BioDivEvo 2014

—

Joint conference

—

15th Annual Meeting

of the Society of Biological Systematics (GfBS)

22nd International Symposium

of the German Botanical Society (DBG),
“Biodiversity and Evolutionary Biology”

—

—

Dresden · March 24 – 27, 2014

Technische Universität Dresden,
Germany

This meeting is funded by
the German Research Foundation

BioDivEvo
2014

The 15th Annual Meeting

of the Society of Biological Systematics (GfBS)

the 22nd International Symposium

“Biodiversity and Evolutionary Biology” of the German Botanical Society (DBG)

March 24 – 27, 2014

on the campus of the Technische Universität Dresden, Germany

Publisher
Senckenberg Naturhistorische Sammlungen Dresden
Königsbrücker Landstraße 159 · 01109 Dresden · Germany

Editor-in-Chief
Uwe Fritz (*Zoology*) on behalf of the German Society for Biological Systematics (GfBS)
Christoph Neinhius (*Botany*) on behalf of Section „Biodiversity and Evolutionary Biology“
the German Botanical Society (DBG)

Distributor
Senckenberg Naturhistorische Sammlungen Dresden
Königsbrücker Landstraße 159 · 01109 Dresden · Germany
+49 351 795841-4264
yvonne.schaarschmidt@senckenberg.de

Conference Logo
Ole Reuter and Andreas Weck-Heimann

Layout
Markward Herbert Fischer

Print
Saxoprint GmbH · Dresden

—

—

—

—

ISBN
978-3-910006-49-2

Abstracts

Posters

—

—

Monday, March 24, 2014

Conference Office — open from 16:00 h

—

Welcome Reception

“Alte Mensa” — TU Dresden
Mommsenstraße 13 · 01069 Dresden

—

Tuesday, March 25, 2014

Conference Office — open from 08:00 h

—

—

Conference Venue

“Trefftz-Bau” · Haus A — TU Dresden
Zellescher Weg 16 · 01069 Dresden

https://navigator.tu-dresden.de/karten/dresden/geb/tre

—

Conference schedule – subject to alterations!

Botany Sessions

Tuesday, March 25, 2014 · TREFFTZ-Bau

09:00

Welcome Address

Dean Prof. Bernhard Ganter,
Uwe Fritz (GfBS), Christoph Neinhuis (DBG)

09:30 ***Plenary Talk*** · Ethnobotany: Monique Simmonds

Kew Innovation Unit, Deputy Keeper & Head of Sustainable Uses of Plants Group

10:30 **Coffee Break**

Session · Biogeography & Molecular Clocks

// 11:00 – 18:00 //

11:00 ***Key Note***: Bernard Goffinet

Dawn in bryophyte genomics: mt genome evolution and phylogenomics of bryophytes

11:45 Will, Classen-Bockhoff; Natural groups in an artificial genus-parallel evolution in *Salvia* s. l. (Lamiaceae)

12:00 Gebauer, Röser, Hoffmann; Molecular phylogeny of the species-rich *Carex* L. sect. *Racemosae* G. Don (Cyperaceae)

12:15 Liede-Schumann, Hartmann; Phylogeny of *Drosanthemum* – a diverse genus of core Ruschioideae (Aizoaceae)

12:30 **Lunch**

12:30

Meeting

// 12:30 – 14:00 //

DBG Section "Biodiversity and Evolutionary Biology"
Venue: Biologie, Raum/Room E33, EG, Zellescher Weg 20b

Tuesday, March 25, 2014 · TREFFTZ-Bau

Welcome Address Dean Prof. Bernhard Ganter, Uwe Fritz (GfBS), Christoph Neinhuis (DBG)	**09:00**
Plenary Talk · Ethnobotany: Monique Simmonds Kew Innovation Unit, Deputy Keeper & Head of Sustainable Uses of Plants Group	**09:30**
Coffee Break	**10:30**
Session · Integrative Taxonomy – Phylogenetics, Systematics (I) **// 11:00 – 12:30 //**	
***Key Note*:** J. Wolfgang Wägele Deep Metazoan Phylogeny: Progress, doubts, and mysteries	**11:00**
Haszprunar, Spies; Naming the crown-of-thornsseastar species in the *Acanthasterplanci* complex	**11:30**
Eulitz, Klass, Bohn, Nehring; Sister where are you? The phylogenetic position of the genus *Attaphila* Wheeler, 1900 (Dictyoptera, Blattodea)	**11:45**
Gaviria, Defaye; Comments on the morphology of a new genus of Parastenocarididae (Crustacea: Copepoda: Harpacticoida) and its phylogenetic relationships	**12:00**
von Döhren; Systematics and Evolution of Nemertea	**12:15**
Lunch	**12:30**

