Zitteliana

An International Journal
of Palaeontology and Geobiology

88

17th Annual Meeting of the Gesellschaft für Biologische Systematik

21.–24. February 2016

Abstracts

Munich 2016

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Professor Dr. Gert Wörheide
Spokesman GeoBio-Center$^{\text{LMU}}$

Welcome Address

Dear Ladies and Gentlemen,

As your host for the next few days, I wholeheartedly welcome you to the 17th Annual Meeting of the *Gesellschaft für Biologische Systematik* (GfBS) in Munich at the Palaeontological Museum of the SNSB-BSPG. This year's meeting is co-hosted by the GeoBio-Center$^{\text{LMU}}$ (GBC), a collaborative platform to facilitate Biodiversity and Geobiology research between scientists from different LMU faculties, the Bavarian Natural History Collections (Staatliche Naturwissenschaftliche Sammlungen Bayerns, SNSB), and other research institutes. The GeoBio-Center$^{\text{LMU}}$ provides trans-disciplinary expertise and access to infrastructure to fertilize new and interdisciplinary approaches that cross geosciences and biological sciences to achieve its overarching goal – to further our understanding of the past, present and future interplay of geosphere and biosphere. Accordingly, the 17th annual GfBS meeting is held under the theme of "Taxa in Time and Space" to highlight the strong ties between Systematic Biology and Palaeontology. In this spirit, we are pleased to welcome more than 150 participants to this conference and look forward to 116 oral and poster contributions and several workshops on progress, perspectives, and pitfalls of systematic research on modern and fossil fauna and flora. I trust you will find the Palaeontological Museum an inspiring setting for this conference!

This volume contains the abstracts for the 116 presentations that have been contributed by more than 300 authors from 29 countries worldwide. This impressive and diverse collection of taxonomic and systematic work at different temporal and spatial levels is clear evidence that taxonomy and systematics of plants and animals are lively, active and much needed disciplines in these challenging times for the biodiversity on this planet. We are also grateful to the following international keynote speakers to present their inspiring work: Gustav Paulay from the Florida Museum of Natural History, Davide Pisani from the University of Bristol, Stacey D. Smith from the University of Colorado, and Katrine Worsaae from the University of Copenhagen. Support for these was provided by the German Research Foundation (DFG, ER611/4-1). Final thanks goes to all members of the local organising committee in Munich and the many helping hands to enable a smooth and enjoyable meeting.

Again, welcome and thank you for coming to Munich – I am looking forward to four inspirational days for organismal taxonomy and systematics!

Gert Wörheide

Chair of Palaeontology and Geobiology, LMU München
Director, SNSB Bavarian State Collection for Palaeontology and Geology (BSPG)
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Professor Dr. Gerhard Haszprunar
Generaldirektor SNSB

Grußwort

Liebe Kolleg/Innen der GfBS, sehr geehrte Gäste,

als ehemaliger Präsident unserer Gesellschaft sowie als Generaldirektor der Staatlichen Naturwissenschaftlichen Sammlungen Bayerns (SNSB) und last but not least als Vorstandsmitglied des GeoBio-Centers der Ludwig-Maximilians-Universität (LMU) München freut es mich besonders, dass so viele von Ihnen unserer Einladung gefolgt sind und sich hier am Paläontologischen Museum der SNSB bzw. am GeoBio-Center der LMU eingefunden haben. Ort und Titel – „Taxa in Time & Space" – unserer Jahrestagung bringen klar zum Ausdruck, dass Biodiversität und Systematik unverzichtbar eine zeitliche Dimension haben, die beachtet werden muss.

Hier kommen die Sammlungen zentral ins Spiel: Wer Veränderung messen bzw. rekonstruieren will, braucht dazu mindestens zwei (aber besser mehrere) zeitlich divergierende Messpunkte. Einer dieser Messpunkte ist die Gegenwart, der zweite und alle folgenden können nur in der Vergangenheit, d. h. in den Sammlungen liegen, da uns der direkte Zugriff zur Zukunft verschlossen ist. Wer immer die Erfassung und Dynamik der Artenvielfalt oder aber Artbildung und Phylogenie im Forschungsfokus hat, kommt an naturkundlichen Sammlungen nicht vorbei, die mit ca. 35 Millionen Inventareinheiten hier in München neben Berlin und Frankfurt ihr drittes großes Standbein in Deutschland haben . Mehr noch: die technische Entwicklung – Stichwort „Museomics" – gibt unseren Sammlungen eine völlig neue und aufregende Dimension, ohne dass dabei aber die phantastischen Möglichkeiten aktueller Morphologie bzw. der neuen Visualisierungstechniken vernachlässigt werden sollten.

Ich denke, dass gerade das „Münchner Modell" – eine enge Verzahnung und Verbindung, aber keine Fusion zwischen Ausstellungseinheiten, Forschungssammlungen und Universität – ein hervorragendes Beispiel dafür liefert, wie sich die Systematik in das Bewusstsein und die Achtung der breiten Bevölkerung aber auch der Universitäten zurückkämpfen kann: nur dort kann der wissenschaftliche Nachwuchs heran gebildet werden, aber die Forschungsmuseen werden sich dazu einbringen müssen.

Lassen Sie uns im Laufe der Jahrestagung auch darüber diskutieren, die Zukunft der Doktoranden und PostDocs, die in so großer Zahl gekommen sind, hängt davon ab.

Ich danke an dieser Stelle dem Organisationsteam und allen Mitwirkenden vor, neben und hinter den Kulissen für die geleistete Arbeit und wünsche Ihnen einen interessanten und stimulierenden Aufenthalt hier in München.

Gerhard Haszprunar

Lehrstuhlinhaber Systematische Zoologie, LMU München
Vorstand GeoBio-Center^{LMU}
Generaldirektor der Staatlichen Naturwissenschaftlichen Sammlungen Bayerns (SNSB)
Direktor der Zoologischen Staatssammlung München (ZSM)

Professor Dr. Uwe Fritz
Präsident der GfBS

Grußwort

Liebe TagungsteilnehmerInnen, liebe GfBS-Mitglieder,

es freut mich ungemein, Sie alle bei unserer Jahrestagung in der schönen bayerischen Landeshauptstadt begrüßen zu dürfen – ein ganz herzliches Dankeschön an die lokalen Tagungsorganisatorinnen und -organisatoren! Ich bin mir sicher, uns erwartet in München eine großartige Tagung!

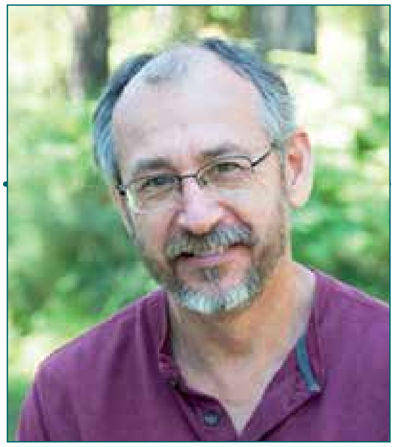
Es ist inzwischen bereits die 17. Jahrestagung der GfBS. Obwohl dies bei weitem kein „rundes Jubiläum“ ist, lohnt es, sich die Entwicklungen seit der Gründung unserer Gesellschaft vor Augen zu führen: Vor rund 20 Jahren stand es nicht gut um die Taxonomie und Systematik. Als „von gestern“ und „nicht drittmittelfähig“ wurden diese beiden Kerndisziplinen der GfBS gern abgetan, mancher sprach gar davon, dass gerade die Taxonomie keine Wissenschaft sei. Unsere Mitglieder haben dem mit der Gründung der GfBS die Stirn geboten und ich entsinne mich gern an das Logo der ersten Jahrestagung in Bonn mit dem jagenden Geparden, der die Aufbruchstimmung der Systematiker symbolisiert hatte.

Mit unserer Gesellschaft haben wir im deutschsprachigen Raum entscheidend dazu beigetragen, dass sich die Wahrnehmung von Taxonomie und Systematik in der Wissenschaftslandschaft geändert hat. Inzwischen sind wir ein fester Ansprechpartner für die DFG in Sachen Systematik und Taxonomie und Mitglieder unserer Gesellschaft waren entscheidend an den DFG-Schwerpunktprogrammen „Deep Metazoan Phylogeny“ und „Radiations“ beteiligt. Zahlreiche weitere DFG-Projekte zu systematischen, aber auch taxonomischen Themen im Normalverfahren zeigen, dass sich etwas geändert hat! In diesem dynamischen Umfeld sind in den letzten 20 Jahren auch mehrere Zeitschriften entstanden, die speziell Taxonomie und Systematik zum Programm haben und ich bin stolz darauf, dass unsere Zeitschrift „Organisms, Diversity & Evolution“ hier eine prominente Rolle spielt.

Im Zeichen der Biodiversitätskrise und der Zeitenwende hin zum „Anthropozän“, die wir leider mit 7,2 Milliarden Artgenossen bereits weit hinter uns gelassen haben, stehen heute ironischerweise die Zeichen für unsere Forschung besser denn je: Mit der zunehmenden Bedrohung der Biodiversität ist „Biodiversitätsforschung“ en vogue geworden und es ist inzwischen eher ein Wettbewerb ausgebrochen, wer diesen Begriff für sich proklamieren darf. Obwohl ich, und bestimmt Sie auch, diese Frage klar mit „wir“ beantworte, glaube ich, dass wir gerade in diesem aktuellen Spannungsfeld die GfBS dringender denn je brauchen: Sie ist die einzige wirkliche Interessensvertretung der Taxonomen und Systematiker, also der „echten“ Biodiversitätsforscher, in Deutschland. Damit ist sie auch der natürliche Ansprechpartner für Zuwendungs- und Drittmittelgeber, aber auch für die Politik, wenn Fragen zur Biodiversität aufkommen. Hier müssen wir in Zukunft allerdings besser werden. Das Totalversagen aller Forscher und Gesellschaften, auch von uns, im Vorfeld des sich seit 20 Jahren abzeichnenden ABS-Debakels, das nur dazu führen wird, dass Biodiversitätsforschung durch eine immense Bürokratie immer schwieriger wird, ohne dass irgendjemand damit geholfen ist, muss uns hier Mahnung sein. Das bedeutet, wir müssen in Zukunft stärker als bisher unsere Kernkompetenz in die Politik hineintragen – denn nur in der GfBS sind die Artenkenner in einzigartiger Weise organisiert. Hier auf der Tagung in München wird es eine Diskussionsrunde über die Zukunft der GfBS geben. Dort sollte auch das Thema erörtert werden, wie die GfBS stärker in die Politik ausstrahlen kann. Eine Gesellschaft lebt aber von ihren Mitgliedern und kann nur so stark sein, wie das Engagement ihrer Mitglieder ist. Tragen Sie dazu bei!

Es grüßt Sie herzlich
Ihr Uwe Fritz

Gustav Paulay
Keynote



Diversification on coral reefs

Coral reefs are the most diverse marine habitats, home to at least hundreds of thousands of animal species. How is this diversity distributed and how did it arise? Our research program is focused on documenting the diversity of reefs and understanding the dynamics of diversification. Through phylogenetic analysis of thoroughly-sampled clades of reef invertebrates, we identify speciation events represented by sister species relationships. We then examine the spatial and temporal context of species divergence across many such cladogenetic events within and among taxa. This approach reveals both strong, recurring patterns of diversification, as well as substantial variation, especially among taxa with different ecologies and life histories.

The geographic scale of speciation ranges from within single reef systems to between ocean basins. Much of this variation is attributable to dispersal ability. Good dispersers can be panmictic from East Africa to West America, while moderate dispersers often differentiate rampantly among archipelagoes. Well-known dispersal barriers and environmental transition zones are sites of recurrent allopatric divergence. The geographic and environmental setting has a great influence on diversification. There is little evidence for single vicariant events being important in diversification. Rather speciation events are broadly dispersed through time at each major barrier, suggesting chance dispersal or recurrent vicariance driving diversity.

While speciation in most groups is fairly slow, taking millions of years, it appears to be rapid in certain contexts and taxa. There is evidence for rapid speciation in several symbiotic taxa, potentially driven by host race formation. Rapid speciation is also a recurrent theme in echinoderms, perhaps facilitated by rapid divergence of gamete recognition proteins. Why reef echinoderms are not more diverse given this capacity for rapid speciation is an interesting question.

Genetic data are also uncovering a large number of cryptic species and showing that endemism is generally much higher than previously appreciated. In many groups color patterns evolve rapidly so that related species are often differentiated only by color and not by structural morphology. Endemics are common virtually everywhere, and not restricted to peripheral and isolated locations.

Davide Pisani
Keynote

Are ctenophores really the sister group of all other animals?

The relationships at the root of the tree of life are still highly debated. While traditionally Porifera (the sponges) were seen as the sister group of all the other animals, recent studies that used genomic information from the first two sequenced ctenophorans suggested this group to be the sister group of all the other animals. Here we shall present recently published results as well as new results illustrating how a sister group relationship between Ctenophora and all the other animals is merely a tree reconstruction artefacts. Further on, I will discuss suggestions that Porifera as the sister group of all the other animals is a tree reconstruction artefact (e.g. caused by an unspecified bias in ribosomal proteins or a compositional artefact) and show that they are invalid. To the contrary, I will present evidence clearly showing that compositional heterogeneity was (at the least in part) responsible for attraction the ctenophores at the root of the animal tree in previous studies.

Stacey D. Smith
Keynote

Connecting genetic mechanisms to phylogenetic patterns: Studies of flower color evolution in Solanaceae

Changes in flower color are among the most common evolutionary transitions in angiosperms and are rapidly becoming among the best understood at the genetic level. This provides an exceptional opportunity to explore how the genetic underpinnings of phenotypic variation shape the distribution of trait differences across the phylogeny. For example, we might predict that character states that can result from simple loss-of-function mutations would arise frequently while those that with a more complex genetic basis would be rare. I will explore these ideas for two particular flower colors, red and white, using the tomato family, Solanaceae, as a model system. White flowers are common in the family, and phylogenetic studies indicate many forward and reverse transitions. Consistent with this pattern, gains and losses of pigmentation in Solanaceae and other taxa commonly involve regulatory mutations, which alter flower color while leaving the underlying pigment pathway intact. By contrast, red flowers have appeared multiple times but remain extremely rare, comprising only ca. 1 % of the 2,800 species in the family. The acquisition of red flowers typically requires mutations at multiple loci, which may in part account for their rarity. However, additional macroevolutionary factors, such as state-dependent diversification and non-equilibrium dynamics, could also contribute to the tippy distribution of red-flowered species.

Overall, these patterns suggest that understanding the genetic mechanisms responsible for different classes of phenotypic transitions may help us to explain why some traits are common and others remain rare.

Katrine Worsaae
Keynote

How small animals provide clues to large scale questions

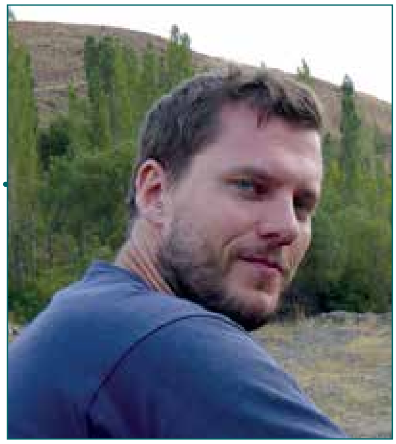
Recent years of progress in molecular phylogenetics have changed the comprehension of ‘the tree of life’, reaching a consensus on three major animal lineages – Deuterostomia (including vertebrates), Ecdysozoa (including arthropods) and Spiralia (many worm-like groups). However, the vast majority of model animals is of macroscopic size and belongs to the two former lineages, neglecting the huge diversity in Spiralia.

Within the third group, Spiralia, several of the understudied, small taxa have shuffled between subgroups, their phylogenetic resolution being critical for reconstructing the evolution of central animal shapes and features such as size, brain and segmentation. In a recent phylogenomic study we assessed the interrelationships among the meiofaunal and macrofaunal members of Spiralia using 402 orthologs mined from genome and transcriptome assemblies of 90 taxa. The meiofaunal ‘problematica’ *Lobatocerebrum* and *Diurodrilus* are found to be deeply nested members of Annelida, and unequivocal support is found for the lastly described phylum Micrognathozoa as the sister group of Rotifera. The formerly platyzoan taxa form separate branches with the gnathiferan clade of Micrognathozoa, Rotifera and Gnathostomulida branching of first, followed by a separate clade of Gastrotricha plus Platyhelminthes. With these several meiofaunal lineages branching off early in the diversification of Spiralia, the concept emerges of a microscopic, acoelomate, unsegmented, direct-developing ancestor of Spiralia.

Whereas most of these traits have been doomed highly variable across Bilateria and their evolution will be difficult to unravel, the nervous system is still often considered highly conservative. So though the presented evolutionary scenario is still debatable, it already leads to further questions on e.g., the complexity and functionality of the early spiralian brain and nervous system – composed of only few cells.

New detailed morphological studies of the neuromuscular systems in the meiofaunal groups Micrognathozoa, Gnathostomulida, and Gastrotricha as well as miniaturized Annelida uncover a comparably low structural complexity of the brain, composed of very few cells. Yet, subdivisions do occur, if not structurally, then in functionality – as indicated by expression patterns of neurotransmitters and neural genes. Whereas the first gene expression studies indicate a functional regionalization within the brain (sometimes possible evolutionary conserved), the neuropeptidergic studies showed high intraspecific variation and indicate that cells can be specific to one neuropeptide and possibly to one function – even in a brain consisting of only 650 cells. A most recent phylogenetic study positioning Xenacoelomorpha as sister to Bilateria adds to the discussion on the origin of the orthogonal nervous system. In this context, our studies confirm a well-polarized nervous system in spiralian meiofauna as well as finding additional nerve bundles and complexity. Most of all, the multiple new data on both brain and nervous system reveal substantial structural variation, even among closely related species, questioning the often-claimed evolutionary conservatism of the animal nervous system.

Martin Husemann
Bernhard Rensch Award



Evolutionary forces driving population differentiation in Lake Malawi rock-dwelling cichlids

The East African cichlids with more than 2000 species represent the most diverse vertebrate radiation known. Lake Malawi harbors the most species-rich flock with more than 700 endemic cichlids. I used a population based approach to study the forces driving the divergence of populations and the factors contributing to the maintenance of species diversity. I examined the effects of genetic drift on population divergence through time and space using an analysis of effective population size. Results indicated that microendemics may have relatively small population sizes (~500 individuals) suggesting vulnerability to drift. Tests for selection indicated an important role of diversifying selection in the divergence of body shape and length in *Maylandia zebra*. Divergence in male color pattern showed weaker evidence for selection. Divergence estimates for body shape and melanophore count were correlated suggesting that both phenotypes may be under correlational selection. Correlational selection is further supported for body shape and male coloration in replicated sympatric species pairs of *Maylandia*.

A common garden experiment using the sympatric *M. zebra* and *M. benetos,* representing a sympatric species pair with divergent coloration, showed that body shape had a strong genetic component, but also exhibited phenotypic plasticity. Hybrid crosses of the two species revealed a complex mode of gene action for body shape and showed high degrees of transgressive segregation. Hence, selection, drift and new variation generated by plasticity and transgressive segregation all contribute to the large diversity observed in cichlids.

Abstracts / Kurzfassungen

Oral Presentation

Poster Presentation

The first author is the presenting author, unless otherwise specified (*)

Podisma pedestris (Acrididae) – one species becoming two?

Oral Presentation Student Prize

Hannes Becher[1], Richard A. Nichols[1]

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In Europe, the grasshopper *Podisma pedestris* occurs widespread in the alpine zone and in Fennoscandia. Throughout most of its range it has an XO sex chromosome system. But individuals in the Southern French Alps posses a neo-X/neo-Y sex chromosome system likely created by an X-to-autosome fusion which subsequently spread through that part of the species‘s range. Both sex chromosome races hybridise, but there is evidence for considerable selection against hybrids and backcrosses. Despite of this selection there seems to be introgression going on between the races. For instance, analyses of allozymes, rDNA sequences, and rDNA distribution found polymorphisms but failed to identify patterns corresponding to the chromosomal races. Apart from the sex chromosome polymorphism there are no molecular, cytogenetic, morphological, or behavioural markers known to tell apart the two races.

The dramatic drop in cost of high-throughput sequencing allows us to address the issue on a much wider scale than ever before (even though *Podisma pedestris*‘s extraordinary large genome size, 1C = 17 pg). One of the aims of my PhD is to investigate whether and to what extent genetic material is being exchanged between the two races. The results might change our notion of whether *Podisma pedestris* is one species and, more importantly, provide insights into how evolution is happening in hybrid zones.

What prevents *Podisma pedestris*’s chromosome races from merging?

Poster Presentation Student Prize

Hannes Becher[1], Richard A. Nichols[1]

[1]Queen Mary University of London, U.K.
h.becher@qmul.ac.uk

The alpine grasshopper species *Podisma pedestris* shows a sex chromosome polymorphism. While the ancestral state is a an XO sex chromosome system (fused race), a neo-X/neo-Y sex chromosome system has become fixed in a part of the species‘s range (un-fused race). Both races meet in the Southern French Alps where they form a narrow hybrid zone suggesting considerable selection against hybrids. Backcrosses homozygous for their sex chromosomes still show reduced fitness indicating the selection against hybrids is not (or not exclusively) due to the sex chromosomes. Despite research going on for more than four decades, no other marker is known to tell apart the two races.

