidae)

11:50 – 12:10

Veitschegger, K.

Intrarelationships of carcharhinid sharks based on molecular data

12:10 – 13:30**Mittagspause**

NOBIS-Preis Beschlussfassung durch die Jury
(U. Aspöck, T. Jerger, A. Kroh, F. Zachos)

13:30 – 15:10**Vorträge 1****Chair: H. Sattmann**

13:30 – 13:50

Agatha, S. & Strüder-Kypke, M.C.

Morphologic data unravel the non-monophyly of the tintinnid genus *Favella* (Ciliophora) in gene trees

13:50 – 14:10

Aspöck, U. & Aspöck, H.

Raphidioptera – an Austrian invention? Austria's contribution to the exploration of the snake-flies (Insecta: Endopterygota)

14:10 – 14:30

Dojen C.

Taxonomie und Biostratigraphie devonischer Ostrakoden

14:30 – 14:50

Zuschin, M., Nawrot, R. & Chattopadhyay, D.

Bivalve diversity in the Northern Red Sea and the role of body size in marine invasion through the Suez Canal

14:50 – 15:10

Thuy, B., Gale, A.S., Kroh, A., et al.

Modern deep-sea faunas much older than previously thought – new data from ODP cores

15:10 – 15:50**Kaffeepause & Poster-Präsentation****15:50 – 17:10****Vorträge 2****Chair: M. Zuschin**

15:50 – 16:10

Kobl Müller, S., Hermann, C.M. & Sefc, K.M.

Recent divergence of an ancient haplochromine cichlid lineage from isolated water bodies in the East African Rift system

16:10 – 16:30

Kropf, M., Hölzler, G. & Parz-Gollner, R.

The origin of the current beaver population in Lower Austria – insights based on mitochondrial DNA sequences

16:30 – 16:50 **Zachos, F.E., Klansek, E., Dekker, J.J., Petersen, B.-S. & Suchentrunk, F**
Contrasting levels of differentiation in Austrian polecats (*Mustela putorius* and *M. eversmannii*) in nuclear and mtDNA

16:50 **U. Aspöck**
Zuerkennung des NOBIS-Preises

17:15 **Führung durch das Landesmuseum Klagenfurt**

Morphologic data unravel the non-monophyly of the tintinnid genus *Favella* (Ciliophora) in gene trees

Agatha, S.¹ & Strüder-Kypke, M.C.²

VORTRAG

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Tintinnids are mainly marine planktonic ciliates that form vase-shaped loricae (houses). Their classification is entirely based on features of these loricae, which are known to vary with environmental conditions and the cell cycle. Phylogenies of the SSU rRNA gene revealed a non-monophyly of the genus *Favella* with two distinctly separate clusters: one branched rather early in the tintinnid evolution, the other grouped with more highly developed genera. Recently, genetic and cytological data on *Favella ehrenbergii*, the type of the genus, were provided (Kim et al. 2010), while own studies were conducted on *F. panamensis* and *F. arcuata*. *Favella panamensis* is similar to *F. ehrenbergii* in morphology and the early branching in the gene trees. Despite a similar-shaped, hyaline lorica, *F. arcuata* clusters distinctly apart from these two congeners, namely, with the more highly developed tintinnids in molecular analyses. Conspicuous differences in the ultrastructure of the lorica walls and in the arrangements of the somatic (body) cilia do not only explain the distant position of the two clusters in the gene trees, but also justify the establishment of a new genus for *F. arcuata*, which is separate from the genus *Favella* on familial level (Agatha & Strüder-Kypke 2012a). It is shown that lorica types (hyaline or with adhered particles) can hardly be used to infer phylogenetic relationships as they indicate natural groupings only at genus level, while rarely at higher ranks. The comparison of cladistic and genetic analyses indicates that the development of the somatic ciliary patterns appropriately reflects the evolution in tintinnid ciliates (Agatha & Strüder-Kypke 2012b). Supported by the Austrian Science Fund (FWF, Project P20461).

Agatha, S., Strüder-Kypke, M.C. 2012a. Reconciling cladistic and genetic analyses in choreotrichid ciliates (Ciliophora, Spirotricha, Oligotrichea). *J. Eukaryot. Microbiol.* 59, 325-350.

Agatha, S. & Strüder-Kypke, M.C. 2012b. Systematics and evolution of tintinnid ciliates. In: Dolan, J.R., Montagnes, D.J.S., Agatha, S., Coats, D.W., Stoecker, D. (eds.) *The Biology and Ecology of Tintinnid Ciliates. Models for Marine Plankton*. Wiley-Blackwell, 42-84.

Kim, S.Y., Yang, E.J., Gong, J., Choi, J.K. 2010. Redescription of *Favella ehrenbergii* (Claparède and Lachmann, 1858) Jörgensen, 1924 (Ciliophora: Choreotrichia), with phylogenetic analyses based on small subunit rRNA gene sequences. *J. Eukaryot. Microbiol.*, 57, 460-467.

Raphidioptera – an Austrian invention? Austria’s contribution to the exploration of the snake-flies (Insecta: Endopterygota)

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VORTRAG

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Raphidioptera are not an Austrian invention, of course – but simply one of the millions of highlights of evolution. However, what we know about snake-flies today has been achieved predominantly by Austrians. The primarily monotypic genus *Raphidia* Linnaeus, 1758, comprising altogether only eight valid species at the end of the first half of the 19th century, was associated with Mantispidae due to a superficial similarity. The young Austrian Friedrich Moritz Brauer (1832-1904) recognised (at an age of 20!) on the basis of larval characters that Mantispidae are related to Chrysopidae, Hemerobiidae, Myrmeleontidae, ... and that *Raphidia* forms a group of its own. Finally this genus became the order Raphidioptera (R.) comprising Raphidiidae and Inocelliidae. In the following 100 years not too many contributions on R. appeared, the knowledge about these insects was summarised by the Austrian authors Anton Handlirsch und Max Beier in the Handbuch der Zoologie (1936). 1963, when we started to study R. intensively, altogether 63 valid species were known. Today 238 species are counted, 166 of them (= ca. 70%) have been described by Austrians (partly together with other authors). Up to the early 1970s it was totally impossible to identify larvae of R. The basis for larval taxonomy was founded by Austrians in 1974. Since 1966 many field trips were carried out by Austrians to almost all important distribution areas of R. resulting not only in the discovery of many new species, but particularly also in uncovering refugial centres of R. Austrian entomologists clarified basic facts on the biology including the remarkable copulation behaviour. In 1968, Austrians proposed a generic classification of R. based on genital sclerites. In 1975, a comprehensive revision of the R. of the Nearctic was carried out (dissertation of U.A.). In 1991, a monograph of the R. of the world (by H.A., U.A. & Rausch) appeared in two volumes. The first report on genital sclerites of fossil R. was published by U.A. & H.A. in 2004. In 2010, the first molecular analysis of Raphidiidae was published – again by Austrians: Haring, H.A., Bartel & U.A. Recently the era of the phylogeny basing on transcriptomes has begun. In an international project on the phylogeny of the Hexapoda Austrians are responsible for the R. The first weighty result corroborates our old hypothesis: Raphidioptera + (Megaloptera + Neuroptera).

Integrative Artabgrenzung in der Felsenspringergattung *Machilis* (Microcoryphia: Machilidae)

Dejaco, T., Gassner, M., Arthofer, W., Schlick-Steiner, B.C, Steiner, F.M

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Alpine Felsenspringer der Gattung *Machilis* eignen sich besonders zur Bearbeitung von biogeographischen und evolutionsbiologischen Fragestellungen, da sie (1) einen hohen Grad an Endemismus aufweisen, (2) verschiedene Fortpflanzungsstrategien verfolgen (sexuell vs. parthenogenetisch) und (3) inner- und randalpin mit ausreichenden Artenzahlen vertreten sind, um spezifische Hypothesen (z.B. Mono- vs. Polyphylye von asexuellen Arten, geografische Parthenogenese, Korrelation von Parthenogenese und Endemismus) zu testen.