Botany Sessions

Tuesday, March 25, 2014 · TREFFTZ-Bau

14:00	Schneider, Hoffmann, Blaner, Winterfeld, Röser; Molecular phylogenetics meets morphology: New insights into classification of the grass subfamily Pooideae (Poaceae)
14:15	Veleba, Bureš, Adamec, Šmarda, Lipnerová, Horová; Genome size and genomic GC content evolution in the miniature genome – sized family Lentibulariaceae
14:30	Hartmann, Rosche, Hensen, Mráz, Schaar, Hochheimer, Lachmuth; Variation in Inbreeding Depression between Geocytotypes of highly invasive *Centaurea stoebe* s. L.
14:45	Ritz, Herklotz; Spontaneous hybrid formation in dogroses: implications for the evolutionary dynamics in a polyploid species complex and its morphology based taxonomy
15:00	Kadereit, Klein; Parallel homoploid and polyploid hybrid speciation in *Sempervivum tectorum* × *S. calcareum* (Crassulaceae)
15:15	Scheriau, Nürk, Koch; Melting gene pools in the *Hypericum perforatum* complex
15:30	Hodac, Scheben, Hojsgaard, Paun, Hörandl; ITS polymorphisms shed light on hybrid evolution in apomictic plants: a case study from the *Ranunculus auricomus* complex
15:45	Schneeweiss, Schönswetter; The role of ecogeographic isolation in the diversification of alpine *Androsace* (Primulaceae)
16:00	**Coffee Break**

Curator's Workshop · Access & Benefit Sharing and other legal aspects of material transfer

// 14:00 – 16:00 //

GIERE; Legal aspects of international specimen transfer – introduction and species protection

---

LÖHNE; Access and Benefit Sharing: The concept, its implementation and its relevance for research and collections management

---

NEUMANN; Bon Voyage ? International exchange of scientific material, legal hurdles and other obstacles

—

—

Discussion.

Coffee Break **16:00**

Tuesday, March 25, 2014 · TREFFTZ-Bau

16:30	Gramlich, Cosendai, Flatscher, Hörandl; Population genetic structure in alpine willow hybrids (*Salix*, Salicaceae)
16:45	N. Wagner, Wöhrmann, Schubert, Weising; Species boundaries in the *Fosterella micrantha* group (Bromeliaceae)
17:00	Schubert, Wagner, Wöhrmann, Weising; A first four-locus plastid phylogeny of *Pitcairnia* (Bromeliaceae)
17:15	Gemeinholzer, Gross, Wissemann, Martens; Flower color evolution within the Cichorieae (Asteraceae) – the Flavonoid-3’5’-Hydroxylase
17:30	Schütz, Quandt, Nebel; Systematics of Pelliaceae (Marchantiophyta, Jungermanniopsida) and the new genus *Apopellia* stat. nov.
17:45	Grossmann, Bock, Schweikert, Boenigk; Small but manifold – hidden diversity in the heterotrophic golden alga *Spumella*
18:00	**Poster Session**
18:15	**Workgroup meeting – Young Scientists** (GfBS)
20:00	**Conference Dinner** at “Alte Mensa” Mommsenstraße, TU Dresden **Bernhard-Rensch-Award** (GfBS), the award winner is Dr. Alexander Blanke; Laudatio (Prof. Dr. Bernhard Misof), Short Presentation (Dr. A. Blanke)

Session · Phylogenomics I

// 16:30 – 18:15 //

***Key Note*: Alan R. Lemmon**; 16:30
Anchored Phylogenomics: Rapidly Expanding Across the Tree of Life

***Key Note*: Oliver Niehuis**; 17:00
Phylogenomics sheds new light on the evolutionary history of insects – results from the international 1KITE project

Weigert, Purschke, Halanych, Struck, Bleidorn; Illuminating the base of the annelid tree using transcriptomics 17:30

Gerth, Gansauge, Weigert, Bleidorn; Phylogenomic analyes of *Wolbachia* Supergroup relationships 17:45

Simon, Sagasser, Brugler, Hadrys, DeSalle; The embryonic transcriptome of the damselfly *Ischnura elegans* and it's impact for comparative insect genomics 18:00

