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## Abstracts

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### **Re-discovery and designation of type material of Brazilian Polycladida: Treasures found in a museum**

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Polyclads are the most charismatic members of the phylum Platyhelminthes. About 1000 species are described in the world and 71 species from Brazil. Among those, 55 species were described by Ernest and Eveline Marcus, between 1947-1968, with no designated type material. Their study material was donated to the Stockholm Natural History Museum. The aim of this work was to designate type material for those Brazilian species. Thus, we considered, following the ICZN, all specimens from an original series as syntypes; in cases it was possible to distinguish specimens, we differentiated into lectotypes and paralectotypes. For species with designated holotype (without museum voucher number at the time), we listed the holotype material, and other material of the original type series as paratypes. We provided information for type series of 52 species, designating lectotypes for 30 species and paralectotypes for 22 species. Among the 261 type vouchers examined, 22 species had material recognized as holotypes and 2 vouchers recognized as paratypes. From 71 species reported from Brazil, 10 species remain without type material information. The re-discovery of Marcus' type material is important for contemporary and future study of Polycladida as the lack of or damaged type material, and poor descriptions are a huge problem for nomenclatural stability. Type material designations and re-descriptions of old species will expand and improve the quality of the knowledge on Polycladida biodiversity. Most of Brazilian polyclad species were described before digital photography and its combination with improvements on microscopy can add new information on internal anatomy characters.

### **Cryptic diversity and habitat connectivity in groundwater dwelling gastropods: preliminary results from *Bythiospeum* versus *Hauffenia* (Gastropoda: Moitessieriidae and Hydrobiidae)**

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Tiny groundwater dwelling gastropods of the families Moitessieriidae and Hydrobiidae were investigated with respect to diversity and population connectivity. Previous results on *Bythiospeum* diversity pointed to a surprisingly lower diversity and thus stronger population connectivity by underground water. This contradicted the traditionally accepted idea that populations would be more or less strongly isolated and represent different species, as they often greatly differ in shell shape. *Bythiospeum* species are mostly found in cave and groundwater environments being blind and mostly unpigmented, while occasional eye pigmentation in *Hauffenia* species seems to indicate a more superficial, but still interstitial life style. Therefore, we wanted to test if the diversification in the two genera is linked to their habitat with respect to the grade of a subterranean life style and thus habitat continuity. Different surfacing groundwaters were sampled in Eastern France and only locations with co-occurrence of both genera were considered here. Per site we ideally sequenced two or three specimens for 16S and partial COI and photographed their shells. Our phylogenetic analyses recovered five well supported clades of *Hauffenia* and only two clades in *Bythiospeum*. In the latter genus so far only a single species was found per site while in *Hauffenia* we found representatives of two clades in three of the 13 sites studied. Overall genetic diversity is higher in *Hauffenia* confirming our hypothesis of less connectivity. These genetic results are only partially reflected in shell morphology, which points to a strong need of revision of characters used to define *Hauffenia* species.

### **Reaching across the ocean of time: A midge morphotype from the Cretaceous of Gondwana found in Eocene Baltic amber**

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Chironomidae, the group of non-biting midges, is a species rich and abundant ingroup of Diptera, with most larval forms being aquatic. There are 6200 formally described species in the extant fauna and a rich geological history stretching back to the late Triassic. Mesozoic forms of Chironomidae are very different in their overall morphology from modern forms, or Cainozoic non-biting midges in general. Mesozoic forms are usually interpreted as representatives of genera that lack Cainozoic representatives, and genera with Cainozoic representatives lack representatives from the Mesozoic. Here we present an exception to this general pattern. The genus *Libanochlites* Brundin, 1976 was based on a species represented by fossils preserved in Cretaceous Lebanese amber. Here we report a new species attributed to this genus from Eocene Baltic amber. While recognizing two species as belonging to the same genus might be considered a mere taxonomic practice, it in this case emphasizes that both species represent the same morphotype. The two species are very similar concerning aspects of the overall habitus, but also minute details such as those of the genital apparatus or wing venation. This record therefore extends the known geological range of this specific morphotype by 80 million years. This provides us with the first confirmed case of the survival of a Mesozoic dipteran morphotype with aquatic larvae into the Cainozoic. This case indicates bradytely, or evolutionary stasis, in insects with aquatic life stages and the impact of the Cretaceous terrestrial revolution on the evolution of insects with aquatic larvae.

### **Phylogeny of Aeolidioidea (Heterobranchia, Gastropoda) based on morphological data with an emphasis on Facelinidae**

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This study presents a phylogeny of the Aeolidioidea (and two of the currently unassigned Embletoniidae) constructed by morphological characters. Information was collected from literature and own investigations of histological slides. Material of 26 different species was examined, with a focus on Facelinidae, which are represented by 13 species here. Twenty-five morphological characters of external and internal anatomy could be compiled and used for tree calculation. This morphological study will provide an independent dataset which is analysed in parallel to a thorough transcriptome study. Although it is by no means complete, this study can be seen as a first approach to understand evolution especially of Facelinidae within Aeolidioidea.

### **Deglaciation time shapes genetic diversity of green algal symbionts in the Antarctic pioneer lichen genus *Placopsis***

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Since ice-free areas in Antarctica are predicted to increase by up to 25% until the end of this century, lichens of the genus *Placopsis* will be important colonizers of these newly available grounds and will still be present in later successional stages of the lichen community. The main symbionts of *Placopsis* species are examined for 56 specimens collected from the South Shetland Islands, Antarctica using molecular (fungal and algal nrITS, fungal RPB1, algal rbcL sequences) and morphological methods. The specimens were collected from soils with different deglaciation times. Uni-algal photobiont cultures were obtained and analysed from two specimens. *Placopsis antarctica* and *P. contortuplicata* proved to be monophyletic and are sister species, only the first one producing vegetative diaspores (soredia). Both share the same photobiont pool and are lichenized with two closely related species, *Stichococcus antarctica* and *S. allas*. Two haplotypes of *S. antarctica* are restricted to areas deglaciated for more than 5000 years and the volcanic Deception Island indicating a shift in the photobionts of *Placopsis* in the course of the soil and lichen community development. These photobiont haplotypes exhibit different ecological preferences, possibly leading to adaptation of the symbiotic entity to changing environmental conditions.

### **New species and hybrids in *Typha* – an example from Austria**

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Newly build waterbodies along a newly built railway in Lower Austria are ideal research sites to examine the spontaneous vegetation of water bodies. Due to their numerous and wind distributed seeds *Typha* are often among the first plants to colonize newly exposed wetland habitats. According to the Flora of Austria there are five species of *Typha* found in Austria. Investigation of herbarium specimen of *Typha*, showed differences between samples referred to be the same species and also not all specimens could be unambiguously referred to a species described in the Flora of Austria. Determination of herbarium specimen and newly collected material from the above-mentioned waterbodies with Floras from other regions showed that there are much more species of *Typha* found in that region than described in the Flora of Austria. Several accessions also showed to be hybrids between species (e.g. *T. × glauca* hybrid between *T. angustifolia* and *T. latifolia*). To be able to find out from where these new introduced species come and also to find the parental species of putative hybrids, a variety of *Typha* samples from nurseries in the examination-region was bought to investigate them. In addition to the morphological extermination of the material, we also conducted flow-cytometry to estimate the genome size of the samples. These analyses showed that all investigated species except those referring to *T. minima* (2C ~ 0.8 pg) have a very uniform genome size (2C ~ 0.54 pg). A similar genome size is an important basis for possible hybrids without polyploidization.



### **The search for the correct species delimitation in protists: from *Monas* to *Poteriespumella* and beyond**

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The genus *Monas* is one of the first scientifically described protist genera. Many of the species originally affiliated with this genus were later transferred to other genera, phyla, taxonomic supergroups and even domains of life. Further, the conceptual idea of species and species delineation changed over time. The electron microscopical era, while providing insights into the morphology and ultrastructure of protist cells, triggered a mechanistic view of species. Consequently, morphospecies were considered the gold standard. Subsequently upcoming molecular phylogenies demonstrated a high microdiversity, i.e. intraspecific variation, and further polyphyly of many lineages. Recently, corresponding eco-physiological, morphological and phylogenetic data seemed to allow for convincingly delineate species. However, whole genome sequencing again calls species delineation into question thus further adding a new perspective to the estimate of protist species diversity and delineation.

### **Opportunities and challenges for natural history collections in the 21st century**

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Biological specimens in natural history collections are primary data and have always played a crucial role as type material and in research documentation. However, with the boost in DNA analyses and global change studies, collections became not only storage but much more the source of material for a wide range of projects. In addition, at least in botany, both number of registered collections and specimens included is constantly growing. For collections, the increased demand is a chance, but also a massive challenge. Access to specimens and related information is an integral component of the convention on biological diversity (CBD). It helps overcoming the taxonomic impediment to CBD-implementation and allows repatriation of knowledge. Virtual access helps to study range dynamics and changes in phenology or traits, but physical access is needed for anatomical, microscopical, chemical and DNA analyses. While the demand of the scientific community for direct and indirect access is massively increasing, most collections, especially those associated with universities, are facing severe problems, including staff and budget cuts, outdated IT infrastructure, and increase in administrative workload due to CBD and Nagoya regulations. These well-known and documented challenges can only be faced with qualified personnel and adequate resources. This would also guarantee data to be compliant with FAIR principles including unique stable identifiers. Proposed benefits like co-authorship or fees for access may help documenting the collections contributions for stakeholders; a better solution would be a stronger commitment of science policy makers towards the development of the collections, including additional funding opportunities.

### **Quantifying morphological diversity in mantis shrimp larvae**

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Since the beginning of the last century, a common theory in the study of larval organisms has been put forward. The idea was largely pushed by Haeckel, and others, suggesting that larval stages (and other immatures) display a rather uniform appearance, leading to an overall low morphological diversity. Adult morphology was thought to be much more diverse and manifold in comparison. This assumption has found backlashes in the course of the last decades. Here, we address this issue at the example of mantis shrimps (Stomatopoda), a group of malacostracan

e crustaceans. About 500 marine species inhabit most parts of the world, with the exception of polar regions. Special about mantis shrimps is the massive raptorial claw that is used in two different ways in adults for preying: a 'spearer' and a 'smasher' type have evolved in the adult benthic stages. The planktic larval stages seem to possess a rather uniform dagger-like morphotype of the claw. We quantified this character among other body features in mantis shrimp larvae from different zoological collections all over Europe (Paris, Copenhagen, Hamburg, etc.) and amended these by data from literature. Statistical analyses reveal that the morphological diversity in larval mantis shrimps in this character is actually higher than in adults. This hints towards a larger diversity in predation strategies and accordingly stronger niche differentiation. In the light of predation on mantis shrimps by commercial fish, this furthermore hints towards a larger ecological and economical relevance of mantis shrimp larvae than expected so far.

### **Reinforcing plant evolutionary genomics using ancient DNA**

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Humans have a vast transformative effect on ecosystems, which keeps shaping plants' distributions, phenotypes and genetic diversity. Tracing these changes over time is central to understand their consequences on plants' adaptability to a changing environment. Although contemporary genomes contain a record of species history, inferences based on them are uncertain, and confounded by, for instance, previous demographic history. Ancient DNA research makes it possible to directly assess historical genomes, refine demographic models, and gauge the role of natural selection in shaping the distribution of phenotypes over time. In the first part of the talk I will present an in-depth description of the biochemical characteristics of DNA retrieved from herbarium specimens. Using herbarium specimens collected in the last 300 years, I will show the temporal patterns of DNA damage and decay kinetics in this type of tissue and suggest approaches to authenticate the historic nature of the retrieved DNA. In the second part, I will present two examples of the dispersal of plants outside of their native range, in which plants changed latitude and required additional adaptation to new ecological conditions.

### **Bridging the gap to conservation genetic application: The importance of globally representative and versatile reference datasets for genetic inventory and monitoring initiatives**

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Forecasts of species' responses under quickly and potentially unpredictably changing climatic and environmental conditions, require reliable and detailed insight into the current state of a species, as well as, the processes shaping its responses to change, inferred from its past evolutionary history. Such knowledge supports long-term sustainable conservation and management strategies and allows societies in dynamic contexts to come to adequate decisions in time and to effectively act. Reference datasets spanning a species' evolutionary relationships and distribution range, its abiotic and biotic environments and all of its genomic record provide the necessary overall evolutionary and ecological context for hypothesis testing and prediction. This is essential, since inferred phylogenetic and population-genetic patterns and summary statistics are, in general, context-dependent. Furthermore, in evolving and highly complex natural systems, information-rich, sequence-based genomic data, optionally sampled repeatedly by monitoring campaigns representing different states across time, is required to support models and inference approaches, which are powerful enough to differentiate multiple processes that are simultaneously acting at different levels and might show continuous variation across space and time. Reference datasets, thus, are at the core of conservation genetic

applications. They provide the versatile and sufficiently informative genetic foundation for accurate, decisive and reliable conclusions. Their implementation requires, first, the in-depth expertise and extensively interconnected and cross-referenced infrastructure of professional specimen and data management, as provided by natural history collections. Second, the development of integrated statistical inference environments that are open-source and user-friendly for quality assurance, complementary, independent analyses and for syntheses.