Der Artstatus mehrerer nomineller Arten wurde allerdings wiederholt angezweifelt (Janetschek 1954, 1970; Christian & Knoflach 2009), und deshalb ist eine sorgfältige Artabgrenzung als Basis weiterer Forschungsarbeit dringend notwendig. Da ein robustes morphologisches Merkmalsystem fehlt, ist die Verknüpfung verschiedener methodischer Ansätze (Integrative Taxonomie) für die Artabgrenzung besonders lohnend. Wir präsentieren hier vorläufige Ergebnisse zu Morphologie, Molekulargenetik und Karyologie und diskutieren insbesondere Widersprüche zwischen den einzelnen Disziplinen, die auf eine komplizierte Evolutionsgeschichte schließen lassen.

Christian, E. und Knoflach, B. (2009). Jumping bristletails (Archaeognatha) in Austria: current knowledge and gaps. In: *Contributions to Soil Zoology in Central Europe III*. K. Tajovský, J. Schlaghamerský und V. Pižl (Eds.), pp. 9-12.

Janetschek, H. (1954). Über mitteleuropäische Felsenspringer (Ins., Thysanura). *Oesterr Zool Z* 5: 281-328.

Janetschek, H. (1970). Über Felsenspringer aus den Alpen und den Pyrenäen (Insecta: Microcoryphia). *Ber Natwiss-Med Ver Innsbr* 58: 277-296.

Taxonomie und Biostratigraphie devonischer Ostrakoden

Dojen C.

VORTRAG

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Muschelkrebse (Ostracoda) sind seit dem hohen Ordovizium wichtige Elemente vieler mariner Faunen. Ihre weltweite Verbreitung aber auch ihre ökologische Abhängigkeit machen sie zu wertvollen Hilfsmitteln in der Biostratigraphie und Paläogeographie, deren Auflösungsvermögen bzw. Zuverlässigkeit jedoch stark von der Qualität der Taxonomie abhängig sind.

Dieser Qualitätsanspruch stößt jedoch schon bei der Erstbestimmung und systematischen Aufstellung neuer paläozoischer Ostrakoden-Taxa auf Probleme wie z.B. verschiedenen Erhaltungszustände (kalkig erhalten, pyritisiert, verkieselt, etc.), die die Oberflächenstrukturen stark verändern können und häufiges Fehlen elementarer Bestimmungsmerkmale wie das Schloss und der Schließmuskelfleck. In Einzelproben mit wenigen Individuen sind zudem Variationsbreiten und Sexualdimorphismus oft nicht erkennbar. In der Literatur zu devonischen Ostrakoden findet man daher oftmals neben offenen Bestimmungen und Art-Gruppierungen neue Artbeschreibungen, die mit hoher Wahrscheinlichkeit auf Morphotypen begründet sind.

Weitere Probleme für die Biostratigraphie liegen in den geographisch und stratigraphisch weit gestreuten Daten sowie ungenauen Fundpunktangaben. Da die Arbeiten teilweise älter 40 Jahre sind, sind zudem die Datierungen oftmals veraltet. Eine Neudatierung ist aufgrund fehlender Zusatzangaben jedoch häufig schwierig.

Das Resultat ist eine relativ chaotische Ansammlung von Informationen, die für eine solide Taxonomie als Grundlage aller weiteren Anwendungen zu entwirren ist. Zu diesem Zweck werden im Rahmen dieser Studie ausgewählte Ostrakodentaxa mit hohem biostratigraphischem Potential auf Sammlungs- und Literaturbasis neu beschrieben und datiert sowie morphologische Varianten geographisch und stratigraphisch abgetrennt.

Acknowledgement: This study is a contribution to the IGCP 596: Climate change and biodiversity patterns in the Mid-Palaeozoic.

Trochulus oreinos and *T. hispidus* (Gastropoda: Pulmonata: Hygromiidae) in the Eastern Alps and adjacent areas: Morphology, ecology and their context to phylogeography

Duda, M.^{1,2,3}, Sattmann, H.¹, Haring, E.^{2,3} & Kruckenhauser, L.^{1,2,3}

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This study investigates the state of *T. oreinos*, a hitherto quite unknown endemic in the Eastern Alps, and of the highly variable *T. hispidus/sericeus* complex. Within the latter many divergent mitochondrial clades were revealed, raising the question whether they represent cryptic species or so far undiscovered morphologically differentiated variants. By combining investigations of shell morphology, genital anatomy and autecology we found high similarity between the two subspecies of *T. oreinos*, which are clearly separated from the *T. hispidus/sericeus* complex, to which they were originally assigned. Some new diagnostic traits allow even the unambiguous separation of the two *T. oreinos* ssp.. Both have the same stenoeocous habitat preferences and are restricted to rocky high alpine areas in the north-eastern Austrian Alps. In contrast, representatives of the *T. hispidus/sericeus* complex are distributed over a wider altitudinal and geographic range, preferring moist areas and scrubby perennial herb vegetation. The nine different mitochondrial clades obtained in the genetic investigations showed neither morphological nor ecological separation. The *T. hispidus/sericeus* clades are intermingled with clades representing morphologically clearly defined species of the genus *Trochulus*, thus rendering *T. hispidus* as currently defined paraphyletic, while *T. oreinos* is clearly monophyletic. A comparison of all data implies different phylogeographic histories and Pleistocene distribution of the investigated species. In *T. hispidus/sericeus* high morphological and genetic variation indicate good dispersal abilities and a broad ecological niche suggesting glacial survival in several refuge areas. In contrast, the small genetic and morphological variation in *T. oreinos* is probably due to specific habitat requirements and poor dispersal ability. We assume that they evolved and outlived the glacial periods in their current restricted distribution range, being adapted to cooler climatic conditions.

Duda, M., Kruckenhauser, L., Haring, E. & Sattmann, H. 2010. Habitat requirements of the pulmonate land snails *Trochulus oreinos oreinos* and *Cylindrus obtusus* endemic to the Northern Calcareous Alps, Austria. *Eco.mont*, 2, 5-12.

Duda, M., Sattmann, H., Haring, E., Bartel, D., Winkler, H., Harl, J. & Kruckenhauser, L. 2011. Genetic differentiation and shell morphology of *Trochulus oreinos* (Wagner, 1915) and *T. hispidus* (Linnaeus, 1758) (Pulmonata: Hygromiidae) in the Northeastern Alps. *Journal of Molluscan Studies*, 77, 30-40.