The problem is now going to be addressed using high-throughput sequencing. *P. pedestris*‘s exceptionally large genome size (1C = 17 pg, approx. 150 times *Drosophila melanogaster*‘s genome) forbids whole genome sequencing approaches. Markers will be selected based on transcriptome sequences of both races. They will then be sequenced selectively to find race-specific SNPs, the segregation of which can be traced across the hybrid zone.

Phylogenetic position, metabolic profile, and antibacterial extracts of the Antarctic lichen *Himantormia lugubris*

Oral Presentation

Andreas Beck[1,2], Veronika Kuhn[3], Wolfgang Eisenreich[3], Pradeep K. Divakar[4], Cinthya Cabrera Rojas[5], Mauricio Cuellar[5], Wanda Quilhot[5], Julia Bechteler[1], Gerardo González Rocha[6], Angélica Casanova-Katny[6]

[1]SNSB-Bavarian State Collection for Botany, Munich, Germany
[2]GeoBio-Center Ludwig-Maximilians-Universität München, Germany
[3]Section of Organic Chemistry and Biochemistry, Department of Chemistry, Technische Universität München, Garching, Germany
[4]Department of Vegetal Biology II, Complutense University of Madrid, Spain
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Lichens produce a tremendous diversity of metabolites, with at least 1,050 metabolites described so far. To elucidate the properties of some of these in more detail, we obtained the metabolomic profile of the Antarctic endemic *Himantormia lugubris*, which based on a six-gene phylogeny (ITS, nuLSU, mtSSU, RPB1, Mcm7 and Tsr1) occupies a basal position within Parmeliaceae. Metabolic profiles were determined by non-targeted 1H-NMR and GC-MS analysis of a methanolic extract. 5,7-Dihydroxy-6-methyl-phthalide was identified as a key marker compound. Specimens growing on either rock or mosses did not differ in their main secondary metabolites. Antibacterial activity of the extracts was screened against multidrug-resistant bacterial strains isolated from clinical specimens in Chilean hospitals. Most of the bacterial strains –Methicillin-resistant *Staphylococcus aureus* (MRSA), Vancomycin-resistant enterococci (VRE), *Escherichia coli* and *Acinetobacter baumannii*– were inhibited in their growth or killed at concentrations >100 mg/mL. *Klebsiella pneumonia*, however, were killed only by concentrations >250 mg/mL.

Phylogenetic significance of the nervous systems of some basally branching Trochozoa

Poster Presentation

Patrick Beckers[1]

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Trochozoa is a taxon of mainly marine invertebrates characterized by the possession of a special kind of larvae. Recent molecular studies recovered this taxon as to consist of Mollusca, Annelida, Brachiopoda, Phoronida, and Nemertea, but morphological data except for the larva supporting this clade are scarce. In order to shed light on the evolution and relationships between these taxa, their nervous systems were investigated using complete series of Azan stained histological sections. Immunohistology and transmission electron microscopy were applied to selected species to clarify fine structural details. To reconstruct the putatively ancestral state several species of different lineages of trochozoans were investigated. For this purpose we predominantly chose species also sampled in current molecular analyses.

The analysis revealed that the central nervous system of basally branching trochozoans (*cns*) most likely is an intraepidermal circular brain with ventro- lateral branching medullary cords which may fuse in their further course. Neurons are homogeneously distributed around the neuropil of the brain and medullary cords, there are no ganglia present. From the brain ring or medullary cords several minor (somata- free) nerves branch off and innervate the visceral organs or body appendages. The current taxon sampling favors the view that a shift of the nervous system into the musculature and an increase of brain complexity (e.g. formation of ganglia, brain compartments and lobes as well as neuron-clusters) must have evolved convergently within certain nemertean, polychaete and molluscan lineages.

A prickly aplacophoran mollusc from deep-sea plains: first record of an abyssal acanthomeniid Solenogaster in the North-West Pacific

Poster Presentation Student Prize

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The deep-sea benthos is one of the largest and continuous habitats on earth, yet its diversity remains largely unknown. The Kuril-Kamchatka Biodiversity Studies (KuramBio) Cruise set out to explore the benthic fauna of the Kuril-Kamchatka trench and its adjacent abyssal plains. Among the organisms collected with an epibenthic sledge were numerous Solenogastres, a small clade of aplacophoran worm-molluscs, which have their peak in diversity on the continental shelf and in bathyal depths. So far only nine lineages are reported from abyssal depths below 4000 m, thus the 18 morphospecies discovered during the cruise present a surprisingly high diversity. Most of the lineages are new to science, and we present a first characterization of one of these morphospecies encountered at 5385–5400 m. We studied the scleritome by scanning and light microscopy, and used histological serial sections for reconstructing anatomy. The retrieved data suggest the specimen to be a representative of the family Acanthomeniidae (order Cavibelonia). However, a unique character mosaic hampers an unambiguous assignment to one of the three existing genera. This study provides the first record of an acanthomeniid *Solenogaster* from the North-West Pacific, considerably expanding the hitherto known distribution of the family from the North and South Atlantic and the Davis Strait (Antarctica). The currently low diversity of Solenogastres from the abyss appears as severely underestimated, owing to the general under-sampling of the deep oceans.

Phylogenetic, bathymetric and onshore–offshore gradients in NE Atlantic cheilostome Bryozoa

Oral Presentation

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Bryozoans form a ubiquitous and occasionally abundant part of the Recent and fossil, sessile epibenthos in shallow-shelf to bathyal environments. Owing to their short-lived larvae, most species have a relatively restricted geographic range of distribution, which makes bryozoans excellent objects for biogeographic and evolutionary studies. However, in the intensified research on NE Atlantic shelf, island and seamount diversity and ecology during the last decades, bryozoans were almost completely ignored.

Based on historical data and recent collections, I will here review the present state of knowledge on the diversity of bryozoans in the Macaronesian seamounts and islands. In combination with information from the fossil record, the timing of invasion of, and the geographic origin of species on, these oceanic islands will be assessed. Moreover, a number of morphological adaptations at the zooid- and colony-level in bathyal species, as well as the common presence of predator-induced damage to the skeleton, reveal depth-dependent selection pressures (e.g. reduction in food availability, predation pressure) that these populations are subjected to.

Pleurobranchoidean sea slugs revisited

Poster Presentation

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The Pleurobranchomorpha (Pleurobranchoidea) are a worldwide distributed and moderately diverse (approx. 90 species) clade of sea slugs, either lacking the shell entirely or internally shelled. As sister to Nudibranchia, the origin and early pleurobranchoidean evolution was suspected to be related to Antarctica and cold deep waters. Traditionally, pleurobranchoideans are divided into two families, Pleurobranchaeidae and Pleurobranchidae, and ten genera. Morphocladistic analyses supported the monophyly of families and of most genera. In contrast, initial molecular analyses did not recover the monophyly of families. Surprisingly, the supposedly pleurobranchaeid *Euselenops*, without mitochondrial data available, clustered within pleurobranchids. In this work, phylogenetic relationships were inferred by analysing partial sequences of up to five mitochondrial and nuclear markers (H3, COI, 16S, 18S, 28S) of more than 30 species, covering all known genera. Novel sequences were generated of the particularly interesting, northern hemispherical cold water taxa *Boreoberthella* and *Pleurobranchella*. Previously missing markers of *Euselenops* and other taxa of both families were supplemented. Multilocus trees from Maximum Likelihood analyses are used for testing and refining earlier hypotheses on pleurobranchoid phylogeny and evolution.

Does the Mid Atlantic Ridge affect the distribution of benthic isopod crustaceans across the Atlantic Ocean?

Oral Presentation Student Prize

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The German Vema-TRANSIT (Bathymetry of the Vema-Fracture Zone and Puerto Rico TRench and Abyssal AtlaNtic BiodiverSITy Study) expedition studied the abyssal fauna inhabiting the African and South American Plates along the Vema Fracture Zone during one cruise. The samples were obtained using a camera-epibenthic sledge from December 2014 to January 2015 on-board R/V Sonne (SO237) at eleven stations along 11° N across the Atlantic Ocean. Aim of the cruise was to investigate whether the Mid Atlantic Ridge (MAR) isolates the fauna of the western and eastern abyssal basins, which may favour allopatric speciation. To address this question, we morphologically and genetically examined two isopod families with different lifestyles. Both families belong to the Peracarida, which is inter alia defined by the presence of a brooding pouch (marsupium). Macrostylidae follow an infaunal (burrowing) lifestyle, Desmosomatidae on the other hand are considered a predominantly epifaunal family with swimming capabilities. Consequently we expected a more limited dispersibility for the burrowing Macrostylidae. Nonetheless, one species of Macrostylidae (*Macrostylis* sp.) sampled with 25 individuals and two species of Desmosomatidae with three (*Prochelator* sp.) and two (*Whoia* sp.) specimens respectively were found to occur across the MAR. This suggests that the MAR does not explicitly act as a distribution barrier to infaunal or epifaunal deep-sea isopods alike.

A step-by-step guide to the digital stippling method

Poster Presentation Student Prize

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Vector-based software has revolutionised scientific illustrating and is well established in crustacean taxonomy.

However, simple line drawings lack depth information. This can be overcome by shading techniques, such as stippling – the application of dots to generate shade. Here we present a step-by-step guide for digital stippling. It comprises two approaches: Manual stippling offers great flexibility to achieve highly realistic results. A round brush is applied to the line art by tapping. Second, to speed up the process and generate homogeneous shades, a semi-automation is shown: the smallest units of symmetric stippling patterns are stored in a brush library. Using macroinstructions, such stored raw patterns are converted into symmetric repetitive patterns. Accordingly, even stippling patterns can be applied quickly across large areas of the underlying template. These methods come with all the advantages of vector illustrations, such as high scalability, reproducibility and easy correction of strokes that have turned out imperfect. The semi-automated stippling was developed during the description of a new deep-sea isopod species from the Kurile-Kamchatka abyssal plain in the Northeast Pacific which is used here as an example.

A new superfamilial taxon of heterobranch snails, and implications for the euthyneuran gastropod tree of life

Oral Presentation Student Prize

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Tjaernoeia exquisita (Jeffreys, 1883) is a millimeter-sized subtidal gastropod from the Eastern Atlantic with a golf-ball like ornamented shell and peculiar head anatomy. It is currently classified as *incertae sedis* among paraphyletic 'lower' Heterobranchia, which link the two major gastropod taxa, Euthyneura and Caenogastropoda. Except for images of the shell, a single radula, and sketches of external morphology, nothing was known about the anatomy of these enigmatic snails, and phylogenetic placement remained elusive.

For the first time, we herein present preliminary phylogenetic data from molecular sequences and data on soft body anatomy derived from 3D reconstruction based on histological serial sections. These results indicate that the genus forms a novel lineage at the base of Euthyneura, together with a similarly enigmatic genus of 'true' euthyneurans, *Parvaplustrum* Powell, 1951.

We highlight potential phylogenetic implications of these results, and discuss them in the light of current hypotheses for the euthyneuran tree of life.

'Using the brain' for phylogenetic and paleobiological inferences in early dinosaurs and sauropodomorphs

Oral Presentation Student Prize

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The 150 Ma of non-avian dinosaur evolutionary history started in the Late Triassic (Carnian). Early dinosaurs were usually gracile and omnivore animals, but the morphological disparity seen in later representatives is astonishing. Sauropodomorpha, one of the three major dinosaur lineages, includes the gigantic herbivorous sauropods, easily recognizable by their peculiar morphology, with long necks and small skull. We conducted a comparative study of braincase evolution in early dinosaurs and sauropodomorph. Based on CT-Scan data, we analysed and virtually reconstructed the braincase of four specimens encompassing distinct geological periods and phylogenetic portions of the sauropodomorph tree: *Saturnalia tupiniquim* (Triassic, Carnian), *Efraasia minor* (Triassic, Norian), *Plateosaurus engelhardti* (Triassic, Norian), and ?*Cetiosaurus oxoniensis* (Middle Jurassic, Bathonian). Some structures previously thought to be exclusive for other archosauriforms are also present in early dinosaurs, showing that information on this structure is still scarce for these taxa. However, some braincase characters provide additional support for dinosaur monophyly and its major sub-groups. Regarding sauropodomorphs, our results show that many of the modifications in the general anatomy of the braincase happened at the basis of the Sauropoda. It remains unclear if these differences might be due to a drastic morphological change at the basis of the group, or if they represent a bias due to the lack of braincase materials of closely related taxa. Overall, braincase anatomy has been demonstrated as an important source of data for phylogenetic and paleobiological inferences in order to better understand the evolution of sauropodomorphs during the Mesozoic.

Phylogenetic reconstruction by means of the development of morphological characteristics: Polyneopteran insects as an example

Poster Presentation Student Prize

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Polyneopterous insects are very diverse, including, e.g., praying mantises, stick insects, grasshoppers, cockroaches and earwigs. The relationships within the group are not fully resolved and still controversial. Therefore, the inclusion of new character sets into the analysis may provide crucial information for resolving these relationships. Developmental data can serve as important clue in this case. Polyneopterans are modern insects with two pairs of wings. Throughout the post-embryonic development of these 'hemimetabolous' (better non-holometabolous) insects the wings grow from little extensions (wing pads) to fully movable wings; this transformation appears rather stepwise with each moult. In early flying insects, the development of the wings is characterised by extreme gradualness. Hence, the ancestral type of wing development has become remodeled in the different lineages of modern insects. To understand the systematics and the resulting phylogeny we tried to reconstruct the evolutionary history of these specialisations. In addition to the unclear phylogeny, also the ontogeny has rarely been documented. As a first step it is necessary to thoroughly document the morphology of the nymphal instars of the species of interest. Here we documented in detail the wing development of the grasshopper *Schistocerca gregaria* (Orthoptera). As known for many years orthopterans show a peculiar change in winglet morphology: the winglet becomes twisted during the moult from nymphal instar III to IV. We compare this specialisation to winglet specialisations of other close related insects and explore whether winglet characters can help to resolve the phylogeny of Polyneoptera.

Geometric morphometric analysis applied to theropod ichnotaxonomy: some examples from the Iberian peninsula

Poster Presentation

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The vertebrate track record is an important source of information that can complement the data provided by the skeletal fossil record. In fact, tracks are the only fossilized evidence in some geological formations so they provide evidence for reconstructing the tetrapod diversity (ichnodiversity). Footprint morphology may vary even within the same trackway as it depends on limb motion, substrate consistency and foot anatomy. Besides, a track produced by the same trackmaker might be slightly different depending on the different mode of preservation. Thus, one of the most intriguing issues in reconstructing the ichnodiversity is how to determine which ichnite represent ontogenetic, extramorphological or preservational variations of others. As a consequence it is often hard to distinguish and classify different tracks just by qualitative descriptions. Recent research in tracks from the Kimmeridgian (Late Jurassic) and Berriasian (Lower Cretaceous) from Spain has shown that geometric morphometric methods are a valuable tool for drawing comparisons between theropod tracks. Principal components analysis and thin-plate spline methods have allowed to quantitatively distinguish between broad groups of tracks in the sample and establishing the main differences between them. Thus, on the one hand at least two different broad groups of theropod tracks have been distinguished in the Berriasian deposits of Huérteles Formation in Soria Province (*Kalohipus bretunensis* and *Iberosauripus* isp.) that are different from other typical theropod ichnotaxa, such as *Eubrontes* and *Grallator*. On the other hand, theropod tracks from the Kimmeridgian deposits of the Lastres Formation in Asturias Province have been classified as *Grallator*.

Mosaic-like polymorphism in two genera of flat millipedes (Diplopoda: Paradoxosomatidae) in southern Australia caused by multiple glacial refugia?

Poster Presentation

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The gonopods of millipedes, which hold the most important taxonomical features for higher and lower taxon levels, are supposed to be very stable within species. In the past, comparably small differences in gonopods have led to the description of several new species in many cases.

Two genera of flat-millipedes – *Somethus* Chamberlin, 1920 from South Australia and *Pogonosternum* (Carl, 1912) from southeastern Australia – are revised using an integrative approach incorporating sequence data and morphology. The majority of these species exhibit a mosaic-like pattern of high intraspecific morphological and genetic variability, and highly localized haplotypes or cryptic lineages. This finding suggests that they are confined to multiple glacial refugia where populations persisted during the cold and dry Pleistocene glacial cycles within suitable moist habitats in southern Australia, which led to isolation and diversification or maintenance of ancient genetic and/or morphological diversity. A similar hypothesis of multiple glacial refugia has been proposed for other southeastern Australian invertebrates with low dispersal ability (e.g., springtails, flatworms, millipedes).

It must be emphasized that in the genus *Somethus* and *Pogonosternum*, but probably also in other Australian

Paradoxosomatidae as well as in other millipedes that are influenced by glacial cycles, gonopod variability and genetic divergence in combination with a poor sampling effort may lead to over-splitting in species descriptions or the presumption of (pseudo-) cryptic species.

Applied molecular taxonomy for the identification and species delimitation of Icelandic deep sea decapods

Oral Presentation Student Prize

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The identification and delimitation of species is a challenging and time consuming task. This is especially true when only juveniles, damaged or incomplete specimens are available. Nowadays molecular methods can help to gain more information from such individuals as well. Many approaches have been proposed to improve molecular species identification in the last years.

Due to the fact that molecular variability is not constant within a species and not always resembles morphology, computational species delimitation methods have been developed to identify species boundaries in molecular datasets. The aim of these methods is to establish primary species hypotheses that can serve as molecular operational taxonomic units and consecutively as a proxy for the 'real' species that are present.

In order to test and refine such molecular approaches we investigated specimens that were sampled during the '**Ice**landic marine **A**nimals: **G**enetics and **E**cology' cruises (IceAGE) in 2011 and 2013. To identify species, the DNA barcode fragment of the cytochrome *c* oxidase 1 gene (COI) was amplified, sequenced and aligned. Sequences were identified using an automated BLAST and BOLD analysis. Species delimitation was conducted following a modified version of the **A**utomatic **B**arcode **G**ap **D**iscovery method (ABGD) and other methods. The results represent a proxy to the number of putative species that are present in the dataset. We will show our latest results and demonstrate how they can be included in an integrative taxonomy framework and discuss the application of additional methods and data to establish a robust workflow for rapid species identification.

Is there any phylogenetic signal in spermatozoa – a case study from nemerteans

Poster Presentation

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Ultrastructure of spermatozoa is widely used as source for phylogenetic inference, since sperm cells are likewise easy to obtain and to analyze ultrastructurally. Spermatozoa on the other hand are highly adapted to the mode of reproduction and thus subjected to sexual selection. Due to these strong functional constrains they should be prone to convergent evolution, given especially that sperm cells are rather poor in characters. If so, sperm cells should not contain much phylogenetic signal and functional constraints shaping their ultrastructure should outperform any influence of historical constraints (evolutionary heritage). Accordingly their inclusion into phylogenetic analyses should increase noise over signal and weaken the quality of such analyses. In order to test whether there is any signal in sperm ultrastructure and to find out whether historical constraints that must underlie functional constrains still influence sperm ultrastructure, we analyzed sperm ultrastructure in 14 nemertean species and added these to our existing matrix. The matrix represents closely related groups and major nemertean lineages. Our study shows that sperm cells possess phylogenetic signal, but this erodes with increasing depth of branching. Although certain nemertean subtaxa can clearly be characterized by specifics in their sperm ultrastructure, this is impossible for the taxon Nemertea or for high ranking nemertean subgroups. Although this result might have been expected, we can show that functional constrains posed upon spermatozoa by sexual selection or the mode of reproduction do not outperform the influence of historical constraints on sperm ultrastructure – at least at lower systematic levels.

Find one, get one free! – The re-description of *Lineus acutifrons* Southern, 1913 results in two species, one of which is new to science

Poster Presentation

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From their beginnings in the 18th century descriptions of nemertean species grew ever more detailed including internal characters over the 19th, and genetic markers by the end of the 20th century. This was to account first, for the perceived structural diversity and later, for suspected cryptic speciation. As a consequence, many descriptions from the early times are nowadays regarded as insufficient rendering the taxonomic status of the respective species obsolete. To solve this taxonomic problem these ‘lost’ species, whenever found, were provisionally identified based on the information from their original description and re-described providing detailed accounts on internal anatomy and complementing genetic marker sequences. One example is the pilidiophoran nemertean *Lineus acutifrons* Southern, 1913 which has been described from the Western coast of Ireland. Having not been found for almost a century the first redescription was performed based on specimens found on the coast of Galicia (Spain). Externally similar specimens collected on the coast of Brittany (France) analyzed by us posses internal characters that differ from the Spanish specimens and advocate grouping the animals into the more recently established genus *Fragilonemertes* Riser, 1998 from the East coast of the USA. Analysis of the molecular markers from both sample sites with markers from *Fragilonemertes rosea* Riser, 1998 indicate that the three sampled populations are closely related but separate species. These results presently do not permit identifying the species corresponding to the original *L. acutifrons*. To solve this problem we consider it essential that specimens from the type locality are sampled.

Bayesian divergence dating with phylogenomic data suggests an ancient rapid radiation of animals prior to Snowball Earth

Oral Presentation

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Knowing the timeframe in which Metazoa and its major subclades originated is crucial to understanding early animal evolution. The fossil record before the ‚‘Cambrian explosion’ is sparse and controversial, but molecular clock methods provide an alternative means of dating the animal tree of life. So far, such studies focussing on Metazoa as a whole have been based on relatively small datasets, questionable phylogenies, and/or incomplete taxon sets. We use a phylogenomic dataset (30,257 aa) including all major groups (Philippe et al. 2009 Curr. Biol.) to date the deep metazoan phylogeny with Bayesian relaxed-clock methods. Our results suggest that crown-group Metazoa originated ~814 Ma, followed by origin of all non-bilaterian phyla and classes, as well as total-group Bilateria, within only ~50 Ma, before the onset of long-term global glaciations (‘Snowball Earth’). These results are robust to molecular clock model choice, root age assumptions, and different fossil calibration sets. Our estimates support some controversial findings interpreted as evidence for (pre-) Cryogenian animal life, and raise questions about the ecology of the earliest animals. Hypotheses about what triggered this ‘pre-Cryogenian explosion’ require a better understanding of palaeoenvironmental conditions during the late Neoproterozoic.