Workgroup meeting – Young Scientists (GfBS) **18:15**

Conference Dinner **20:00**

at "Alte Mensa" Mommsenstraße, TU Dresden

Bernhard-Rensch-Award (GfBS),

the award winner is Dr. Alexander Blanke;
Laudatio (Prof. Dr. Bernhard Misof),
Short Presentation (Dr. A. Blanke)

Botany Sessions

Wednesday, March 26, 2014 · TREFFTZ-Bau

Session · Plant Form & Function

// 09:00 – 10:30 //

09:00	***Key Note*: Karl Niklas;** A Biophysical Perspective on Evolutionary Developmental Biology
09:30	Jerominek, Classen-Bockhoff; Insights into the inside – Anatomical studies of the explosive style movement in Marantaceae
09:45	S. Wagner, Isnard, Rowe, Wanke, Neinhuis; Growth form shifts in the genus Aristolochia
10:00	Bull-Hereñu, Ronse de Craene, Pérez; The enigmatic development of the androecium of *Eucryphia* Cav. (Cunoniaceae)
10:15	Schüssler, Freitag, Kadereit; Evolution of C4 photosynthesis and diversity of C4 and C3 leaf anatomy in Salsoleae s.s. (Chenopodiaceae/Amaranthaceae)
10:30	**Coffee Break**
11:00	***Key Note*: Stanislav Gorb;** Contact Mechanics at the Insect-Plant Interface: How Do Insects Stick and How Do Plants Prevent This?
11:30	Frenzke, Samain, Symmank, Goetghebeur, Neinhuis, Wanke; Evolution of fruit structures correlates with species richness and transition to epiphytism in Peperomia
11:45	Erbar; The nectary diversity in Brassicaceae: phylogenetic trends

Session · Morphology, Development & Evolution

// 09:00 – 14:00 //

***Key Note*:** Andreas Hejnol; The mouth, the anus and the blastopore: Open Questions about questionable Openings	**09:00**
***Key Note*:** Alexander Gruhl; Evolutionary developmental biology of Myxozoa	**09:30**
Wanninger, Scherholz, Redl, Todt, Wollesen; Molluscan evodevo: ancestral states and phylogenetic implications	**10:00**
H. Wägele, Schmitt, Martin, Gregor; Longevity of plastids in sacoglossan sea slugs – what counts in this unique association?	**10:15**
Coffee Break	**10:30**
Martin, Mayer; Oral innervation in a velvet worm provides insights into the evolution of the ecdysozoan brain	**11:00**
de Sena Oliveira, Lüter, Wolf, Mayer; On the evolutionary changes in the integument of the onychophoran *Plicatoperipatus jamaicensis* (Peripatidae)	**11:15**
Koch; Evolution of life habits in silverfish (Insecta, Zygentoma)	**11:30**
Vegliante, Nuss; Functional morphology of the genitalia of Anania hortulata (Lepidoptera: Crambidae).	**11:45**

Botany Sessions

Wednesday, March 26, 2014 · TREFFTZ-Bau

12:00	Kempe, Lautenschläger, Neinhuis; Reorientation in tilted stems of papaya by differential growth
12:15	Ajani, Classen-Bockhoff; Breeding system in andromonoecious *Dorema aucheri* Boiss. (Apiaceae – Apioideae), endemic to Iran
12:30	**Lunch**
14:00	Klein, Kadereit; Phylogeny, biogeography and evolution of edaphic association in the European oreophytes *Sempervivum* and *Jovibarba* (Crassulaceae)
14:15	Kondraskov, Schütz, Thiv; Macaronesian island biogeography: inter- and intra- archipelago relationships of laurel forests
14:30	Masson, Lauterbach, G. Kadereit; Following the track of aridification – biogeography and adaptation to drought in *Anabasis* L. (Chenopodiaceae)
14:45	Tkach, Röser, Hoffmann; Phylogeny and biogeography of the highly diverse genus *Pedicularis* (Orobanchaceae)
15:00	Luebert, Moreira-Muñoz, Dillon; Contrasting two Neotropical radiations in the Asteraceae: *Plectocephalus* (Cynareae) and the *Lucilia*-group (Gnaphalieae)
15:15	Ley, Dauby, Köhler, Wypior, Röser, Hardy; Comparative phylogeography of eight tropical herbs and lianas (Marantaceae) in central African rainforests
15:30	Wölk, Röser; Polyploid evolution, intercontinental biogeographical relations and morphology of the newly described African oat genus *Trisetopsis* (Poaceae)
15:45	Mráz, Barabas, Lengyelová, Turis, Schmotzer, Janišová, Ronikier; Pattern of vascular plant endemism in the Western Carpathians and its relation to geography, environmental factors and taxon traits