### **Evolutionary history of the megadiverse Neotropical genus *Philodendron* Schott (Araceae): Out of Amazonia and back again**

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*Philodendron* is one of the most characteristic components of the Neotropical rainforests ranging from tropical Mexico to southern Brazil, and the Caribbean islands. With an estimated ~700 to 1,000 species, *Philodendron* is the second largest genus in the family Araceae. We performed the largest phylogenetic reconstruction for *Philodendron* to date based on a molecular dataset of three non-coding plastid DNA regions (*petD*, *rpl16* and *trnK/matK*) including 173 taxa (221 accessions). Our results indicate that *Philodendron* and its three subgenera *Meconostigma*, *Philodendron* and *Pteromischum* are monophyletic. Divergence-time estimates and inferences of the geographic range evolution revealed that *Philodendron* originated ~29 mya in the pan-Amazonian region. Overall, the current geographic distribution of *Philodendron* is the result of multiple geographic range expansions: since the middle Miocene onwards from Amazonia to northwest South America and southeast Brazil; and more recently during the Miocene-Pliocene transition from the Chocó ecoregion to Central America, and from South America to the Caribbean islands. Time-dependent diversification rate shift analyses revealed that the diversification process of *Philodendron* combines elements of the two models used to explain the origin of the species diversity in the Neotropics: the 'cradle' model, which postulates a more recent and faster diversification rate (subgenus *Philodendron*), and the 'museum' model, which assumes an older and more constant diversification rate (subgenera *Meconostigma* and *Pteromischum*). Furthermore, we demonstrate a potential indirect impact of the rise of the Andes from the middle Miocene onwards on the diversification process of plant lineages distributed in the adjacent lowlands of the northern Andes.

### **The use of environmental amplicon NGS sequencing, well-curated DNA databases from vouchered collections and type material in the discovery of the Dinophyte biodiversity in Bavarian lakes (Germany)**

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Reliable determination of organisms is a prerequisite to explore their spatial and temporal occurrence, and to investigate their evolution and ecology. The identification issue is

challenging for the study of unicellular organisms, but the development of sequencing techniques has helped to overcome the limitations intrinsic to their microscopic size. In this study, we obtained highthroughput rRNA amplicon sequence data from environmental water samples collected from thirteen localities in Upper Bavaria (Germany), to investigate the diversity and distribution of freshwater dinophytes in this region. The Bavarian lakes provide a great study system due to the presence of extensive lake districts and ice age river valleys, which are ecologically very diverse. We found 186 operational taxonomic units (OTUs) associated with Dinophyceae that were further classified by means of a phylogenetic placement approach. The phylogeny was inferred from a well-curated reference alignment and comprised a systematically representative set of 251 dinophytes, covering the currently known molecular diversity, and considering DNA sequences linked to type material. Environmental OTUs were scattered across the reference tree, but accumulated mostly in freshwater lineages, with 79% of OTUs belonging to the most frequently encountered taxa in Bavaria based on morphology. Twenty-one OTUs showed identical sequences to already known vouchered accessions, two of which are linked to type material, namely *Palatinus apiculatus* and *Theleodinium calcisporum*. Our approach highlights the importance of high throughput sequencing of environmental samples coupled with well-curated reference databases including vouchered collections and type material in the species determination of freshwater dinophytes in Bavaria.

### **Preliminary Insights into the Phylogeny of the Paleotropical Dioecious Clade of Guettardeae (Rubiaceae): New Perspectives and Challenges**

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The generic boundaries within the tribe Guettardeae of Rubiaceae (~750 species in ca. 20 genera) remain unresolved, and taxonomic stability is still far from being reached. Majority of its Old-World members belong to *Antirhea* Comm. ex Juss., *Guettarda* L. and *Timonius* Rumph. ex DC. In the first and only broad phylogenetic study of Guettardeae, *Antirhea* and *Guettarda* were revealed to be para- and polyphyletic, respectively; however, no new generic delimitations were proposed. On the other hand, *Timonius* was considered to be a natural assemblage, but this is uncertain due to the limited sampling, neither representing the morphological nor geographical variation in the genus. Here, we revisited the ITS-based phylogeny of Guettardeae by focusing on the 'Paleotropical dioecious clade' with an expanded sampling and addition of nuclear ETS and chloroplast (*atpB-rbcL*, *trnT-F*) molecular datasets. Our preliminary findings revealed that the nuclear regions resulted in almost fully resolved Guettardeae, while the chloroplast markers exhibited low sequence variability resulting in unresolved trees. Even though there were no phylogenetic conflicts observed between the two genomes, the reconstruction presented here is based on nuclear markers only. The phylogeny validates previous hypotheses for *Antirhea* and *Guettarda*, but *Timonius* is polyphyletic and forms three well-supported lineages: 1) *Abbottia* group, 2) *T. auriculatus* group, and 3) *T. timon* group. Although the results reported here are considered as preliminary, we reviewed clade-specific morphological characters supporting these lineages to highlight potential implications for the much-needed taxonomic clarification in this scarcely investigated group.

### **Are Sacoglossa sea slugs able to 'live from the sun'?**

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Sacoglossa sea slugs are truly fascinating. They are the only animals that are able to incorporate the chloroplasts of their food algae in their own cells. In some species the 'stolen' chloroplasts – the kleptoplasts - are photosynthetically active for weeks or months. This intriguing phenomenon is described by the term functional kleptoplasty and is also interesting for the popular press, because there are 'Slugs that eat the sun', 'Slugs that become a plant', and 'Slugs that are photosynthetic'. These headlines are eye-catching but also problematic in many ways, because the impression is created that the slugs are actively involved in the process of keeping the kleptoplasts active and that they need them for their survival – just like a plant. But is this really the case and what is the evidence? Can Sacoglossa sea slugs actually be called 'photosynthetic'? Besides uncertainties about the mechanisms involved in the uptake and maintenance of the kleptoplasts in the cell, it is still unknown how the kleptoplasts stay photosynthetically active and if and how much the alien organelles support the physiology of the slugs. Many studies concluded that the kleptoplasts are important to overcome starvation periods and boost the slugs' physiology. Yet, often results rather support the idea that the plastids might serve as some kind of larder than having the same function as in their native algal cytosol. Sacoglossa sea slugs should not be called 'photosynthetic', but functional kleptoplasty remains fascinating.

### **Delimitation of sexual species in the *Ranunculus auricomus* complex (Ranunculaceae): evidence from RAD-seq and morphological data**

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The *Ranunculus auricomus* complex is a Eurasian agamic complex consisting of 12 described sexual taxa and 750 to 800 morphologically described apomictic lineages. Some sexual species have been safely identified as progenitors of the complex and allopolyploidy has been demonstrated for at least one apomictic lineage, but a comprehensive picture of the complex's evolutionary history does not yet exist. Implementing a 'diploids first' approach with the aim of better understanding species delimitations in the sexuals of the complex has been suggested as an essential step towards this goal. Ploidy measurements and flow cytometric seed screening (FCSS) were used to confirm populations as di- and tetraploid sexuals. Restriction-associated DNA sequencing (RAD-seq) and target enrichment of nuclear genes were used to reconstruct phylogenetic relationships and genetic clusters. Geometric morphometrics based on fresh and herbarium material was employed to identify distinguishing morphological characteristics. Based on those results the current number of described sexual species may overestimate the actual diversity. Genomic structure and morphometric data identified just five distinct lineages. Shape and size of the basal and stem leaves and the trichome density of the receptacle distinguished between lineages most successfully.

### **Heterostyly in Connaraceae - a first herbarium-phylogenomic analysis of an understudied tropical clade**

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Until recently, herbarium specimens had limited utility for molecular phylogenetics because of the poor quality of DNA preserved in specimens. As a result, clades where sample acquisition has proven particularly burdensome (such as in chiefly tropical families), remain poorly known although they may offer exceptional opportunities for addressing particular evolutionary questions. Here, we leverage recent advances in herbarium-phylogenomics to address the evolution of heterostyly in the pantropical plant family Connaraceae (Oxalidales, ca. 200 spp.). Heterostyly is a widely studied model for the ecology, evolution, and genomic organisation of plant reproductive systems. According to textbooks, heterostyly comes in two flavors: populations contain two (distyly) or three (tristyly) floral morphs that differ in the spatial position of male and female sexual organs within flowers, combined with a sporophytic self- and intramorph incompatibility system. However, contrary to this predominant view, early morphological studies suggested at least seven different types of heterostyly in Connaraceae, including tristily, distily, several intermediate forms, and monomorphic species. Thus, Connaraceae offers the potential to reconstruct the evolutionary pathways that lead to and from various types of heterostyly, but a molecular-phylogenetic framework is lacking. We present the first molecular phylogeny for Connaraceae, including 45 species representing all accepted and dubiously synonymized genera, sampled almost exclusively from herbarium specimens. We used a targeted enrichment approach for 353 putatively single copy genes that are conserved across angiosperms. Based on the results, we evaluate supra-familial classification and generic circumscription and present implications for the evolution of the heterostylous syndrome.

### **Simultaneous speciation in the European high mountain genus *Facchinia* (Caryophyllaceae)**

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*Facchinia* (Caryophyllaceae) comprises seven species and two subspecies of high mountain plants restricted to the European Alpine System (EAS). Five species occur in the Alps, one in the Pyrenees and one in smaller mountain ranges near Valencia (Spain). While six of the seven species are restricted to relatively small areas, *F. rupestris* has a larger distribution range and occurs in sympatry with other species of the genus. We used Sanger sequencing and genotyping-by-sequencing (GBS) to reconstruct the phylogeny of *Facchinia* and to explore possible mechanisms of speciation in the genus. We sampled all taxa for Sanger sequencing and all but the Pyrenean *F. cerastiifolia* for the GBS analyses. Data was analysed using a variety of methods to reconstruct species trees and phylogenetic networks. All analyses resulted in a basal polytomy that could not be resolved with any method. Our approach allowed us to exclude hybridization, incomplete lineage sorting and character saturation as explanations for our results. This led to the hypothesis that speciation in *Facchinia* took place simultaneously. Thus, the basal polytomy found is not an artefact of sampling or analysis but illustrates a biological reality. The flora of the Alps and the EAS were highly impacted by glaciation and deglaciation during glacial/interglacial cycles of the Quaternary. A plausible scenario for the evolution of *Facchinia* and for the phylogenetic pattern found is that a widespread ancestor of the genus was forced into different and geographically isolated refugia in Quaternary glacials, where simultaneous speciation took place in allopatry.

### **Towards a worldwide revision of the digger wasp genus *Sphex***

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*Sphex* Linnaeus, 1758 is one of the most well-known digger wasp genera. Many of its members are large and conspicuous and are often collected. Over 130 species have been described. Despite this, the genus is generally in poor taxonomic condition. Especially high-diversity tropical regions are only sparsely covered. Sub-Saharan Africa, South America with the exception of Argentina and Chile, and South East Asia are the most salient areas. The few available revisions for those regions are outdated and often focus on diagnostically dubious characters. Identification keys are incomplete, images are lacking for the majority of species, and virtually no molecular data exist. This project aims to remedy the aforementioned issues by revising the members of the genus *Sphex* from each of the important regions. Having completed Australia, a revision of the Afrotropics is currently underway. Morphological characters, some of which have not been studied before, are used for initial species attribution, and subsequent genetic analyses reveal species identities as well as phylogenetic data and enable a substantiated assignment of males and females. Over 1600 pinned specimens belonging to at least 38 different species were already examined morphologically by us, with nine of them likely being undescribed. We have reliably amplified a partial region of the CO1 mitochondrial gene from specimens collected up to 35 years ago. In conjunction with sequence data from various other sites, we will be able to reconstruct the evolutionary history of *Sphex* all over the world and propose the first phylogeny within this genus.

### **Next-Generation Sequencing of Chloroplast Genomes in *Leucanthemum* (Compositae, Anthemideae) using long-range PCR**

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The genus *Leucanthemum* Mill. (oxeye daisies, marguerites) represents a polyploid complex in the chamomile tribe Anthemideae of the sunflower family (Compositae) with approximately 42 frequently hybridizing species. To elucidate evolutionary relationships within such closely-knit groups, the analysis of whole chloroplast genomes has become increasingly common. Apart from being used for whole-chloroplast phylogenies, plastomes can be mined for phylogenetically informative markers, which permit more cost-effective, yet still reliable delimitation of species. However, to date only very few chloroplast genomes are available for tribe Anthemideae, and none for the genus *Leucanthemum*. In the present study, we designed a comprehensive and effective workflow for next-generation sequencing of whole chloroplast genomes in the genus, which is based on Illumina sequencing of 16 long-range PCR amplicons [Uribe-Convers et al. 2014, Applications in Plant Sciences 2(1): 1300063]. The chloroplasts of two *Leucanthemum* species, *L. virgatum* (Desr.) Clos and *L. vulgare* Lam., have been successfully sequenced and annotated this way. The two plastomes differ in 272 substitutions, 56 deletions and 43 insertions. A search for mutation hotspots revealed that the *trnE-rpoB*, *ndhF-rpl32*, and *rpl32-trnL* intergenic spacer regions show the highest variability, making them useful candidates for lower-level phylogenetic studies in the group.