Exploring the paleobiology of Ediacara-type organisms in carbonate environments: The Shibantan Member (South China) and the Khatyspyt Formation (Arctic Siberia)

Oral Presentation

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The Ediacaran Period (ca. 635–541 Ma) is characterized by the first global occurrence of complex soft-bodied macroscopic life forms (Ediacara biota). The biological affinity of these organisms is still puzzling, but some forms might represent stem-group metazoans (e.g. *Kimberella*, *Dickinsonia*). A comprehensive appraisal of their diversity and ecology is commonly hampered as the fossils are usually preserved as imprints in siliciclastic or volcaniclastic facies, potentially causing taphonomic biases. Carbonate settings appear to provide a more complete picture of these communities, but there are only two known settings known so far: The Shibantan Member in South China and the Khatyspyt Formation in Arctic Siberia. In this talk we will provide an overview about the diversity of organisms in these two fossil lagerstätten and discuss their palaeoecology.

Diversification of big plant genera in space and time: insights from phylogeny, biogeography, morphology and karyotype evolution of the genus *Ranunculus*

Oral Presentation

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The genus *Ranunculus* comprises about 600 species and is distributed in all continents. The evolutionary success of the genus was so far enigmatic as the species show neither a pronounced differentiation of flowers, nor specialized fruits, nor growth forms. Phylogenetic analyses based on plastid and nuclear DNA sequences enabled us to reconstruct phylogeny, biogeographical history, morphological and chromosomal evolution within the genus and related genera. The genus originated in the early Miocene and started to diversify c. 18 Ma into nine well-supported big clades. Several events of transcontinental dispersal enhanced colonization of all continents and speciation via geographical isolation. Many clades diversified in mountain ranges via regional adaptive radiations during the Pliocene and Pleistocene. Rapid, mosaic-like evolution of successful character combinations rather than specific autapomorphies enabled buttercups to adapt to aquatic and terrestrial habitats in all altitudinal zones. Karyological analysis of 125 species revealed eight karyotypes within the genus that appeared congruent and ancestral to major clades. Chromosomal evolution showed increasing asymmetry within the phylogeny of the genus, and several incidences of polyploidy. Strikingly, species with different karyotypes from different clades appear to be reproductively isolated even in the same habitat and in crossing experiments. We conclude that karyotypes established efficient crossing barriers among members of early diverged major clades which enable extant species to coexist in the same habitat. The success of *Ranunculus* appears to be based on a flexible, highly adaptive generalist morphology, and on a pronounced diversification of chromosomal features.

Can the morphology of deep sea shark teeth reveal sex and species? (Chondrichthyes, Squaliformes)

Oral Presentation Student Prize

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Lantern sharks, or Etmopteridae, display a distinct dentition pattern with multi-cusped upper and overlapping, single-cusped lower teeth. Tooth morphology in Elasmobranchs is often used as taxonomic character for species identification. However, the upper tooth morphology of etmopterids may display sexual dimorphism as already confirmed for *Etmopterus granulosus*. We analysed the morphology of upper and lower teeth of three lantern shark species, *Etmopterus brachyurus*, *E. molleri* and *E. spinax,* regarding their intra- and interspecific variability and to test dental characters for taxonomic content. Additionally fossil etmopterid lower teeth were analysed to compare their morphology with analysed extant species and to gain information about the etmopterid phylogenetic background.

Teeth of extant specimens (n = 150) were extracted from preserved jaws. Fossil teeth have been collected from a clay pit in Mitterdorf (Bavaria). All teeth were digitally documented, measured and analysed with morphometrics. Results from statistic evaluation of data indicate that fossil teeth are distinct from the extant species analysed; based on the height to width ratio fossil teeth stem from several species or represent different ontogenetic stages. Furthermore, the results suggest that the upper teeth of *E. molleri* and *E. spinax* are sexually dimorphic and display high intraspecific variability. Tooth characters analysed herein did not reveal species specific characters and call species level information of etmopterid shark teeth into question.

Early developmental traits demonstrate deep homologies in two distinct galeomorph sharks

Poster Presentation Student Prize

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Chiloscyllium punctatum (Müller & Henle, 1838), the brown banded bamboo shark, belongs to the Orectolobiformes, which is a basal group of Galeomorphii. It is a small species of benthic, oviparous sharks, similar to *Scyliorhinus canicula* (Linnaeus, 1758), a well-studied carcharhiniform shark, which also is oviparous. Both species are bred in captivity all around the world and resemble each other in their life histories, habitat preferences and diet. This project compares the early development of the bamboo and lesser spotted dogfish sharks to identify similarities and differences in early ontogeny and when adult morphological traits are established.

It was shown that the developmental patterns of the lesser spotted dogfish and bamboo sharks are comparable. Hence staging of the embryonic development of *C. punctatum* was conducted starting with a late pharyngula stage following the protocol established for *S. canicula*. Through additional examination of the internal morphology of *C. punctatum*, the staging sequence was amplified by several traits.

Comparison of developmental sequences of both sharks demonstrate that most morphological changes occur until stage 30, when the overall adult shape is reached. Both species ingest their yolk sack in stage 34, characterizing the end of embryology, and still feed on it several days after hatching.

These results show, that *C. punctatum* and *S. canicula* share similar developmental patternings, which indicate homoplasy between these two species and are the results of similar life histories in phylogenetically distinct shark clades but, simultaneously, portend deep homologies probably representing the basic pattern in galeomorph sharks.

How do adult brachiopods sense light?

Oral Presentation

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Adult brachiopods have been observed to be light sensitive. Retraction into the sediment (linguliforms), fast closure of the valves, and jerking movements of the animal (rhynchonelliforms) are behavioral responses to changing light conditions. However, in contrast to lecithotrophic larvae of some rhynchonelliform taxa, adult animals throughout the phylum have never been reported to have visible light sensitive organs such as eyes, pigment spots or similar structures. Using tailor-made antibodies against ciliary opsin based on transcriptomic data from the laqueoid brachiopod *Terebratalia transversa*, we were able to detect a regular distribution of c-opsin expressing epidermal cells along the mantle margin in adult *T. transversa*. This is in line with the occurrence of ciliary photoreceptors in the apical lobe of the larvae of this species and enables the sessile adult to detect changes in light intensity over the whole length of its shell commissure. As adult rhynchonelliforms are firmly attached to the substrate with their pedicle and, therefore, are unable to move away from their attachment site, this marginal epidermal light sense may preferably be used to detect shadowing events caused by approaching predators and accordingly trigger protective behavior. The detection of light intensity change in adult brachiopods could even be possible when the valves are firmly closed, as hundreds of setae ('bristles') fringing the shell margin may serve as optical fibres guiding the light stimulus towards the photoreceptive epidermal cells protected inside the shell.

Flower-color evolution within the DYCs (damned yellow Composites)

Poster Presentation

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Cichorieae are also called DYCs, due to the predominant flower color of the ~1,400 species in 93 genera and their limited availability of morphologically diagnostic characters, which renders plant identification difficult. Easy to determine are the few bluish to pinkish Cichorieae in systematically quite unrelated subtribes – e.g. *Catananche* in the Scolyminae, *Cichorium* in the Cichorieae, *Lactuca seriola* in the Lactucinae, and *Prenanthes* in the Hypochaeridinae. The flower colors are due to anthocyanins in the petals and the anthocyanin biosynthetic pathway is well known. Two enzymes, flavonoid 3‘ hydroxylase and flavonoid 3‘, 5‘ hydroxylase, determine the hydroxylation pattern of the anthocyanins which exhibit three classes: cyanidins (redish/pink flowers), delphinidins (bluish flowers), and pelargonidins (one possibility to exhibit orange flower color). We sequenced the F3‘5‘H of *Catananche caerulea, Cichorium intybus* and *Lactuca seriola* and the phylogenetic analysis revealed high similarity of the bluish Cichorieae F3‘5‘H with other Asteraceae F3‘Hs and F3‘5‘H, however it is paraphyletic to the F3’5’H of other groups. This pinpoints to a neofunctionalization of the F3’5’H enzyme, to enable the Asteraceae to produce delphinidins again. The q-RT PCR expression pattern revealed *F3’5’H* to be expressed in different species at different times and developmental stages during flower development andthe flavonoid composition, analyzed via LC-MS and HPLC, was quite inconsistent. The initial enzymes (caffeic acid, p-coumaric acid and 3‘ hydroxylated flavonoids like quercetin derivatives) were found in all screened taxa, whereas delphinidin, pelargonidin and cyanidin was sometimes missing, which might be indicative for an inactivation of the DFR enzyme (dihydroflavonol 4-reductase).

Development of thermogenesis in pouch young of *Monodelphis domestica* (Didelphidae, Mammalia) and the evolution of endothermy in mammals

Oral Presentation

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Endothermy of mammals is regarded as a key innovation in the evolution of mammals allowing sustained body temperatures. Heat production in eutherian newborns and subsequent developmental stages depends on the progressive recruitment of non-shivering thermogenesis which is fueled by brown adipose tissue (BAT). BAT is rich in mitochondria and exclusively expresses the mitochondrial uncoupling protein 1 (UCP1). Through UCP1, chemical energy of nutrients bypasses ATP production and thereby is directly dissipated as heat. This mechanism is documented in many placental mammal taxa but unknown from marsupials. However, a UCP1 orthologue with uncharacterized function is present in marsupials. Since endogenous heat production is essential for the survival of hairless neonates, non-shivering thermogenesis is considered a potential mechanism of marsupial heat generation. Especially in pouchless marsupials such as the grey short-tailed opossum (*Monodelphis domestica,* Didelphidae), independent heat production that compensates for heat loss of the neonates and early 'pouch young', is considered as essential for survival. However, there is no convincing evidence for non-shivering thermogenesis in marsupials. This ongoing study examines different WAT depots in a series of developmental stages of *Monodelphis domestica*, searching for thermogenic BAT in marsupials using a range of molecular, biochemical and morphological techniques to examine indicators for non-shivering thermogenesis in this marsupial species.

Mouse-deer (Mammalia, Artiodactyla, Tragulidae) diversity disparity in the past and the present: lessons from fossils

Poster Presentation

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The Tragulidae is an ancient group of ruminant artiodactyls, which originated in the Eocene or Oligocene; long before other members of the crown ruminants came into existence. Their fossil remains are widely occurring in Eurasia and Africa with a total of more than 30 species described so far and document peak of species during the Middle Miocene. Today the extant members comprise the three genera (*Hyemoschus*, *Tragulus, Moschiola*) with ten species distributed over the tropical climate zone of Asia and Africa only, which are selective browser, i.e. exclusive intake of food items with a high content of protein that requires minimal fermentation. All of the latter range among small living ruminants with a body mass from 0.7 to 16 kg. Their small size and related biological variables were generally interpreted as ancestral ruminant traits, but recently authors provided data evident of a much wider adaptational spectrum in the past. Here we present the current knowledge on past tragulid diversity and demonstrate that comparison between phenotypes of living and fossils tragulids allows for inference of a much higher hidden taxonomic diversity in fossil tragulids when measured at scales of extant tragulid α-taxonomy. This supports the recently established hypothesis on a secondary ecological adaptation of living tragulids as an evolutionary response to a highly competitive situation among ruminants of the Neogene.

Xenacoelomorpha - from enigmatic turbellarians to kingpins of bilaterian origin

Oral Presentation

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Up to the 1990s Acoelomorpha (Nemertodermatida & Acoela) have been uniformly classified as archoophoran 'Turbellaria' or Plathelminthes respectively. In 1995 the first serious doubts on the turbellarian resp. plathelminth nature of Acoelomorpha have been published which became confirmed by molecular data in 1999. Nowadays phylogenomic studies on Xenacoelmorpha (*Xenoturbella* plus Acoelomorpha) are ambivalent and regard the phylum either as degenerated and progenetic Deuterostomia or as a quite plesiomorphic first extant offshoot of Bilateria. A recent thorough review of morphological data as well as principal considerations on assumptions of 'reduction' by the author suggest that several features of the free-living and mostly predatory Xenacoelomorpha are plesiomorphic rather than secondarily reduced: smallness, non-metameric and acoelomate condition; an intraepidermal nervous plexus being independently evolved several times towards subepidermal 'brains'; lack of a stomatogastric nervous system; lack of circulatory and excretory (ultrafiltration) system; lack of true gonads; few Hox-genes and micro-RNAs. The specific interconnected ciliary root system, the presence of free statocytes with intracellular statoliths within the statocyst vesicle, and the direct development are regarded as phenotypic synapomorphies of Xenacoelomorpha. In contrast, the acoel condition of the gut (a syncytial amoeba) is considered as a secondary condition within the subgroup Acoela.

Resolving a super-species complex in the past: 300 million years old 'sword tails' as an example

Oral Presentation

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Species delineation has become a major issue in modern extant taxonomy. Identifying cryptic species appears currently a hot topic. While this may be challenging in modern species, it is even more so in fossils ones. Fossils usually offer less characters than modern forms, molecular tools cannot be applied, and direct observations of behaviour are impossible.

I will present here an example in which ontogenetic data provide important characters for discriminating between different species of Carboniferous xiphosuran chelicerates (c. 300 Ma), generally known as horseshoe 'crabs', but the old-fashioned name 'sword tails' is more appropriate.

Two well established species are *Euproops danae* from North America and *Euproops rotundatus* from Great Britain. Numerous finds of *Euproops* sp. from North-Western Germany revealed first difficulties here. The German form is known from 10 instars of which the early stages resemble the American species (*E. danae*), while the later stages are virtually indistinguishable from the British species (*E. rotundatus*).

The case may be even more problematical involving also sword tails assigned to different genera. I present here reconstructions of ontogenetic sequences of American, British and German forms of fossil sword tails. I will demonstrate that 1) it is not possible to provide a reliable diagnostic differentiation based on adult characters alone, 2) also specific immature stages do not provide reliable characters for a diagnostic differentiation, 3) only a comparison of ontogenetic patterns can identify distinct species. This emphasises that a hapantho-type concept is urgently needed for arthropod systematics.

Character transformation in mantis shrimps: the rise of 'super-sized' raptorial larvae

Poster Presentation

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Mantis shrimps (Stomatopoda) are impressive raptorial crustaceans. While still comparably rare in the fossil record, parts of their evolutionary history leading to the highly specialised adult forms is quite well understood due to exceptionally preserved fossils especially from the Upper Carboniferous (c. 320–300 Ma), Upper Jurassic (c. 150 Ma) and Upper Cretaceous (c. 90 Ma).

Even more alien-like than the adult forms are the larval forms of modern mantis shrimps. These are impressively large for larvae, reaching sizes of several centimetres. Due to this impressive size such larvae have evolved numerous specialisations, facilitating these large forms to remain longer in the pelagic realm, more precisely as ‚super-sized‘ plankton. A reconstruction of the evolution of these highly specialised larvae is even more challenging than the reconstruction of the adult morphology as fossil mantis shrimp larvae are even rarer than well preserved adults; less than a dozen specimens are known so far.

We present a detailed reconstruction of the evolution of mantis shrimp larvae incorporating also fossil forms. The oldest stomatopod larvae are known from the Upper Jurassic Solnhofen limestones. In these deposits, different larval types coexist: Small larvae but with an already more adult-like morphology occur next to large larvae with a rather modern, derived morphology. Especially the larger extension of the head shield and the shield spines characterise the more modern-type larvae. These data contribute to our understanding of character transformation in the stomatopod lineage and how modern giant stomatopod larvae with their specialised morphology evolved.

The inclusion of ontogenetic data of fossil and extant species increases the explanatory power of phylogenetic reconstructions

Oral Presentation

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Phylogenetic systematics is in many aspects an adult-centered biological discipline. With this, the discipline is by no means an exception. Yet, it is important to point out that ontogenetic data, i.e. information also of the earlier life phases, may provide important additional aspects for different areas:

1) Species delineation:

a) Knowing the ontogeny of a species decreases the risk of mistaking a morphologically differing juvenile or larva as a separate species. While this has been an issue for extant species especially in the past, it is still a major issue in palaeontological studies.
b) Adults of different species may appear very similar or character-poor while immatures may be very distinct, providing a more reliable base for species delineation.
c) Besides simple characters of specific stages developmental trajectories may provide important clues for species delineation.

2). Reconstruction of relationship:

a) Data from immatures increase the number of available characters.
b) Some species, also in presumably important phylogenetic positions, are known exclusively by immatures. For including these into phylogenetic frameworks only the comparison to corresponding stages will allow a reliable reconstruction.
c) The same holds true for species or groups presumed to have evolved by heterochrony.

3). Character reconstruction:

a) Fossils may provide important additional 'steps-in-between'.
b) Ontogenetic data may decrease morphological gaps by identifying supposed 'novelties' as simple results of ontogenetic shifts.
c) Evolutionary key adaptations of a specific group may not be coupled to innovations of the adult morphology, but to larval novelties, remaining unidentified if excluded from the analysis.

Systematic approaches beyond phylogeny: sharpening our logical tools

Poster Presentation

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Phylogenetic systematics is in its core a historical science. Its goal is nothing less than reconstructing the history of an evolutionary lineage based on available observations. Yet, as this history is not directly observable, it needs to be somehow 'extracted'. For doing so, logical tools have been established (e.g., character-based approaches, matrices, coherence, predictability). With these tools a first step in the process of reconstructing history is usually a process of sorting, more precisely of systematic sorting. This last aspect, 'systematic', needs to be emphasised as opposed to a mere 'classification'.

Aspects of sorting or classifying are also important in scientific disciplines outside phylogeny. Hence we can ask: is it possible to substitute classificatory approaches by systematic ones also in other fields? Phylogenetic systematics may be seen as a pioneer here that could act as an example for other fields as well.

Yet, not all fields that make use of classificatory approaches have a historical component as does phylogenetic systematics. Hence, transferring logical tools from phylogenetic systematics into other fields demands for a detailed analysis. In principle, the challenge can be broken down to the question: how can we distinguish between mere classifications and true systematic approaches?

We present examples of different fields for which such an approach has been or is about to be explored, among them ecology, classical geometry and historical martial arts. Based on these different examples we give a first evaluation of the applicability of certain logical tools used in phylogenetic systematics for other scientific disciplines.

Population genomics of the Pyrenean desman (*Galemys pyrenaicus*) in the Western Pyrenees

Poster Presentation

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We are studying the population genomics of the Pyrenean desman (Lipotyphla: Talpidae: *Galemys pyrenaicus*), a small semi-aquatic mammal endemic to the Iberian Peninsula and the Pyrenees. This species is listed as Vulnerable on the IUCN Red List and as Critically Endangered in parts of its range and is therefore of high conservational importance. Previous studies based on analyses of mtDNA have shown that the overall genetic diversity of the Pyrenean desman is low, and only large-scale populations could be delimited. Our goal was to study the connectivity of populations and the influence of landscape on gene flow in a delimited study area in the Western Pyrenees. We used ddRAD sequencing to generate several thousand SNPs (single-nucleotide polymorphisms) per individual. This dataset provided sufficient resolution to delimit sub-populations, roughly corresponding to specific river systems. We will next use landscape data to study the impact of landscape and riverscape features on the gene flow and therefore also the dispersal of the Pyrenean desman in the study area.

DNA barcoding of orthopterans from Germany, Austria, and Switzerland

Oral Presentation

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The DNA barcoding approach uses a short fragment of the mitochondrial COI gene as a standard for reliable species identification of metazoans. A comprehensive DNA sequence database based on reliably identified voucher specimens is a prerequisite for the successful application of the DNA barcoding method for species identification. Most barcoding projects worldwide are coordinated within the framework of the International Barcode of Life Project (iBOL) and the Consortium for the Barcode of Life (CBOL). We present the results of the collaboration of four major European barcoding projects, i.e., the Barcoding Fauna Bavarica (BFB), German Barcode of Life (GBOL), Austrian Barcode of Life (ABOL), and Swiss Barcode of Life (SwissBOL). Concerning orthopterans, barcodes have been made available for 117 of the 145 species (81 %) recorded in Germany, Austria, and Switzerland, representing 97 % of German, 79 % of Austrian, and 88 % of Swiss species. Our study highlights some pitfalls of the barcoding of orthopterans. Nuclear mitochondrial pseudogenes (numts), a common source of misidentification, were detected in at least four species. This number is very low compared to some previous studies on orthopterans. Some species in the genera *Chorthippus*, *Gomphocerippus*, *Omocestus*, and *Stenobothrus* cannot be distinguished using DNA barcodes because their barcodes form clusters, possibly due to incomplete lineage sorting and / or hybridization. We conclude that DNA barcoding is a reliable tool, with some caveats, for species identification in orthopterans. We also point out directions of future research and set a starting point for the collaboration of European barcoding projects.