Eocene lamniform sharks from Antarctica with special reference to sandtiger sharks (Odontaspidae)

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The known Eocene elasmobranch fauna from Antarctica (La Meseta Formation) currently comprises 24 taxa in 15 families with sharks representing the majority of taxa. Diversity patterns of these sharks are rather irregular throughout the Eocene section. Generally, shark remains are very rare in the lowermost portion of the sequence (Telm 1), which characterizes the start of the sedimentary sequence. The depositional environment is interpreted as low-energetic and/or protected lagoon or estuary during warm, wet, and seasonal climatic conditions until the middle Eocene. Gradual cooling towards the top of the La Meseta Formation correlates with abrupt drops in sea surface temperatures. The highest diversity of sharks seemingly occurs in Telms 4 and 5 when climatic conditions changed to strongly seasonal and cool-temperate. The lamniform shark, *Striatolamia macrota*, is the dominant shark species from Telms 1–5 according to all available data. The lamniform shark, *Palaeohypotodus rutoti*, is very abundant in Telms 4–5, which generally is considered a Palaeocene relict form. The fauna of Telms 4–5 is characteristic for a cool-water assemblage. New chondrichthyan material from the middle and uppermost parts of the Eocene sequence (Telms 5–7) on Seymour Island allows to revise the distribution of sharks in the Eocene of Antarctica. An Argentine-Swedish field party as a joint project of the Instituto Antártico Argentino (IAA) and the Swedish Polar Secretary (SPFS) collected the material of this study during the Antarctic summer campaigns 2011 and 2012. The fossiliferous upper horizons of the La Meseta Formation are composed of poorly consolidated, marine sandstones and siltstones, which were deposited in a coastal and/or deltaic environment. The small assemblage includes teeth of benthopelagic lamniform sharks, a batoid and a chimeroid. The low diversity of this assemblage agrees well with the observed trend of a general decrease in taxonomic diversity of chondrichthyans throughout the middle part of the depositional sequence, which might correlates with habitat loss on the upper shelf of Antarctica due to shelf ice development. The newly collected material includes abundant teeth of a large, hitherto unknown odontaspidae shark from Telms 4–7. This species differs in several aspects from other contemporaneous odontaspidae and provides new insights not only into the systematic of Palaeogene odontaspidae but also into their distributional patterns. This new odontaspidae was a common faunal element of the Antarctic Eocene chondrichthyan fauna during Telms 4–5 but seemingly disappeared at the end of the sedimentary sequence (Telm 7). This suggests that this shark might have been endemic to the Southern Hemisphere. The new odontaspidae occupied an upper position in the Eocene Antarctic food-web based on the size of its teeth.

Phylogenetic relationships within the “South African Clade”, a subclade of Eremiadinae (Squamata)

Engleder, A.^{1,2}, Haring, E.^{1,2} Kirchhof, S.³ & Mayer, W.¹

POSTER

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Eremiadinae are one of three subfamilies of lacertid lizards predominantly distributed throughout Asia and Africa. Previous phylogenetic studies did not result in a highly supported topology (Mayer and Pavlicev 2007), especially with respect to one group of Eremiadinae which we designated “South African Clade” because of its geographical distribution. It includes the genera *Pedioplanis*, *Meroles*, *Ichnotropis*, *Tropidosaura* and *Australolacerta*, but support for this group was quite low. In the present study we wanted to test the monophyly of this group and to clarify the relationships among the five above mentioned genera. We also included representatives of “East African” Eremiadinae (genera *Nucras*, *Heliobolus* and *Latastia*) and some distantly related genera (*Atlantolacerta*, *Ophisops*, and *Lacerta*). We sequenced sections of the widely used mitochondrial genes for 16S rRNA, 12S rRNA and *cytochrome b* as well as the nuclear genes *c-mos* and *RAG-1*. To obtain additional sequence information we also tested four new nuclear markers which were already used for other reptiles, but so far have not been widely tested: *PRLR*, *KIF24*, *EXPH5* and *RAG-2*.

Altogether, the sequence information is 4473 bp for nuclear and 2045 bp for mitochondrial marker sequences. The results provide strong support for the “East African Clade” and the “South African Clade”. The results confirm the genus *Tropidosaura* as a monophylum. Furthermore, our findings show that *Ichnotropis* is paraphyletic, as *Ichnotropis squamulosa* appears more closely related to *Meroles* than to *Ichnotropis capensis*. Thus, the monophyly of *Meroles* is questionable as well. Moreover, the two species (*A. australis* and *A. rupicola*) of *Australolacerta* are very distantly related and thus the genus is probably not monophyletic.

Mayer, W., Pavlicev M. 2007 The phylogeny of the family Lacertidae (Reptilia) based on nuclear DNA sequences: convergent adaptations to arid habitats within the subfamily Eremiainae. *Mol Phylogenet Evol*, 44, 1155–1163.

A molecular approach to resolve the biodiversity of the Digenea of selected freshwater snails in Eastern Austria

Gaub, L.^{1,2,3}, Feix, A.S.^{1,3}, Hörweg, Ch.¹, Sattmann, H.¹ & Walochnik, J.²

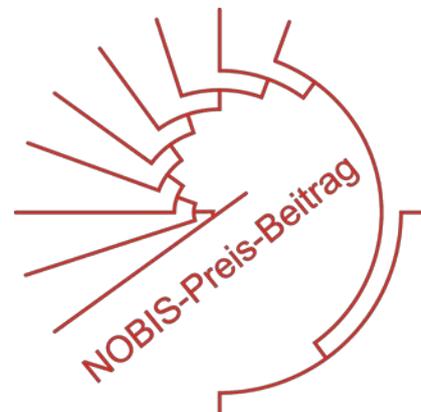
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Digenean trematodes (= Digenea) are widespread endoparasites. The aim of the current study is to reveal the digenean diversity in freshwater snails in the floodplains of the Leitha, Austria. This screening programme for Digenea is focused on taxa of potential medical and veterinarian significance, including fascioloids, echinostomatids and schistosomatids. Until now, a total of approximately 1.300 snails of different species (*Galba truncatula*, *Lymnaea stagnalis*, *Planorbarius corneus*, *Planorbis planorbis*) have been collected, measured and examined under a microscope for the presence of digenean trematodes. Samples from affected snails were tested by PCR and further identified by sequencing. In 4 out of 687 collected *G. truncatula*, digeneans were detected by microscopy as well as by molecular methods.

Also several *L. stagnalis* were positive for trematodes. Xiphidiocercariae were recorded, could however, not yet be further identified. Larval stages of *Trichobilharzia*, *Bilharziella*, and Echinostomidae were detected and assigned by morphological methods to genus or family level respectively. This determination was also proved and samples were identified to the species level by molecular methods. Altogether it was shown that potentially pathogenic trematodes do occur in this region and that morphologically undeterminable larval stages can be assigned to described species if sufficient reference data are available in DNA databases (e.g. NCBI GenBank, BOLD).



Application of taxonomic actualism to fossil benthic foraminiferal communities reveals the history of the Burdigalian Seaway

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From c. 20.4 to 17.5 Myrs the Burdigalian Seaway connected the western Mediterranean Sea and Atlantic Ocean with the Central Paratethys Sea via the North Alpine Foreland Basin (NAFB). The resulting changes in paleoceanography and paleogeography initiated a wave of macro- and microfaunal immigration from the Atlantic and Mediterranean into the Central Paratethys and had a severe impact on marine ecosystems. In the present study, the concept of taxonomic actualism is applied to fossil assemblages of benthic foraminifers in order to reconstruct paleoceanographic changes in the trough of the Puchkirchen Basin (located in the central NAFB) as a result of the developing Burdigalian Seaway. The sample material originates from drill-sites and outcrops in Upper Austria. Based on the data, four major phases in the development of the Puchkirchen Basin can be distinguished:

1. The global sea-level rise at the base of the Burdigalian (c. 20.4 Ma) initiated a marine transgression in the NAFB. In the Puchkirchen Basin, a long-lived basin-axial channel system was reactivated resulting in turbiditic and mass-flow deposition. The unstable upper bathyal environment is reflected in a low diverse autochthonous benthic foraminiferal fauna mainly composed of *Bathysiphon filiformis*.
2. The perpetuating transgression flooded large shelf areas and established the Burdigalian Seaway. As a result the channel belt in the Puchkirchen Basin was cut off from its sediment sources and shut down. Subsequently, sedimentation was primarily controlled by large delta fans prograding into the basin. High sedimentation rates and strong terrestrial input led to the development of diverse foraminiferal faunas that are largely composed of agglutinated species.
3. At c. 19 Ma the Burdigalian Seaway became a vast shelf sea when increasing sedimentation rates led to the upfill of the deep-marine Puchkirchen Basin. At the same time marine sedimentation reached its maximum extent in the NAFB. Characteristic hyaline shelf faunas composed of species of *Lenticulina*, *Amphicoryna*, *Melonis*, *Cibicidoides* and *Ammonia* developed.
4. The beginning of a regression at c. 18 Ma heralded the closure of the Burdigalian Seaway. Biofacies distribution shows a prograding tide-influenced shelf and widespread shallow water environments largely dominated by *Ammonia*, *Elphidium* and *Cibicidoides* developed. The closure of the Burdigalian Seaway initiated a major reorganization of paleogeography resulting in the final retreated of the Central Paratethys towards the east.