### **More than meets the eye: Comparative phylogeography of the North Sea/Baltic Sea environmental gradient**

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The Baltic Sea is a unique habitat because of its strong salinity gradient and young age (ca. 8000 years). However, the organisms inhabiting the Baltic Sea were long thought to be but depauperate extensions of their North Sea ancestors. Only recently have we begun to appreciate the genetic distinctiveness of Baltic Sea populations, which can be the result of adaptations to the unique environmental conditions of the Baltic Sea, or of limited gene flow between North and Baltic Sea. To gain a more comprehensive view of Baltic Sea diversity, I compared population-wide mitochondrial sequence data from several prominent marine invertebrates of the macrozoobenthos from North and Baltic Sea. I find that following our expectations, genetic diversity is lower in some, but not all species. Moreover, a number of species, all of which are crustaceans, have higher genetic diversity in the Baltic Sea than the North Sea. About half of the species are genetically indistinguishable from their North Sea ancestors, including several recent colonizers of the Baltic Sea. This result is not surprising but raises the question if the other undifferentiated species are also recent additions to the Baltic Sea. I investigated this hypothesis in a comparative phylogeographic framework using a hierarchical approximate Bayesian computation model, implemented in the program 'msBayes'.

### **The longer the better or short and accurate? Collinearity and synteny in *Tethya* (Porifera: Demospongiae)**

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For comparative genomics and DNA taxonomy, the identification of orthologous genes, those that are derived from a last common ancestor by speciation, is crucial. The correct identification of orthologs can be difficult, because a gene could have originated by gene duplication and not speciation. Those so-called paralogs, therefore, may prove misleading in a taxonomic context due to their non-orthologous origin and evolutionary history. Whole genome assemblies can provide useful information on the genomic makeup of a species, including collinearity and synteny, the arrangement of genes in the same order or their co-location on the same chromosome, respectively. Collinearity and synteny information may help to detect and support ortholog identification by comparing gene order and chromosomal location. Gene prediction, comparison, collinearity and synteny reconstruction usually require accurate DNA sequence information over long stretches, ideally chromosome-scale scaffolds. Here we present a pipeline that combines existing gene prediction and alignment tools with custom perl scripts to identify ortholog genes even in long reads with a relatively high error rate. We use an improved assembly of the recently published genome of the sponge *Tethya wilhelma* and genome drafts of two congeners (*Tethya minuta*, *Tethya citrina*). The existing *T. wilhelma* genome was improved by including information from CHICAGO and HiC libraries, and the latter two were assembled either from Nanopore (MinION, Oxford Nanopore) or Illumina paired-end sequencing data. With these datasets, we show how collinearity can be visualized on fragmented but accurate sequences as well as on much longer but error-prone Nanopore based assemblies. We discuss the advantages and disadvantages of including collinearity and synteny information in the different steps of ortholog identification.



## Evolution of carnivory in angiosperms and diversification of trap types

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Carnivory has evolved at least ten times in flowering plants, resulting in 19 carnivorous plant genera containing a total of at least 800 species. Five basic trap types are found among carnivorous plants (pitfall traps, adhesive traps, snap traps, eel traps, and suction traps), and the former two types have evolved at least three times in parallel in distantly related groups. On the other hand, suction traps, snap traps, and pitfall traps at least in the case of Nepenthaceae, have evolved by modification of passive flypaper-type traps. The orders Lamiales and 'non-core Caryophyllales' (Nepentales) are of special interest regarding trap evolution, as within each of these two groups, different trap types have been realized from a common carnivorous ancestor. Within Nepentales, loss of carnivory has occurred in two families of rainforest lianas (Dioncophyllaceae and Ancistrocladaceae). Carnivory dates back to c. 85 Mya in Nepentales and to c. 44 Mya in crown Lamiales (stem ages of carnivorous clades). The evolution of carnivory did not affect diversification rates in any lineage where this has been tested with modern comparative methods, rejecting botanical carnivory as a 'key innovation'. Most early-branching carnivorous lineages are species-poor (often monotypic), and those genera which are species-rich today (*Drosera*, *Utricularia*, *Nepenthes*) already were carnivorous long before they diversified - here it was rather modification of a given trap type in adaptation to different habitat niches (or prey spectra), but also geographic radiation, that led to the present species diversity.

## Think global, act local - what the seemingly increasing number of Austrian animal species can tell us

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In 1998 Geiser published that 45870 species of animals occur in Austria. An update after 20 years on behalf of Zoological Botanical Society Austria (Geiser 2018) resulted in 54125 animal species reported for Austria. Insects alone account for 40 000 species. This increase by 8255 species or 18 % is first and foremost due to an improved level of scientific knowledge. On the one hand, several projects of pure and applied science provided a lot of new data and lists which can be analysed to gain species numbers of animal groups in Austria. On the other hand, these numbers will be always fuzzy and disputable, to mention only the problems caused by alien species or subspecies status. Also, there are a considerable number of species for which only few individuals have been recorded in Austria. Others have not been recorded in Austria for more than 50 years. Although the species number has seemingly been magnified, it does not mean that pressure on biodiversity has decreased. To the contrary – biomass is shrinking. Therefore, it is necessary to consider that this seemingly encouraging number of animal species in Austria only reflects a status which includes an increasing number of endangered species.

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### **The importance of the epitype concept for reliable species determination in protists such as dinophytes**

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For unicellular organisms, the biodiversity assessment did not start until the late 18<sup>th</sup> century using light microscopy. Type material, particularly of older taxa, consists of specimens mounted permanently on glass or mica slides (a historically important example is the Ehrenberg Collection in Berlin) or of illustrations only. In many cases, type material is ambiguous and makes reliable species determination problematic because of various sources of error, including imperfect documentation of subcellular diagnostic traits or insufficient morphological differentiation within cryptic species complexes. For a correct application of such ambiguous scientific names, the Shenzhen Code (ICN) provides a tool for an epitype designation. In our ongoing research, we clarify the taxonomic identity of dinophytes (such as *Durinskia oculata* from Prague, Czech Republic; *Palatinus apiculatus* from Berlin, Germany; *Heterocapsa steinii*, *Prorocentrum micans* and *Scrippsiella acuminata* from Kiel, Germany; *Parvodinium mixtum* and *Spiniferodinium limneticum* from Tatra Mountains, Poland) by collecting samples at corresponding type localities. If establishing living strains are morphologically consistent with corresponding protologues, then they are used for designation of interpretative epitypes in form of permanent slides for light microscopy. The significant difference from the historical types is that epitypes correspond to living material enabling DNA sequencing, deep morphology study as well as experiments in ecology. Thus, epitypification is a key tool for a stable taxonomy and reliable species determination ensuring unambiguous link between a scientific species name, its protologue, morphology, ultrastructure, genetic characterisation and spatial distribution, all of which are of great importance especially for character-poor, unicellular organisms such as dinophytes.

### **The monophyly of the water lilies remains uncertain – How standardized data collection and automated bioinformatic processing is key to plastid phylogenomics of early-diverging angiosperms**

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The comparative analysis of complete plastid genomes has become a method-of-choice for evolutionary botanists. Both sequencing and phylogenetic analysis of dozens, if not hundreds, of plastid genomes per investigation have become commonplace. Thus, thousands of novel plastid genomes are being released each year, creating a valuable resource for biological research. However, the ease and speed of sequencing complete plastid genomes are leading many researchers to forego established data collection and analysis procedures, including the preservation of plant source material, automated – and, thus, standardized – bioinformatic data processing, the case-specific selection of phylogenetic reconstruction methods, and the continued curation of published sequences. As a result, a considerable portion of existing plastid genomes cannot be linked to – and, thus, re-created from – plant material stored in herbaria,

botanical gardens or DNA banks, re-assembled from original read data, or trusted as having been updated upon the identification of assembly or annotation errors. Here, I discuss the impact that these factors can have on evolutionary research of early-diverging angiosperms. Specifically, I report on a series of plastid phylogenomic investigations of the water lilies (Nymphaeaceae) and relatives that differ in their conclusions due to differences in data collection, automated bioinformatic processing, customized phylogenetic analysis, and the use of curated genome sequences. I particularly highlight the finding that different genes of the plastid genome support different phylogenetic relationships at statistically significant levels, challenging the idea of linkage among all plastome genes and highlighting the importance of customized tree reconstruction strategies in plastid phylogenomics.

### **Old, but still en vogue – how closely do fossil may fly larvae resemble their modern counterparts?**

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Mayflies (Ephemeroptera) are flying insects, easily identifiable by (usually) three thread-like structures arising from their terminal ends. Within Pterygota, the group of flying insects, modern mayflies are representatives of an old lineage, with their sister lineage leading to Odonoptera (dragonflies, damselflies and fossil relatives). Most of their lives, ephemeropterans spend as aquatic larvae. Also, the larvae can be easily recognised, by the presence of three thread-like posterior structures, but additionally by prominent gills on the abdomen. In modern river ecosystems may fly larvae play an important role as herbivores and detritivores; few species are predators of other insects, or prey for various fish species. Most important, many of them are bioturbators. Fossil mayflies seem to resemble modern ones already to a large degree, not only as adults, but also as larvae. Connecting larvae and adults of fossil species is often challenging, making biodiversity estimations of the past tricky, as most mayfly taxonomy bases on adults. Here we compare morphological traits of mayfly larvae through time to evaluate possible changes in ecological role of the larvae. Fossil may fly larvae are known from down into the Permian. Especially beautiful examples are known from Mesozoic deposits, and they are especially abundant in Cretaceous faunas such as the one from the famous Crato formation. Despite the theoretically good data base, especially from different museum collections, preservational differences still provide challenges for comparative studies. We present first attempts to this morphological approach and discuss possible ways to overcome outlined difficulties.

### **Thinking beyond the adult paradigm benefits from thinking beyond the taxonomic paradigm, or: the long path towards new approaches for understanding diversity**

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Taxonomy has for quite some time been considered an old-fashioned discipline. This has changed tremendously. In the age of conservation biology, biodiversity loss and the ‘extinction of insects’, measuring diversity has become crucial, and the basic starting point for inferring biodiversity is still counting of taxonomic units. In many groups of organisms, taxonomy is therefore still the ‘science of the adult male’, not least in most areas of entomology, as for adult males it is usually least difficult to identify them to species. Yet, it is important to note that the adult male is in most cases the most short-lived morphology within a species. This simply means that larvae (or other immatures) or females usually interact longer with other ecosystem components. Especially in species with long-lived larvae, mayflies may serve here as a simple example, the ecological impact of an individual is on the larval side. Yet, many immature forms cannot be easily determined. New molecular tools have greatly improved the situation, but still

fail regularly in historical collections (which are full of material of immatures) and totally in fossils. Hence, we need to develop concepts that allow us to abandon the common practice of ignoring immatures and include them into diversity assessments. A major challenge for doing so is that larvae can often not be easily identified to a narrow taxonomic group. The key to reach the realm beyond the adult paradigm is therefore going beyond the taxonomic paradigm. I discuss possible first steps in such a direction.

### **Insect monitoring 2.0 based on metabarcoding**

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Nature conservation strategies and environmental monitoring are often focused on vertebrates and plants which allow for comparatively easy monitoring. Most insects - although covering 70-80% of the terrestrial animal diversity - are ignored in environmental and ecological research as well as in monitoring approaches: Just 1-2% of our insect fauna can be regarded as well-established indicator groups, including butterflies (Rhopalocera), ground beetles (Carabidae), dragonflies (Odonata) and 'grasshoppers' (Orthoptera). The identification of most other insects was severely hampered by the 'taxonomic impediment', that is, the time-consuming morphological analysis and lack of experts. We show that large-scale insect monitoring - which has become an imperative considering the worrying facts of insect decline in Central Europe - is now possible through DNA barcoding based on the sequencing of the COI 5' gene fragment: In two major projects, German Barcode of Life and Barcoding Fauna Bavarica, we have assembled DNA barcodes for some 24,000 German animal species. Based on this comprehensive genetic library, lists of thousands of species can now be generated from huge mixed bulk samples through quick, efficient and cheap metabarcoding approaches. For this purpose, we improved sampling strategies and bioinformatic workflows. We present promising results from two insect monitoring projects establishing an 'early warning system for pests and invasive species' and investigating 'insect responses to organic and intensive farming.'

### **Admixture and fast speciation in species complexes of phytophagous Hymenoptera and Orthoptera: A MuseOMICS approach**

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Clusters of molecular OTUs, like mitochondrial haplotypes or DNA barcodes, generally correspond closely to biological species, but exceptions exist. In particular, phytophagous Hymenoptera and acridid Orthoptera exhibit haplotype sharing across species complexes, even comprising different genera, and/or barcode divergence within species. This phenomenon was detected in >20% of species studied in the former (N=822) and 41% in the latter group (N=70). Sawflies (Hymenoptera: 'Symphyta') and grasshoppers (Orthoptera: Acrididae) represent different type of organisms, such as holo- vs. hemimetabolan, species-rich vs. species-poor, and taxa with small vs. very large genomes. Possible causes for haplotype sharing between species are hybridization, incomplete lineage sorting, nuclear mitochondrial pseudogenes (numts), and the influence of *Wolbachia* bacteria on the reproductive system of the host organisms. We studied a selection of species of the two aforementioned groups from Central Europe and employed RAD sequencing to generate genomic data sets with the aim of detecting genetic admixture. Specifically, we used the hyRAD approach for low-quality DNA samples, as many species were only available as historical specimens from museum collections. To study numts in Orthoptera, we first isolated mitochondria from tissue to extract the barcode ortholog and then ran an amplicon sequencing to study the diversity of numts.