Zoology Sessions

Wednesday, March 26, 2014 · TREFFTZ-Bau

Tietze, Päckert; Coevolution of plumage pattern and migratory behaviour with range in swifts (Aves: Apodini)	**12:00**
Lunch	**12:30**

Session · Integrative Taxonomy – Phylogenetics, Systematics (II)

// 14:00 – 16:00 //

***Key Note*:** George Sangster Integrative taxonomy and the nature of species	**14:00**
Franke, Schumann, Mayer; Phylogeny and expression of Pax genes in the onychophoran Euperipatoides rowelli	**14:30**
Baer, de Sena Oliveira, Mayer; Slime protein profiling: A non-invasive tool for species identification in Onychophora	**14:45**
Tippelt, Schwentner, Richter; New insights into spinicaudatan diversity (Crustacea: Branchiopoda) – identification and differentiation of several undescribed Eocyzicus species	**15:00**
Mally, Korycinska, Agassiz, Hodgetts, Nuss; Discovery of a species complex in the *Leucinodes* genus group damaging Solanaceae fruits in Sub-Saharan Africa and moving in trade (Insecta: Lepidoptera)	**15:15**
Päckert, Martens, Sun; Phylogeography and systematics of Himalayan and Chinese birds - multiple lines of evidence	**15:30**
Ohl; Should we register and name all species on Earth, and if we should, how can we achieve it?	**15:45**

16:00	**Coffee Break**
16:30	Dillenberger, Kadereit; Evolution of edaphic association in the European high mountain genus *Adenostyles* Cass.
16:45	Hoffmann, Gebauer, Röser, Tkach; Evolution of the Arctic Flora
17:00	Appelhans, Jun Wen, W. L. Wagner; A molecular phylogeny and biogeographic analysis of the *Euodia* alliance (Rutaceae) reveals key innovations for species richness
17:15	Lehnert, Noben, Weigand, Krug, Quandt; Phylogeography of the tree fern genus *Sphaeropteris* (Cyatheaceae)
17:30	Bartha, Sramkó, Volkova, Surina, Ivanov, Banciu; Transylvanian basin: novel extra – Mediterranean refuge and source of diversity for the temperate herb *Erythronium dens-canis* (Liliaceae)
17:45	Möller, Huettel, Wöhrmann, Weising; Veni, vidi, vici: genetic bottlenecks and clonal propagation accompanied the introduction of *Vinca minor* L. (Apocynaceae) to Central Europe
18:00	**Meeting of the members GfBS** (Mitgliederversammlung) **&** **Postersession**

Coffee Break & Postersession 16:00

Meeting of the members GfBS
(Mitgliederversammlung)
&
Postersession 18:00

Thursday, March 27, 2014 · TREFFTZ-Bau

Session · Phylogenomics II

// 09:00 – 15:15 //

09:00	***Key Note*: Jim Leebens-Mack;** Resolving Ancient Genome Duplications Across the Angiosperm Phylogeny
09:45	Albach, Mayland-Quellhorst; 454 sequencing of ITS1 in the analysis of polyploid species – Challenges, prospects and lessons
10:00	Meudt, Mayland-Quellhorst, Albach; Insights into polyploid transcriptomics of non-model plants: An example in *Veronica* (Plantaginaceae)
10:15	Bernhardt, Willing, Schneeberger, Kilian, Blattner; Phylogenetic analysis of Hordeeae (formerly Triticeae): sequence capture of 400 single – copy genes and Illumina sequencing
10:30	**Coffee Break**
11:00	Brassac, Blattner; Supermatrix or coalescent-based phylogenies? Analysis of next-generation sequenced multilocus data in *Hordeum* (Poaceae)
11:15	Naumann, Salomo, Der, Wafula, Bolin, Maass, Samain, Neinhuis, dePamphilis, Wanke; Single – copy nuclear genes place haustorial Hydnoraceae within Piperales and reveal a Cretaceous origin of multiple parasitic angiosperm lineages
11:30	Wicke, Müller, Quandt, de Pamphilis, Schneeweiss; Physical and functional plastome reduction coincides with major shifts of substitution rates and relaxation of purifying selection in photosynthetic and nonphotosynthetic parasitic Orobanchaceae