Systematic positions and evolution within trentepohlialean algae living in symbiosis with lichen-forming ascomycetous fungi

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Unusual for typical green algae adapted to aquatic habitats, Trentepohliales do occur in non-aquatic environments such as tree trunks, fruits, old concrete, etc. In free-living state they often completely cover the substratum forming numerous orange, cushion-like or crustose colonies. The orange colour arises due to the agglomeration of carotenoid pigments (e.g. haematochrome) in the algal cells which protect the filaments against high UV irradiation. The systematics of this algal group is incomplete and show unresolved positions within genera or species, e.g. within *Printzina lagenifera* and *Trentepohlia arborum*. The reasons are due to the fact that the taxonomy was established basically on morphological and sparse molecular data (18S rRNA and rbcL gene) of free-living Trentepohliales. Trentepohliales frequently contribute to species-rich and highly diverse cryptogamic associations living together with mosses, fungi and ferns. In our investigation we were interested in trentepohlialean algae living in symbiosis with ascomycetous fungi, forming lichens. Lichenized Trentepohliales were not well investigated until recently. To contribute new molecular data sets, we started to collect diverse lichen species with trentepohlialean photobionts in temperate and tropical habitats. As universal primers were not applicable to amplify the DNA of this type alga, we prepared photobiont isolations under axenic conditions according the Yamamoto-method specified by Stocker-Wörgötter of selected lichen species. Specific Trentepohliales-primers (18S rRNA gene, rbcL locus and ITS region) were designed on the basis of the sequences from the trentepohlialean algal cultures and various sequences of algal genera and lichenized fungal strains from the NCBI GenBank. Individual phylogenetic analyses of each marker with around 128 trentepohlialean photobionts and 13 strains of free-living representatives were performed to compare the relationships, the support of branches and resolution of the tree constructions. The maximum clade credibility tree of the 18S rRNA gene showed a low resolution and genetic variation by contrast with the other two markers. Relationships within the trentepohlialean genera were also not fully clarified if each single analysis was considered. The phylogenetic analysis of the concatenated molecular data demonstrated higher resolution and support of the algal relationships. The identification of most trentepohlialean photobionts was also possible. Our results showed that lichens collected in tropical regions offered higher photobiont diversity than lichens living in temperate habitats. A time-calibrated BEAST will clarify the relationship between free-living and lichenized Trentepohliales.

ABOL – the Austrian Barcode of Life project

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Austria is due to its geographic position and a high variety of distinct biotopes considered as a biodiversity hotspot in Europe. Despite continuing extinction of species and human induced global changes of the environment we are far from having obtained complete catalogues of all taxa in all groups of organisms.

ABOL (Austrian Barcode of Life) is a collaborative project of several scientific institutions in Austria with the objective to register all species occurring throughout the country (animals, plants, fungi) by means of DNA barcoding. To record the diversity taxonomically and to make the obtained information accessible for scientific research and practical use is one of the primary aims of ABOL. An important prerequisite for this attempt is the development of a data base connecting genetic identifiers with taxonomically reliably determined reference specimens. As it is the case with similar global and national projects ABOL will set a decisive step to explore and finally secure biodiversity. The need for such an initiative is also demanded by the *Convention on Biological Diversity*, which has been signed and ratified by Austria as well.

Objectives of our initiative are: (1) to record the current biodiversity in Austria both at the level of species and at the level of intraspecific diversity as measured by genetic marker sequences; (2) to enhance the significance of taxonomic research and collection based research and to boost collaborations between scientists from various institutions using various methodological strategies; (3) to enhance the visibility of research on biodiversity in Austria which will contribute to its value in the public view and to opinion formation concerning the conservation of nature; (4) to develop reliable, fast and reasonably priced barcoding methods for certain applications of determining species from unknown samples.

Lake bottom settlement by bivalves as result of astronomical forcing

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POSTER

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Settlement by bivalves in offshore areas of lakes is limited by bottom water oxygenation and availability of nutrients. Information from sediment-cores suggests that the formation of appropriate ecological windows seems to follow predictable and repetitive patterns through time. To test this hypothesis a high-resolution multi-proxy analysis was conducted on a 6-m-long core of Tortonian age (~10.5 Ma; Late Miocene) from Austria (Europe). Sediments of Lake Pannon were studied with a 1-cm-resolution to detect all small-scale environmental variations. Based on an already established age model for a longer interval of the same core, the study covers about eight millennia of Late Miocene time with a resolution of ~13.7 years per sample. Herein we extend the study on molluscs, which were picked from the samples. As the shells were fragmented during washing, no individuals could be counted. Therefore, the abundance of molluscs was evaluated by using semi-quantitative categories. Generally, molluscs are rare from most samples, indicating hostile conditions for bivalve settlement. The coquina layers are formed mainly by the small-sized, thin-shelled dreissenid bivalve *Sinucongeria primiformis*. It forms moderately dense pavements by monospecific gregarious assemblages. Most specimens are articulated and fully grown whereas juveniles are very rare. The assemblages represent characteristic “boom and bust” populations, which formed during sporadically established suitable conditions for settlement. Shell cavities are commonly incrustated with pyrite, pointing to anoxia as a reliable cause both for their sudden death. Hence, the formation of bivalve pavements on the bottom of Lake Pannon was only possible for extreme r-strategists during “time windows” of improved ecological conditions. These opportunities are interpreted here to correlate with cyclic shifts in the epilimnion/hypolimnion relation and the corresponding oxygenation of bottom waters. Indeed, Lomb-Scargle periodograms and REDFIT analyses of the data revealed highly significant signals with periodicities of c. 11, 37 and 75 cm. These cyclicities are expressions of the upper Gleissberg cycles, the 500-years-cycle and the 1000-years cycle. This indicates that bottom water oxygenation and nutrient supply were strongly influenced by these solar cycles.

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PCA resolves species level taxa within the European Neogene *Persististrombus*-lineage (Gastropoda: Strombidae)

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POSTER

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Strombids are among the most eye-catching gastropods, which attract a broad community of scientists and collectors. The phylogeny and the generic affiliations of the various fossil and extant taxa, however, is only slowly resolved. After early attempts of Abbott (1960), a major breakthrough was achieved not before the 21st century when a set of papers tried to clarify the validity of genus-rank taxa and to allocate species groups to these genera. Molecular data support these considerations and suggest very complex phylogeographic patterns. The newly established system is gradually also applied to the fossil taxa. As the strombids experienced their first main radiation during late Oligocene and Miocene times, the correct allocation of these taxa is crucial for supporting molecular data with the fossil record. One of the most wide spread and specious genera in the European fossil record is *Persististrombus*, which is still represented by two species along the tropical western and eastern Atlantic coasts. We have gathered morphometric data on 219 Oligocene to Pliocene shells representing 6 species level taxa of this genus. A principal component analysis on the full data set documents that all juvenile shells of the *Persististrombus inflexus*-flock are very similar and features for a specific separation arise later during ontogeny. Adult shells, however, cluster clearly in separate fields, being separated mainly by the characters “spire angle”, “height of the last spire whorl” and “height/width (max)”. Members of the European *Persististrombus*-species-flock display a tendency to produce strongly sculptured populations with marked spines or to form populations with elongate shells and reduced sculpture. The development of sculptured morphs is an iterative process as exceptionally sculptured taxa occur in stratigraphically and geographically discrete phases and areas. These taxa are at least chrono-subspecies and form no continuous evolutionary lineage leading to the Pliocene *Persististrombus coronatus* with which they were intermingled so far.