New cervid cytochrome b sequences, new conundrums in cervid systematics

Oral Presentation Student Prize

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Cervid systematics has been puzzling researchers for over 150 years. For many parts of the phylogeny results from comparative anatomy and molecular data are in consensus; however, systematic relationships of some taxa, particularly within Odocoileini (American clade of New World deer), remain difficult to solve. This is likely partly due to the incomplete taxon sampling in current cervid phylogenetic data sets. Although molecular approaches contributed largely to increase the data available for phylogenetic analyses, a comprehensive species sampling could not yet be achieved. For almost 20 % of cervid species we still lack molecular data, because they are difficult to access in the wild. In this study, we obtained partial mitochondrial cytochrome b sequences for *Mazama bricenii*, *Mazama chunyi*, *Muntiacus atherodes*, *Pudu mephistophiles*, and *Rusa marianna* from 13 museum specimens, including three holotypes. These new sequences were combined with available cytochrome b sequences to the most taxonomically complete data set yet known for cervids. The newly sequenced species were placed within the topology and provide new insights into the evolutionary history of these five species.

Re-analyses of the previously available sequences in combination with the new sequences confirmed monophyly of Odocoileini, Capreolini (*Capreolus* and *Hydropotes*), and Cervinae (Old World deer) including Muntiacini (*Muntiacus* and *Elaphodus*) and Cervini. However, systematic uncertainties within *Cervus* and *Muntiacus* remain, new systematic issues were discovered, and solving the phylogenetic relationships within *Pudu*, *Hippocamelus*, *Mazama*, and *Odocoileus* remain challenging.

Endocranial anatomy of a marine crocodylomorpha (Thalattosuchia): a preliminary study

Poster Presentation

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Thalattosuchians were Mesozoic marine crocodylomorphs known from deposits of the Lower Jurassic through the Lower Cretaceous, and without close extant relatives. Thalattosuchia comprises an assemblage of basal forms, the teleosaurids (shallow coastal forms), and the fully pelagic forms known as the Metriorhynchidae. Their fossil record is abundant, and most of them have been recovered from marine deposits in Europe and South America. Despite their abundant fossil record, the phylogenetic placement of Thalattosuchia in crocodyliform systematics is still debated. During the last few decades digital techniques to study fossils have been used to visualize the internal morphology of the skull, and to generate virtual cast of the internal cavities and/or bones. Neuroanatomical studies in Thalattosuchia are scarce, even though they are important for two main reasons: they provide further insights into the palaeobiology of these animals and therefore contribute to understand secondary marine adaptations; and, second, internal anatomical exploration provides features of potential phylogenetic value. As part of a project that includes the internal anatomical exploration of several specimens or Thalattosuchia and other crocodyliforms, I studied the teleosaurid *Steneosaurus bollensis* (SNSB-BSPG 1984 I 258) based on micro-CT scanning. Results show that some endocraneal features that were believed to be exclusive to Metriorhynchidae are present in *Steneosaurus bollensis*. Their presence in this taxon suggests that certain endocraneal features were more widely distributed within Thalattosuchia and not restricted to Metriorhynchidae. The preliminary information obtained here will be useful to expand character information/sampling related to the braincase anatomy of marine crocodylomorphs.

Navelseeds in the New World

Oral Presentation

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Fruit is widely used as an important character in Boraginaceae systematics. Recently, however, many taxa, such as the navelseeds (*Omphalodes*) have been shown to be polyphyletic. The Japanese species have been placed into a new genus, *Nihon* Otero et al., and also for our native *O. scorpioides*, an own genus, *Memoremea* Otero et al., was created. By expanding the taxon sampling, we can show that the remaining *Omphalodes* are still paraphyletic and split into four clades: two in the Old World, and two in the New World. One of the latter consists of mainly high mountain annuals in Mexico while the fourth clade contains the two monotypic island genera *Selkirkia* (Juan Fernandez) and *Myosotidium* (Chatham Island) plus three continental South American species currently assigned to *Cynoglossum*. The three South American species of '*Cynoglossum*', together with the island shrub *Selkirkia berteroi* (Colla) Hemsl. and the subantarctic 'megaherb' *Myosotidium hortensia* (Dcne.) Baill. are distinct from the remaining *Omphalodes* s.l. in fruit morphology, thus we argue that the taxa of this latter clade are best combined into an expanded genus *Myosotidium*. The considerable differences in vegetative morphology are easily explained by the highly divergent habitats the respective taxa occupy.

The evolution and diversity of sauropods from the early Middle Jurassic Cañadón Asfálto Formation, Patagonia, Argentina

Oral Presentation Student Prize

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Sauropod dinosaurs represent important components of Jurassic and Cretaceous terrestrial ecosystems. However, the origin and early radiation of sauropods, thought to have occurred during the Early Jurassic, remains poorly understood. The latest Early to early Middle Jurassic Cañadón Asfálto Formation, Chubut, Patagonia, Argentina, is one of the few units globally that yields sauropod remains from the time of early sauropod diversification. The most common taxon is *Patagosaurus fariasi*, known from more than eight individuals, preserving axial and appendicular skeletal elements. *Patagosaurus* is a derived, non-neosauropodan eusauropod, on the basis of having complex vertebral lamination, high neural arches and non-camerate pneumatic fossae in dorsal vertebrae, among others. It is recovered as more basal than *Mamenchisaurus* and *Omeisaurus*, but more derived than *Shunosaurus*. It often is recovered as sister-taxon to *Cetiosaurus*. Some material originally referred to *Patagosaurus* represents a different, undescribed taxon, which is also recovered as a non-neosauropodan eusauropod, but possibly more derived than *Patagosaurus*. *Volkheimeria* is only known from fragmentary remains (dorsal and caudal vertebrae, pelvic girdle, femur, tibia), discovered together with remains of *Patagosaurus*. Preliminary phylogenetic studies indicate that *Volkheimeria* is a more basal sauropod than *Patagosaurus* and might not even be a eusauropod. Another sauropod has more recently been uncovered from the locality El Bagual. Several autapomorphies confirm these remains to represent a new taxon. Preliminary phylogenetic analysis recovers it as sister taxon to *Patagosaurus*. These finds show that early sauropod faunas were already surprisingly diverse and included a mixture of basal and derived forms.

New insight into the ontogeny of mesothelan spiders and its impact on character evolution in early araneaens

Poster Presentation Student Prize

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Mesothelae is an ingroup of true spiders, Araneae. More exactly, Mesothelae is the sister group of all remaining spiders, and its representatives have retained numerous plesiomorphic features, even more so than mygalomorph spiders, or bird spiders, which they largely resemble. Due to this position, mesothelans are important for reconstructing ingroup systematics of Araneae, as well as for the systematic position of Araneae within Arachnida. Yet, it needs to be carefully evaluated which characters of Mesothelae indeed represent plesiomorphic traits retained from the ground of Araneae and which ones represent autapomorphic traits of Mesothelae.

We present here new aspects of the post-embryonic ontogeny of mesothelan spiders. The sternum of adult mesothelan spiders is characterised by a very narrow shape. Sternal plates of other spiders and whip spiders (supposed sister group of Araneae) are rather wide. Interestingly, hatchlings of mesothelans do not have a narrow sternum, but a rather broad rounded one. The characteristic narrow shape develops during ontogeny. The narrow adult sternum is therefore most likely an autapomorphy of Mesothelae, having evolved by heterochrony.

Other newly observed features include an ontogenetic differentiation of male chelicerae, which become significantly smaller with their last moult, and morphological details of the spinnerets. The latter appear overall rather leg-like and long and consist of numerous articles; yet, they lack true pivot joints between the articles. This makes the spinnerets more flexible and possibly facilitates the spinning of complex structures. With these new findings we can partly resolve the character evolution of early araneaen spiders.

Testing species delimitation with larval morphology: SEM analysis of protonymphon larvae of two closely related pantopods, *Pallenopsis patagonica* (Hoek, 1881) and *Pallenopsis yepayekae* Weis, 2014

Poster Presentation

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In Pantopoda, different types of protonymphon larvae, and also cases of direct development have been described. Detailed analyses of protonymphons that provide diagnostic features for distinction between species are however rare. We have used the scanning EM to establish species-specific sets of characters for protonymphons of two species of the ‘patagonica’ species group of *Pallenopsis*, *P. patagonica* and *P. yepayekae*. Despite the close relationship of the two species, we observed numerous features that allow very well to differ between them, e.g. the number, arrangement and branching type of Gabelborsten, their associated slit glands, armature of the movable and immovable cheliphore fingers, shape of dactylus and setae, and the general habitus. These features can be visualized with the high resolution power of the scanning EM. Our results suggest that protonymphons can be identified to species level when adequate imaging techniques are used, as is also the case for larvae of other arthropods, e.g. decapod zoeas. Moreover, the status of the two studied species of *Pallenopsis* is fully supported by protonymphon morphology.

[Supported by grant of Sea Life Center Munich given to R. Melzer]

Unexpected lack of genetic and morphological divergence in the widespread tortoise *Indotestudo elongata* (Blyth, 1854).

Poster Presentation Student Prize

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The Elongated Tortoise *Indotestudo elongata* occupies a wide distributional range in Southeast Asia covering several well-known zoogeographic barriers. Across its range, the species shows a high variability in size, shape, and coloration.

We examined 163 adult tortoises (76 males and 87 females) from Vietnam, Cambodia, Myanmar, and Thailand for morphometric and coloration-related characters. Multivariate statistical analyses were performed to quantify morphological variation and to identify potential underlying geographic patterns. Intraspecific genetic differentiation of 17 specimens of *I. elongata* was assessed by analyzing mitochondrial DNA (COI, ND4, and cyt *b*) obtained from fresh samples as well as from historic collection material from throughout the species' range. For historic samples PCR primers for the amplification of variable regions of the respective genes were developed using sequences from fresh samples and Genbank. Samples were subsequently amplified in series of short fragments of 160–270 bp and all precautions for aDNA work were taken (DNA extraction in a clean room, etc.).

Morphological analyses revealed no differences between geographic groups. Concordantly, there was only minor genetic variation within the examined samples of *I. elongata*, lacking a clear geographic pattern.

Although we found high morphological and moderate genetic variability, the Elongated Tortoise exhibits no variation that is correlated with the geographic origin of the samples. Considering its wide distributional range, it is surprising that none of the current zoogeographic barriers in Southeast Asia (e.g. the Isthmus of Kra or the Annamite Mountains) seems to have had a major influence on intraspecific variability.

Integrative taxonomy of Southeast Asian Snail-eating Turtles (Geoemydidae: *Malayemys*) reveals a new species and mitochondrial introgression

Oral Presentation Student Prize

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Based on an integrative taxonomic approach, we examine the differentiation of Southeast Asian Snail-eating Turtles using information from 1863 bp of mitochondrial DNA, 12 microsatellite loci, morphology and a correlative species distribution model. Our analyses reveal three genetically distinct groups with limited mitochondrial introgression in one group. All three groups exhibit distinct nuclear gene pools and distinct morphology. Two of these groups correspond to the previously recognized species *Malayemys macrocephala* (Chao Phraya Basin) and *M. subtrijuga* (Lower Mekong Basin). The third and genetically most divergent group from the Khorat Basin represents a previously unrecognized species. Historic fluctuations in potential distributions were assessed using species distribution models (SDMs). The Last Glacial Maximum (LGM) projection of the predictive SDMs suggests two distinct glacial distribution ranges, implying that the divergence of *M. macrocephala* and *M. subtrijuga* occurred in allopatry and was triggered by Pleistocene climate fluctuations. Only the projection derived from the global circulation model MIROC reveals a distinct third glacial distribution range for the newly discovered *Malayemys* species.

Lettuce (*Lactuca*) diversity; Eurasia to north America independent lineage migration and allopolyploidization

Poster Presentation

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Flowering plant intercontinental disjunctions have long been believed to result from land connections between Eurasia and North America across Beringia and the North Atlantic. The lettuce alliance (Lactucinae, Cichoreae, Asteraceae) is distributed in Europe, Africa, Asia and North America with two centres of diversity; one in the E Mediterranean-SW Asian region, the other in the Sino-Himalayan region. Our phylogenetic studies are the first to sample the entire alliance and disentangle generic diversity. Using this background we aim to decipher the origins of the North American lettuce (*Lactuca*) taxa. Chloroplast, ITS and low copy nuclear sequence analyses, combined with biogeographic studies have revealed novel insights into the origin of these taxa. Presenting the results of molecular phylogenetic, biogeographic and molecular dating analyses, we show that the North American taxa are members of two distinct monophyletic *Lactuca* lineages, representing two independent migration episodes from Eurasia to North America. One of these North American lineages is unique in *Lactuca* for its chromosome number of n=17, likely being of allopolyploidization origin; all other taxa are diploids with n=8 and n=9. We hypothesise two contrasting geographic routes to explain the origin of the two North American *Lactuca* lineages.

The worms among the gastropods: phylogeny and evolution of Rhodopemorpha (Heterobranchia, Gastropoda)

Oral Presentation

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Turbellarian-like Rhodopemorpha have puzzled taxonomists for over 150 years. Ontogenetic studies finally settled them within molluscs, as one of the most aberrant free-living gastropod clades lacking otherwise typical morphological characters (such as foot, shell, head tentacles and radula) while presenting uniquely modified excretory and digestive systems. However, the sister group relationships of this small clade of microslugs have remained largely unstudied, owing to their comparable rarity and a general undersampling of meiofaunal forms. The present study includes material from a decade of dedicated sampling efforts in tropical and temperate zones demonstrating that current rhodopemorph diversity with only seven valid species in the two established genera *Rhodope* and *Helminthope* considerably underscores the still hidden diversity of this enigmatic clade. We present morphological and computer-based 3D-microanatomical data on some of the most divergent new lineages, including new color morphs of *Rhodope* and a characteristic novel clade with conspicuous cruciform spicules. Multi-marker molecular data reveals additional, morphologically cryptic but genetically distinct, lineages within *Helminthope*. Our molecular phylogenies, in which we analyzed all these lineages in a broad gastropod framework, contradict earlier hypotheses of pulmonate or opisthobranch relationships and supports our previous, initial data, in revealing affinities of Rhodopemorpha with shelled, basally branching Heterobranchia. Potential morphological characters supporting this intuitively surprising placement are reviewed providing further insights to the evolutionary history of the clade as well as indications of a progenetic origin.

Senecio L. (Asteraceae-Senecioneae) and the colonization of the Palaearctic from southern Africa

Oral Presentation

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Several studies have postulated that the colonization of the Palaearctic by plants from southern Africa has taken place either by long-distance dispersal or by stepping-stone dispersal via two different migration pathways, the arid and high-altitude corridors.

We present a biogeographical analysis of *Senecio*, one of the largest genera of angiosperms with about 1000 species and a nearly cosmopolitan distribution, which is well represented in the two potential migration corridors. It had been shown before that the genus is of sub-Saharan origin and has colonized the Palaearctic twice. We expanded previous sampling of the genus in the two focal regions and reconstructed molecular phylogenies based on two nuclear ribosomal (ITS and ETS) and three chloroplast markers (*trn*L, *trn*LF and *trn*C-*ycf*6). Due to phylogenetic conflict between the two genomes, historical biogeographic reconstruction is based on nuclear markers only.

We can show that *Senecio* originated in western southern Africa (WSA) in the mid to late Miocene. *Senecio* differs from most other species-rich lineages in WSA which are not well represented in the Palaearctic. The two independent colonizations of the Palaearctic started from different source areas in southern Africa. An annual lineage most likely originated in lowland areas of WSA and is found mainly in lowland areas of the Palaearctic, and a perennial lineage most likely originated in mountainous regions of sub-Saharan Africa and grows mostly in mountainous regions in the Palaearctic. While the first lineage very likely colonized the Palaearctic via long-distance dispersal, the latter most likely migrated via the high-altitude corridor.

The neural tube of chordates and the tubular collar cord of enteropneusts: homology or homoplasy?

Oral Presentation

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Gene expression analyses within the last years have revealed that the neural tube of chordate deuterostomes and the ventral nerve cord of polychaete protostomes exhibit a highly similar mediolateral architecture. On that basis, a likewise complex CNS has been proposed in the urbilaterian. Hemichordate enteropneusts, a group of non-chordate deuterostomes, possess a much less complex nervous system, yet a part of the dorsal nerve cord forms a hollow tube resembling the neural tube of chordates. Putative homology of this collar cord and the chordate neural tube is supported by ultrastructural resemblances. However, recent gene expression analyses are less conclusive and revealed contradicting results. The majority of data has been collected from *Saccoglossus kowalevskii*, a species showing a derived mode of development. In order to clarify this issue, we investigated the expression of neuronal regionalization genes in the indirect developing enteropneust *Balanoglossus misakiensis*. We focused on the development of the collar cord and studied anteroposterior (*six3/6, otx, engrailed*) and mediolateral (*pax6, dlx, nk2.1/2.2*) patterning genes. Expression analysis shows that the tubular collar cord of *B. misakiensis* is positioned anteroposteriorly in a region corresponding to the vertebrate midbrain. However, mediolateral patterning of *pax6, dlx,* and *nk2.1/2.2* is completely aberrant in comparison and has no corresponding domain in the chordate neural tube, neither in the midbrain region nor in the trunk. Under consideration of all available data (morphology, gene expression, and phylogenomic analyses), putative homology of the collar cord and chordate neural tube are discussed.

A new phylogeny of copepod (Crustacean) orders based on 18S rDNA

Oral Presentation

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For the first time phylogenetic relationships between representatives of all 10 copepod orders (Platycopioida, Calanoida, Misophrioida, Harpacticoida, Gelyelloida, Monstrilloida, Cyclopoida, Poecilostomatoida, Siphonostomatoida and Mormonilloida) were investigated using nucleotide sequences of the nuclear small subunit ribosomal DNA. Phylogenetic trees generated by bayesian and maximum likelihood analysis supported the three main monophyletic subgroups of Copepoda, the Progymnoplea, Gymnoplea and Podoplea. The Progymnoplea (Platycopioida) are basal to the two others and the results of both phylogenetic methods supported the monophyly of seven copepod orders: Platycopioida, Calanoida, Misophrioida, Monstrilloida, Siphonostomatoida, Gelyelloida and Mormonilloida. In contrast to previous phylogenetic hypotheses based on morphology, the order Cyclopoida shown to be paraphyletic enclosing Poecilostomatoida as a derived inner clade. Within harpacticoids, the Polyarthra (families Canuellidae and Longipediidae) clustered basal to Oligoarthra, suggesting its removal from the Harpacticoida as a separate order, whereas Oligoarthra placed as sister group of Gelyelloida. Misophrioida concurred basal within Podoplea. This molecular phylogeny is based on a single gene fragment and therefore needs to be considered as preliminary.

Integrative re-description of *Turbanella hyalina* (Gastrotricha: Macrodasyida) as baseline for future phylogeographic studies

Poster Presentation

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Recently, it could be proven that genetic cryptic species do exist among morphologically defined species of the phylum Gastrotricha. An early study of the genetic distances between three geographically separated Atlantic populations of the species *Xenotrichula intermedia* shed some initial light on the reported cosmopolitan distribution of many meiofaunal species. Later, distinct differences in the muscle arrangement were detected in two other populations of *X. intermedia* as an indication for the presence of further 'cryptic species'. A molecular taxonomic survey of some species of the genus *Turbanella* unravelled two independent mitochondrial lineages within *Turbanella hyalina*, the first described marine gastrotrich species of the taxon Macrodasyida. This result has been confirmed by further analysis of a slowly evolving nuclear marker. Hence, there are at least two cryptic genetic species within the nominal species *T. hyalina*. Since the original description by Schultze (1853) is incomplete and does not contain, for instance, data of variability of important taxonomic characters, a re-description was overdue. We conducted an integrative description of *T. hyalina* covering light microscopic, SEM (internal and external morphology), and CLSM investigations (muscular system). Furthermore, an analysis of COI gene sequences obtained from specimens of the original type locality was used to identify the corresponding genetic lineage. The results will serve as baseline for all upcoming phylogeographic and integrative taxonomic studies including this species.

Integrative taxonomy provides evidence for the species status of the Ibero-Maghrebian grass snake *Natrix astreptophora*

Oral Presentation Student Prize

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The grass snake (*Natrix natrix*) is Europe's most widely distributed and, in many regions, most common snake species, with many morphologically defined subspecies. Yet, the taxonomy of grass snakes is relatively little studied and recent investigations have shown major conflicts between morphologically defined subspecies and phylogeographic differentiation. Using external morphology, osteological characters, information from 13 microsatellite loci and two mitochondrial markers, we examine differentiation of the subspecies, *N. n. astreptophora* from the North African Maghreb region, the Iberian Peninsula and neighbouring France. Our analyses show that *N. n. astreptophora* hybridizes with the neighbouring taxon *N. n. helvetica* only exceptionally. Even though many morphological characters are highly variable and homoplastic in grass snakes, *N. n. astreptophora* differs consistently from all other grass snakes. Based on these results we conclude that *Natrix astreptophora* (Seoane, 1884) should be recognized as a distinct species.

Incipient hybrid speciation of door snails in previously glaciated areas in the Caucasus

Oral Presentation

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Homoploid hybrid speciation, speciation by hybridization without a change in chromosome number, may be the result of an encounter of closely related species in a habitat that is different from that usually occupied by these species. In the northwestern Caucasus the land snail species *Micropontica caucasica* and *M. circassica* form two distinct entities with little admixture at low and intermediate altitudes. However, at higher altitudes in the Lagonaki plateau, which were repeatedly glaciated, *Micropontica* populations with intermediate characters occur. Admixture analyses based on AFLP data demonstrated that the populations from the Lagonaki plateau are homoploid hybrids that now form a cluster separate from the parental species. The Lagonaki populations are characterized by a mtDNA haplotype clade that has been found in the parental species only once. The fixation of this haplotype clade in most hybrid populations suggests that these haplotypes are better adapted to the cooler conditions in high altitude habitats and have replaced the haplotypes of the parental species in a selective sweep. The fixation of a presumably adaptive mitochondrial haplotype clade in the Lagonaki populations is an important step towards speciation under the differential fitness species concept.