### **The diversity of mantis shrimp larvae – adding new extreme forms**

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Loss of diversity has become an important key word, also for non-scientists. Marine diversity is heavily represented by planktic organisms. Among them, crustacean larvae form a large part of the plankton. Mantis shrimps (Stomatopoda, Verunipeltata) are among those crustaceans with very long-lasting larval phases. Similar to their adults, mantis shrimp larvae live as predators feeding on other planktic organisms. They can reach formidable sizes of several centimeters and are an important food source for planktivorous fishes. Hence, they are of potentially significant ecological importance. Despite this, their development and diversity remain largely understudied. Recent findings of previously unknown, 'extreme' morphotypes of stomatopod larvae have highlighted how limited our knowledge especially concerning the morphological diversity of such larvae is. It also demonstrates that diversity in an ecological sense reaches beyond taxonomic diversity. Herein, we report two novel specimens of extreme stomatopod larvae. They can be considered 'extreme' both in terms of their size and their rather aberrant shield morphology. They were found in the crustacean collection of the Centrum für Naturkunde (CeNak) of the University of Hamburg. Representing erichthus-type larvae, they belong to the extreme morphotype termed 'spiny balloon'. We discuss the functional morphology and possible connection of the new specimens in relation to the single previously known 'spiny balloon' larva. With this, we contribute further insights into the still very limited knowledge of stomatopod larval diversity and development.

### **Comparing the morphological diversity of larvae and adults of neuropteran insects through time**

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Larvae of many insects possess different morphological features and lifestyles when compared with their adults. This is especially the case in holometabolan insects, such as neuropterans (lacewings). Lacewing larvae have a predatory lifestyle and have a clear morphological specialization in their elongated mandibles. In fact, the mandibles form complexes with parts of the maxillae, combining them to a pair of piercing-sucking stylets. In most lacewing larvae these are used for injecting venom into the prey and then for sucking the body fluids. Larval diversity of extant species is astonishing concerning their ecological differentiation, including for example: 1) parasite-like forms (later larval stages of Mantispidae); 2) aquatic, almost worm-like, flexible active hunters in nevrothiids; 3) sand-buried ambush predators, partly with sand funnel pits as in ant lions (Myrmeleontidae), with sometimes sharp, enlarged stylets. There is also a rich fossil record of such larval forms, mostly from several kinds of amber. Morphological diversity seems to be higher in fossils than in extant forms. However, fossil holometabolan larvae are challenging to be included into evolutionary reconstructions and diversity assessments, as identifying their species is, at best, an educated guess. We therefore use a morphology-oriented approach. Ten dimensions were measured in extant and fossil neuropteran larvae and adults. Differences in morphology can be recognised and can be correlated to specific time slices (100 mya, 50 mya, today) allowing us to reconstruct changes of larval and adult morphology through time and to compare the morphological diversity of adults versus that of larvae.

### **Tracking of 2600 individuals in an urban garden shows that small European solitary bees have mean foraging distances below 185 m**

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Bees are important pollinators, but they are in decline. In order to protect wild bees, conservationists and politicians are in need of data about bee flight distances and possibilities for effective resource enhancement. In the Munich Botanical Garden, we assessed the flight distances of some 2600 individually marked individuals from six species in a flower-rich environment in an urban context. Data collection involved several student projects as well as a citizen science approach. Most females forage within a range of less than 200 m if they are not forced to fly further due to food shortage. Therefore, flower patches 150-200 m from nesting sites conservatively support wild bees. We also investigated eight flower strips established in different sections of Munich in 2017, again involving teacher and bachelor students to document floristic and faunistic biodiversity, including the preparation of herbarium sheets.

### **Limno-terrestrial meiofauna in amber: discovering an ignored layer of the palaeodiversity**

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Ambers and other fossil and subfossil resins such as copals were long thought as a primary source of the well-preserved fossil invertebrates from Triassic up until Holocene. Up to now amber deposits around the world yielded thousands of species of insects, numerous cheliceratans, some crustaceans, also vertebrates like frogs, snakes, birds, non-avian dinosaurs feathers, mammal hairs as well as numerous plants, fungi, unicellular parasitic eukaryotes, and even some prokaryotes. It is notable however that representatives of the meiofauna, water films dwelling organisms (63-1000 µm long) are largely absent from the amber records, represented chiefly by the free-living Nematoda, mostly relegated to the artificial genus *Vetus*, and by smaller Collembola. Waterbears (Tardigrada) and rotifers are considered extremely rare in ambers, both being represented by the two occurrences each – in Cretaceous and Miocene ambers respectively. I would like to challenge the paradigm of the rarity of the terrestrial meiofauna in amber, and back up this contention with multiple new records of the Rotifera, Nematoda and Tardigrada from the Baltic amber.

### **The evolution of carbon-concentrating mechanisms, C<sub>4</sub> and CAM photosynthesis, in a changing world**

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In numerous lineages of land plants, the ancestral C<sub>3</sub> pathways has been supplemented independently by two different carbon concentrating mechanisms (CCM) in order to compensate for low carbon supply, high levels of photorespiration and drought stress, all factors that changed frequently during earth history and that likely will change in the future. Both CCMs, C<sub>4</sub> photosynthesis and Crassulacean Acid Metabolism (CAM), require complex structural, biochemical and gene regulatory changes. They share a number of features, for example key genes, but they also differ in many aspects and rarely occur in closely related plant lineages. Although less than 10% of land plants engage in CCMs, they account for over 25% of the primary terrestrial biomass and constitute a major fraction of the vegetation in subtropical (C<sub>4</sub>) and arid (C<sub>4</sub> and CAM) regions. We profit from the enormous productivity of C<sub>4</sub> photosynthesis and also from the drought tolerance of CAM species by a number of crop species, and an immense research effort is launched to engineer C<sub>4</sub> and CAM traits into C<sub>3</sub> species to meet the ever-increasing food and energy demands of the coming decades. The success of this scientific

challenge is highly dependent on our understanding of the evolution and functioning of these complex traits. Considering the structural diversity of C<sub>4</sub> and CAM and their independent origins at different times and under different selective pressures, it is difficult to imagine that they evolved along a common evolutionary trajectory (as proposed in current models). Only a sufficient number of in-depth non-model group case studies will be able to reveal the diversity of C<sub>4</sub> and CAM evolution, and botanical collections are essential to conduct these studies. Apart from obtaining DNA samples for phylogenies, herbarium material can be used for carbon isotope screenings, a fast way to detect CCMs, and for anatomical studies as well as species distribution modelling. Living collections are valuable resources for further insights into the physiological and biochemical diversity of C<sub>4</sub> and CAM, as well as for gene regulatory studies. I will use examples from Chenopodiaceae, Aizoaceae and Zygophyllaceae to illustrate the diversity of C<sub>4</sub> and CAM evolution and show the adaptive value of CCMs.

### **Understanding phylogenetic relationships in Cladobranchia (Mollusca, Heterobranchia, Nudibranchia) using RNA-seq data**

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The species-rich taxon Cladobranchia, which is sister to Anthobranchia in the exclusively marine group of Nudibranchia (Gastropoda, Heterobranchia), currently comprises approximately 98 genera from 22 families. Despite attempts to shed light on the evolution of Cladobranchia, the phylogenetic position of most families within the group is still subject to debate. While past efforts of gaining a better understanding of their relationships using approaches with barcoding genes did not result in phylogenies with satisfactory resolution, the first phylogenies using transcriptomic multi-gene approaches only covered a limited number of species omitting many families whose positions are still uncertain. To take further steps towards overcoming this problem we sequenced the transcriptomes of 21 species of heterobranch sea slugs and combined our data with raw reads from 40 species of Heterobranchia available from public databases. In order to obtain a high number of genes suitable for phylogenetic analyses, we assembled the raw reads using six different transcriptome assembly tools. For each species we identified the best assembly using a variety of descriptive parameters. We then searched the assemblies for orthologous genes that are presumed to be single-copy in molluscs and combined them in a phylogenetic analysis using a supermatrix approach. Our preliminary results expand the knowledge about the evolution of Cladobranchia by increasing the number of taxa examined in a transcriptomic multi-gene approach.

### **A new, chimera-like species of the Macrodasyida (Gastrotricha) discovered in deep sublittoral sand off Flores Island (Azores, Portugal) and affiliated with integrative taxonomy**

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In the course of the BIODIAZ project, a multitude of sediment samples from various depths were obtained during cruise M150 of R/V METEOR in the area of the Azores Archipelago. In order to gain preliminary insight into the community of marine Gastrotricha, a subset of samples was cultivated aboard (vented and stored at 5°C) and meiofauna was subsequently extracted with a 7% aqueous solution of MgCl<sub>2</sub> for microscopic investigation and extraction of genomic DNA. This initial study yielded 19 species from 13 genera of the taxon Macrodasyida. Amongst these, there

was a peculiar specimen from a species so far unknown to science. This exceptional morphotype looks like a chimera of two known genera. Its front end possesses characteristic features of the genus *Ptychostomella* such as a funnel-shaped mouth opening formed by an oral hood, sensory papillae and an unarmed cuticle. The posterior trunk is distinctively shaped as an elongated, unpaired appendage featured with characteristically arranged paired posterior adhesive tubes like in species of *Dendrodasys*. A cladistics analysis of a fragment of the 18S rRNA gene definitely places the new morphotype among other sequenced species of the genera *Ptychostomella* and *Tetranchyroderma* (Thaumastodermatidae). Hence, the new species will be described as a member of *Ptychostomella* while its *Dendrodasys*-like rear trunk is a nice example of convergent evolution within Gastrotricha. An additionally sequenced fragment of the mitochondrial COI gene will guarantee a secure identification of this new species during future biodiversity surveys using standard procedures as well as metabarcoding approaches.

### **Clarifying the taxonomy of *Gymnodinium fuscum* var. *rubrum* Baumeister from Bavaria (Germany) and placing it in a molecular phylogeny of the Gymnodiniaceae (Dinophyceae)**

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The taxonomy of *Gymnodinium* and the Gymnodiniaceae is inconsistent, also because the systematic position of the type species, *Gymnodinium fuscum*, is elusive at present. Historical names of microscopic species are frequently ambiguous that a reliable determination is impeded, although crucial to fully explore the biology of organisms. The epitypification approach is a powerful tool provided by the ICN to overcome identification problems. We therefore collected material at the type locality of *G. fuscum* var. *rubrum* and established a strain for morphological (light and electron microscopy) and molecular studies. The motile cells showed a obovate shape in outline, with an acute antapex, and a fishhook-shaped apical structure complex, which is characteristic for many Gymnodiniaceae. Older cultivated material further exhibited red granules in the cell, being the name-giving diagnostic character of the variety. We also generated ribosomal RNA sequences that were included in a comprehensive molecular phylogeny. Monophyletic Gymnodiniaceae segregated into seven clades at high taxonomic level. *Gymnodinium fuscum* and *G. fuscum* var. *rubrum* were placed in one of these clades, which also contained other unarmoured dinophytes and organisms parasitizing on copepod eggs. The phylogenetic resolution of the molecular DNA provides evidence for a dynamic evolutionary scenario of Gymnodiniaceae and might be helpful for an improved classification of the group. As taxonomic result, we validate and epitypify the historical name, *G. fuscum* var. *rubrum*, showing diagnostic traits such as a descending (but not straight) cingulum and a reciprocal size ratio between episome and hyposome in comparison to the original form.

### **Early-Mid Pleistocene genetic differentiation and range expansions as exemplified by Eurasian *Bunias orientalis* (Brassicaceae): the Caucasus as key region**

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Turkish Warty cabbage (*Bunias orientalis*) is a conspicuous perennial herb from the Brassicaceae family and known for its 250 years of invasion history into Europe and worldwide temperate regions. Putative centers of origin were debated to be located in Turkey, the Caucasus or Eastern Europe. We studied genetic variation from the nuclear and plastid genomes and identified two major gene pools in the Caucasian/Irano-Turanian region and close to the Northern Caucasus, respectively. These gene pools are old and started to diverge and expand approximately 930 kya in the Caucasus. Pleistocene glaciation and deglaciation cycles favoured later expansion of a European gene pool 230 kya, which was effectively separated from the



Caucasian/Irano-Turanian gene pool. Although the European gene pool is genetically less diverse, it largely serves as source for colonization in modern times with rare observations of genetic contributions from the Caucasian/Irano-Turanian gene pool such as in North-East America. This study largely utilized herbarium material to take advantage of a biodiversity treasure trove providing biological material and also giving access to detailed collection information; we demonstrate its particular value for setting an evolutionary, spatiotemporal framework as prerequisite for future studies.