Successfully reproducing populations of extant species of *Persististrombus* in the Panamic Province and the African-Eastern Atlantic Province are limited in their distribution by the 20°C isotherm. This value may thus be a realistic estimate for the cool-season sea surface temperatures for *Persististrombus*-bearing formations. Minimum sea surface temperatures of 16°C were probably the final barrier for reproduction.

Clausilia dubia – a (bio)diverse alpine land snail

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In the present study the subspecies classification of *Clausilia dubia* DRAPARNAUD, 1805 was reassessed by morphological (various shell characters) and molecular analyses (partial sequences of the mitochondrial gene for COI). In Austria 17 subspecies of *C. dubia* are described, 13 of them occur in the investigated area of the Northern Calcareous Alps of eastern Austria. In this region some subspecies occur sympatrically or even syntopically.

The results of the morphological analyses showed that a determination by qualitative characters is possible, but we could not separate any subspecies only by quantitative characters. For an easier classification the subspecies can be merged into four morphogroups. Unfortunately, none of these morphogroups formed a distinct group in the morphometric analyses too. The phylogenetic analyses showed five clear distinct clades, but none of them corresponds solely to any of the described subspecies or morphogroups. Furthermore, no geographic pattern could be detected in the phylogenetic trees. Altogether it was not possible to distinguish any subspecies neither by morphometrics nor by the genetic data. Due to the sympatric/syntop occurrence and the difficult determination of the subspecies the validity of the described subspecies is doubtful.

Alpine populations of *Pyramidula pusilla*: A closer look into the species phylogeography

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The pulmonate land snail *Pyramidula pusilla* (VALLOT, 1801) is a rather small and inconspicuous species of the monotypic family Pyramidulidae. It inhabits sun-exposed calcareous rocks from the Mediterranean area to Western and Central Europe and feeds on endolithic lichens. Even though it is a quite common and by far the most widespread species among the European representatives, nobody has taken a deeper look into its phylogeography so far. To learn more about *P. pusilla*, we extracted DNA and performed a DNA sequence analysis of a ~650 bp section of the mitochondrial *cytochrome c oxidase subunit 1* (COI) gene. To date, we investigated 357 individuals collected at 98 different sampling sites, which were mainly located in the Eastern Alps.

The phylogenetic tree calculated with the sequence data revealed that *P. pusilla* is subdivided in at least two distinct clades. Due to the lack of a geographic pattern and high genetic diversity in the different clades, we decided to add morphological data to address the question of potential cryptic species. Photographs were taken of 143 individuals and morphometric analyses were performed. Although these results indicate differences between clades, none of the results offer a clear conclusion whether those findings can be interpreted as speciation or merely expresses a high degree of genetic variation within the Alpine populations of *P. pusilla*.

Recent divergence of an ancient haplochromine cichlid lineage from isolated water bodies in the East African Rift system

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The Haplochromini are the most specie-rich cichlid tribe and are the dominant cichlid lineage in eastern and southern Africa, where they are found in all riverine and lacustrine systems. Phylogenetic analysis of mitochondrial DNA identified haplochromine cichlids from isolated water bodies in the eastern branch of the East African Rift system as an ancient lineage separated from their western sister group in the course of the South Kenyan – North Tanzanian rift system formation.

The close phylogenetic relatedness among taxa of this lineage indicates a recent common ancestry and historical connections between now separated water bodies. In connection with a total lack of local genetic diversity attributable to population bottlenecks, the data suggest cycles of extinction and colonization in the unstable habitat provided by the small lakes and rivers in this geologically highly active area.

Taxonomy and faunal relationships of Early Miocene neoselachians (Chondrichthyes, Elasmobranchii) of the western Paratethys

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POSTER

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Sharks, rays and skates (Elasmobranchii, Neoselachii) experienced at least three major radiation events during their long evolutionary history. The third and most recent one, which gave rise to all living forms occurred in the Cenozoic. The Miocene (23.03–5.33 Ma) is crucial in the evolution of living neoselachians, because it was then that they achieved an astonishing diversity. Despite all progress accomplished in the last decades our understanding of Miocene neoselachian taxonomic diversities and faunal relationships is very incomplete. After the Tethys Ocean had nearly completely vanished by the end of the Eocene, the Paratethys Sea developed an isolated basin in the latest Eocene – earliest Oligocene, which was separated by the Alpine mountains from the Mediterranean Sea. Marginally to the Paratethys, the Molasse Basin developed during the Oligocene – Miocene. The neoselachian assemblage that forms the focus of this study comes from the Burdigalian (middle Ottnangian, Early Miocene, ca. 17.8 Ma) Achen Formation of Bavaria (S. Germany). This fauna is more or less the same age as the famous one described from the Baltringer Horizon in Baden-Württemberg. The Simsee assemblage, however, is less diverse. Faunal relationships with contemporaneous elasmobranch faunas in the Mediterranean and slightly older assemblages from the North Sea are established based on qualitative (presence/absence) data. Additionally, we established the beta (local) diversity for the studied localities. These three measures allow a more profound comparison of neoselachian assemblages. We used genera rather than species for minimizing taxonomic biases. Accordingly, the closest taxonomic similarities exist to Miocene faunas of South France (18 taxa) and the Vienna Basin (11 taxa). Closest faunal relationships exist to the North Sea and Vienna Basin assemblages (Jaccard Coefficient of Community), and Vienna Basin and South France (Coefficient of Closeness), respectively. The highest beta diversity of neoselachians during the Miocene is found in south-eastern Spain. Western Paratethyan neoselachian diversity, conversely, is rather low but still higher than that of the Vienna Basin. Reconstructing migration patterns based on these results are rather ambiguous. However, the majority of data might indicate that neoselachians migrated into the Molasse Basin either from the South. Comprehensive taxonomic and systematic revisions of Paratethyan neoselachian assemblages are obviously necessary to better understand evolutionary and migration patterns of sharks, rays, and skates during the Cenozoic in general and the Miocene in particular.

The origin of the current beaver population in Lower Austria – insights based on mitochondrial DNA sequences

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The known history of the successful beaver reintroduction in Austria proves that between 1976 and 1988 about forty individuals of *Castor fiber* mainly from Poland, Russia and Sweden have been released east of Vienna to the Danube watershed. However, it is also noted that this stock included twelve individuals of the North American Beaver, *Castor canadensis*. Therefore, the genetic status of the current beaver population in Austria is still under discussion. Previously published results and investigations of more than 100 life trapped or dead beavers during the years 1997–2005 (Sieber, pers. comm.) showed no evidence that *C. canadensis* has successfully established or survived in the overall rapidly expanding Austrian beaver population.

During the last 10 years increasing conflicts with landowners and different interest groups (e.g. agriculture, forestry, fishponds, hydraulic engineering) forced the implementation of a new beaver conflict management. This management, following a stepwise action plan, started in the winter season 2006/07 in Lower Austria. In this federal state, derogation rules from the strict protection of the species according to the European legislation (FFH, Habitats Directive) allow the trapping and killing of beavers under controlled conditions on locally restricted sites. In parallel, a monitoring system was established to collect morphometric data and organic material from all under derogations killed individuals for further scientific studies including genetics. So far 124 tissue samples from 47 locations widely distributed over a variety of river systems in Lower Austria are available for respective studies.