Session · Integrative Taxonomy – Phylogenetics, Systematics (III)

// 09:00 – 10:30 //

Key Note: MICHAEL RAUPACH; Modern integrative taxonomy: new methods, techniques and applications **09:00**

KINDLER, BÖHME, CORTI, GVOŽDÍK, JABLONSKI, JANDZIK, METALLINOU, ŠIROKÝ, FRITZ; How many species of grass snakes are out there? Phylogeography, gene flow cross contact zones and taxonomy of *Natrix natrix* **09:30**

STRUTZENBERGER, PÄCKERT; DNA-barcode-assisted biodiversity assessment of passerine birds on the Qinghai-Tibetan Plateau **09:45**

Coffee Break **10:30**

Workshop · "Scientific literature"

// 11:00 – 12:30 // **11:00**

DÄHNE, KASPEREK; All Literature on Biology Online!? Supply of literature for biodiversity research in transformation.

Thursday, March 27, 2014 · TREFFTZ-Bau

11:45	Appelhans, Hojsgaard, Pellino, Schmutzer, Scholz, Vogel, Sharbel, Hörandl; Genome evolution and speciation in polyploid complexes: insights from transcriptomics studies in *Ranunculus auricomus*
12:00	McCann, Schneeweiss, Stuessy, Weiss-Schneeweiss; The impact of reconstruction methods, phylogenetic uncertainty and branch lengths on inferences about dysploidy in *Melampodium* (Asteraceae)
12:30	**Lunch**
14:00	Moreira-Muñoz; “Plant geography of Chile”, written by Karl Reiche
14:15	Bouman; Tree diversity and stand dynamics at varying proportion of balsam fir (*Abies balsamea* L.)
14:30	Nolzen, Albach, Rezk, Shrestha, Kuhnert, Schepker, Ullrich; Phylogeny ploidal variation and antimicrobial activity of *Rhododendron* (Ericaceae)
14:45	Kunzmann, Dolezych, Wilde, Uhl, Brocke, El Atfy; Innovation in palaeobotany: the Whole-Plant concept
16:00	**Coffee & Plenary Farewell**, GfBS Poster Award

Lunch	**12:30**
Session · Biogeography & Molecular Clocks (Zoology) **// 14:00 – 15:15 //**	**14:00**
Key Note: Thomas Schmitt; Genes in Space and Time: The molecular Biogeography of Europe	
Stelbrink, de Bruyn, Albrecht, Hall, von Rintelen; Sulawesi – A biogeographic melting pot No session in parallel	**14:30**
Lüter, Ebeling; Some like it cold – hybridization in Atlantic sister species of Terebratulina (Brachiopoda)	**14:45**
Letsch, Ware; Ancient biogeography and evolution of dragonflies (Odonata: Anisoptera)	**15:00**
Coffee & Plenary Farewell, GfBS Poster Award	**16:00**

Session · Biogeography & Molecular Clocks

11:00

Key note:

Dawn in bryophyte genomics: mt genome evolution and phylogenomics of bryophytes

—

BERNARD GOFFINET

University of Connecticut, USA

—

Among extant lineages of land plants, mosses compose the second most ancient divergence. The evolutionary history of extant mosses spans approximately 350 mya (Yang), and is ultimately marked by several rapid radiations. Satisfactory reconstructions of the affinities of mosses to other land plants, of the macroevolutionary relationships within mosses and of the most recent diversifications have been hindered by the putative paucity of morphological traits and extensive reverse or parallel transformations. Inferences from discrete genetic loci raised new phylogenetic hypotheses but their robustness remains to be tested, including based on larger data sets. Recent major developments in sequencing and analytical tools have dramatically enhanced our ability to target genomic data from field collected bryophytes, and bryology is now entering the phylogenomic era.