Current views on the early evolution of the insect head revisited

Oral Presentation

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Reconsideration of insect morphology by microtomography in the past decade has contributed tremendously to an improved understanding of the skeleto-muscular system and its evolution in Ectognatha (Hexapoda). The Basal-Hexapods-Team of the 1Kite- project now focused on entognathan hexapods (Collembola, Protura, Diplura) to infer homologies and ancestral states of the insect head. Insights of their studies by µCT remarkably contrast against previous interpretations, especially with regard to the early evolution of entognathy and of the head endoskeleton in hexapods. In order to reveal whether previous descriptions really failed to provide proper interpretations, the respective data inferred from classic invasive studies are presented, including dissection, histology, transmission electron microscopy, and confocal laser scanning microscopy. These data demonstrate that several aspects of the contemporary interpretations based on µCT are unsupported by either topography or parsimony. Misinterpretations particularly consider skeletal elements of the mouthparts and preoral chamber that are partly confused or entirely dismissed; incomplete reconstructions based on improper claims of absence of components that can unambiguously be visualized with histological stains; misrepresentation of unpaired formations as paired structures; and a redundant misinterpretation of excretory organs as salivary glands under disregard of their actual homologues. Main reasons for such flaws are highlighted, including missing taxonomic profoundness and artifacts apparently caused by automated 3-D segmentation algorithms. Current insights do not question the high value of microtomography in evolutionary morphology but corroborate the view that this technique still requires complementary invasive studies to achieve a maximum of accuracy in morphological descriptions.

A comparative anatomical study of *Dermechinus horridus* (Echinoidea: Echinidae) and its echinid relatives

Poster Presentation Student Prize

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Morphological and molecular studies suggest that the Echinidae Gray, 1825 are composed of one fossil (*Stirechinus*) and five Recent (*Dermechinus*, *Echinus*, *Gracilechinus*, *Polyechinus*, *Sterechinus*) genera. From a morphological point of view, echinids can be considered 'typical' sea urchins, i.e. they are composed of a globular endoskeleton and their internal anatomy follows the basic echinoid pattern. However, a single species stands out from this group: *Dermechinus horridus* (A. Agassiz, 1879), also known as the cactus urchin. So far, only little information has been obtained regarding the anatomy and evolutionary history of this charismatic deep sea species. Using a set of invasive and non-invasive imaging techniques, we gathered novel morphological data on numerous specimens. Our ontogenetic series show that the conical shape of the corona is attained relatively late in development. Furthermore, the feeding apparatus displays allometric growth on an unprecedented scale, while spination differs significantly in size from other echinid taxa. Finally, the internal anatomy of *Dermechinus* shows particular adaptations to the vertical elongation of the corona. The data obtained during this study are compared with results based on invasive and non-invasive imagery from all other Recent echinid taxa. Using these novel as well as previous findings, a tentative evolutionary history of the Echinidae is presented.

The *Limacina helicina* (Phipps, 1774) complex: splitting one model organism into three

Oral Presentation Student Prize

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Shelled pteropods (Thecosomata) form a monophyletic clade of holopelagic euopisthobranch gastropods. The aragonite shell of euthecosomes has been demonstrated to be vulnerable to lowered sea water pH, rendering them a suitable bioindicator for ocean acidification research. In particular the 'species' *Limacina helicina* with its extraordinary delicate shell bears a high indicative potential and is thus frequently used to monitor rising acidification in polar and subpolar regions. It is also one of the most abundant pelagic organism, of major ecological importance, and threatened by ocean chemistry change.

The actual taxonomic status of *Limacina helicina* is confusing. There is a conglomeration of subspecies and 'formae' characterized by hardly perceptible differences restricted to shell morphology. Most of these descriptions left the soft body unrewarded. Still there is little information on internal morphology and organ functions. Initial single gene approaches indicated high genetic divergence between Arctic and Antarctic clades, which is suggesting the presence of a species complex. Different species may have different ecological preferences and tolerances to changing environments.

This integrative taxonomical study combines modern microanatomical investigation techniques with a multilocus molecular analysis of an extended set of newly generated sequences from specimens representing both hemispheres. 3D-reconstructions based on semithin histological sections revealed an astonishing anatomical resemblance of northern and southern clade. Molecular analyses support the presence of a species complex with at least three species. To provide a reliable taxonomic foundation for any ecological work, it is eminent to explore the actual species diversity of *Limacina helicina* covering its entire geographic range.

Evaluating the origin of xerophytic leaf characters in SW Asian wild pears (*Pyrus*, Rosaceae)

Oral Presentation

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Pyrus is a Eurasian genus of trees that inhabits two different types of habitat: mesophilic and xerophytic forests. The genus is especially diverse in SW Asia and the Caucasus ecoregion, where 25 endemic species are recorded. In the Caucasus, wild pears are found predominantly in the xerophytic open forests, which represent a unique vegetation type for the region. Our general goals are to better understand the evolution and biogeography of *Pyrus*, and especially species limits and species distribution in the Caucasus.

This study addresses the evolution of xerophytic adaptations in *Pyrus*. We reconstructed the phylogenetic relationships in *Pyrus* using a dense taxon sampling of the Caucasian species. Our dataset comprised ten plastid regions, totalling c. 9000 nt sequenced per sample. Moreover, we estimated the divergence times of the major *Pyrus* clades and reconstructed the ancestral states of mesophilic and xeromorphic leaf shapes using a novel set of software scripts. Our results indicate a highly supported monophyletic *Pyrus* with two major clades: one East Asian and one Western-Eurasian. The latter includes species from Europe, Southwest Asia, and the Caucasus. Both clades were estimated to have originated in the Miocene. Character reconstructions revealed that the transition of leaf shape in *Pyrus* likely occurred from broad to narrow-shaped leaves via the mediation of intermediate-shaped leaves. We conclude that the evolutionary history of *Pyrus* in SW Asia and the Caucasus is more complex that previously assumed and may be best explained by multiple arrivals of ancestors and subsequent speciation with adaptations to dry habitats.

LARGE (taxonomic) confusion in MICROscopic organisms – Examples for the need of reliable species determination for a robust taxonomy in dinophytes

Oral Presentation Student Prize

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For unicellular organisms such as dinophytes, the biodiversity assessment started in the late 18th century using light microscopy, and also *Peridinium* (≡ *Goniodoma*) *acuminatum* Ehrenberg was described 180 years ago. However, no original specimen could be relocated, and the identity of the species was doubtful. It was also involved in several historical pitfalls when used as type of *Heteraulacus* Diesing and *Goniodoma* F. Stein. Previous authors emphasised that the organisms investigated by Ehrenberg and von Stein were not conspecific, but never performed the necessary taxonomic conclusions. In order to clarify the identity of *P. acuminatum*, we investigated the species from the type locality. To avoid further confusion, we designated an epitype, which is not in conflict with the protologue. The species is, moreover, morphologically indistinguishable from epitype material of *Glenodinium* (≡ *Scrippsiella*) *trochoideum* F. Stein and exhibits the identical sequence of the Internal Transcribed Spacer. Thus, we consider both names referring to the same species, namely *Scrippsiella acuminata* (Ehrenb.) Kretschmann, Elbr., Zinssmeister, S. Soehner, Kirsch, Kusber & Gottschling as member of the Peridiniales. However, *P. acuminatum* is correctly assigned, nomenclaturally, to *Heteraulacus* at present, resulting in *Scrippsiella* Balech becoming a later heterotypic synonym of *Heteraulacus*. In consequence, all species names accepted under the well-established name *Scrippsiella* would have to be transferred to *Heteraulacus*, explicitly assigned to the Gonyaulacales. Given the ecological importance and wide distribution of *Scrippsiella*, we consider a conservation of *Scrippsiella* against *Heteraulacus* and *Goniodoma* to preserve its current usage as further step towards a robust nomenclature of dinophytes.

Evolutionary organ pipes in full blast: Do snails dance to the Hutchinson tune?

Oral Presentation Student Prize

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One of the most compelling topics in biology is the origin of biodiversity and species diversification. In this context George Evelyn Hutchinson (1959) proposed that species sharing the same habitat and niche differ in body size averaging at a ratio of 1.3, suggesting that competition is minimized by differences in body size, as it has been approved for many different taxa. Unfortunately, the Hutchinson rule has never been tested extensively and has been treated as evolutionary biology's orphan, though it might hold crucial information about speciation. Especially closely related taxa in adaptive radiations are most suitable models that promise deeper insight into evolutionary processes. Prominently known, is for example African's Lake Tanganyika, mostly for its cichlid radiation. In addition, it also harbors an even larger species flock of paludomid gastropods. These lacustrine and 'thalassoid' (i.e. marine-like) paludomids exhibit, next to most distinct radula morphologies potentially indicating trophic specialization, a striking array of shell sizes. Based on the biometry of 50 named species of these thalassoid paludomids we tested the Hutchinson 1.3 rule for size-related parameters and discuss here our findings in context of species diversification and the question of a truly 'adaptive' radiation.

Chloroplast activity and degradation in solar-powered sea slugs

Oral Presentation Student Prize

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Solar-powered sea slugs (Sacoglossa: Gastropoda) represent the only known animals capable of stealing chloroplasts from their algal food, retaining them for months while undergoing extended starvation periods. These stolen chloroplasts, termed kleptoplasts, are stored within their digestive gland tissues and can remain photosynthetically active for months after ingestion. Recent research has investigated this activity using Pulse Amplitude Modulated Fluorometry, a technique that measures the chlorophyll a autofluorescence originating from photosystem II. The effective quantum yield values obtained from PAM Fluorometry provide a relative value of the number of reaction centers actively involved in photosynthesis, a qualitative assessment. Very few quantitative measurements have been attempted and they fail to examine chlorophyll content throughout starvation periods. Here, we present a detailed, quantitative look at chlorophyll degradation in sacoglossan tissues, examine chloroplast digestion in situ and explore the correlation between chlorophyll breakdown and the degradation of the kleptoplast itself. Chlorophyll degradation was monitored in the long-term plastid retaining species *Elysia timida*, the ambiguous *Elysia viridis* and the short-term retaining *Thuridilla hopei.* Chlorophyll a content was measured using confocal microscopy to detect the autofluorescence and compared to Acridine Orange stained lysosomes detailing an inverse relationship with a strong correlation between decreasing chlorophyll content and lysosome abundance. The relationship between chlorophyll a breakdown and the degradation of the plastid is currently being examined to determine if there is any correlation and / or causation.

The morphology of the trionychian respiratory apparatus and its phylogenetic implications

Oral Presentation

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The phylogenetic relationships among cryptodiran turtles often appear controversial depending on the approach followed (morphological *vs.* molecular). One of these controversies concerns for instance the placement of the Trionychia (Carettochelyidae + Trionychidae), which usually is treated as the sister taxon of the Kinosternidae and thereby nested well within Cryptodira (morphology), or as the sister taxon of all remaining cryptodirans (molecules). Lungs and associated structures of the respiratory system (extrapulmonary airways, coelomic integration of the lungs, respiratory musculature) of *Carettochelys insculpta* and that of several representatives of the Trionychidae were examined macroscopically. The anatomy of the respiratory musculature among trionychians is in agreement with that recently inferred for turtles as a whole. The principal coelomic compartmentalization by the post-pulmonary septum agrees with previous studies on other turtles as well, but suggests the convergent development of a completely separated pleural cavity in Trionychidae. Our data support the evolutionary distinctiveness of the taxon Carettochelyidae with its sole extant member *C. insculpta* based on a unique intrapulmonary branching mode. Most important, however, is that our data provide morphological support for the predominantly molecular-based hypothesis of an early split of the Cryptodira into the Trionychia and the remaining lineages (Durocryptodira). The dextrad displacement of the trachea among trionychians contrasts with the situation found in durocryptodirans, in which the trachea lies to the left of the neck (or as in Testudinidae exhibits an extreme reduction accompanied by long extrapulmonary bronchi). This anatomical ‘dichotomy’ appears functionally related to the evolution of the specialized neck retraction among cryptodirans.

Building-up of a DNA barcode library of aquatic true bugs for Germany

Poster Presentation

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With more than 80,000 known species world-wide and app. 8,000 species documented for Europe, true bugs (Insecta: Hemiptera) are an economically and ecologically important taxon. Whereas true bugs are primarily terrestrial, various taxa can be considered to be aquatic or semi-aquatic. The Nepomorpha (backswimmers, water boatmen, water scorpions) have at least one life stage that is truly aquatic; the Gerromorpha (water skaters, water measures) are semi-aquatic and live on the water surface. The extant aquatic and semi-aquatic species of the Hemiptera fall into 19 families with app. 4,800 species in more than 300 genera. In Central Europe, more than 74 species of aquatic Hemiptera are known. Nevertheless, the identification of many species using morphological traits only is challenging and time-consuming. In many cases, only males can be identified. In this context, DNA barcoding represents an efficient and straightforward approach to analyse biodiversity and to determine specimens. Recent studies already demonstrated the usefulness of DNA barcoding to identify true bugs species. However, the number of analysed aquatic and semi-aquatic species was low. As part of this project we started to build-up a DNA barcode library for aquatic and semi-aquatic Hemiptera of Central Europe, with a focus on Germany. In total, 237 specimens representing 42 species were analysed, whereas 172 (73 %) barcode sequences from 30 (71 %) species were successfully obtained until now. Additional specimens will be studied in the near future to increase the number of analysed species. All data will become part of the GBoL project.

Comparative morphology of the mouthparts of lophogastrids

Oral Presentation Student Prize

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Historically the phylogenetic position of Lophogastrida has ever been controversial. They are included in the Mysidacea, together with Mysida, or considered as the sister taxon to all other Peracarida. Since lophogastrids are deep-sea dwellers, they have rarely been subject to extensive studies, little is known about their behaviour and feeding preferences. In my study I took a closer look at especially their mouthparts in order to document their morphology for further comparative purposes. SEM work was undertaken of the mouthparts of *Lophogaster typicus*, *Gnathophausia zoea* and *Eucopia grimaldii*, as well as light-microscopic studies using Alizarin red staining of the mouthparts of *Gnathophausia gigas*. In all examined specimens the mandibles possess large sharp incisors and molar processes with varying secondary setation, but lack a fully formed lacinia mobilis. The presence of oostegites clearly indicates the inclusion of Lophogastrida in the Peracarida, while lack of a distinct lacinia mobilis in adult lophogastrids may be a secondary loss, hence an autapomorphy (structure present already in the ground pattern of Neocarida, so being plesiomorphic in Peracarida). The lack of fine setae and the setal row of their mandibles between molar and incisor processes indicates a predatory lifestyle where the mandible is mainly used to shred and crack large pieces of food particles. The morphology of labrum and paragnaths supports this hypothesis by exhibiting large grooves and even molar-like structures perfectly fitting the gnathal edges of the mandibles. Maxillulae, maxillae and maxillipeds do not seem to possess structures deviating from the plesiomorphic form.

Taxonomic study of *Oedothorax*, a hopeful dwarf spider genus for investigating the evolution of sexual dimorphic male head structures

Oral Presentation Student Prize

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Previous studies have shown that the dimorphic cephalic structures in dwarf spiders are related to nuptial gift secretion. In most dwarf spider genera there is little intrageneric variety among these structures. However, the genus *Oedothorax* comprises species with elaborate hunch, sulci, pits and/or grooves as well as species that lack such structures, and therefore lends itself in particular for investigating the evolutionary history of dimorphic head structures. The inspection of somatic and genitalic characters of both sexes from 49 of 76 known *Oedothorax* species and several outgroup taxa suggest a preliminary phylogenetic hypothesis which will be presented here. Our results shed light on the evolutionary pattern of dimorphic structures in these spiders, and also provide a new insight into the taxonomy of this enigmatic genus.

Exploring the third dimension of the early Cambrian Chengjiang arthropods

Oral Presentation

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Fossil evidence plays an irreplaceable role in the evolutionary biology research, as it is the only way to bring evolutionary biologists into direct contact with the extinct animals that have been an essential part of evolution. The 520 million-year-old early Cambrian Chengjiang biota located in southwestern China documents the earliest known fossil evidence of the so-called ‘Cambrian Explosion’ – a significant bio-radiation event in which the oldest known representatives of the major animal groups known from today appeared within a relatively short geological time window. Studies on Chengjiang fossils, however, have mainly been limited to the information exposed on the surface of the slabs. As a consequence, understandings of the origin and evolution of those early Cambrian animals have been based on such two dimensional data. Here, we take Chengjiang arthropods as an example and show that X-rays of a micro-CT can penetrate the fossil slabs and extract brand-new information from the third dimension. Such information is key to understanding many aspects of those early arthropods, including evolutionary developmental biology, ecology, and phylogeny.

Habitat partitioning of two fish species from the Middle Triassic of the Monte San Giorgio (Canton Ticino, Switzerland)

Oral Presentation

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A new neopterygian genus including two new species is described from Middle Triassic deposits of the Monte San Giorgio. The fish shows a mosaic of typically halecomorph and ginglymodian anatomical characters. It might thus represent a basal holostean and its mosaic morphology challenges the monophyly of both Halecomorphi and Ginglymodi, which together with Teleostei represent the three main crown neopterygians lineages.

During the latest Anisian to earliest Ladinian the two new species coexisted in the intraplatform basin represented by the uppermost Besano Formation, but only the type species inhabited the more restricted basin represented by the Ladinian Meride Limestone, except for the ‘Kalkschieferzone’. The different distribution of the species is interpreted as a result of habitat partitioning and different adaptability to palaeonevironmental changes. The more widely distributed type species shows interesting patterns of intraspecific variation including ontogenetic changes and morphological variation over time. The second species presents anatomical features that strongly indicate a strictly durophagous diet.

The partition of habitat and the trophic specialization of the second species suggest a previous event of sympatric speciation, which together with the presence of top predators indicate the existence of well-stablished ecosystems. Therefore, following the rapid recovery during the Anisian immediately after the end of the coral and coal gaps, the ecosystems of the upper Besano Formation at around 10 Ma after the Permo–Triassic mass extinction had already entered the third phase of recovery proposed for the Triassic biotas, which is in agreement with the model of ecosystem stepwise recovery pattern.

Kleptoplasts – starch storage factories in solar-powered sacoglossan sea slugs?

Oral Presentation Student Prize

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The incorporation of chloroplasts in enigmatic sacoglossan sea slugs has been known and studied for a long time. Previous work has shown that both the slugs and their stolen chloroplasts (kleptoplasts) survive for weeks to months when the slug enters a starvation period. Carbon fixation is performed by these plastids, a process which is affected by temperature, irradiance and even slug behavior. The particular algal species also affects kleptoplast survival. Active carbon fixation could prolong a starving slug’s life span, likely due to the photosynthates produced, although photosynthate accumulation and degradation have only recently been considered. Therefore, the aim of this study is to investigate the relative amount of photosynthates in sea slugs during starvation. The long-term plastid retaining form, *Elysia timida* and its sole food source, the chlorophyte, *Acetabularia acetabulum* were examined. The main photosynthate produced by *A. acetabulum* is starch, a polysaccharide comprised of amylose and amylopectin. We present here for the first time, a significant increase in amylose concentration, within the slug’s digestive gland cells during a starvation period, followed by a sharp decrease. This suggests that kleptoplasts function as both, a nutritive producer and storage device, holding onto the polysaccharides they produce for a certain time until they are finally available and used (as indicated by the concentration decrease) by the starving slug. This directly indicates some benefits provided by functional kleptoplasty to a long-term retaining species.

Comparative morphology of the cephalic tentorium in millipedes (Diplopoda)

Poster Presentation Student Prize

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The monophyly of Myriapoda is morphologically supported mainly by a distinct cuticular formation of the head called the tentorium and its involvement in movements of the mandibles. The traditional assumption that the myriapod tentorium primarily is a mobile formation yet remained contentious and is currently challenged by new insights on the head morphology of centipedes (Chilopoda) and symphylans. The composition of the tentorium in millipedes (Diplopoda) still remains poorly understood based on the few descriptions presently available. In order to clarify its nature and evolution among millipedes, we started re-examinations of their head anatomy based on serial histological sections used for 3-D reconstructions. First results of our studies are presented for the ring-forming millipede *Polydesmus angustus* (Polydesmida). In this species the skeleto-muscular system of the head shows remarkable correspondence to its state in juliformian millipedes. The tentorium proved to mainly represent an exoskeletal formation. Tentorial mobility is achieved by intracuticular flexibilities not known from other myriapods thus far. The articulation of the tentorium with the head capsule involves a cuticular protuberance that has been misidentified as a sensorial organ in previous descriptions, indicating that Tömösvary organs are generally lacking in Polydesmida. Insights obtained question the current view that among the helminthomorph millipedes Polydesmida is more closely related to Nematophora than to Juliformia.