Based on 81 individual samples collected between 2007 and 2011, our first aim was to document and to verify the genetic origin of the beavers currently found in the Lower Austrian population. Mitochondrial DNA sequence data of the frequently used control region were obtained to confirm species affiliation of these individuals (i.e. *C. canadensis* or *C. fiber*), and to uncover regional origin of European Beavers (i.e. western and/or eastern European Beaver representing several subspecies). Outcome of these genetic analyses will be presented here. In the future, genetic data obtained will also be used assessing possible hybridization events among intraspecific lineages of beavers in Lower Austria, uncovering local family sizes and for the identification of the relationships between individuals with respect to (family) range size and patterns of (individual) dispersal.

'Septal compass' and 'septal formula' – a new method for phylogenetic investigations of the ear region in sciuriforms (Rodentia, Mammalia)

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POSTER

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Bei morphologischen Untersuchungen der Ohrregion von Nagetieren lag bisher der Fokus auf den Gehörknöchelchen oder dem knöchernen Labyrinth. Septen als knöchernen Trennwände in der Mittelohrregion, wurden lediglich beschrieben, ihre phylogenetische Bedeutung jedoch nicht erkannt. Um die Anatomie der Mittelohrregion zwischen einzelnen Taxa zu vergleichen und gegebenenfalls ein phylogenetisches Signal der Septen erfassen zu können, wurden in dieser Studie der 'Septenkompass' und die 'Septenformel' entwickelt. Mit Hilfe dieser beiden methodischen Werkzeuge kann die Anatomie und die jeweilige Verlaufsrichtung der knöchernen Septen graphisch und numerisch erfasst werden, wobei sich 'primäre' und 'sekundäre' Septen unterscheiden lassen. Zusätzlich zum 'Septenkompass' beschreibt die 'Septenformel' numerisch das Auftreten der knöchernen Septen und wird entsprechend der Zahnformel benutzt.

Werden der 'Septenkompass' und die 'Septenformel' auf die Sciuriforma angewandt, eine Gruppe von Hörnchen deren Verwandtschaftsverhältnisse nicht eindeutig geklärt sind, so zeigen sich deutliche phylogenetische Signale innerhalb der Mittelohrregion. In Sciuridae treten ventral und dorsal gelegene 'primäre' und 'sekundäre Septen' auf. Gliridae zeigen im dorsal gelegenen Recessus epitympanicus keinerlei solcher Strukturen, besitzen jedoch posteromedial gelegene Divertikel. Die Anatomie der Ohrregion bei *Aplodontia rufa* ist völlig anders gestaltet, indem viele kleine Knochenbälkchen in einem Netzwerk vorliegen, was nicht mit der Septenuhr erfasst werden kann. Dies findet sich ebenso bei *Ischyromys typus*, was für ein Grundplanmerkmal innerhalb der Rodentia spricht. Durch die zukünftige Anwendung des 'Septenkompass' und der 'Septenformel' wird die Klärung weiterer phylogenetischer Fragestellungen innerhalb der Nagetiere erwartet.

Modern deep-sea faunas much older than previously thought – new data from ODP cores

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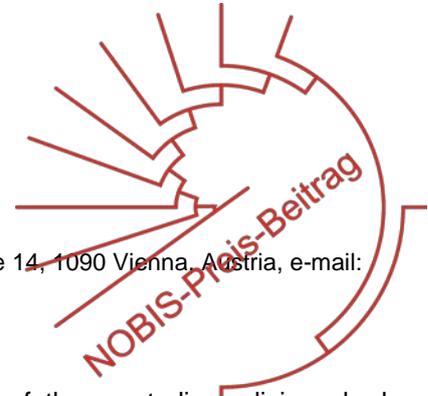
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The origin and possible antiquity of the spectacularly diverse modern deep-sea fauna has been debated since the beginning of deep-sea research in the mid-nineteenth century. Recent hypotheses, based on biogeographic patterns and molecular clock estimates, support a latest Mesozoic or early Cenozoic date for the origin of key groups of the present deep-sea fauna (echinoids, octopods). This relatively young age is consistent with hypotheses that argue for extensive extinction during Jurassic and Cretaceous Oceanic Anoxic Events (OAEs) and the mid-Cenozoic cooling of deep-water masses, implying repeated re-colonization by immigration of taxa from shallow-water habitats. Here we report on a well-preserved echinoderm assemblage from deep-sea (1000–1500 m palaeodepth) sediments of the NE-Atlantic of Early Cretaceous age (114 Ma). The assemblage is strikingly similar to that of extant bathyal echinoderm communities in composition, including families and genera found exclusively in modern deep-sea habitats. A number of taxa found in the assemblage have no fossil record at shelf depths postdating the assemblage, which precludes the possibility of deep-sea recolonization from shallow habitats following episodic extinction at least for those groups. Our discovery provides the first key fossil evidence that a significant part of the modern deep-sea fauna is considerably older than previously assumed. As a consequence, most major palaeoceanographic events had far less impact on the diversity of deep-sea faunas than has been implied. It also suggests that deep-sea biota are more resilient to extinction events than shallow-water forms, and that the unusual deep-sea environment, indeed, provides evolutionary stability which is very rarely punctuated on macroevolutionary time scales.

Intrarelationships of carcharhinid sharks based on molecular data

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Carcharhinid sharks (Chondrichthyes, Carcharhiniformes) are one of the most diverse living shark families with about 53 described species. The fossil record of Carcharhinidae extends back into the Eocene with the oldest records coming from the Southern Hemisphere. In the Miocene, they seemingly diversified rapidly and all living lineages within Carcharhinidae appeared. The genus *Carcharhinus* is the most speciose within the family displaying a wide range of morphotypes and trophic adaptations. The monotypic blue shark, *Prionace glauca*, is among the most wide-ranging large-open ocean predators and probably is the most abundant pelagic shark. However, little is known about the differentiation of blue shark populations and despite all progress accomplished in recent years, the relationships of the blue shark within Carcharhinidae but also the intrarelationships of Carcharhinidae are far from being resolved. This, however, is essential to trace their evolutionary history. Based on morphological evidence, the blue shark, e.g., is placed in its own genus, which is sister to *Carcharhinus*, whereas molecular evidence occasionally suggested in the past that it might be member of *Carcharhinus*. Here, CO1 data from GenBank and different approaches were employed to review the intrarelationships of Carcharhinidae and the systematic position of *Prionace glauca* as well as some other carcharhiniforms within this family. The European hare, *Lepus europaeus*, and the eagle ray, *Myliobatis aquila*, were used as outgroups. The first three methodological approaches yielded very similar arrangements of terminal taxa and support the monophyly of carcharhinid sharks. The Bayesian approach, conversely, provided very different arrangements with [*Carcharhinus acronotus* + *Carcharhinus isodon*] being the most basal carcharhinids outside remaining members of *Carcharhinus* and *Galeocerdo cuvier* (tiger shark) forming a sister group with *Lepus europaeus*. This indicates some major problems in using CO1 data for inferring interrelationships with Bayesian approaches. Neighbor joining and Bayesian approaches placed the blue shark, *Prionace glauca*, within the genus *Carcharhinus*. Nevertheless, the position within *Carcharhinus* depends on the method employed with *Prionace glauca* either being sister of *Carcharhinus plumbeus* (neighbor joining) or *Carcharhinus falciformis* (Bayesian approach). Consequently, it seems mandatory to combine morphological and molecular data for identifying the systematic position of the blue shark, *Prionace glauca* within Carcharhiniformes and Carcharhinidae, respectively and resolving the intrarelationships of Carcharhinidae.