We have assembled the organellar genomes for a phylogenetically broad sample of mosses to characterize the evolution of these genomes, and assess the significance of the mosses in the evolutionary history of vascular plants, and are now targeting exons from all genomic compartments to built extensive data sets to reconstruct the macroevolutionary tree of life of mosses and resolve critical rapid diversifications, such as that of the Funariaceae ± 20 mya. The mitochondrial genome of mosses varies in size among the deepest lineages but remained extremely stable structurally during the last 350 mya: only two genes and three introns have been lost, no gene has been acquired from the chloroplast genome, and rearrangements are completely lacking, due likely to the complete absence of scattered repeat. Phylogenetic inferences in the context of land plant evolution from concatenated mt exons confirm, once saturation, compositional heterogeneity and codon bias are taken into account, that bryophytes s. lato are paraphyletic, that hornworts share a unique ancestor with extant vascular plants, liverworts marked the successful colonization of land, and mosses diverged from a liverwort type ancestor. Preliminary inferences from organellar exons sampled via gene enrichment and the entire nuclear ribosomal DNA repeat obtained as a leaking by-product, for exemplars of Funariaceae, yield a backbone phylogeny of the family congruent with that inferred from discrete loci, further underline the high homoplasy in morphological traits, and will provide a phylogenomic framework within which to critically revise concepts of homology of morphological traits and reconstruct their transformational history.

11:45

Natural groups in an artificial genus – parallel evolution in *Salvia* s. l. (Lamiaceae)

—

Maria Will[1] · Regine Classen-Bockhoff[2]

[1] Institut für Spezielle Botanik und Botanischer Garten, Johannes Gutenberg Universität Mainz, Germany — [2] Institut für Spezielle Botanik und Botanischer Garten, Johannes Gutenberg Universität Mainz, Germany

—

Salvia L. (Lamiaceae) is a good example to study parallel character evolution. Its lever-like stamens were largely regarded as synapomorphous character supporting the monophyly of the genus. However, molecular data tell a different story: *Salvia* is not monophyletic! Its species fall in four independent evolutionary lineages (Clade I – IV) some of them coveringeven additional genera. Clade I (*Salvia* s. str.) covers exclusively *Salvia* species including the type species *S. officinalis* L. In contrast, Clade II, III and IVare distinct evolutionary lineages (*Salvia* s. l.) having similar morphological characters than *Salvia* s. str.

The formation of lever-like stamensis the most striking but not the only example of parallel evolution in *Salvia*.This is evident by phylogenetic data based on a broad taxon sampling. We provide an overview of the evolution of *Salvia*s.l. with a focus on Old World (OW) *Salvia* which are represented with 196 (57%) of its 345 species.Our study representsthe whole phenotypic diversity, distributional and ecologicalrange of OW *Salvia*.Nuclear (*nr*ITS) and chloroplast (*rpl*32-*trn*L) data were used to identify natural lineages which were compared to the morphological groups (sections) recognized in *Salvia*.

Based on an ancestral character state reconstruction,a repeated colonization of America, Africa, and the Canary Islandsis documented. Furthermore, parallel evolution of different characters has been discovered, i.e. (1) growth forms, (2) colored papery calyces, (3) stamen types, and (4) different pollination syndromes. As a consequence, similar character states in unrelated clades result from convergent evolution. This leads to the question:Are there any morphological preconditionsin the common ancestor of *Salvia* and closely related generawhich have triggered the evolution of lever-like stamens or the frequent shift towards bird-pollination?

12:00

Molecular phylogeny of the species-rich *Carex* L. sect. *Racemosae* G. Don (Cyperaceae)

Sebastian Gebauer · Martin Röser · Matthias H. Hoffmann
Institute of Biology, Martin Luther University Halle-Wittenberg, Germany

The genus *Carex* (Cyperaceae, ca. 2,000 species) belongs to the most species-rich genera of angiosperms. Section *Racemosae* (ca. 60 species) is one of the largest infrageneric groups within subgenus *Carex*, whose species are mainly distributed in high mountain systems of the northern hemisphere and the Arctic but also in parts of the southern Andes in South America. Some species are widely distributed, showing a circumboreal distribution (e.g., *C. buxbaumii*, *C. media*), others have more restricted ranges in isolated high mountain areas (e.g., *C. orestera*). To address the molecular phylogeny, systematics and evolution of section *Racemosae*, we sampled nearly 80 % of the species from all biogeographical groups and related sections and studied them using Maximum Parsimony, Maximum Likelihood and Bayesian Inference analyses of a combined sequence data set of four nuclear (ITS, ETS 1f) and chloroplast (*trn*K-*mat*K, *rps16*) markers. Our results corroborate that sect. *Racemosae* is not monophyletic in its current circumscription as already suggested by previous molecular studies. However, the majority of species forms a well-supported clade that is sister to the monophyletic sections *Bicolores* and *Paniceae*. Eight major clades could be resolved, some of them were supported by morphological characters and, particularly, by biogeography. Former classifications of subsections (e.g., Egorova 1985) were supported only for some morphologically well-defined groups (e.g., *Atropictae*, *Papilliferae*). Polyphyly of most traditionally defined taxonomic groups and morphological analyses of many discrete and continuous characters revealed extensive morphological homoplasy. Vegetative and generative characters were both affected by homoplasy. An unusual vicariant distribution pattern of some presumably closely related species between south-western North America and Central Asia (e.g., *C. melanocephala*, Central Asia; *C. nova*, North America) suggested by previous studies could not be corroborated by this study. The overall similarity among these species is a good example of an extreme morphological parallelism in high mountain areas.