Diverse admixture patterns in the *Hyles euphorbiae* complex (Lepidoptera: Sphingidae): Ambitious Integrative Taxonomy

Poster Presentation

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Based on colour pattern morphotypes, the Western Palaearctic spurge hawkmoths can be sorted into two species, the Eurasian *Hyles euphorbiae* and Afro-Macaronesian *H. tithymali*. These species had been postulated to have merged into several hybrid swarm populations, although a mitochondrial phylogeography revealed a different substructure with local differentiation. We analysed a comprehensive mitochondrial sequence dataset of about 900 specimens and additionally assessed nuclear population structure by means of 12 microsatellite loci. Mitochondrial polymorphisms retained in *H. euphorbiae* indicate incomplete lineage sorting within the species complex. Microsatellite analyses revealed an overall weak differentiation but generally corroborated the superordinate division into two entities. Diverse patterns of extensive mito-nuclear discordance in the Mediterranean and the Middle East presumably evolved by more recent introgression. This discordance indicates massive introgressions of *tithymali*-related mitochondrial haplogroups, accompanied by a minor introgression of nuclear alleles, into the Italian and Aegean *H. euphorbiae* populations, which appear to have taken place as recently as the late Holocene. The complex mosaic of divergence and reintegration is assumed to have been mainly influenced by locally differing barriers to gene flow. Taken together, the data indicate that the populations studied belong to only one species according to the biological species concept, although the populations sampled in this study are currently treated under five valid species names: *H. cretica*, *H. euphorbiae*, *H. robertsi*, *H. sammuti* and *H. tithymali*.

Morphology and phylogeny of Chaetognatha: evaluation of newly discovered and traditionally used characters

Oral Presentation

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Arrow worms (Chaetognatha) have been and still are problematic animals concerning their assumed position in the tree of bilaterian animals. Even to date chaetognaths are tagged 'incertae sedis' in current textbooks referring to their hitherto unknown rooting and sister group relationships. Both morphologists and molecular biologists have so far failed to deliver a clear-cut hypothesis. Chaetognaths share many different apomorphies, such as the multilayered, dual-type epidermis, cephalic grasping spines, heterosarcomeric muscles, specific neuromuscular innervation patterns, or heterocoely, strongly supporting them as a monophyletic taxon. Potential synapomorphies, if at all proposed, were rare and treated with extreme care, because a long, independent evolution of this group was assumed to have occurred at least from the early Cambrian onwards. However, progress has been achieved in past 10 years, especially with regard to developmental genetics and morphology. Discussion now place chaetognaths as either the sister group of the Protostomia or an early off-shoot among protostomians, thus representing the sister group of Lophotrochozoa and Ecdysozoa (soft polytomy). This contribution presents some of these new morphological characters (CNS, sense organs, epidermal glands) that have been contributed recently to this debate.

The shaft organ of *Scutigera coleoptrata* (Linné, 1758) (Chilopoda): tracing scolopidia back to ground pattern of Mandibulata?

Poster Presentation

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In Myriapoda, many cuticular sensilla or even complex sense organs are still unknown. One example of the latter is the shaft organ at the antennal base of scutigeromorph centipedes. There wasn't a single study since its first discovery by Heinrich Fuhrmann (in 1922) who noticed minute sensory cones inside a cuticular cavity on the scape of *Scutigera coleoptrata*. We provide a comprehensive description of the shaft organ. SEM and TEM revealed that the 10–15 sensory cones sitting in the cuticular cavity are surprisingly complex. Each sensory cone bears a huge terminal pore and includes three biciliated receptor cells and three sheath cells. The cilia emitted by receptor cells are different in length and possibly transduce mechanical stimuli via different mechanisms. Two receptor cells extend long cilia that project into the sensory cone where they adhere to a presumably expandable secretion pin plugging the terminal pore. This pattern is reminiscent of hygroreceptors found in various insects. The cilia of the third receptor cell are much shorter and terminate within depressions of the thickened dendritic sheath deeply below sensory cone. The dendritic sheath is connected to a scolopale-like structure built by the third sheath cell which strongly resembles scolopale cells in hexapod/crustacean scolopidia, except for the absence of an internal cuticular cap. For the first time, sensilla with scolopidial elements are recorded in Myriapoda. This finding may allow to add bimodal cone-/peg-like sensilla with scolopidial elements to mandibulate ground pattern, whereas unimodal, internalized, cap-enforced scolopidia remain a synapomorphic character state of Tetraconata.

Outlier loci correlate to precipitation: indications for micro-geographic adaptations at the species' range edge of *Geropogon hybridus* (L.) Sch. Bip. (Asteraceae)?

Poster Presentation

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As species approach their ecological limits their populations typically become smaller and more fragmented (Bridle & Vines 2007). These range-edge populations are more likely to maintain specialized genotypes that are particularly well-adapted to their harsh or extreme climates. (Rehm et al. 2015). We found evidence for this by investigating the genetic pattern (AFLP) of 12 fragmented *Geropogon hybridus* populations at their range-edge in Israel along a very strong precipitation gradient. In the investigation area within a distance of 45 km the annual rainfall changes rapidly from 450 to 300 mm per year without significant temperature changes. Our AFLP data (3 different primer combinations, 91 taxa, 123 polymorphic loci) revealed strongly structured populations and comparatively strong differentiation along this micro-geographic scale. Significant isolation-by-distance (IBD) patterns suggest differentiation as result of drift and dispersal limitation. Next to IBD we also found very significant isolation by environment (IBE), precipitation here. Applying the spatial analysis method (SAM) to correlate annual precipitation with AFLP data revealed 3 outlier loci to be potentially under selection, which were also found by other softwares (BAYESCAN, MCHEZA). Populations distributed across climatic gradients commonly show high levels of local adaptation but rarely on this micro-geographic scale with IBD to be in force. Furthermore, IBD-IBE- associations by means of climatic variables on larger geographic scales commonly comprise temperature and precipitation changes without the possibility to detangle one cause from another. In contrast, on our micro-geographic scales only precipitation changed along the gradient implying that the detected outlier loci are most probably linked solely to reduced water availability.

Morphological adaptations to freshwater habitats in the circulatory and excretory systems of the limnic slug *Acochlidium* (Acochlidia, Panpulmonata, Gastropoda)

Oral Presentation

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Habitat shifts from marine to freshwater or terrestrial environments and *vice versa* are rare within the Metazoa due to high adaptive costs. An exception form euthyneuran gastropods, which succeeded to colonize all aquatic and terrestrial habitats; in particular, pulmonate taxa show numerous independent habitat shifts. Among those the small clade of Acochlidia unites a remarkable variety in habitats: acochlidian slugs invaded marine, limnic and even (semi)terrestrial environments. Interestingly, Acochlidia comprise the only slugs inhabiting freshwater systems. We assume morphological adaptations in the circulatory and excretory systems to enable the limnic life style. A complex kidney in basal marine *Hedylopsis* and *Pseudunela* is considered a prerequisite to inhabiting freshwater systems in their limnic relatives of Acochlidiidae.

In the present study we provide the first detailed micro-anatomical data of the circulatory and excretory systems of a limnic *Acochlidium* based on modern histological 3D-reconstruction. The circulatory and excretory systems in *Acochlidium* resemble that of limnic *Strubellia* in showing a complex kidney and a long, looped nephroduct. Striking is the unique multiplication of up to 41 renopericardioducts connecting the pericard as site of ultrafiltration with the kidney. Ultrastructural analyses reveal the mysterious 'dorsal vessel system' to be the extended pericard with podocytes. We compare the circulatory and excretory systems of limnic *Acochlidium* with (semi)terrestrial Aitengidae, in which the 'dorsal vessel system' is connected to the kidney.

Remarkable differences in the 'dorsal vessel system' of closely related Acochlidia underline the need of comparative reinvestigation of similar systems in other panpulmonates for reliable homology assumptions.

Early evolution of the gastropod superfamily Cerithioidea and the systematic significance of the shell slit

Oral Presentation

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Cerithioidea are a predominantly marine group of gastropods. They are diverse in modern seas and have a rich fossil record. They occupy a basal position within Caenogastropoda and living cerithioids have many plesiomorphic characters. Modern cerithioids commonly have complex and characteristic shells including small carinate or heliciform larval shells in species with planktotrophic larval development. Based on this complex shell morphology, undoubted members of Cerithioidea are as old as Late Triassic. Adult and larval shell morphology suggests that the Palaeozoic stem- or sister-group of Mesozoic to modern Cerithioidea are probably to be found amongst Murchisonioidea which unites high-spired shells with a labral sinus or shell slit. Apart from murchisonioids, shell slits are wide-spread in Palaeozoic gastropods, especially in Pleurotomarioidea which were highly diverse until the Mesozoic but have only few living representatives. The slit serves the ventilation of the mantle cavity and is commonly associated with the presence of a pair of bipectinate gills which is seen as the original condition in Gastropoda. However, the phylogenetic distribution of shell slits and a large variation in their position on the labrum suggests that this character complex is not homologous in the various gastropod groups. Presence and position of shell slits, larval shell morphology and shell microstructures are used to discuss whether murchisonioids were early cerithioids.

Quantification of phylogenetic incongruence between organellar and nuclear genomes

Poster Presentation Student Prize

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Phylogenetic relationships inferred from organellar and nuclear DNA data are often difficult to resolve because of evolutionary conflicts among gene trees. Conflicting associations or 'outliers' (i.e., linked pairs of terminals in two phylogenies) among these data sets often provide valuable information about evolutionary processes responsible for these conflicts (e.g., chloroplast capture, retention and sorting of ancestral polymorphism). Statistical tools that to date have been used in cophylogenetic studies have the potential to test for the degree of topological congruence between organellar and nuclear data sets.

Two distance-based methods, namely ParaFit and PACo, were used to detect reliably those outliers contributing to conflicting phylogenies. We explored their efficiency, and the impact of input data (i.e., cladograms *versus* additive trees) between data sets, by using several simulation approaches and analyses of real data sets. Particularly, we inferred the phylogenetic relationships of Catasetinae (Orchidaceae), which is a suitable group to investigate phylogenetic incongruence because of documented hybridisation between some of its constituent species. The comparison between trees derived from chloroplast and nuclear sequence data reflected strong, well supported incongruence within Catasetinae. As a result, outliers among chloroplast and nuclear data sets (and in experimental simulations as well), were successfully detected by PACo when using distance matrices obtained from phylograms, but not from cladograms. The performance of ParaFit was overall inferior compared to PACo. We provide a pipeline to statistically identify outliers with high reliability and display them in plots and trees by using the software R.

Further support for the species status of Ibero-Maghrebian grass snakes (*Natrix astreptophora*) by morphological and osteological findings

Poster Presentation Student Prize

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The grass snake (*Natrix natrix*) occurs in many morphologically defined subspecies throughout its range from North Africa over whole Europe to Asia. This widely accepted subspecies concept was recently challenged by the molecular phylogenetic analysis of Kindler et al. (2013), who identified a high number of clades that do not match previous subdivisions of this species. In this study, we used 18 external morphological characters for multivariate analysis and examined cranial and vertebral osteology to test for support of the genetic lineages. We found consistent morphological differences between the westernmost subspecies, *Natrix n. astreptophora*, and all other subspecies. Most notably, *Natrix n. astreptophora* shares its skull structure with the fossil *Natrix longivertebrata*, while all other recent grass snakes show a different, presumably derived condition. Additionally, this form features significantly lower ventral scale counts, a distinct coloration within this group and mostly lacks hybridization with the geographically adjacent *Natrix n. helvetica*. These results support the deep genetic split between Ibero-Maghrebian grass snakes and their siblings and further strengthen the proposed species status for *Natrix astreptophora* (Seoane, 1884).

New discoveries and the radiation and faunal replacements in tetanuran theropod dinosaurs during the Jurassic

Oral Presentation

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Tetanurae is the major clade of theropod dinosaurs, which also includes recent birds. The clade is subdivided into three major lineages, the Megalosauroidea, Allosauroidea and Coelurosauria (including birds), with the latter two lineages forming sister taxa to the exclusion of the former. Tetanurans originated in the Early Jurassic and experienced their first major radiation in the Middle Jurassic. Unfortunately, the Middle Jurassic is the most poorly sampled epoch of the Mesozoic. Two new taxa from the Middle Jurassic provide new data but also highlight several problems associated with understanding the Middle Jurassic evolution of tetanurans. A basal tetanuran from the early Middle Jurassic Cañadón Asfalto Formation of Argentina shows an unusual combination of megalosauroid and allosauroid characters and thus challenges the currently accepted interrelationships between the major lineages of tetanurans. A new megalosaurid from the late Middle Jurassic (Callovian) of northern Germany underlines the great diversity of this clade in the Middle Jurassic. Taking into account the phylogenetic relationships of these taxa and the Early and Middle Jurassic theropod fossil record, an almost ‘explosive’ radiation of tetanuran theropods at the end of the Early and the beginning of the Middle Jurassic is indicated. The current fossil record furthermore indicates a faunal turnover from megalosauroid-dominated Middle Jurassic to allosauroid/coelurosaurian dominated Late Jurassic faunas. However, the fragmentary nature of many known taxa, poor dating of many Middle Jurassic localities and biases of the fossil record make both the interpretation of the phylogenetic relationships as well as faunal changes during the Jurassic problematic.

Unusal calcareous ring morphology in molpadid sea cucumbers (Echinodermata)?

Poster Presentation

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A unifying synapomorphy of all Holothuroidea is the calcareous ring (CR) which surrounds the mouth internally, gives support to the pharynx, water vascular system and tentacles, radial nerve ring, and muscle bands. Accordingly, this structure is one of the most important morphological characters in the whole group. Yet, it is heavily understudied.

A detailed anatomical description of the CR of several small molpadid sea cucumbers (members of the Caudinidae, Eupyrgidae, Molpadiidae) is presented. The latter are typically infaunal ovoid or more or less sausage-shaped echinoderms, known today from the subtidal zone down to abyssal and hadal depths, where they can form a large part of the biomass of macro- and mesobenthos.

High-resolution x-ray computed tomographic (CT) analysis of the calcareous ring of *Cherbonniera utriculus* (Molpadiidae), *Eupyrgus scaber* (Eupyrgidae) and *Hedingia albicans* (Caudinidae) reveals internal details not previously observed or probably overlooked. This includes several bilateral symmetrical patterns, dorsal/ventral differences, merged anterior processes in radial elements (R) of the CR, slit-like foramina for the passage of the radial nerve, and furthermore left/right patterns of these foramina, formerly known only from some apodid sea cucumbers.

Thus, the CR appears to be a more complex structure than formerly thought by most echinodermologists, offering characteristics most potentially useful in understanding the phylogeny and diversification of 'holothuriacean' sea cucumbers (Aspidochirotida + Molpadida + Dendrochirotida).

Paleobiology of a new giant protist-type vendobiont from the Ediacaran Shibantan Member (Southern China)

Oral Presentation

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A new group of Ediacara-type fossils was observed in black laminated limestones of the Shibantan Member in the Huangling anticline (South China). The facies consists of microbial mat layers and tempestites, deposited in a shallow subtidal environment. Bedding surfaces are commonly characterized by disrupted and shrunken biofilms, and horizontal trace fossils occur below the microbial mats in some places. The new Ediacara-type fossils are closely associated with microbial mat layers, relatively large (up to 60 cm in diameter) and generally more or less circular in shape. The best-preserved specimen shows a fine circular ribbing and a distinctly structured outer margin, resembling the morphology of modern giant deep-sea protists (*Stannophyllum*). As the specimens exhibit no mouth or anus, nutrients were may obtained via direct uptake and phagocytosis, being for instance known from recent amoeboids. Given the large body sizes, however, a close association with symbiotic microorganisms also occurs plausible. All observed specimens are associated with conspicuous traces on the bedding surfaces, suggesting moving, feeding or shrinkage of the organisms. As organic biomarkers and trace elements indicate a temporarily stratified sulfidic water body, the organisms could probably tolerate low oxygen concentrations in the water column.

The potential role of sexual selection for deep-sea diversity

Oral Presentation

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The deep sea is inhabited by a specialized and highly diverse fauna. The drivers responsible for the evolution and maintenance of this diversity in the oligotrophic deep oceans are controversially discussed. A potential influence of the age and vast dimensions of the abyssal environment, for example, has been contradicted by the depth-diversification and source-sink hypotheses attributing speciation predominantly to the continental slopes. Recently, the importance of small-scale spatial and temporal variability in food supply has been focused on to explain deep-sea diversity. While previous attempts were dedicated to environmental factors, we want to introduce an ecological perspective on this matter exemplified by sexual dimorphism.

Sexual dimorphisms impede biodiversity, as they can lead to misallocation of conspecifics, which have therefore often been classified as different species. They evolve through a combination of natural and sexually selection acting differentially on males and females. Consequently, sexually dimorphic characters may serve to improve our understanding of speciation processes. Especially in deep-sea habitats, where behavior can hardly be observed *in situ*, this phenomenon may help to illuminate potential selective forces and thus the high diversity.

We studied extremely dimorphic isopods collected during the German Vema-TRANSIT (Bathymetry of the Vema-Fracture Zone and Puerto Rico TRench and Abyssal AtlaNtic BiodiverSITy Study) expedition with R/V Sonne. It is concluded that the observed sexual dimorphisms are related to a different use of microhabitats which reduces niche overlap between the sexes. This in turn promotes niche variation within the population, potentially leading to ecologically mediated disruptive selection and adaptive speciation.

What is a deer and what is an antler?

Oral Presentation

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Members of the Cervidae, or deer, are known to share antlers as an autapomorphy. While extant cervids are clearly characterized by the unique traits of these cranial appendages like their branched structure, their burr and their regenerative nature, the origin of the clade and antlers respectively has a long tradition as an issue. The fossil record of antlers is excellent, but hitherto comprehensive investigations basically considered external anatomy only and neglected histological information. Here, we review the conflicting hypotheses and (distinctive) underlying data as well as systematic consequences. Further, we present novel research results based on µ-CT imaging of earliest fossil antler-like appendages. By examination of longitudinal histological traits we are able to reconstruct growth patterns and to demonstrate their correspondence with principle structures in extant antlers and underlying physiological processes respectively. Beyond that, our results allow for a critical assessment of stem cervid systematics. Overall, we can present evidence for an at least 20 Ma lasting evolution of Cervidae (contradicting and predating previously suggested 16 Ma, 11 Ma, and others) as well as an early diversification of stem cervids comprising different kinds of beam-less antlers.

Rapid identification of meiofauna species (Copepoda: Harpacticoida) using MALDI-TOF MS

Poster Presentation Student Prize

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The term meiofauna refers to organisms with a size of 45 µm to 1 mm found in marine and freshwater sediments. In marine environments they inhabit all depths from the intertidal zone down to the hadal (deeper than 6,000 m). Second to nematodes, the Harpacticoida are the most abundant meiofauna group found in marine sediments with a typical density of 200,000 to 300,000 individuals per m^2 (Huys & Boxshall 1991). To date there are more than 50 families containing around 3,000 described species. Because of their small size, species identification is taxonomically very challenging and laborious. While DNA Barcoding provides a suitable tool for identification, it is still very time consuming and cost-intensive, since single sediment samples can contain up to 1,000 specimens. An alternative to DNA Barcoding might be the analysis of proteome fingerprints using MALDI-TOF MS (**M**atrix-**a**ssisted **l**aser **d**esorption/**i**onization **m**ass **s**pectrometry), which is commonly used for rapid identification of bacterial colonies and over the last years was tested for some metazoans as well (e.g. Laakmann et al. 2013). Now, for the first time, we successfully applied this technique to meiofauna organisms. To use this technique for species identification in further studies, we are currently establishing a mass spectra library for harpacticoid copepods from the North Sea and are going to present the current state of work.

Understanding modes of character transformation: intermediate larval stages of decapod crustaceans as an important source

Poster Presentation Student Prize

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Decapod crustaceans occur in various ecological systems and occupy numerous ecological niches, inhabiting the oceans, freshwater, as well as terrestrial environments all over the world. Most decapod crustaceans spend a large part of their life as larvae. Reconstructing the character evolution by means of Hennigian phylogenetic systematics must therefore not be limited to the reconstruction of adult morphologies, but also larval morphology needs to be included (holomorph approach).

Selective pressures appear to favour stronger morphological differences between specific larval phases with different life habits (e.g. pelagic and benthic phase). Therefore, such phases are usually coupled to distinct morphological specialisations. An interesting source of information for understanding the character evolution leading to such distinct larval types are intermediate forms that show a mixture of morphological traits generally accepted as characterising two different larval phases.

Such intermediate stages are well-known in fossil representatives of various lineages of decapods. These forms include cases in which larvae have not yet evolved all characteristics of their modern counterparts, but also true developmental steps-in-between. In many lineages these latter forms have been lost, most likely due to strong selective pressures against morphologies neither fully specialised for the one nor the other environment, but representing true transitory forms.

Yet, larvae with intermediate morphologies also occur under unfavourable environmental conditions in modern forms. Such cases demonstrate how easily external factors may lead to unexpected, seemingly ‘new’ morphologies. With this, intermediate forms offer interesting insights into the mode of character transformations within the various decapod lineages.

Status of the German Barcode of Life initiative: first results, outlook and an example for the usage of the reference library

Poster Presentation

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GBOL (www.bolgermany.de) is currently the largest barcoding campaign in Europe, financed by the German Federal Ministry for Education and Research. The initiative is flanked by complementing projects (Barcoding Fauna Bavarica (BFB), FREDIE for European freshwater fishes and invertebrate taxa, barcoding of the North Sea Fauna) and supported by more than 200 external experts. The latter play a crucial role, because the taxonomic workforce and expertise in natural history museums and universities is insufficient. Here, we present statistics and first results for the work achieved within the first three years (2011–2015) and give an outlook for the recently approved second funding period (2016–2018) introducing new partners and organism groups. Addressing the motto of this conference (Taxa in Time and Space) we also present first results from a cooperation with the Canadian Global Malaise Trap Program (GMP), where two collection localities in Germany were chosen for an annual sampling, in order to assess the diversity of flying arthropods. Applying the DNA barcode reference library we were able to assign species names to 35 % of the detected molecular units (5368 BINs) via reverse taxonomy. Furthermore, 7 and 26 % were assigned to genus and family level. These findings illustrate the potential of a comprehensive DNA barcode library to identify unknown samples, and reveal the gaps that need to be filled in the coming years. As the corresponding voucher specimens are available for morphological determination, we invite all taxonomic experts to explore the unnamed species and enhance the reference library by giving names to them.