Molecular phylogeny of the genus *Staphylea* L. (Staphyleaceae) with special reference to the European species

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POSTER

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Staphyleaceae is a family within Crossosomatales traditionally including three genera defined by the morphology of their fruits: *Staphylea*, *Turpinia* and *Euscaphis*. Recent classifications included all New World species of *Turpinia*, *T. cochinchinensis* (paleotropical) and the monotypic *Euscaphis japonica* into the genus *Staphylea*. All other paleotropical species of *Turpinia* were included in the genus *Dalrympelea*. Our aim was to get insights into the relationships of the European bladdernuts, *Staphylea pinnata* and *S. colchica* within the “classical” *Staphylea* species, characterized by inflated capsules. Moreover we wanted to test the hypothesis of an allotetraploid origin of *S. colchica* from *S. pinnata* and *S. emodi* from the Himalayas. Poyarkowa (Flora of U.S.S.R. 1989) had denoted *S. emodi* as the most closely related species to *S. colchica*. We applied DNA sequencing of the markers ITS (nuclear genome) and trnL-F (chloroplast) using 25 samples of 8 species from Europe, Asia and North America. Material was obtained from own collections, from herbarium specimens and supplemented by gene bank data.

The phylogeny of the ITS sequences showed that *S. colchica* from the Russian Black Sea coast near Sochi contained only one copy that included an insertion of three nuclear bases (TTG) compared to all other accessions including *S. pinnata* which lacked this insertion. Georgian *S. colchica* contained both types of copies whereas *S. emodi* lacked the insertion and showed slight affinities to other Asian *Staphylea* species. Thus, there is no indication that *S. emodi* was involved in the allotetraploid formation of *S. colchica*. The other Asian and American *Staphylea* species differed considerably from the European ones. It is striking that *S. pinnata* SW of the Danube (Serbia, 60 km SW of the Iron Gate; Slovenia; Eastern Austria) showed two copies, one of it with a deletion of nine nucleotides (AACCACACTCCCA). On the contrary the deletion was not present in accessions from Georgia, Turkey, Serbia at the Iron Gate and Poland in the West Carpathians. It might be that the nine nucleotides got lost on the species’ colonization back to Central Europe after the Ice Age.

A simple method to preserve fish material over many decades if not centuries in finest overall quality

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POSTER

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In his publication on treated formalin as a permanent preservative, Miller (1952) observed that specimens of top-minnows fixed in this solution for over eight years “appeared to the writer as if they had been preserved only a few days”. He noted the absence of long-range tests to determine the time scale of unimpaired conservation for borax buffered formaline solutions. Our contribution is intended to close this gap. Specimens of *Cyprinodon* (Teleostei: Cyprinodontiformes) that had been collected more than four, seven or even ten decades ago were burrowed from the Museum of Zoology in Michigan (UMMZ) and the Natural History Museum of Paris (MNHN) for micro-CT based morphological studies. Except for the structural colour blue of male specimens of some populations, all pigment based colour patterns (black to brown, yellow to orange and white) were found to be preserved in a wondrous, near life quality of preservation. Fine structural elements such as fin rays, scales and even fine bony elements such as fish bones were found to be conserved without widespread deteriorations (e.g. decalcification) commonly found in differently treated material when micro-CT scanned at the TU Munich. This holds true for all material including the oldest specimens collected in 1905. Formalin has been used in natural history collections since the late 19th century and the preservative effect is brought about by cross-links of protein and DNA molecules. Formalin is another name for formaldehyde in aqueous solution (CH₂O) and if not buffered produces an acidic ph. In addition, formaldehyde generates formic acid under the influence of light. Acid leads to decalcification of hard tissues such as bones and a general deterioration of collection material and is therefore undesirable. For this reason, the standard histological fixative is neutral buffered formalin, which often is used in natural history collections. However, the buffer capacity of this solution is limited and fish material treated in this way partially loses its colouration and becomes rather stiff after a short period of time. As exemplified by the material partially collected more than hundred years ago, a near life quality of preservation can be archived when 10% formalin solutions are treated with borax as a buffer. Such ten percent formalin solutions equal 4% formaldehyde solutions as the commercially available stock solutions usually contain 40% formaldehyde by weight. The original receipt was to add a level teaspoon (ca. 5 ml) of household borax to ½ gallon (about 2 l) of 10 percent formalin. The above observed different effects of formalin additives are readily observable after a few weeks. To further test this treatment, 10 neon tetra (*Paracheirodon innesi*) with their iridescent blue colour stripe and their intense red colouration of the tail were fixed in neutral buffered formalin and borax treated formalin. The identical effect was observed. This method thus provides a good method for preserving taxonomically important characters in collection material.

Miller, R. R. 1952. Treated Formalin as a Permanent Preservative. *Turttox News*, 30, 178- 179

Morphologische und genetische Unterschiede zweier Unterarten der Maskenammer *Emberiza spodocephala*. (Aves, Emberizidae)

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Die Familie der Emberizidae ist in Bezug auf die Beziehungen zwischen den Subfamilien und Genera eine recht gut untersuchte Gruppe, auf Ebene der Subspezies gibt es aber vor allem bei ostasiatischen Arten noch erhebliche Wissenslücken (Alström et al. 2008). Dies trifft insbesondere auf die verschiedenen Unterarten der Maskenammer *Emberiza spodocephala* zu. Als Vogel der Ostpaläarktis wurde diese Singvogelart vor allem in neuerer Zeit nur spärlich untersucht. Die meisten Arbeiten zu Verbreitung, Verhalten und taxonomischem Status sind vor 1980 durchgeführt worden, Untersuchungen zur Phylogenie auf molekulargenetischer Basis sind noch nicht vorhanden. Drei Unterarten sind derzeit beschrieben, zwei davon – *E. s. spodocephala* und *E. s. personata* – überlappen sich teilweise in ihrem Brutgebiet. In der russischen Literatur werden diese beiden Taxa bisweilen sogar als separate Arten geführt. Literaturangaben sind hinsichtlich der morphologischen und morphometrischen Unterscheidbarkeit allerdings z.T. widersprüchlich, und vor allem die feldornithologische Zuordnung von Weibchen und vorjährigen Männchen ist problematisch. In dieser derzeit noch laufenden Arbeit wird versucht, durch die Kombination von morphologischen, morphometrischen und molekulargenetischen Merkmalen, den taxonomischen Status der Unterarten *E. s. spodocephala* und *E. s. personata* zu klären. Zu diesem Zweck wurden im Frühjahr 2011 im Zuge eines dreimonatigen Aufenthaltes in Fernost-Russland 99 Maskenammern vermessen, fotografiert und beprobt, zusätzlich wurden an der Birdcollection des NHM London in Tring noch insgesamt 317 Bälge aus allen drei Unterarten (zusätzlich zu *E. s. spodocephala* und *E. s. personata* auch noch *E. s. sordida*) vermessen, von 20 Individuen wurden DNA-Proben genommen. Die biometrischen Daten werden nun, kombiniert mit den den Fotografien, dazu verwendet, um die Taxa nach morphologischen Kriterien zu trennen. Um diese Zuordnung mit der Unterscheidung auf molekulargenetischer Ebene zu vergleichen, wurden Sequenzen des mitochondrialen NADH-Dehydrogenase-Gens (ND2) und des Cytochrom-Oxidase (COI) Gens untersucht. Die Individuen konnten eindeutig der jeweiligen Unterart zugeordnet werden. Die Analyse der Morphometriedaten ergab einen signifikanten Unterschied zwischen *E.s.spodocephala* und *E.s.personata* in Schnabel- und Tarsuslänge, der Unterschied der längsten Handschwinge (P8) war nicht signifikant. Die derzeit noch laufenden Untersuchungen an nukleärer DNA werden helfen, phylogenetische und biogeografische Muster in diesem Unterartkomplex weiter aufzuklären.

Diese Untersuchung wird durch die Forschungsförderung der DO-G unterstützt.