### Using herbaria to track global environmental change

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Global change is affecting our environment at a rapid pace – but how are species responding? Answering this question is crucial to understand the long-term consequences of global change. Herbaria store vast time-series data to address this challenge, centuries of ecological and evolutionary plant responses to four of the main drivers of global change: pollution, habitat change, climate change, and invasive species. Historical specimens track changes not only at the morphological, but also at the genetic level, now accessible through sequencing. Such data can for example unveil the genetic basis of successful colonization or deadly plant pests. It can also tell if plant changes reflect acclimatization via morphological plasticity, or actual long-term evolutionary responses through genetic change. Optimally, such genetic analyses are based on temporally (and geographically) spread samples. This is however straightforward only for model species with small genomes and a reference sequence – hence, for a minority of species. Further, the fragmentation of ancient herbarium DNA (aDNA) precludes use of restriction-enzyme based sequencing traditionally used in ecology. We have refined a method for reduced representation sequencing and hybridization-capture to efficiently compare contemporary and historical specimens. For both *Arabidopsis thaliana* and the non-model plant *Cardamine bulbifera*, our homemade baits, based on fresh-sample libraries, enrich historical libraries for the same genomic fraction represented also in fresh libraries. With this, we will now investigate shifted flowering and associated genome-wide genetic trends in historical and modern samples across three species and ~200 years, to understand the role of genetic changes for climate change responses.

### Evolution of substrate specificity and fungal symbiosis in filmy ferns (Hymenophyllaceae): a Bayesian approach for ambiguous character state reconstruction

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We used a Bayesian approach for a comparison of the ambiguous character of preferred substrate with the incompletely known mycorrhization status for an ancient lineage of ferns, the Hymenophyllaceae or filmy ferns. The majority of the analysed 167 species prefers either the saxicolous, terrestrial or epiphytic habitat (differentiated into low and high epiphytic), but there are also many generalists without clear preference. For the whole family Hymenophyllaceae, the terrestrial habitat and AMF (Arbuscular Mycorrhizal Fungi; prevalent in habitats directly connected to the soil) but are largely absent in the high epiphytic habitat), received the highest probability for representing the ancestral state. For the subfamily Hymenophylloidae, the low epiphytic habitat and DSE (Dark Septate Endophytes; a morphological class of mostly unspecified fungi that may include potentially symbiotic ascomycetes) received the highest probability as ancestral state, whereas that for AMF was very low. The subfamily Trichomanoidae was found most likely to be originally terrestrial, but the probability value did

not differ much from the values for low epiphytism, with all values around 50±5 %. The high epiphytic habitat, which in its present condition is thought to be possible only in angiosperm-dominated vegetation, did not receive high probability to be the ancestral state in any clade. This decouples the evolution of epiphytism in filmy ferns in time from the advent of the angiosperms, which is hypothesized to have triggered the radiation of all other major epiphytic fern lineages.

### **Change of radula morphology and plastid-turnover upon food change in the sea slug *Elysia viridis***

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Sacoglossa sea slugs feed on a variety of ulvophyte algae. Characteristic for this marine slug group is their specialized radula, which is made out of single teeth organized in a row with the leading tooth facing forward. The leading tooth is used to cut a slit in the cell wall of the algae. Then the slugs suck out the cell content of the algae and incorporate the chloroplasts in their own cytosol (kleptoplasts). In some species like 'sap-sucking' slug *Elysia viridis*, the kleptoplasts stay photosynthetically active during starvation, a phenomenon known as functional kleptoplasty. *E. viridis* is one of the few species feeding on at least three different algae to which the morphology of the radula adapts. In many photo-physiological studies that tried to understand kleptoplasts photosynthesis, specimens of *E. viridis* were collected in the field from *Codium* spp., transferred to *Bryopsis hypnoides* for one month, and then used for experiments. Yet, it is unknown whether this feeding period guarantees a complete exchange of *Codium* plastids with those of *Bryopsis* (plastid-turnover) and how fast the radula adapts to the food switch. Knowing the kleptoplasts source is important to exclude biases in photo-physiological experiment caused by kleptoplasts from different sources. Thus, we analyzed the time frame in which the radula morphology changes and how fast the plastids are turned over in *Elysia viridis* upon food switch. Our results should serve as a guide when working with *E. viridis* to ensure unambiguous results when it comes to understanding kleptoplast photosynthesis.

### **Description of a new species of the genus *Peronia* from Persian Gulf with a discussion on the family Onchidiidae (Panpulmonata, Heterobranchia, Gastropoda)**

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The family Onchidiidae, air-breathing sea slugs living in the Eu – and Supralittoral, currently contain 14 genera, which are considered as valid. However, there are incongruencies with regard to names and species features used in published descriptions. Here we investigate the affiliation of ten genera of Onchidiidae based on DNA barcoding. Furthermore, we describe a new species collected from Persian Gulf belonging to the genus *Peronia* J. Fleming, 1822, based on anatomical, histological, and scanning electron microscopy data. Species delimitation test of available sequences of the genus *Peronia* were performed by ABGD, GMYC, and bPTP analysis of the 16S rDNA and Cytochrome oxidase I (CO1) sequences. These tests provide further evidence

for this new species along the Iranian shorelines, but also show the presence of further cryptic speciation and wrong affiliation within this genus.

### **What grows where? An online-data portal for living collections of Botanical Gardens**

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Botanic gardens sustain unique living resources for research, conservation and education. The scientific value of these collections depends on documentation quality and accessibility. To date, the heterogeneity of collection databases used by botanic gardens still hampers obtaining an up-to-date overview of the global representation of plants in living collections. Therefore, we initiated a joint project that combines evolutionary research with developing an accession-based botanic garden database. Seven German<sup>s</sup> botanic gardens with important collections of bromeliads and epiphytic cacti combine their databases in an online portal. Both plant groups are highly attractive to the general public and ideal models for studying the evolution of biodiversity. Genomic markers will be explored that can aid to identify species and additionally investigate reticulate evolution. Relevant accessions are linked to herbarium vouchers and DNA samples making them more sustainably accessible for research. The data portal will be open-access, although different user groups (members, researchers, public) will see different details. The local databases will be combined in an index through the BioCASE Provider Software and the indexing tool B-HIT, which map their content into the ABCD data standard. Through this infrastructure, the data portal enables a 'live' view of the collections irrespective of the management software, and data providers retain complete ownership over their data. Analyses of collection data will generate insights, which could be used to develop collection priorities and strategies for maintaining genetic diversity in collections. The project will highlight the role of living collections in knowledge gain and promote the importance of botanic gardens as a resource for documented plant material for research and conservation.

### **Transcriptomic evidence that photosymbiont recognition in cnidarians and sacoglossans depends on pattern recognition receptors (PRRs)**

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Among metazoans, many phyla are able to associate with photosynthetic organisms and are thus benefiting passively from photosynthesis. In sea slugs (Gastropoda), the animal host either forms a symbiosis with unicellular algae, usually *Symbiodinium*, (Nudibranchia-Dinoflagellates) or retains only the chloroplasts of its food resource (Sacoglossa). The cellular and molecular mechanisms behind the establishment and the maintenance of the symbiosis and chloroplast retention remain largely unknown in these mollusks. In cnidarians, however, it is accepted that proteins involved in immune response known as pattern recognition receptors (PRRs), such as scavenger receptors and thrombospondins, are involved in the recognition of the symbiont, and

hence, in the establishment of the symbiosis. For the sacoglossan sea slug *Elysia chlorotica* the role of PRRs in chloroplasts incorporation has been recently suggested, but detailed analyses for this species and other sea slugs on PRRs are absent. We studied the transcriptomic expression profile of three Sacoglossan species (two starving, one feeding) and compared them to the expression in two cnidarian taxa that were introduced to *Symbiodinium* after a bleaching event. Our results show that the general expression profile among the different taxa and conditions are similar, but the expression of specific PRRs differs. These findings contribute to understanding the genomic basis involved in the establishment of the photosymbiosis in cnidarians and the chloroplast retention in sacoglossans.

### **Taxonomic re-evaluation of tiny, interstitial slugs in the cryptic family Pseudunelidae based on anatomical and molecular data**

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The mesopsammon is a changing habitat under pressure from anthropological changes and marine pollution. The effects of those trends result in changes in species diversity as well as shifts in dispersion and population patterns. The basis for wildlife conservation, however, is robust knowledge of prevalent species and their distribution. Micromollusks are a common, but understudied representative of marine interstitial life. In tiny, interstitial slugs like Pseudunelidae (Acochliidiomorpha) species are commonly cryptic and often impossible to distinguish on a species level by studying external features and microanatomy. In the present study, we re-evaluated the existing taxonomic knowledge within the meiofaunal Pseudunelidae of the Indo-Pacific via 3D reconstructions from histological section series comparing recently collected, ambiguously identified specimens of the genus *Pseudunela* to described species deposited in museum collections. Traditionally used characters such as external morphology and radula are insufficient for unambiguous species delineation. The different features of the reproductive system like female glands and copulatory organs, formerly believed to be robust characters for identification, depend largely on individual ontogenetic stage. In contrast, the excretory system provides distinct specific characters. Additionally, we critically compared available methods of molecular species delineation (i.e. ABGD, statistical parsimony, GMYC, BPP) to analyze species boundaries based on mitochondrial markers. A resulting minimum consensus matched anatomical and geographical patterns.

Integrative methods can resolve complex relationships of previously ambiguous specimens by granting insight into their cryptic diversity. The correct assessment of species numbers and dispersions may be crucial to accurately estimate effects of man-made changes in a given habitat.

### **Phylogeny, evolution and classification of *Sedum* (Crassulaceae) and related genera**

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The classification of *Sedum* (Crassulaceae-Sempervivoideae) and related genera remains controversial, and three decades of molecular phylogenetic work have provided evidence for non-monophyly of many of these genera. We present a broadly sampled and dated molecular phylogeny of Crassulaceae-Sempervivoideae. Based on this phylogeny we hypothesize that after colonization of the Northern hemisphere (from the Southern hemisphere) in the area of the former Tethys and Paratethys Seas a rapid radiation of Sempervivoideae took place. A biogeographic pattern emerges in which migration out of this ancestral area is linked to pronounced morphological evolution which led to the recognition of segregate genera thought to be derived from *Sedum*. These segregate genera, however, have been defined on the basis of

strongly homoplasious characters such as degree of petal fusion, petal coloration or flower merosity. Moreover, there exists no single character state used for the delimitation of any segregate genus which is not also found in at least one species of *Sedum* in its current circumscription. Extensive literature work led to the result that only very few of the monophyletic clades found can be defined by phenotypic characters. Mainly for these two reasons we propose to combine all 13 genera currently recognized in tribe Sedeae into *Sedum* which then comprises c. 705 spp.

### **Mountains as evolutionary arenas: Patterns, approaches and paradigm shifts in the Tibeto-Himalayan region**

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Recently, the 'mountain-geobiodiversity hypothesis' (MGH) was proposed as a key concept for explaining the high levels of biodiversity found in mountain regions of the Tibeto-Himalayan region (THR), comprising the Qinghai-Tibetan Plateau, the Himalayas, and the biodiversity hotspot known as the 'Mountains of Southwest China'. In addition to the MGH, which covers the entire life span of a mountain, a complementary concept, the so-called 'flickering connectivity system' (FCS) was recently proposed for the period of the Quaternary. The FCS is putting a focus on connectivity dynamics brought about by repetitive climatic changes during the past ca. 2,6 million years, emphasising that fragmentation and allopatric speciation are not the sole factors for accelerated evolution of species richness and endemism brought about by climatic oscillations and accompanying shifts of elevational belts. I will provide a review of the current state of knowledge concerning geological uplift, Quaternary glaciation, and main phylogeographic patterns of seed plant species in the THR. In addition, I will suggest which factors future avenues of phylogeographic research should take into account on the basis of the fundamentals presented by the MGH and FCS, and related complementary paradigm shifts.

### **Battling the global antimicrobial crisis: the importance of collections for investigating the phylogenetic and spatial distribution of anti-infective metabolites in the flora of Java**

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The continued high rates of use of antibiotics in healthcare and agriculture has led to a dramatic increase in antimicrobial resistance, with multidrug-resistant bacteria emerging as a major public health problem worldwide. However, despite the urgent need for new antibiotics, many pharmaceutical companies have largely suspended their antibiotic drug discovery efforts, mainly due to very high investment but low returns. To help battle the global antimicrobial crisis, we here evaluate the phylogenetic patterns of anti-infective compounds across taxonomic and biogeographic scales in one of the most species-rich regions on Earth and assess the predictive power of phylogenies to identify clades with naturally occurring substances potentially suitable for the development of new active pharmaceutical compounds. Specifically, we (1) estimate the degree of phylogenetic signal of anti-infective compounds using a genus-level phylogeny of the flora of Java, and (2) identify 'hot nodes' in the phylogeny, indicating overrepresentation of anti-infective compounds in a given clade. Finally, we (3) assess the spatial patterns of plants with anti-infective compounds relative to total plant diversity across the region. By identifying clades of overrepresentation, drug discovery can be guided into promising clades with high possibilities of finding more plant species useable for drug production. Clades underrepresented with activity might constitute lineages with low numbers of activities or poorly-studied lineages, these clades are therefore high risk - high reward clades.

This is the first full approach combining bioactivity of all angiosperm genera on Java with spatial and phylogenetic data and based on nearly 400,000 herbarium vouchers.