The invasive freshwater jellyfish *Craspedacusta sowerbii* – is there only one clone present?

Poster Presentation Student Prize

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The introduction of alien species into ecosystems is a consequence of increased human mobility. The freshwater jellyfish *Craspedacusta sowerbii* originating from China represents a recently globally distributed species. First reports in Germany are from 1905. Today it is widespread in standing and slow-flowing waters. *C. sowerbii* has a metagenetic life cycle with sessile polyps predominantly reproducing asexually. Occasionally, male or female medusae are budded off, allowing for sexual recombination. Notably, outside China, jellyfish within local populations are mostly unisexual and assumed to be genetically identical suggesting the spread of only one or few successful clones. After screening 30 lakes in 2015, it emerged that *C. sowerbii* is more widespread than assumed in the polyp stage. In case of medusae occurrence, all medusae from German and Austrian sites were females. Besides COI-barcoding to assign individuals to species, we just develop microsatellite markers to test for population structure and evolutionary dynamics. Moreover we are interested in the functional role of *Craspedacusta* within freshwater communities. Although mass occurrences of medusae have been recorded and effects on aquatic food web dynamics are likely, the consequences of *C. sowerbii* being introduced to freshwater systems are unknown. Therefore, we also designed field mesocosm experiments to identify the trophic position of medusae combined with laboratory experiments regarding polyp establishment.

Passing the buck in systematics – the case of the water deer (*Hydropotes inermis*)

Oral Presentation Student Prize

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Male deer (Cervidae, Mammalia) are typically characterized by their autapomorphic antlers and small to lacking upper canines. The monotypic water deer (*Hydropotes*) is the only living deer, whose males show the opposite pattern with no obvious trace of antlers but presence of enormously sized upper canines. Systematics based on morphological and cytogenetic data of extant cervids suggests that *Hydropotes* is sister taxon to all other species, i.e. represents the most ancient crown cervid lineage. In contrast, recent molecular phylogenetic studies suggest a more complex evolutionary history and derived position of *Hydropotes*, being sister taxon to the roe deer (*Capreolus*), i.e. secondary adaptation comprising the loss of antlers and repeated saber-like enlargement of upper canines as known from stem cervids. Unfortunately, the fossil record of *Hydropotes* is scarce and doubtful and doesn‘t contribute to solving the controversy.

In our presentation we aim to demonstrate the conflicting hypotheses including resulting problematic issues in terms of the current knowledge and opinions on behaviour, anatomy, development, and genetics. Further, we introduce our approach in order to unravel the phylogenetic position of *Hydropotes* and related evolutionary aspects of the genus.

Comparative morphology of the head kidneys and salivary glands of jumping bristletails (Insecta: Archaeognatha)

Poster Presentation Student Prize

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The head of apterygote hexapods houses a variable number of salivary glands in addition to one pair of labial nephridia called the head kidneys. Their structure and composition have not received much attention in modern studies of insect morphology thus far. In order to explore their systematic value and early evolution in hexapods, we started comparative studies on their anatomy based on serial histological sections used for 3-D reconstructions. In jumping bristletails (Archaeognatha) the head glands and labial kidneys proved to be largely conservative. Salivary glands consist of paired lateral, bilobed anterior glands and one unpaired median posterior gland equipped with paired efferent ducts. Both anterior and posterior glands open into the preoral chamber, the former laterally below the mouth opening and the latter medially below the hypopharyngeal lingua via a large, unpaired bowl-shaped duct into which the labial nephridia open as well. The paired head kidneys are apomorphic in Archaeognatha in showing a bilobed sacculus (sac-shaped in other apterygotes), each with a dorsal lobe (absent in other apterygotes) that is tightly enveloped by a strongly convoluted labyrinth. The opening of the labyrinth into the bowl-shaped efferent duct is positioned on paired lateral extensions of the bowl. The large size and distinct shape of the common bowl-shaped efferent duct of both posterior salivary gland(s) and head kidneys are primarily shared by silverfish (Zygentoma) and represent apomorphies of insects (Ectognatha) not encountered in previous considerations of their ancestral states thus far.

Mobile genetic elements in sponge mitochondria: vertical transmission, independent colonization, and consequences for systematics

Oral Presentation Student Prize

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Introns, known as 'selfish' and 'mobile' genetic elements, intermit coding regions of genes. In eukaryotic mitochondrial genomes they are divided into Group I and Group II introns according to their splicing mechanisms and secondary structures. In metazoans (animals) they have so far only been detected in sponges, cnidarians, placozoans and one annelid species. Within demosponges, Group I and Group II introns are present in six families. Based on their different insertion sites within the cox1 gene and their secondary structure, four types of Group I and two types of Group II introns are known, which can harbor up to three encoding homing endonuclease genes (HEG) of the LAGLIDADG family (Group I) and/or reverse transcriptase (Group II).

In the current study we analysed the largest dataset to date on sponge mitochondrial introns (95 taxa), encompassing 11 different sponge genera. We provide strong evidence that one LAGLIDADG encoding gene was vertically transmitted within the subtropical- tropical genus *Cinachyrella* (Tetillidae) for which we analysed 73 samples comprising 13 species. Additionally, the extent of independent horizontal gene transfer between different demosponge groups was observed. Furthermore, we detected for the first time up to two introns in sponge lineages for which no intron had been reported before (Scleritodermidae).

Our study highlights the potential biases and consequences of using standard cox1 barcoding primers in demosponge systematics and DNA barcoding.

A first evaluation of RAD-Seq to address phylogenetic questions within demosponges

Poster Presentation

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Next Generation Sequencing (NGS) applications such as '**R**estriction Enzyme **A**ssociated **D**NA **Seq**uencing' (RAD-Seq) have proven valuable in molecular ecology but phylogenetic analyses of non-model organisms remain relatively underexplored. Genome-wide multilocus data are particularly promising when attempting to resolve shallow phylogenetic relationships among recently diverged taxa, where existing molecular markers are insufficient to untangle phylogenetic relationships at and below family level, such as in the class Demospongiae (Porifera). Library construction for genomics in sponges generally is challenging due to their often high numbers of microbial symbionts.

Therefore, this study aims to evaluate laboratory procedures to generate high-quality genomic DNA libraries for RAD-Seq from various demosponge taxa. In addition, the value of different bioinformatic approaches to establish and phylogenetically analyse alignments of orthologous loci and to discard symbiont reads will be discussed.

This study provides the first insights into the complexity of RAD-Seq library preparations from high-microbial abundance (HMA) demosponges and suggests that the ezRAD method might become a powerful tool to address phylogenetic questions among closely related demosponge species.

Cryptic lineages in DNA barcoding and how to assign them to classical morphology

Oral Presentation

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Especially in animal groups with highly differentiated genitalia due to sexual selection (e.g. Araneae and Diplopoda) DNA barcoding provides an excellent possibility to confirm morphological delimitations.

In contrast we face an unexpected diversity of cryptic mitochondrial lineages in animal groups that lack clearly discernible genitalic modifications, such as Chilopoda, Symphyla or Pseudoscorpionida, exactly those groups, with sperm transfer via spermatophores.

After decades of synonymisation we now face the possibility, that many old names might be justified. But how to correlate these taxa with the discovered mitochondrial lineages? Are we still able to determine with morphology solely? A vision for possible solutions for these questions will be presented.

Conservation genetics of the Northern river terrapin (*Batagur baska*) breeding project

Oral Presentation Student Prize

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Around 100 years ago, the Northern river terrapin *Batagur baska* aggregated in big groups on the river banks of eastern India, Bangladesh and Myanmar for breeding. Nowadays the distribution is restricted to small separated regions. Fewer than 30 wild animals are confirmed to survive. To mitigate this extreme decimation, a breeding project was launched in 2010 in Bangladesh by the Vienna Zoo and the Turtle Survival Alliance (TSA). First random reproduction in the breeding seasons 2012 and 2013 resulted in 84 juveniles. To preserve as much genetic diversity as possible, a genetic supervision of future breeding is currently established. For doing so, all captive individuals of *B. baska* were genotyped using on 13 polymorphic microsatellite loci to reveal individual relationships to avoid mating of closely related terrapins.

Threat or fiction: is the pond slider (*Trachemys scripta*) really invasive in Central Europe? A case study from Slovenia

Poster Presentation

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Using samples of non-native pond sliders (*Trachemys scripta*) from three different climatic zones in Slovenia, we perform parentage analyses and use population genetic approaches to find out whether they successfully reproduce and are able to establish populations. Based on 14 highly polymorphic microsatellite loci, we provide evidence for successful reproduction and invasiveness of pond sliders not only for the Mediterranean and sub-Mediterranean regions of Slovenia, but also for the central part of the country having a temperate continental climate. Our results suggest that the pond slider should be classified as an invasive species (introduced species spreading in a non-native region) for Slovenia and other European regions with similar climatic conditions. Since the negative impact of pond sliders is out of question for native European turtle species, we suggest the immediate removal of pond sliders from all habitats. Our study provides for the first time hard evidence for the capability of pond sliders to reproduce in Central Europe. Thus, it contributes to the understanding of the invasiveness of pond sliders in Europe and delivers an important foundation for decision-makers in conservation.

Hook-bearing sea cucumbers (Apodida, Echinodermata) – the need for modern and detailed investigations

Oral Presentation Student Prize

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The undisputed fossil history of sea cucumbers begins in the Middle Ordovician (466 Ma), mostly known by isolated microscopic material only. However, also the anatomical features of living holothurian species used as taxonomic characters, rely heavily on the morphology of calcareous hard parts. Therefore, detailed analyses of modern ossicle characters can help us in determining a firm placement of fossil sea cucumber taxa. Unfortunately, microscopic ossicles of modern species are often still documented by conventional 2D-drawings and light microscopy. Although SEM and ESEM methods, invented in the early 1930s and late 1980s, have taken on an important role in documenting and analysing zoological and palaeontological material. However, actually less than 20 % of modern sea cucumber species were investigated with the help of SEM, which often hindered a satisfactorily interpretation of fossil taxa.

Here we present a detailed analysis of two members of the hook-bearing holothurian genus *Taeniogyrus* (Apodida: Chiridotidae: Taeniogyrinae). We found that even very small morphological details, formerly neglected or overlooked by echinodermologists, are present in specimens of different sizes and ages. In combination with the study of fossil hook-bearing taxa these results indicate that there has been a long chiridotid holothurian evolutionary lineage, at least since the Middle Devonian (385 Ma).

Integrative taxonomy and niche partitioning of sympatric *'Gibbula'* species (Trochidae, Vetigastropoda)

Oral Presentation

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Roughly two dozens species of the genus *Gibbula* s.l. inhabit Mediterranean rocky coasts. Considerable intraspecific variability of these abundant, biofilm-grazing snails causes problems in identification and delineation of several species. We attempted to resolve these using DNA-barcoding and geometric shell morphometrics on 8 taxa. Some species, e.g. *G. varia* and *G. rarilineata*, separate nicely with CO1 and ITS data, even if shell shapes do not differ. On the other hand, genetic separation of *G. varia* and *G. divaricata* is ambiguous, although shell shape is highly diagnostic. Thus, combining both methods is the most effective approach to characterize these species. Integrating geographical and habitat data reveals unresolved ecological questions: Why is there no genetic differentiation among disjunct populations in some species, whereas in other, closely related species, deep genetic and morphometric differences are evident? Are there different microhabitat preferences of sympatric species? Does wave exposure influence shell shape? Preliminary data and observations on the distribution in the lower intertidal and shallow subtidal as well as on the scarcely investigated reproductive biology of these common species point out future directions of research beyond the much needed resolution of their systematic problems.

Chasing the Unknown: The role of larvae in SE-Asian Odonata taxonomy, with case studies of larva descriptions from Borneo

Poster Presentation Student Prize

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Odonata are model organisms for evolutionary research. Furthermore, many Odonata species are colorful, easy to observe and identify, and occur in standing as well as running waters, making them the ideal bioindicators to assess the quality of all freshwater habitats.

South-East Asia is the species richest region for Odonata worldwide. Although new species are discovered frequently in SE Asia, Odonata probably represent one of the best studied insect groups in the region. However, for most species only the adults are known, even though nearly all species spend by far the greatest part of their life as larvae.

Describing the larvae of species for which only the adult stage is known helps to assess the water quality of freshwater bodies, since the adults of some Odonate species can only be found at certain times in the year, whereas the larvae can be found at any time. Finding larvae in a given water body demonstrates that the habitat is suitable for reproduction of this species. Moreover, morphological characters of Odonata larvae can be included in phylogenetic analyses. Last but not least, many elusive species exist in SE-Asia, especially in the families Gomphidae and Chlorogomphidae. To record such elusive species, and sometimes to discover undescribed species, rearing of larvae is the most practical method. DNA barcoding is an additional method, for fast assignment of a larva to a species for which only the adult is known.

Here, we present examples of larval taxonomy using species from Borneo.

MicroCT Analysis as a tool for taxonomic research in Odonata

Poster Presentation Student Prize

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For the identification of many dragonfly species, it is necessary to examine the secondary copulatory organ of the males. Dissecting out the genital ligula, however, entails the risk of damaging the specimen. This is especially problematic with old and thus frail specimens, such as type material. A method that allows the investigation of internal structures without the need for dissection would therefore be highly advantageous. The Micro-Computer Tomography Analysis (microCT) offers a non-dissipative way of visualizing and scrutinizing internal morphological characters. We tested the potential of microCT Analysis for investigating the genital ligula in Odonates. Particularly, we applied microCT Analysis for a taxonomic revision of seven members of the damselfly genus *Coeliccia* (Steinhoff & Uhl, Zootaxa 2015).

Hybridisation capture targeting exons across highly divergent fish species

Oral Presentation

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In the era of second generation sequencing, targeted gene capture has evolved into a useful tool to collect molecular data for phylogenomic purposes. Here, RNA baits are used to capture in DNA libraries for a maximum of 14,000 exons, which are promising to be phylogenetically informative. Sequence information for the RNA bait design was attained from publicly available genomes of bony fishes, i.e. *Danio rerio*, *Gasterosteus aculeatus*, *Oryzias latipes*, and *Tetraodon nigroviridis.* The efficiency of the capturing is reviewed using custom scripts. We are aiming for collecting a subset of loci common to all target species, which will subsequently used for reconstructing phylogenetic inferences of highly divergent species of fishes, which phylogenetic interrelationships are still unsatisfactorily resolved.

Phylogeny and systematics of *Jurinea*, a large Eurasian genus of the Cardueae (Compositae)

Oral Presentation Student Prize

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Jurinea is a genus of herbaceous plants with 150–200 species which form a characteristic element in steppe and high mountain vegetation. Species diversity concentrates in Central and Southwest Asia and in the eastern Mediterranean region. Regional taxonomic treatments are available for parts of the genus, but a comprehensive monograph as well as a phylogenetic analysis with a representative sampling are hitherto lacking.

We have addressed phylogenetic relationships within *Jurinea* and between its closely related genera by analysing DNA sequences of nuclear (ITS, ETS) and plastid (*petD*, *trnL-trnF*) regions. Our dataset includes 70 species and covers most of the geographic distribution of the genus and its sections.

Jurinea in its actual circumscription is not found monophyletic, since *J. cartilaginea* and *J. gedrosiaca* are placed within subtribe Centaureineae of the Cardueae, while all other analysed species form a well-supported clade. The segregate genus *Jurinella* is entirely nested within *Jurinea*. A clade including the genera *Himalaiella* and *Lipschitziella* is sister to *Jurinea.* Within *Jurinea,* two main lineages correspond to the western and eastern range of the distribution area. The current sectional classification is not always reflected by the clades found. Instead, there is an overall geographic pattern. For example, two clades containing predominantly Caucasian species were resolved, yet it is unclear whether they result from a single diversification in the region or form successive branches.

This first phylogenetic framework for *Jurinea* offers interesting perspectives for further analysis of biogeography, speciation, niche evolution and character evolution of the genus.

Another kind of annelid hook – on the fine structure of sipunculan introvert hooks

Poster Presentation

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Sipunculans are unsegmented worms that inhabit a wide diversity of marine benthic habitats. Their fossil record can be traced back to the early Cambrian which seems to corroborate the idea that Sipuncula are the sister group of Annelida (based on the body organization) or Mollusca (based on the cleavage pattern). Recent molecular studies, however, provide convincing evidence that Sipuncula are an annelid ingroup. Since chaetae are characteristic for Annelida, one would expect to find such structures at least in some sipunculan species as well. In fact, a number of species bear hooks extending from the cuticle of the introvert. Other annelid taxa possess hook shaped chitinous chaetae. Since identically termed structures are characteristic for annelid subgroups, we studied the fine structure of sipunculan hooks in *Aspidosiphon muelleri* and *Golfingia* cf. *vulgaris* using different morphological techniques, like histology, electron microscopy, and confocal laser scanning microscopy. Our data provide evidence that the sipunculan hooks are entirely cuticular structures which have nothing in common with annelid chaetae. Sipunculan hooks, thus, presently do not contain any phylogenetic signal to unravel their annelidan sister group. We assume that similar functional constraints might have forced the evolution of such hooks.

How to organise, process and archive collection and occurrence data using GFBio services provided by Germany’s major natural history and culture collection data repositories

Oral Presentation

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Environmental and biological research is becoming central to major societal challenges related to the Earth‘s ecosystems and climate dynamics. To handle the scale and complexity of the scientific questions being addressed, there is a strong need to integrate knowledge because biological data are currently scattered and difficult to share. The DFG funded infrastructure project ’German Federation for Biological Data (GFBio, www.gfbio.org)’ is going to set up a coherent infrastructure to improve scientific data integration and preservation. It brings together national key players providing environmentally related biological data and services. The overall goal is to provide a sustainable, service-oriented, national data infrastructure facilitating data sharing, and stimulating data intensive research in the fields of biological and environmental sciences.

Germany‘s major natural history and culture collection data repositories are involved in GFBio. With their experience they contribute in the long-term management, curation and storage of physical and digital collection units, and any kind of taxon-related primary biodiversity data from monitoring and ecological projects originating from DFG research projects. These GFBio data centres integrate existing components and management systems for organising data and workflows within the common GFBio technological framework.

Besides this, GFBio fosters researchers and research groups with training resources, graduate courses, education modules, technical and content services. The use of database systems and workbenches for managing and integrating biodiversity data is recommended to keep complex data coherent and get them ready for GFBio submission. The involved data centres are active in the development of best practises and new standards for sharing and archiving of biodiversity data.

Morphology and anatomy of osmophores in *Cycnoches* Lindl. (Orchidaceae, Catasetinae) and their utility in phylogenetics

Poster Presentation Student Prize

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Pollination effectiveness in *Cycnoches* is directly dependent on osmophores. Euglossine-bee pollinated orchids produce a bucket of fragrances acting as attractant and reward for pollinators, which collect these fragrances and use them during courtship. Despite the importance of scent glands in orchids, few studies on their anatomy and morphology have been published. They conclude that osmophores are diverse among orchid taxa at various taxonomic levels, yet provide stable characters within species. Phylogenetic relationships of *Cycnoches* (Catasetinae) were investigated using DNA sequences, and three statistically strongly supported clades were recovered, but no morphological/anatomical traits supported the internal relationships. To achieve a better understanding of the morphological-anatomical relationships within *Cycnoches*, we investigated osmophores by means of location and presence staining, as well as using light and scanning electron microscopy. Our results indicated that within Clade B, *C. chlorochilon*, *C. ventricosum* and *C. warszewiczii* were more similar to each other regarding the smoothness of the osmophore surface and the presence of a thick cuticle, characters that distinguish them from *C. lehmannii*. Additionally, we demonstrated close similarities between *C. egertonianum* and *C. rossianum* (Clade C) uniquely showing convex osmophores with deeply wrinkled surfaces and a thick cuticle as well. In contrast, *C. peruvianum* displays rippled folded osmophores with smooth surface. Furthermore, *C. dianae* and *C. guttulatum* (also Clade C) exhibited convex osmophores with cells of different sizes (one big cell surrounded by smaller ones) indicating their close relationship. These results provide an additional but independent support of the internal phylogenetic relationships within *Cycnoches.*

A DNA-barcoding inventory of Red Sea calcareous sponges (Porifera, Calcarea)

Oral Presentation

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The Red Sea is a biodiversity hotspot for marine animals. Nonetheless, for many taxa like sponges little is known about the diversity, distribution and abundance of species. This especially holds true for the sponges of the class Calcarea, which in many cases are small and inconspicuous compared to other sponge species. Most of the 23 known species of the Red Sea were described over 100 years ago, and only few studies on their distribution or abundances were conducted since. More troublesome, molecular phylogenies suggested in general that the morphology-based classification of calcareous sponges is highly artificial on the order, family and often even the genus level. Applying a recently proposed DNA-barcode, the C-region of the 28S rDNA, we screened 87 specimens of calcareous sponges collected in the Red Sea (coast of Egypt and Saudi Arabia) between 2004 and 2013. We identified 25 operational taxonomic units (OTUs; subclass Calcinea: 10 OTUs; subclass Calcaronea: 15 OTUs), which presumably include new species for this region. A molecular phylogeny elucidates their relationships to other Calcarea. Morphological descriptions and reference sequences for these OTUs will be made available through the Sponge Barcoding Database (www.spongebarcoding.org) for future DNA-based biodiversity studies in the Red Sea.