12:15

Phylogeny of *Drosanthemum* – a diverse genus of core Ruschioideae (Aizoaceae)

—

Sigrid Liede-Schumann[1] · Heidrun E. K. Hartmann[2]

[1] Dept. of Plant Systematics, University of Bayreuth, 95440 Bayreuth, Germany —
[2] University of Hamburg, Germany

—

Within the „core Ruschioideae“, more precisely in the core group named also Ruschieae, *Drosanthemum* takes a position as sister group to the remaining c. 130 genera of the tribe. The genus comprises c. 120 species and occurs throughout western and central South Africa and into Namibia. Subgenera overlap widely in parts of their distribution areas, with a centre of diversity in the southwestern Cape. In the genus eight subgenera can be distinguished based on differences in flower and capsule morphology. Molecular phylogenetic analyses confirmed most of these morphological groups, but also suggest some taxonomic adjustments at subgeneric level, such as the establishment of a new subgenus as a home for taxa that have been shifted between *Drosanthemum* and *Delosperma* until now. Furthermore, taxa with characters intermediate between subgenera can now be re-assessed, resulting in a new arrangement of species and subgeneric taxa. With the help of our phylogeny, character evolution in *Drosanthemum* will be re-assessed and interpreted with reference to the geographical distribution patterns of the taxa. The hypothesis that adaptations to arid habitats have evolved independently in several clades will be evaluated.

14:00

Molecular phylogenetics meets morphology: New insights into classification of the grass subfamily Pooideae (Poaceae)

—

Julia Schneider · Matthias H. Hoffmann · Anne Blaner
Grit Winterfeld · Martin Röser

Institute of Biology, Martin Luther University Halle-Wittenberg,
Neuwerk 21, 06108 Halle (Saale), Germany

—

The grass subfamily Pooideae comprises approximately 220 genera and 4,200 species, including a large number of crops and forage plants. This study deals with the molecular phylogeny and systematics of Pooideae. In order to gain a deeper insight into the evolutionary patterns of this subfamily, we analysed a representative number of genera from all recognised tribes. Some of these genera have been insufficiently studied or were placed differently in previous classifications.

Molecular phylogenetic analyses were carried out using the chloroplast (cp) gene region *mat*K–3'*trn*K, the nuclear internal transcribed spacers (nrITS) and the nuclear single-copy locus topoisomerase 6 (*Topo*6). Furthermore, morphological characters were extensively examined and discussed with respect to molecular data.

The DNA data yielded a comparatively robust molecular phylogenetic hypothesis of Pooideae, which is largely in agreement with the newly obtained morphological information mainly based on inflorescence characters. Some of these taxonomically relevant morphological traits have apparently been considered to be less meaningful or have simply been overlooked in the past. The new findings give strong evidence to modify the taxonomic treatment of major lineages within this subfamily. We suggest to merge some widely accepted traditional tribes of Pooideae and propose the following preliminary classification: 1) Brachyelytreae; 2) Nardeae with subtribes Nardinae and Lygeinae; 3) Meliceae with subtribes Brylkiniinae and Melicinae; 4) Phaenospermateae; 5) Duthieeae; 6) Stipeae with subtribes Ampelodesminae and Stipinae; 7) Diarrheneae; 8) Brachypodieae; 9) Hordeeae with subtribes Brominae, Hordeinae and Littledaleinae; 10) the Aveneae/Poeae tribe complex.

Interestingly, we identified a new morphologically well-defined group among the early evolutionary lineages encompassing all 'primitive' members (*Danthoniastrum*, *Duthiea*, *Metcalfia*, *Pseudodanthonia*, *Sinochasea*, *Stephanachne*) of the previous tribe Aveneae and *Anisopogon,* which was formerly sometimes placed outside of the subfamily Pooideae. Based on cp data the genus *Phaenosperma* is closely related with this group, but differs strongly in morphological characters. We proposed to keep *Phaenosperma* under the monotypic tribe Phaenospermateae and to unify the other genera under the newly described tribe Duthieeae, which is strongly supported by recent DNA sequence information of the nuclear single-copy locus *Topo*6.