### **Viva la evolución! Discovery of a third lineage of freshwater slugs (Acochlidimorpha, Panpulmonata) from Cuba**

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Tropical species diversity is endangered by man-made habitat change or habitat loss. Small panpulmonate slugs of the clade Acochlidimorpha occur in terrestrial, marine, brackish and freshwater habitats of the tropics, but often exhibit narrow distribution ranges. While several benthic freshwater species colonized rivers on different Indo-Pacific Islands, only one single Western Atlantic species is described from St. Vincent Island. *Tantulum elegans* Rankin, 1979 was described living interstitially in a mountain spring march. Recent attempts of re-collecting fresh material for molecular analyses at the type locality failed due to habitat change - the mountain spring has been transformed into banana plantations. Recently, several specimens of a small freshwater acochlidimorph were discovered in a coastal river on Cuba, which is the first discovery of a 'hedylopsacean' Acochlidimorpha in the Western Atlantic since *Tantulum elegans*. Here we present the slug in microanatomical detail including 3D-reconstructions of all organ systems and scanning electron microscopical analysis of the radula. The Cuban slugs show a mix of characters of the marine *Pseudunela* and the freshwater genera *Tantulum* and *Strubellia*, and additionally are characterized by a unique comb-like structure in the reproductive system. Different evolutionary scenarios are discussed. In a first scenario, the colonization of freshwater systems could have taken place twice independently, once in the Caribbean and once in the Indo-Pacific. In a second evolutionary scenario, the Western Atlantic was conquered twice, once by the ancestor of *Tantulum* and second by the common ancestor of the Cuban species and a yet undescribed species of the Indo-Pacific.

### **Phylogenetic relationships and biogeography of gray mullets (Mugilidae)**

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Gray mullets are characterized by a generalized morphological conservatism, which results in confusion in species classification among different studies, thus leading to disagreements on the inferred evolutionary history of the group. Due to their commercial relevance, in order to establish proper management actions, it is imperative to 1) identify the number of independently evolving lineages, in addition to taxonomically recognized species, and 2) understand the timing and geographic context of diversification of these lineages. We compiled sequencing data from all published studies including the genus *Mugil*, and closely related genera. Based on three mitochondrial genes and fossil data we estimated a comprehensible time-calibrated phylogeny for the whole genus and tested the monophyly of several taxonomically recognized species. Our results show that the diversification of *Mugil* began nearly 31.8Ma, during a period of large temperature fluctuations. *Mugil cephalus*, *M. curema* and *M. rubrioculus* are paraphyletic clades, containing several independently evolving lineages that started diversifying about 24Ma. In addition, we found that morphological conservatism has resulted in

specimen miss-identification and consequently in a significant overestimation of the distribution of *M. hospes* in the Atlantic Ocean, which southern range is actually restricted by the Amazon river flow. Our results show that morphologically and ecologically similar species may have long and independent evolutionary histories that must be considered when establishing sustainable management actions.

### **Island woodiness accelerates disparification in plant radiations**

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The evolution of secondary (insular) woodiness and the rapid disparification of plant growth forms associated with island radiations, show intriguing parallels between oceanic islands and tropical alpine montane sky islands. However, the evolutionary significance of these phenomena remains poorly understood and the focus of debate. We explore the evolutionary dynamics of species diversification and disparification of plant growth forms across evolutionary radiations compared to their non-island close relatives, in these contrasting island systems. We estimate rates of species diversification, growth form evolution and phenotypic trait space saturation for the classical oceanic island plant radiations – the Hawaiian silverswords and Macaronesian *Echium* - and the well-studied tropical alpine radiations of *Lupinus* and *Hypericum* in the Andes. We show that secondary woodiness is closely associated with dispersal to islands and with accelerated rates of species diversification, accelerated disparification of plant growth forms, and occupancy of greater phenotypic trait space for island clades than their non-island relatives, on both oceanic and sky islands. We conclude that secondary woodiness acts as a key innovation, manifest as the potential to occupy greater trait space, for plant radiations on island systems in general, further emphasizing the central importance of ecological opportunities in driving adaptive radiations.

### **Lack of coverage limits the value of protist collections**

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Protists are a diverse group of organisms which are of major importance to our ecosystems since they influence metabolic pathways, microbial community structure and population size. They are e.g. dominant primary producers but also primary agents of top-down control of bacteria and thus determining the transport of organic matter. Despite their importance we still do not completely understand the whole diversity and functional aspects they combine overall, but also within one species. Ecophysiological lab-experiments as well as genome analyses of different Chrysophytes showed an immense diversity within this group comprising various nutritional strategies and morphologies even between closely related species and between strains affiliated with the same species. For instance, different clonal strains of the heterotrophic Chrysophyceae *Poteriospumella lacustris* showed a huge diversity regarding ecophysiological aspects but also regarding genome size and ploidy level. These differences are presumably conditioned by the origin of the different strains but a lack of reference strains and taxa limits knowledge gain. Using heterotrophic chrysophytes as an example we will discuss the coverage of protist diversity in collections and the prospects and limits of collections due this lack of coverage.

### **Hybrid species recognition using ‘Next Generation Sequencing’ (NGS) of museum specimens**

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Hybridization between species combines divergent genomes and can produce new species when genome fusion is accompanied by reproductive isolation from the parents. Genetic variation in hybrid species is primarily not acquired by mutation, but by recombination. Hybridization is frequent in the Palearctic Hyles species and intermediate phenotypes occur regularly. As non-model organisms, genomic analyses of these moths provide a promising opportunity to document and understand changes in biodiversity, gaining insight into the evolutionary process of speciation. To compare the genomic compositions of the Palearctic Hyles species, we used two different approaches of the hyRAD protocol (Hybridization Restriction-Associated-DNA sequencing) to obtain single nucleotide polymorphisms from museum exemplars. We further compared these two protocols to shotgun sequencing to determine the differences in endogenous DNA content, contamination and detected single nucleotide polymorphisms. This comparison will help to further evaluate and utilize modern high throughput techniques for the use of museum samples in phylogenomic studies in Lepidoptera.

### **Combining RNA-seq, target DNA enrichment, and Sanger sequences results in a strongly supported comprehensive cuckoo wasp phylogeny**

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Cuckoo wasps are a stinging wasp (Aculeata) family with an obligate kleptoparasitic or parasitoid lifestyle. In a recent study, we used Sanger sequence data of eleven genes in order to resolve the phylogenetic relationships between 187 cuckoo wasp species. Our results revealed inaccuracies within cuckoo wasp taxonomy, since we showed that multiple cuckoo wasp genera are para- or polyphyletic. However, these results were insufficiently supported to resolve the early diversification of major cuckoo wasp lineages (*i.e.*, subfamilies and tribes). In this study, we infer a phylogenetic tree from a supermatrix comprising amino acid sequence data of 492 single-copy genes with a total of 230,915 informative sites of 94 ‘Chrysidioidea’ (*i.e.*, cuckoo wasps and their closest relatives) and 45 outgroup species by combining transcriptomic and target DNA enrichment data. Our results show, opposed to previous morphological studies, a sister group relationship between Amiseginae and Cleptinae, which together comprise the sister group of Chrysidinae. On tribal level, Allocoelini are the sister group of all remaining Chrysidinae, while Elampini are the sister group of a group comprising Chrysidini and Parnopini. Additionally, our study confirms the results of a recent phylogenomic study that found Chrysidioidea to be paraphyletic, however our data suggest that Dryinidae are the sister group of all remaining Aculeata and not the sister group to Aculeata excluding the former Chrysidioidea. Ultimately, we obtained an almost completely resolved phylogeny of 196 species of cuckoo wasps and 104 outgroup species by using the new topology as constraint while reanalyzing previous Sanger sequenced data.



### **Exceptional crustacean fossils in two lineages of Peracarida emphasize the convergent evolution of subchelate grasping appendages**

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From very early on in their evolutionary history, crustaceans developed mechanisms that allowed them to explore practically all aquatic environments, and even terrestrial ones. The great adaptive success of crustaceans has a lot to do with the specialization of the large number of appendages for specific tasks. Similar selective pressures seem to trigger the phenomenon of convergent evolution, explaining very similar morphological traits found, for example, in extant malacostracan crustaceans. Subchelate grasping appendages are among the specializations that can be found in many different lineages within Eumalacostraca, including Peracarida (including opossum shrimps and woodlice), Hoplocarida (mantis shrimps) and Decapoda (shrimps, lobsters and crabs). A subchela is formed by a distal element, dactylus, that folds inwards towards the penultimate element, propodus, forming a claw-like appendage. This appendage can be used for grabbing food, holding on a partner during mating, or grasping on a host in parasitic forms. Here we will present two exceptional fossils of Peracarida that exhibit subchelate morphology on thoracic appendages, an amphipodan from the Permian (around 280 million years old) and a lophogastridan from the Jurassic (around 150 million years old). Both show massively developed subchela that, based on comparison with extant forms, function on the first to facilitate copulation, and on the latter as part of the feeding apparatus. The fossils provide insights on how the morphology of a grasping appendage was transformed in deep time, by comparisons with extant representatives of these two different ingroups of Peracarida.

### **Divergence and gene flow during radiations of cryptic species: insights from *Chorthippus* grasshoppers**

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Adaptive radiations provide a great opportunity to understand the evolutionary processes contributing for species formation. Theoretical and empirical studies have shown that radiations are facilitated when a trait under divergent natural selection is also involved in mating cues (i.e. magic traits). It is yet unclear how quickly and effective are adaptive radiations of species lacking eco-morphologic divergence. We address this question using grasshopper species of the genus *Chorthippus* that have evolved assortative mating but can hybridize readily in the laboratory without noticeable intrinsic incompatibilities. Using transcriptomic tools, we show that different species share the same mitochondrial lineages but already show significant differences in their nuclear genomes, suggesting that they split relatively recently. We show that ancestral gene flow has occurred following species formation, probably before postglacial expansion to central and northern Europe. Nevertheless, species do not show ongoing gene flow in current sympatric localities, showing that complete reproductive isolation is currently established. These results suggest that rapid radiations can occur due to divergence in mating cues and in the absence of strong divergence selection, resulting in cryptic species that are genetically, morphologically and ecologically identical but otherwise behave as good biological species.

### **Generic revision in Marsdenieae (Asclepiadoideae, Apocynaceae)**

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The Marsdenieae is a tribe belonging to Apocynaceae subfam. Asclepiadoideae distributed pantropically and contains well known taxa such as wax plants (*Hoya*). In the last 200 years, the ca. 730 species in Marsdenieae have been classified in more than 110 genera, but most are synonymized to at least 26 genera currently accepted. A severe challenge in Marsdenieae is low intergeneric variation and obvious absence of diagnostic characters, making the assessment of monophyletic units difficult. Here, we revisit the taxonomy of Marsdenieae using molecular phylogenetics and morphological studies on available herbarium material. For phylogenetic analyses we sequenced both cpDNA (*trnT-trnL*, *trnL-trnF*, *rps16*, *psbA-trnH*), nrDNA, and nuclear single copy (At2g06530a, At2g34620b) loci for 205 different accessions. In order to recognize monophyletic taxa, phylogenetic hypotheses are supplemented by identification of diagnostic apomorphic characters and compared to biogeographical evidence. Obtained phylogenetic trees indicate several genera as polyphyletic, such as *Marsdenia* R.Br., whose species group in several different clades. Interestingly, all neotropical species are revealed in a single clade distant from the type species *M. tinctoria*.

### **New insights in the character evolution in the lineage towards modern dragonflies and damselflies**

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Insects and especially larval insects play a major role in freshwater ecosystems. One of the easiest recognisable group of insects with aquatic larvae is Odonata. Larvae of Odonata possess a specialised form of the labium with which they grab and adduct their prey ('Fangmaske'). Within Odonata two major ingroups, Damselflies (Zygoptera) and dragonflies (Anisoptera) can be distinguished from by the presence of three long processes on the posterior abdomen in the first. In dragonflies and the related damsel-dragonflies (Epiophlebia), on the other hand, corresponding processes are condensed to a cone-like structure ('anal pyramid'). Information about fossil larvae is strongly limited and, with little exception, restricted to ingroup odonatans. The phylogenetic framework in the lineage towards Odonata is mainly based on wing characters. Thus, the affinity of fossil larvae is often problematic. We report the first dragonfly related larvae from Cretaceous Burmese amber (100 million years old). The fossils represent small sized early larval instars without wing pads that could allow to integrate the fossil into the existing phylogeny of dragonfly relatives. The morphological features in the fossil do not allow for a narrow interpretation of the systematic affinity. However, presence of a specialized labium along with a plesiomorphic morphology in the posterior abdomen, within the same animal, provides unique information about the character evolution along the lineage towards dragonflies and damselflies.

### **What's the madder? Disentangling the complex evolutionary and taxonomic history of Mediterranean *Rubia* (Rubiaceae)**

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The genus *Rubia* (Rubiaceae) comprises c. 80 accepted species distributed throughout the temperate and tropical regions of the Old World. Due to their high Alizarin content, the roots of several species, including *R. tinctorum*, *R. cordifolia*, and *R. peregrina*, have been important sources for purple dye since the Bronze Age. These madder root dyes were traded throughout the Old world, competing on the dye market with purple derived from shellfish (e.g., *Hexaplex trunculus*) and kermes dye produced from crushed scale insects (e.g., *Kermes vermilio*). Madder roots have also been used in Ayurvedic and Traditional Chinese medicine as an anti-inflammatory agent. As a consequence of the trade and local cultivation of several species, original distribution ranges are somewhat obscure for several *Rubia* species and the status of populations on islands like Madeira and the Azores was unclear. We studied morphology in combination with sequence data of 7 plastid DNA regions plus nuclear ITS for 109 herbarium samples, representing 54 *Rubia* species. A biogeographic analysis reveals frequent long-distance dispersal and independent natural colonization of isolated islands like the Azores, probably facilitated by frugivorous birds, who eat the fleshy *Rubia* fruits. The concept of a widespread variable *R. peregrina* is not supported. Instead, we argue for splitting *R. peregrina* into several more locally distributed taxa. For most of them, a validly published name is already available. Our study highlights the strength of an integrative herbarium-based approach to analyze plant groups with a complex evolutionary and taxonomic history.