Contrasting levels of differentiation in Austrian polecats (*Mustela putorius* and *M. eversmannii*) in nuclear and mtDNA

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Hybridisation and reticulate evolution at and around the species level are common and widely spread phenomena. The complete substitution of parts of the genome of one species by that of another, introgressing species, however, are comparatively rare. We studied 142 specimens of the two mustelid sibling species *Mustela putorius* (European polecat) and *M. eversmannii* (steppe polecat) in an area of sympatry in Austria in Central Europe, together with specimens of the former species from areas where steppe polecats do not occur. Initial species assignment was performed based on phenotypic characters (pelage colour and pattern, potentially diagnostic skull traits). We then sequenced a part of the mitochondrial control region and generated genotypes at 12 nuclear microsatellite loci.

While there was a clear split between the two species in the nuclear genome with only ambiguous evidence of recent hybridisation in very few individuals, comparisons with *M. eversmannii* sequences from Serbia and Mongolia (taken from GeneBank) showed that all nuclear steppe polecats exclusively harboured *M. putorius* mtDNA haplotypes, suggesting the complete substitution of the mitochondrial genome ("mitochondrial capture") in the area of sympatry in Austria. This is probably due to introgressive hybridisation in the more distant past, whereas the nuclear microsatellites did not yield evidence of frequent extant hybridisation. Our results furthermore show that caution must be exercised when using phenotypic characteristics in discriminating these two species. This particularly holds with respect to pelage colour and is of conservation relevance because the steppe polecat is a protected species, while the European polecat is not. In order to understand the possible evolutionary mechanisms which have led to the observed unilateral transmission of mtDNA in these sibling species, further molecular and evolutionary analyses are necessary, e. g. with respect to a potential adaptive advantage of *putorius* mtDNA in Central Europe as compared to the more continental distribution range of *M. eversmannii* and the possible influence of intraspecific (sexual) dimorphism and interspecific size differences in the area of sympatry.

Wild bees (Apidae) in a secondary habitat in Vienna

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Wild bees play a vital role in pollination. However, destruction of natural habitats, and also overuse of pesticides decimate bee populations or even drive species to extinction. On the other hand, wild bees are known to easily re-colonize even small habitats like private gardens as soon as they suit their needs (Zurbuchen & Müller, 2012). Requirements for the presence of wild bees are certain climatic conditions and the availability of adequate host flowers (or host bees for the cuckoo bees) and nesting sites which can be highly species-specific.

The present study reports on a survey of the bee species composition of Donaupark, a recreation area in the 22nd district of Vienna, in 2011 and 2012. Formerly, the study area was part of the Danube inundation area, later partly a dumping ground, and in 1964 designed for hosting the international garden exhibition. Nowadays, it is a park with lawns and various flower beds, but with "Irissee" and "Schmetterlingswiese" it includes two re-naturalized habitats, "Irissee" is a pond (3 ha) with natural vegetation on its banks; "Schmetterlingswiese" (1 ha) was previously a clover meadow and since 2003 it is altered and managed for the propagation of butterflies. Wild bees were collected during a "biodiversity day" on 4 June 2011 and on 14 days during the entire bee season in 2012.

Altogether 119 bee species were recorded (17 % of the Austrian fauna; comp. Gusenleitner et al. 2012), including the first record of *Hylaeus intermedius* for Vienna. 12 % of the species were cuckoo bees using resources of host bees; 45.5 % burrow ground nests; 7.6 % nest exclusively in plant stems; 5.9 % exclusively in beetle boreholes in wood. Concerning pollen preferences most species (64 %) were generalists, followed by species that are oligolectic on Asteraceae (8.5 %).

In comparison, a similar study performed on the Wiener Donauinsel (Pachinger & Hölzler, 2006) yielded a total of 144 bee species and a relatively high number (19 %) of parasitic bees. An explanation might be the significantly larger size (390 ha vs. 1 ha) that accommodates larger and stable populations of the host bees.

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Geographische Variation in der Schalenmorphologie, Anatomie und Histologie von *Cylindrus obtusus* (Gastropoda: Pulmonata: Helicidae)

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In *Cylindrus obtusus* (Draparnaud, 1805), a land snail endemic to the north-eastern Calcareous Alps of Austria, preliminary investigations revealed geographic differences in shell size and the genital tract (Adensamer 1937; Edlinger 1999; Schileyko 1997). Moreover, in a recent investigation by Kruckenhauser et al. (2010) genetic groups were detected that correspond to certain differences in genital anatomy. Microsatellite analyses indicated that only in the western populations the genotypes are in Hardy-Weinberg equilibrium, whereas eastern populations show a strong deviation from HW equilibrium at all loci displaying an extreme excess of homozygotes. Altogether these results suggested an altered mode of reproduction in eastern populations where selfing seems to occur predominantly.

In the present study a morphometric analysis of the shell revealed that there is a significant difference in shell-size (height) between two geographical groups (east, west), in which eastern populations are slightly smaller than western. Although geographical differences in the genital tract were highly significant, there was no correlation between shell-size and size of the mucous glands and the stylophore. In the eastern populations the mucous glands were significantly shorter and asymmetrical and the stylophore was also shortened compared to the western populations, where mucous glands were long and symmetrical. A comparative histological analysis did not reveal any significant differences in the cell-structure between the two groups. Altogether, the results indicate that size reduction of the mucous glands and the stylophore may not influence the mucous secretion, nor the general production of a love-dart, since there was a love-dart present in all individuals of the eastern populations. However, it might influence the amount of secrete-product. The lack of a love-dart in many individuals of the western populations may be explained by the fact that it had been shot already during copulation and had not been reproduced. This would not be the case for most of the individuals of the eastern populations. The significant geographic differences support the former hypothesis of Kruckenhauser et al. (2010) that eastern populations mainly reproduce via selfing. Nevertheless, as the knowledge about the reproductive cycle of *C. obtusus* is very limited, an extended histological investigation covering seasonal variation would be necessary to clarify functional aspects.

Bivalve diversity in the Northern Red Sea and the role of body size in marine invasion through the Suez Canal

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The opening of the Suez Canal in 1869 re-established the link between the Mediterranean and Indo-Pacific realms, allowing hundreds of species to spread from the Red Sea (RS) to the Eastern Mediterranean (EM), with mollusks being one of the most prolific groups. The present study evaluates shallow-water bivalve diversity in the Northern Red Sea and the role of bivalve body size in Lessepsian migration. Bivalve species richness from a coral-dominated coastal area that covers approximately 75 km² was assessed through original collecting activity in water depths from the intertidal to >50m and by incorporating selected literature records. 243 bivalve species were recognized and this high species richness can be related to the great habitat variety and major sampling effort, which enabled us to detect many rare species. Species accumulation curves suggest that the full range of species in the bay was considerably under-estimated. Additional species would most likely be detected at depths from 20 to 50 m, where sampling intensity was much lower than in shallower parts of the bay. Additional species are also likely to be small and rare; they will probably have unusual life habits and will probably be detected in bulk samples from soft substrata, from systematic sampling in cryptic habitats and from commensal associations. Body size correlates with many key life history traits and it has been long proposed to play an important role in mediating dispersal and establishment success of species. Our data suggest that successful RS invaders are a random sample of their source species pool in respect to body size, but they are significantly larger than native Eastern Mediterranean (EM) species. Explanation of this pattern can be found in distinct shapes and modal values of the regional body-size frequency distributions (SFD) in the two areas. A left-skewed SFD characterizes the RS species pool and differs significantly from the more log-normal Mediterranean counterpart. The causes of this discrepancy are not clear and may be related to different biogeographic affinities of the two biotas or to the late Neogene extinctions and history of recolonization of the EM basin. These preliminary results suggest that greater competitive abilities of the RS invaders contribute to the asymmetry of the interchange and in spite of the apparent lack of size-selectivity among invaders, continued inflow of the RS species will progressively shift the Eastern Mediterranean SFD towards values typical for the Indo-Pacific realm.

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