Monitoring of opisthobranch biodiversity in Indonesia – and its applied aspect

Oral Presentation

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Coastal areas of Indonesia are considered as the most diverse marine habitats in the world. This comprises also opisthobranch taxa (Gastropoda, Mollusca), which exhibit highest species numbers and also highest diversity with regard to life styles in these tropical areas. Not only scientists are interested in opisthobranch diversity. Tourists, a major economic factor in these areas, are highly attracted by these beautiful gastropods. Actually, many diving centers advertising during the International Exhibition BOOT in Düsseldorf use large pictures of slugs for attraction. Less known is there importance in the search of new drug leads. Antibiotic resistance to traditional products is one of the biggest threats in human health and therefore these organisms have come into focus as novel producers of bioactive metabolites. Mollusk-derived molecules are most promising drug leads and especially opisthobranchs contribute already to several new medical therapies. When the Bundesministerium für Bildung und Forschung (BMBF) advertised their program in spring 2014 (Identifikation und Nutzung in Indonesien natürlich vorkommender Substanzen für die Arzneimittelentwicklung), the authors successfully applied and we started with our project (*Indonesian Opisthobranchs and associated microorganisms – From biodiversity to drug lead discovery*) in summer 2015. Here we present first results from our first collecting efforts.

Ultrastructure and phylogenetic evaluation of the Tömösváry organ in *Craterostigmus tasmanianus* Pocock, 1902 (Myriapoda: Chilopoda)

Poster Presentation

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All centipedes share cuticular sensilla of various morphologies and functions. However, more complex sense organs are only present on the head and associated appendages of some chilopod subgroups. For instance, postantennal organs, termed Tömösváry organs in Myriapoda, were only known from Scutigeromorpha and Lithobiomorpha. Here, Tömösváry organs are located in small excavations/depressions of the cuticle at either head flank, posterior to the antennal base and, if present, the anterioventral margin of the eye. Tömösváry organs were assumed to be present in Craterostigmomorpha but solid anatomical evidence was missing. With the present contribution, its existence in *Craterostigmus tasmanianus* is documented for the first time, based on light and electron microscopy. TEM reveals that two distinct groups of altogether 8-12 biciliated receptor cells are nested in an epithelium made up by hundreds of sheath cells surrounding and supplying a huge common but strongly diversified receptor lymph space. Each receptor cell projects two elongated, locally convoluted cilia that pass through a pore canal in the cuticle, branch and finally abut to the sensory plate lining the pore canal with a very thin cuticle. Axons of receptor cells project into the nervus tömösváryi, which innervates the lateral protocerebrum. Homology of Tömösváry organs in Chilopoda is further strengthened by common presence of receptor cells each projecting two cilia that branch apically. However, many characters, such as lacking a cuticular excavation or the asymmetric distribution pattern of receptor cells and their cilia represent further apomorphies of Craterostigmomorpha.

Comparative Trunk Research: SEM studies of bisected proboscides of Pantopoda

Poster Presentation Student Prize

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One of the most striking traits of Pantopoda is their highly developed proboscis. The shape varies from short and roundish (e.g., in *Pigrogromitus timsanus*) to slim and elongated (e.g., in *Austrodecus glaciale*). The proboscis' inner structures involved in food uptake include a filter apparatus and an armature made of denticles. However, these structures have been studied in the past only in a few species. Therefore a comparative analysis of representatives of all pantopod lineages is required. In this study we bisected proboscides of *Achelia langi* (Dohrn, 1881)*, Anopodactylus californicus* Hall, 1912*, Ascorhynchus castellioides* Stock, 1957*, Austrodecus glaciale* Hodgson, 1907*, Callipallene margarita* (Gordon, 1932), *Colossendeis macerrima* Wilson, 1881*, Endeis spinosa* (Montagu, 1808), *Nymphon macronyx* Sars, 1877*, Pallenopsis patagonica* (Hoek, 1881), *Pantopipetta* sp., *Pigrogromitus timsanus* Calman, 1927 *and Pycnogonum litorale* (Stroem, 1762), and analysed them with SEM, µCT and fluorescence microscopy. Sets of 'inner trunk' characters that vary between taxa were established. These traits included length and width of proboscis, shape and structure of the mouth opening, borders and armature of the antimeres, shape and position of denticles, length of filter apparatus, and structure of the filter bristles indicating a high variability of structures on the pycnogonid proboscis' inner surface probably related to modes of food uptake.

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Shifts in ontogeny: Species delineation of fossil and extant tadpole shrimps

Poster Presentation Student Prize

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The tadpole shrimp *Triops cancriformis* (Branchiopoda, Eucrustacea) is often referred to as a 'living fossil', implying that the morphology of the species has barely changed since some hundred million years. In 1938, Trusheim reported fossil tadpole shrimps (235–200 Ma, Upper Triassic) which he interpreted as representatives of *Triops cancriformis*, differing from modern forms only by the smaller size of the fossils (termed by him *Triops cancriformis minor*).

We compared the ontogenetic sequence of the fossil forms with that of modern ones. Fossil material comes from the same layers as that of Trusheim (which is considered lost) from the museum Terra Triassica in Euerdorf. Fossil specimens were documented under cross-polarized light and processed into high-resolution images. These fossils were compared with exuviae of extant specimens documented with fluorescence microscopy.

Both forms show a distinct elongation of their prominent shield during ontogeny. Concerning the length/width ratios of the shield, fossil and extant forms show parallel trajectories. Yet, these trajectories differ significantly in their y-intercept: fossil forms start out with a distinctly more rounded shield shape, becoming more elliptical, while extant forms already start with a more elliptic shape. Further differences are also apparent in ratios of shield versus trunk. All differences are highly significant.

These differences cast severe doubt on the interpretation that *Triops cancriformis* has remained unchanged since 235 million years. The term 'living fossil' is in general a problematic one, but seems especially inappropriate in the presented case.

Septum by septum to evolutionary history of glirids

Oral Presentation Student Prize

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It is possible to divide the middle ear of several mammal groups into the dorsally positioned epitympanic recess and the ventral tympanic cavity. In rodents, both the epitympanic recess and the tympanic cavity are divided into chambers by bony septa. For comparative analyses, the ‘septal compass’ and ‘septal formula’ were invented as a new method for phylogenetic investigations of the middle ear in the squirrel-related clade (sciurids, glirids, and aplodontids). Conclusions on the phylogenetic relationships can be drawn between the investigated species, as the combinations of septa are even family specific (Pfaff et al. 2015). When molecular studies fail to explain phylogenetic relationships, morphological investigations might share light on that question to reveal the true origin of glirids. Here, we re-analyse the morphology of the middle ear region of almost all genera of extant glirids and also extinct species. A new phylogenetic tree will be suggested for glirids, followed by a discussion on how the unique middle ear region of *Glirulus japonicus* might be a distinct structure of glirids.

A digitalisation project on four major fish collections at the Bavarian Natural History Collections reveals differences in data patterns determined by historical, domain-specific and preservation-related parameters

Oral Presentation

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The DFG-funded research infrastructure project IDES (http://ides.snsb.info) was designed to set up high performing digitalisation stations and integrated work and data flows to be used by four institutions belonging to the Staatliche Naturwissenschaftliche Sammlungen Bayerns (SNSB). The project focuses on collection specimens of the fish group Actinopterygii from Europe and adjacent seas, starting from the Mesozoic era (Trias) until collections of extant fishes. One of the challenges was to address various types of preservation, like dried collections of skeletons, wet collections, micro- and macrofossils, DNA and tissue collections, otoliths and fish scales. After three years, IDES is successfully organizing and processing occurrence (space-time) data of about 28,000 fish specimens (fossil and recent), measurement data of about 5,200 fishes and more than 41,000 high-resolution images. The 8,000 fossil objects (mainly from the late Jurassic) have much information on collecting, collectors and publication history, paleontological excavation sites and stratigraphies available. Beside the primary biodiversity data the extant fish object data is phenotypic and genotypic trait data and – to a minor part – data on habitat information. We use Diversity Workbench tools for statistics and data visualisation to analyse data quality and completeness, to create taxonomic profiles and document data patterns, e. g. on kind of preservation, object type and space-time distribution. Most of the IDES data are accessible via the GBIF and BiNHum portals. In the future, they will also be available via other portals like GFBio (http://www.gfbio.org), GeoCASE, FishBase and FishNet 2.

Testing the power of the Papillomavirus Episteme

Poster Presentation

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Papillomaviruses (PVes) are a diverse taxon of pathogens with a circular genome of double stranded DNA, which infect epithelial tissue of various amniotes. The Papilloma Virus Episteme (PaVE) has been established to provide highly organised and curated papillomavirus genomic information and tools to the scientific community. The power of the Papilloma Virus Episteme has not been tested so far. We downloaded all available complete viral genome sequences, and reconstructed papillomavirus phylogeny under different approaches, including single- and multi-gene analyses of nucleotide and amino acid alignments using Maximum Likelihood and Bayesian criteria. We also compared phylogenies independently derived from the L1 gene with the gene combinations E1+E2+L1 and E1+E2+L1+L2. All phylogenetic reconstructions yielded similar results, retrieving four consistent PV groups at higher taxonomic level, but the relationships between them were unclear. However, several internal nodes of such groups are supported by high if not maximal statistical values. Using resulting phylogenies, we calculated the degree of congruence between virus and host phylogenies with the program PACo. Heterogeneous results indicated that overall similarity between virus and host trees was low and that evolutionary mechanisms other than co-divergence (e.g., zoonotic events) may contribute to PV diversification. Our results are in striking agreement with previous studies, and the service provided by the Papilloma Virus Episteme significantly accelerates phylogenetic reconstructions. We propose extended services such as evolutionary placement of short reads and novel virus sequences into the existing PV tree topology and automated tests of the widely accepted, but frequently challenged assumption of close virus-host co-divergence.

Climatic niche characteristics of the butterflies in Europe (CLIMBER) – a new database for measuring the response of butterflies to climatic changes

Poster Presentation

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CLIMBER is a database providing information on the position and breadth of major climatic niche characteristics for almost all European butterfly species (Schweiger et al. 2014). It includes the mean annual temperature which forms (as ‘species temperature index’ = STI) the basis to calculate the ‘community temperature index’ (CTI). This index already proved to be a powerful indicator in the context of climate warming. In addition to temperature-based climatic indices, the database also includes several indices for water availability.

Here, we present new applications of this dataset, which help to assess how butterfly communities react to climatic change. A phylogenetic analysis of the CLIMBER dataset using a newly assembled Maximum Likelihood phylogenetic tree (COI & ef1-α) revealed that adaptations to cold thermal limits are phylogenetically conserved while adaptations to the warm limits are not. We assume that the phylogenetic signal for cold-adaptation is a legacy of the ice ages. The lack of evidence for phylogenetic conservatism of warm-adaptations may indicate different evolutionary or ecological processes at cold and warm range margins probably caused by increased importance of biotic interactions under warmer conditions. A potential quicker adaptation to warmer conditions or a lack of range-filling at the warm ends due to biotic interactions together with anthropogenic landscape barriers to dispersal might lead to the observed climatic debts of butterflies.

From bycatch to main dish! Spines of irregular echinoids as monitors for diversity trends in the deep sea during Cenozoic critical intervals. A pilot study.

Oral Presentation

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IODP sites U1334C (tropical Pacific, Upper Oligocene) and U1405B (boreal Atlantic, Lower Miocene) yielded more than 5,500 (very) good preserved atelostomate spine fragments. Pore orientation in the spines (helicoidal: Spatangoida *versus* horizontal: Holasteroida) enables a distinction between both groups. Further classification is attempted based on shaft morphology (e.g. curved, straight, kinked, pointed tip), arrangement and frequency of thorns, pore shape, and tip shape (e.g. pointed, spatulate, forked, serrated, spoon-like, leaf-like). Variable spine morphologies demand a kind of fuzzy systematics, uniting transitional morphologies into clusters. U1334C is dominated by Holasteroida. At least two Holasteroida spine assemblages occur. One consists of spatulate to forked and serrated tips with almost identical shafts; the other yields leaf-like to spoon-like tips, with spines thinning at the junction to the tip. Thick (ca. 1 mm diameter) Spatangoida spine fragments are less common. Miocene U1405B is dominated by Spatangoida, sharing almost no similarities with the Oligocene tropical Pacific. Accordingly, the excellent atelostomate spine record in DSDP/ODP/IODP cores enables the recognition of time-specific spine assemblages, which have the potential to monitor the deep sea Atelostomata response to critical intervals in Cenozoic re-organisation in palaeooceanography and palaeobiogeography (mid-Eocene Climate Optimum to the late Oligocene warming, ca. 20 Ma, deep sea bottom water oscillation: ca. 7°C). This pilot study aims to etablish Atelostomata spine assemblages as a new proxy to reconstruct deep sea diversity changes, deep-sea benthic–pelagic coupling and palaeobiogeography. This is the first time ever that a macrofossil group is used for this purpose.

Snails in space: Diversity and distribution patterns underlined by intertidal planaxid gastropods

Oral Presentation Student Prize

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Finding and explaining patterns in diversity and distribution of and within species is one of modern biogeography's most important issues. When conducted with well revised phyla, it can reveal their evolutionary history and thereby allows to decipher diversification processes. For an evolutionary systematics study we revised the Planaxidae Gray, 1850 (Gastropoda, Mollusca), a family of intertidal snails that is distributed worldwide throughout tropical and warm temperate marine regions. It comprises seven genera with at least eleven species. By reconstructing the geographic distribution of each constituent taxon we found an overall pattern of species diversity, corroborating those found in other costal taxa. In addition, based on findings on the type species, viz. *Planaxis sulcatus* (Born, 1780), we studied its unique reproductive mode. So far, this ovoviviparous species has been proposed as a case of poecilogony, i.e. a single species with two distinctly different reproductive modes. Instead of two rather distinctive modes, an evaluation of the species' reproductive biology throughout its distribution range suggests the transition from one mode to another with several intermediate stages. This transition of reproductive modes is in accordance with salinity concentration shifts of the sea water in certain parts of the range, proposing an explanation for the putative poecilogony. We anticipate that the case of *Planaxis sulcatus* allows for new insights in intraspecific diversity of reproductive modes in marine invertebrates, implying a higher complexity of modes than traditionally thought.

Phylogenetic relationships, divergence times and evolution of host plant use in the weevil tribe Apionini (Apioninae, Brentidae, Coleoptera)

Oral Presentation

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The taxonomic and systematic examination of the weevil subfamily Apioninae is constantly challenged by their relatively uniform appearance. Traditionally, almost all Palearctic apionines, belonging to the tribe Apionini, were assigned to one genus, *Apion*. Most Palearctic taxa live monophagous or oligophagous on Asteraceae and Fabaceae, but many are associated with other plant families, like Lamiaceae, Malvaceae and Polygonaceae and others. According to the host associations in addition to morphological characters, *Apion* is now divided into several genera, which are further grouped into eleven subtribes. However, a comprehensive hypothesis of the phylogenetic relationships within the tribe Apionini is still missing to date. The present study is therefore the first formal phylogenetic attempt to test the monophyly of all Apionini subtribes, to resolve their relationships and to estimate the times of their divergence. We further examined the consequences of differential host plant associations in apionine weevils: a) is host plant use generally conserved, meaning that related taxa feed on related plants; b) are there phylogenetic patterns in the use of particular host plant tissue types (e.g. flowers, seeds etc.); and c) are particular host plant affiliations or shifts to specific host plants associated with enlarged species richness. Our first preliminary phylogenetic analyses propose most subtribes being monophyletic, except of Oxystomatina, Kalcapiina and Aspidapiina. Aplemonina appear as sister group to all remaining Apionini. Divergence time estimations indicate their occurrence in the Upper Cretaceous. Host plant use is generally conserved, with Fabaceae and Polygonaceae and Malvaceae being colonised at least two times.

Archaeotherioiconology

Poster Presentation

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Archaeotherioiconology is the combined archaeological and zoological study of prehistoric mammal depictions. Mammals have been the first objects depicted by man in a recognizable manner, and they remained a key issue of artistic interest since. Naturalistic animal depictions often allow for a recognition of physical traits which can be used from the viewpoints of systematic zoology. A typical result of such a study would be the identification of species or other taxa, including such ones which where not known to have thrived in the respective area and, if circumstances suggest so, may consequently be added to the region‘s faunal list. In various cases, identifiable traits may not be known from other available zoological or paleontological evidence, such as skin colours or fur markings of extinct animal races, so that their investigation would provide a valuable addendum to the understanding of important microevolutionary processes. The paper exemplifies some instances of such archaeotherioiconological studies and concomitantly introduces the work area of the recently-formed ‘Center for Rock-Art Studies and Archaeotherioiconology'. The center is open for all sorts of co-operation projects in its fields of research, which are mainly the Holocene and Later Pleistocene larger mammals of the Palaearctic region, as conventionally understood, yet there are no restrictions to these.

Towards an integrative and comprehensive standard for meta-omics data of collection objects (MOD-CO)

Poster Presentation

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With the advent of advanced molecular techniques and methods, a new era for analyzing and characterizing historic collection specimens, as well as freshly collected environmental samples has started. Sequencing (nucleic acids, proteins) based analyses allow for the recognition of identity, provenance, and even the physiological status of a given object or organism. The fact that microbial organisms can colonize virtually any substrate makes their composition a valuable marker for any kind of deposited dead, deep-frozen or living collection objects. It is of highest importance, to elaborating a standard (schema and vocabulary) for the assignment of any kind of metagenome, metatranscriptome, metaproteome, and metametabolome data to reference samples in natural history and living culture collections. Such Meta-Omics Data (MOD) from analyses, referenced by environmental samples, are necessary for (a) basic research on biodiversity and functional diversity of microbial communities, (b) applied research, e.g. environmental control projects, biotechnology, diagnostics, and monitoring projects.

The aim of MOD-CO (http://www.mod-co.net) is to select and categorize relevant descriptors from a wide range of analysis protocols, and to set up a standard that avoids structural redundancy. The concept is product-oriented, hierarchical, and based on elementary processes. The MOD-CO schema consequently focuses on the description of every individual intermediate of work- and data flows: It describes all relevant procedural steps of an intermediate since the establishment of the preceding one ('retrospective view'). The schema will be published and implemented in the relational database application *DiversityDescriptions* with a generalized data model. All data elements will be organized as descriptors, their dependencies and descriptor trees.

Could tiny dinos take over big waters of the world? – Spatial distributions of unicellular dinophytes

Oral Presentation Student Prize

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The question, whether protists have mostly limited geographical distribution or are cosmopolitan organisms, has recently become a controversial topic, causing much debate between researchers. As a result, many scientific papers were published, supporting either a moderate endemicity model or ubiquitous dispersal hypothesis. Several reasons for the controversy have been proposed – for example, species misidentification and unclear naming of protistan species, including dinophytes. Additionally, due to a lack of generally accepted basis for species delimitation, biogeography of dinophytes is still not well understood. Floating debris, shellfish seed stocks and animal hosts were, together with ballast waters, proven to present a rather common distribution vector for motile dinopyhtes or their coccoid cells. Despite the imminent absence of seawater exchange with, for example, the Mediterranean and the Black Sea, observations of several invasive species, including dinophytes, brought to the Black Sea accidentally, have been made. This data is alarming and demands immediate attention, as those invasive species could be the cause of biodiversity depletion. Moreover, composition of freshwater dinophyte communities may result from both a) radiations after recent transitions from the marine into the freshwater environment as well as b) adaptation to freshwater prior to the formation of the Baltic Ridge older then the Plesitocene and subsequent dispersal to the current habitats. The general aim of the research is to perform a molecular phylogeny analysis with further interpretation of spatial distributions, based on additional new data from samples, collected on several locations across Europe.

Evolutionary and functional implications of gastric caecum diversity among irregular sea urchins (Echinoidea: Irregularia)

Oral Presentation

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Morphology-based inferences of sea urchin (Echinodermata: Echinoidea) phylogeny have traditionally been conducted by incorporating skeletal (usually external) characters only. However, recent studies show that features of sea urchin soft parts – in particular digestive tract components – display sufficient variation among taxa to serve as phylogenetic characters. The present study aims to illustrate evolutionary and functional implications of the diversity observed in the gastric caecum, a specialized organ branching from the gut in most members of the largely infaunal irregular sea urchins (Echinoidea: Irregularia). Using dissections, magnetic resonance imaging and micro-computed tomography, novel developmental, morphological, and morphometric data were gathered from several hundred specimens representing almost 150 Recent species from 35 families in the Irregularia. Three major conditions of the gastric caecum occur among irregular sea urchins: fragmentation of a single caecal lobe into numerous sacculi in lamp urchins (Cassiduloida), presumed loss in most sand dollars (Clypeasteroida) and hypertrophy in many holasteroids (Holasteroida) and heart urchins (Spatangoida). These observations on gastric caecum diversity are discussed with regard to possible correlations with variable expressions of other morphological structures (e.g. Aristotle‘s lantern, internal organs, test, respiratory structures) as well as available life history data (e.g. mode of life, ambient sediment composition, biogeography, bathymetry). The novel morphological data presented here provide a more precise picture of the evolution of infaunal sea urchin taxa, and corroborate the monophyly of major clades.

List of all Authors