### **The molecular evolution of hemocyanin genes as indicator of Tectipleura habitat shifts?**

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Comprising approximately 3,400 amino acids, Molluscan hemocyanin is one of the largest proteins described in nature. Therefore, the genes of these oxygen transport molecules offer great possibilities as a new molecular marker addressing multiple phylogenetic issues within Mollusca, the second largest phylum within the animal kingdom. Presently, we use hemocyanin genes as a tool to trace phylogenetic relationships within Heterobranchia, a gastropod clade which covers over 30,000 species living in all kinds of habitats. During the last years, the phylogeny of Heterobranchia has been much debated and the monophyly of the two traditional groups Opisthobranchia and Pulmonata has been rejected. The currently accepted systematic classifies Heterobranchia in 'Lower Heterobranchia', Ringipleura, Acteonacea and Tectipleura, but the exact phylogenetic relationships within those clades are far from being resolved. Our present analyses focus especially on Tectipleura, a clade that represents the most diverse Heterobranchia group in terms of habitat variation and comprises Euopisthobranchia and Panpulmonata. Numerous habitat shifts occurred independently from each other during the evolution of the respective lineages and led to the colonization of marine, limnic and terrestrial environments. These habitat shifts were accompanied with adaptations of their respiratory systems to their new habitats, which enhances hemocyanin as an excellent phylogenetic marker to enlighten the jumbled systematics of Tectipleura: As the primary respiratory protein, hemocyanin represents a link between living conditions and the physiologies of the animals and therefore can be used to reflect their evolution by analyzing the adaption of these proteins to diverse habitats.

### **Why is Northern Siberia dominated by larch forests? – Illuminating the history of Siberian larch using target-enriched sedimentary ancient DNA**

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Although the climatic conditions in Siberia are similar to those in Northern Europe and North America, the latter regions are dominated by evergreen needle-leaf forest in comparison to the deciduous larch (*Larix* MILL.) forests in Siberia. This is even more peculiar as *Larix* is a poor competitor with evergreen needle trees in mixed stands. The basic mechanisms controlling the distributions of these two biomes are still not well understood and future alterations due to climatic changes are uncertain. Previous work has failed to provide insights into long-term biogeographic patterns of *Larix* species, as established methods (pollen analysis, metabarcoding) cannot distinguish ancient *Larix* below genus level. In this study, we want to sequence whole ancient chloroplast genomes of *Larix* from lake sediment samples originating from southern Taymyr peninsula (72.399° N, 102.289° E). We will do this by enriching sedimentary ancient DNA (*seda*DNA) extracts for *Larix* chloroplast DNA using hybridization-capture prior to high-throughput sequencing. In a second step, we will extend the capture target to informative mitochondrial and nuclear SNPs. Preliminary results from shotgun sequencing of *seda*DNA from a sediment core dated back to 7000 years BP show that, although most of the sequences are of bacterial and archaeal origin, *Larix* chloroplast DNA was recovered. The enriched data set will enable us to trace distribution changes of Siberian *Larix* lineages in Northern Siberia through time.

### **Did the Australasian genus *Coriaria* (17 species) reach Chile and Central America independently or not?**

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*Coriaria* (Coriariaceae, Cucurbitales), a genus of 16-17 species in the New World, Asia and Australia, and the Mediterranean, is one of 23 unrelated genera of angiosperms (in 8 families) whose species form symbioses with *Frankia* bacteria. It is sister to *Corynocarpus* (Corynocarpaceae), 5 species from Vanuatu, New Guinea, Australia, and New Caledonia. A phylogeny of *Frankia* (2014) tested for a possible geographic match between *Coriaria* and *Frankia* but found none. Two phylogenies of *Coriaria* (2000, 2014) reported a split of the previously single New World species into two lineages, one from Mexico to Peru, the other from Chile/Argentina, which seemingly arrived independently, from New Zealand and from somewhere in Asia. Most sequences, however, are unvouchered. Using DNA from herbarium specimens, we are reanalyzing the biogeography of *Coriaria* and will test for possible geographic correlations among the symbionts. So far, clades from Australasia, the New World, and Central and Eastern Asia (including the Mediterranean species *C. myrtifolia* L.) each are well-supported. This rejects the previous phylogeny, since all American specimens of *C. ruscifolia* subsp. *microphylla* and subsp. *ruscifolia* form one clade. Dating is ongoing, with one calibration coming from a fossil of *Coriaria longaeba* from the Armissan strata near Aix en Provence in Southern France, dated to ca. 33 mya.

### **Assessing the future of German insect diversity by applying species and community distribution modelling through time and space**

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The decline of insect diversity and abundance has gained public recognition over the last years, and is expected to provoke cascading effects on food webs and jeopardize ecosystem services. To mitigate the effects of global changes, conservation science must consider the organization of biodiversity in space. Thus, it is particularly relevant to characterize species community composition and turnover, as they directly relate to ecosystem functioning. In an exploratory analysis, we utilize primary biodiversity data available on the Global Biodiversity Information System (ca. 2 million occurrence records), to assess the beta diversity of the entomofauna community within Germany, to reveal spatial scaling of diversity loss and illuminate mechanisms of its regional maintenance. We generate presence absence matrices, to describe patterns of beta, alpha, gamma diversity, sampling effort, and use generalized dissimilarity modelling to predict and characterize the  $\beta$ -diversity turnover in response to environmental changes over the remainder of this century. Preliminary results indicate there will be biotic homogenization along with northern distributional shifts, and we can detect serious knowledge gaps on the distribution of insects. Future steps include investigating the functional diversity within communities, along with species distribution modeling to assess areas that should be prioritized for conservation purposes within Germany.

### **Giant spermatozoa of *Lonchoptera lutea* (Lonchopteridae, Diptera) – Structural and ultrastructural aspects**

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Light microscopic dissections of the female reproductive tract of Lonchopteridae (Diptera, Brachycera) revealed spermatozoa apparently much wider and possibly also much longer than the average dipteran spermatozoon. Subsequent studies with more elaborate methods such as serial sectioning, SEM, TEM, and micro-CT substantiate this finding and reveal new and interesting details. The micro-CT reconstructions show bundles of maturing spermatozoa running along the inner wall of the spherical testes in several turns. Their full length could not yet be reconstructed but definitely exceeds 2000  $\mu\text{m}$ . While in other Diptera the number of spermatocytes per bundle is generally 64, semi-thin sections reveal that in *L. lutea* the bundles comprise a variable number of spermatocytes, ranging from 62 to 89 with an average of 76. TEM studies of mature spermatozoa show that the sperm tail has a width of about 1.6  $\mu\text{m}$  along much of its length. The commonplace axoneme (0.2  $\mu\text{m}$  wide) is accompanied by a single large mitochondrial derivative (1.2  $\mu\text{m}$  wide) and a large band-shaped accessory body (1.3  $\mu\text{m}$  x 0.2  $\mu\text{m}$ ). The ultrastructure of the accessory body shows up to 50 evenly spaced electron-light tubules embedded in an otherwise homogenous electron-dense matrix. This condition is unique among all Diptera studied to date and we cannot even speculate on the cellular origin, molecular composition and function of this peculiar structure. The ongoing study will add considerably to the hitherto scarce information on the diversity of spermatozoa structure and ultrastructure in the Aschiza section of the higher Diptera.

### **First survey of heterobranch sea slugs (Mollusca, Gastropoda, Heterobranchia) from Sangihe Island, North Sulawesi, Indonesia**

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North Sulawesi, Indonesia with its many islands is famous for the underwater biodiversity which attracts many tourists. This holds also true for a small island located in the Northern most part of Sulawesi along the Sangihe ridge, Sangihe Island. However, this island is much less known and has come into focus only recently through an increase in tourism. Other activities, such as mining, are planned, which will probably have a large impact on the environment. Recently, monitoring projects started around Bunaken National Park (North Sulawesi) using marine Heterobranchia as indicators for the health of coral reefs. No information about this taxon exists around Sangihe Island. We started monitoring of marine Heterobranchia around Sangihe Island in 2016. A total of 250 specimens that could be assigned to 23 species were sampled by diving and snorkelling at 7 sites around Sangihe Island. At least eight species (35%) are not recorded from Bunaken National Park, indicating probably habitat differences. However, the biodiversity of sea slugs around Sangihe Island is certainly under-sampled. Species composition indicate also a higher trend towards Anthobranchia. We also report here the first species mimicry in Indonesia, with *Chromodoris annae* mimicking *C. elisabethina*.

### **The importance of undescribed material from collections for biodiversity: *Elthusa* Schioedte & Meinert, 1884 (Eucrusea, Isopoda, Cymothoidae) from South Africa as an example**

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Cymothoid isopods are well known parasites of marine and freshwater fishes, most often attaching to the external surface, branchial chamber or buccal cavity of their hosts. Within this group, the branchial attaching genus *Elthusa* Schioedte & Meinert, 1884 is a world-wide genus in distribution with 35 species including the three species described here. Only a single species, *Elthusa raynaudii* Milne Edwards, 1840, has been described from the coasts of South Africa. Although it is expected that the biodiversity of these isopods would be much higher in this region than what is currently recorded, there are many challenges that obstruct the advancement of their taxonomy and systematics. These challenges have hindered the research of cymothoids in many regions, leaving numerous species undiscovered or undescribed. All South African material held at the National Museum of Natural History, Paris, France (MNHN) and the Iziko South African Museum, Cape Town (SAMC) identified as, or appearing to belong to *Elthusa*, was examined. Four species were identified, three of which proved to be undescribed and are fully described here. Diagnostic identification criteria are provided, along with an identification key to simplify and aid in the correct identification of species in future collections. The

description of three new species provides evidence that it is the lack of collecting, as well as undescribed preserved material, rather than a lack of new species, that accounts for the low number of branchial cavity-attaching cymothoid species from the South African region.

### **The Global Caryophyllales Initiative – Towards dynamic monographing of a major group of plants**

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The Global Caryophyllales Initiative aims at creating a global synthesis of species diversity in the Caryophyllales. The order constitutes up to 6% of flowering plants – about 12,500 species in >30 families, and includes ecologically diverse, economically important, invasive, and threatened species.

The initiative uses a collaborative and informatics-supported approach towards a monographic synthesis: The international Caryophyllales Network was initiated in 2011 and quickly gathered specialists from across the world (to date, more than 150 scientists from 37 countries). The network is recognized by the World Flora Online Council as its Taxonomic Expert Network for Caryophyllales.

The continuous advances of the network are presented in the open-access Caryophyllales Portal (<http://caryophyllales.org/>) that provides up-to-date phylogenetic and taxonomic information. The systematic treatment is powered by the EDIT Platform for Cybertaxonomy (<https://cybertaxonomy.eu/>), with the generic checklist (<http://caryophyllales.org/Checklist>) and some family treatments already publicly available. The checklist is regularly updated in consultation with family editors. A species-level taxonomic backbone incorporating all names and pertinent nomenclatural acts and evaluations is being compiled. Nepenthaceae serves as a case study for the accommodation of descriptive and other published factual data. This synthesis is to go beyond simple one-off publications – the aim is to integrate base information with globally available primary biodiversity data, especially specimen information. Here, we are going to summarize, in particular, contributions from Austria, Germany, and Switzerland.

The ongoing implementation shows that a dynamic online monograph requires to rethink several aspects of editorial workflows. We believe that the taxonomic community is ready to meet that challenge.

### **Dealing with reticulate evolution and polyploidy in times of big data – evolution of Eurasian shrub willows (*Salix*, subg. *Chamaetia/Vetrix*)**

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Plant evolution is shaped by a bunch of different processes, for instance hybridization, introgression and polyploidization. Especially polyploidization seems to be an important factor that is supposed to be responsible for about 15% of speciation of land plants. However, despite this knowledge, dealing with taxa that underwent processes of reticulate evolution and/or polyploidization in molecular systematics is still challenging, even at the rise of NGS tools. To understand these processes, we study genus *Salix* (c. 400 species), which is an interesting model system to analyze the effects of ancient and recent hybridization, reticulate evolution, and polyploidization. Especially the big and species-rich clade of northern hemisphere shrub willows (subg. *Chamaetia* and subg. *Vetrix*) is interesting due to morphological plasticity of the species contrasting the molecular purity, a high degree of polyploidy and frequent interspecific hybridization. The clade contains tiny shrub willows adapted to arctic-alpine regions as well as bigger shrubs and trees. We used the next generation sequencing approach RAD sequencing (Restriction site Associated DNA sequencing) to analyze the phylogenetic relationships of about 50 Eurasian and Asian species representing the *Chamaetia/Vetrix* clade. By mining a large number of single-nucleotide polymorphisms (SNPs) we could reconstruct the phylogenetic history of the genus including a rapid radiation in the Pan Himalaya region. We will further present the applicability of this genomic marker system to understand evolutionary origin, parentage and diversification of the polyploid willow species. Finally, we will present our preliminary results of whole-plastome sequencing on eight species.

### **Differentiation of trunk segments in scorpions: First results of an evolutionary historical approach with an emphasis on collection work**

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Scorpions are predatory euechelicerates with about 2,300 extant species, their evolutionary history dating back to the Silurian (about 430 mya). Scorpions are known from terrestrial habitats all over the world, their sizes ranging from about 1 cm body length (*Typhlochactas mitchelli*) to the largest representatives with over 20 cm body length (*Pandinus imperator*). However, morphological diversity is not only represented by size differences, but also by differences of body organization. Scorpions, as all arthropods, possess a segmented body, with several segments being organized into functional units, termed tagmata. These tagmata are specialized in their morphology to perform different functional tasks, such as walking or food uptake. In euechelicerates, especially the transition area between the anterior and the next tagma shows a high morphological variability. Segments may have undergone compression, functional integration into one tagma while usually interpreted to be part of the other one, but also appendage differentiation. In scorpions, this transition area shows a combination of all three processes leading to a highly compressed area with obscured segment borders. We are aiming at reconstructing the evolutionary history of this transition area in scorpions. We use a combination of several methods including measurement-based morphospaces, investigations of inner structures, e.g., muscles, using  $\mu$ CT and histological sectioning, but also of ontogenetic and fossil data. Here we present first results and also highlight the importance of collections to this project as they offer access to numerous extant and extinct specimens, allowing to cover a broad phylogenetic range.



## **Morphologically Diskint: Comparing Island Populations of Skinks in the Comoros Archipelago**

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A previous barcoding study focusing on squamate lizards in the Malagasy region found an unexpected relationship between two fossorial skink species; despite observed morphological variation between the species, *Flexiseps ardouini*, native to northern Madagascar, was found genetically nested within the four island populations of *Flexiseps johannae* endemic to the Comoros Archipelago. This study looks at the morphological and genetic relationship between the island populations of *F. johannae* and its mainland counterpart. To do this, two segments of nuclear DNA were sequenced from both species and compared to previously obtained mitochondrial DNA sequences. Next, we collected morphological data from morphometrics, pholidosis, and osteology to identify and compare geographic morphological variation between the two species and among the four island populations. Significant morphological distinction was found both between the two species and among the four island populations of *F. johannae*. Many of the morphological differences between the species are size-related with *F. johannae* presenting similar characteristics to *F. ardouini* just on a smaller scale. This is perhaps evidence of incipient speciation and insular dwarfism. The molecular data, on the other hand, showed no divergence at all between the species. This incongruence between genetic data and morphology perhaps indicates a historical human introduction or a recent natural dispersal of *F. johannae* from Madagascar that included rapid morphological adaptation to the insular environments of the Comoros. *Flexiseps johannae* in the Comoros Archipelago is, therefore, a useful system for the study of island biogeography of terrestrial reptiles.

## **Combining data from major German natural science collections with GFBio data curation and network services supports taxonomists and biodiversity researchers with re-using existing and publishing new high-quality data.**

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The German Federation for Biological Data (GFBio, [www.gfbio.org](http://www.gfbio.org)) is a DFG-funded project of 20 institutions running an infrastructure to support scientists in all steps of the data life cycle. The most important goal is to support researchers in producing FAIR data (Findable-Accessible-Interoperable-Reusable) and to provide an infrastructure for archiving and publishing these data. Among the GFBio partners are seven major German natural science collections with their IT departments and data centers. They contribute their long-term expertise in offering archiving and publication services as well as permanent access to large amounts of biodiversity and geodiversity data essential for earth systems research. The collection partners in GFBio provide user-friendly spreadsheet templates for data processing and submission, describe community standards and technical approaches for data exchange, offer taxonomic thesauri and ontologies

via the GFBio Terminology Service and give advice in the correct use of property rights, licenses and other legal issues. GFBio is committed to building a national infrastructure for research data management with GFBio e.V. as the legal entity for ensuring sustainability of the services. Two GFBio e.V. data scientists already support researchers like taxonomists and biodiversity researchers in the publication and (re-)use of terminologies as well as high-quality biodiversity, collection and molecular data.

### **Leaf beetle (Coleoptera: Chrysomelidae s.l.) decline and range changes in Central Europe as represented in data from private and museum collections**

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The database ChryFaun contains over 171,000 records of leaf beetles s.l. in Central Europe, compiled from private and museum collections, from faunistic publications and from other publicly available databases. Based on 168,674 records in the database for the period from 1900 to 2009 we analyzed changes in distribution and frequency of records. From the first quartile (1900-1929) to the last (1990-2017) 25 of 715 species extended their range towards North. The number of records per decade increased by factor 26 from 1498 to 39,162. The number of reported species increased from 395 in decade 1 to 636 in decade 10, but only 550 were reported in decade 11 (2000-2009). The number of species with declining records increased since 1990 from 263 to 475 in 2009, despite the continuously increasing total number of records. Decrease and increase of records is found likewise in mono-, oligo-, and polyphagous species. 34 species (5.3%) have not been reported since 1990, and even 84 (13.2%) since 2000. 72% of all species reported between 2000 and 2009 had fewer records than in the preceding decade. Our data correspond with previous studies that found severe declines in several insect taxa over the last decades. We conclude that data from private and public collections are useful for the retrospective analysis of numbers and distributions of leaf beetles as well as other taxa.

### **Independent evolution of viviparous modes: An overview of reproductive diversity of Cerithioidean snails with an emphasis on Australian freshwater Thiaridae**

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Reproductive modes of organisms are a major focus in many biological disciplines as they can hold information on mating systems and morphological traits of both adults and offspring. Insights on the latter are consequential for our perception of a species' dispersal ability and thereby of utmost importance for biogeographic and evolutionary research. However, the focus of studies on reproductive modes is oftentimes concentrated on the adult stages, neglecting differences in offspring morphology and behaviour. This 'adultocentric' view can hamper taxonomic and biogeographic insights. The high diversity of viviparous modes found within aquatic Cerithioidean snails exemplifies this problem. Though most marine taxa are oviparous, several freshwater lineages of this superfamily independently developed different modes of (ovo-)viviparity. At least four distinct morphologies of brood chambers can be differentiated, even though freshwater habitats were colonised two to three times independent of reproductive mode evolution. In addition to this diversity, within a particularly diverse family of cerithioidean freshwater gastropods, the Thiaridae, two modes of viviparity are known. One is an ovo-viviparous mode, where offspring are nourished exclusively by the egg's yolk before numerous individuals of highly dispersive free-floating larval stages are released. The other is an eu-viviparous mode, where a smaller number of offspring is directly nourished by the mother and are released at a less mobile developmental stage. These distinctions are of high explanatory value for the biogeography of Australian thiarid taxa, illustrating the important role

reproductive modes and offspring mobility play for species distribution and their evolutionary history.

### **Mining herbaria and roaming the forests: Plant phenology advances since the industrial revolution.**

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Ongoing anthropogenic global change influences species and ecosystems. One of the most compelling types of evidence for this are shifts in the timing of phenological events. Plants, in particular, may respond e.g. with advanced flowering due to warmer climatic conditions. So far, long-term data on phenological changes are scarce - especially for Europe. We are currently mining German herbaria to gather historical phenological data, dating back from the beginning of the industrial revolution until today. We focus on 20 early-flowering herbs that grow in forest understories, because these species have a distinct flowering period and are particularly suited for studying phenological changes. Data from the herbarium surveys of historical specimens will be tested for long-term trends and climatic correlates and will be compared to data from field surveys in 2017. First results indicate that for almost all species flowering time advanced within the last two centuries. This suggests that climatic changes affect plant phenology. Such ecological as well as evolutionary responses of plants to anthropogenic environmental change can have far-reaching consequences for ecological communities and long-term evolution.

### **They are young, and they are many: Dating freshwater lineages in unicellular dinophytes**

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Dinophytes are one of the few protist groups that have an extensive fossil record and are therefore an appropriate group for time estimations. However, insufficient sequence data and strong rate heterogeneity have been causing setbacks with putting dinophyte evolution into a time frame until now. Marine→freshwater transitions within this group are considered geologically old and evolutionarily exceptional due to strong physiological constraints that hinder such processes. Phylogenies based on concatenated rRNA sequences of two major dinophyte lineages, Gymnodiniaceae and Peridinales, were carried out using RAxML and MrBayes approaches and were dated with BEAST package using an uncorrelated molecular clock and five calibration points based on fossils. All analyses recovered highly congruent phylogenetic tree topologies and time spans. Contrarily to previous assumptions seemingly supported by scarce fossil record, marine→freshwater transitions are more frequent in dinophytes (i.e., approximately 15 such processes were inferred for the subset of Peridinales and Gymnodiniaceae), and none of them occurred as early as 140 MYA. Furthermore, most marine→freshwater transitions, and the diversifications that followed, took place after the Cretaceous–Paleogene boundary. Not older than 40 MYA, the youngest marine→freshwater transitions within Gymnodiniaceae and Peridinales occurred under the strong influence of the Eocene climate shift. Our evolutionary scenario indicates a more gradual diversification of dinophytes without noticeable impact of catastrophic events, and that their freshwater lineages have originated several times independently at different points in time.

**Placing the florogenetic patterns of the Eurasian steppe belt in time and space: Phylogeography and historical biogeography of the false flax (*Camelina* Crantz, Camelinaeae, Brassicaceae)**

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The Eurasian steppe belt is the vastest grassland region in the world, stretching 8,000 km from the Pannonian basin and the Danube delta in the west to the Manchuria region in the East Asia. However, despite its sheer size, little is known about the temporal and spatial patterns of flora origin and evolution of the Great Steppe. The study subject of this project was *Camelina* – a taxon, which occupies open dry habitats in temperate zones of Eurasia. To infer the evolutionary history of this taxon, maximum likelihood optimization in RAxML and Bayesian Inference approach were carried out. Furthermore, we performed a secondarily calibrated time estimation analysis using Bayesian optimization in BEAST to infer potential influence of climatic shifts on the distribution patterns of *Camelina*. Our study resulted in a well-supported phylogeny that corresponded with the species' morphology. Furthermore, we uncovered several genetically distinct inter- and intraspecific lineages that can be but are not necessarily geographically correlated. Time estimation analysis recovered the diversification of *Camelina* to have taken place only around the transition from Pliocene to Pleistocene (approximately 2.6 MYA), and its dynamics being under a strong influence of several glacial periods and their outcomes. Its young age also explains the subtle morphological character differences among species and high interspecific hybridization potential. We further discuss the rediscovery of wild *Camelina sativa* populations and propose the ETS region as a barcode for species delimitation in this group.

**Behavioral and morphological adaptations to the use of a new nest substrate in the pollen wasp genus *Quartinia* (Masarinae, Vespidae)**

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Pollen wasps are a monophyletic lineage of Vespidae, most obviously united by the provisioning of the larvae with pollen. While many pollen-wasps nest in muddy soil or rigid sand or use these kinds of substrates to build aerial earthen cells, all species of *Quartinia* observed until now construct their nests in habitats with loose sand. A silky excretion is applied on the inner surface of the burrow, stabilizing the walls. Representatives of the genus *Quartinia* and of other pollen wasp taxa were studied comparatively to recognize the structures correlated with this behavior. This way we could identify a hitherto unknown maxillary gland, as well as a process of the galea that likely serves the formation of the silky threads from the gland excretion. The newly found structures are key adaptations of the genus *Quartinia* that allowed it to inhabit new habitats and likely facilitated the species diversity of this genus.

**A deep phylogeographic division within the young, widespread pioneer tree *Macaranga tanarius* (Euphorbiaceae) in Sundaland, Southeast Asia**

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\* We dedicate this talk to our good friend and long-term collaborator Brigitte Fiala who sadly passed away in Nov. 2018.

*Macaranga tanarius* (Euphorbiaceae) is one of the most widely distributed pioneer tree species in lowland rain forests of Southeast Asia. According to molecular dating analyses, the species is less than five million years old and most likely originated on the island of New Guinea. We are studying the population structure and phylogeography of *M. tanarius* in Sundaland, a region with a quite complex paleogeographical history. Climatic fluctuations during the Pleistocene led to sea-level changes and repeated cycles of exposure and inundation of the Sunda shelf. We would like to know (1) how often and along which routes *M. tanarius* colonized into Sundaland, and (2) how changing conditions during the Pleistocene influenced gene flow across the Sunda shelf. To address these questions, six plastid and eleven nuclear microsatellite markers were analysed in a total of 329 specimens from 36 populations. With both marker types, we found a clear differentiation between Borneo in the east and Java, Sumatra and the Malay Peninsula in the west of Sundaland. These findings suggest that two independent colonization events into Sundaland took place. Furthermore, our data suggest that despite recurrent exposure of the Sunda shelf during the Pleistocene no gene flow has occurred between populations in east and west Sundaland. This observation is quite surprising, given that *M. tanarius* otherwise colonized very quickly almost all regions of Southeast Asia.