Furthermore, the study revealed the small grass tribe Hainardieae as highly polyphyletic and showed its genera in different groups among the Aveneae/Poeae tribe complex.

14:15

Genome size and genomic GC content evolution in the miniature genome-sized family Lentibulariaceae

Adam Veleba [1] · Petr Bureš [1] · Lubomír Adamec [2] · Petr Šmarda [1]
Ivana Lipnerová [1] · Lucie Horová [1]
[1] Department of Botany and Zoology, Masaryk University, Kotlářská 2, 61137, Brno, Czech Republic — [2] Institute of Botany, Dukelská 135, Třeboň, 37982, Czech Republic

Carnivorous family Lentibulariaceae comprises plants with absolutely smallest genome size (GS) so far known for vascular plants. Until now, the data has been known only for about 8 % of its species richness, which limits the understanding of evolution of such highly miniaturized genomes. Genome miniaturization is assumed to significantly affect overall genomic DNA base composition (GC content), however the data has been known only for two species so far.

GS and genomic GC content were analyzed with flow cytometry in 119 species of Lentibulariaceae. The evolution of both genomic parameters was reconstructed and the key events of their changes were detected. The correspondence of the measured genomic parameters with ecological traits was tested using sequence-based phylogeny.

GS ranged from 1C = 73 Mbp in *Genlisea nigrocaulis* to 1C = 1471 Mbp in *G. subglabra*. Genomes of 19 species were found to be smaller than *Arabidopsis thaliana*. The reconstruction of GS evolution revealed multiple miniaturization events in *Utricularia* and a miniaturization trend in *Genlisea* sect. *Recurvatae* and *G.* sect. *Genlisea*. The GC content of *Genlisea* and *Utricularia* species was extremely variable (34.0%–45.1%). Its variation is the highest among any family or genus of vascular plants analyzed so far. There were detected two clades with increasing portion of GC bases, one in *Utricularia* and one in *Genlisea*, as well as a clade with the opposite tendency in each of these genera. No correlation between measured genomic parameters and ecological traits was found.

Because of multiple independent genome miniaturization events and associated high GC content variation, Lentibulariaceae represents an interesting model group for future detailed genomic studies. The absence of any relationship with ecological traits suggests that the reasons for the genome miniaturization could be associated with an intrinsic process rather than with external selective pressure.

14:30

Variation in Inbreeding Depression between Geocytotypes of highly invasive *Centaurea stoebe* s. L.

—

Matthias Hartmann [1] · Christoph Rosche [1] · Isabell Hensen [1]
Patrik Mráz [2] · Adrian Schaar [3] · Janine Hochheimer [4]
Susanne Lachmuth [1]

[1] Institute of Biology/Geobotany and Botanical Garden, Martin Luther University Halle Wittenberg, Am Kirchtor 1, 06108 Halle, Germany — [2] Herbarium PRC & Department of Botany, Charles University in Prague, Benátská 2, 12801 Praha, Czech Republic — [3] Institute of Zoology, Martin Luther University Halle Wittenberg, Domplatz 4, 06108 Halle, Germany — [4] Institute of Biology/Geobotany and Botanical Garden, Martin Luther University Halle Wittenberg, Neuwerk 21, 06099 Halle, Germany

—

The spotted knapweed (*Centaurea stoebe*) is considered one of today's worldwide top invaders. In its native range, two cytotypes (i.e. diploid and tetraploid) are frequent, whereas, so far, only the tetraploid cytotype has been reported in the invaded range. Hence, three geocytotypes can be characterized: native diploid, native tetraploid and invasive tetraploid, respectively. This cytotype shift has already been described for other invasive species and may partially be explained by the assumption that polyploids maintain a higher heterozygosity. Tetraploids may thus buffer inbreeding depression better than their diploid conspecifics. This may particularly lead to better colonization ability for primary colonization as well as secondary invasion as inbreeding is assumed to occur in the course of serial colonization events during range expansion.

We conducted a breeding experiment (outcrossing and halfsib-mating) including lineages from 39 *C. stoebe* populations. In order to investigate differences in inbreeding depression between the geocytotypes, we compared germination success and growth between inbred and outbred offspring of the three geocytotypes.

Across all traits, we observed different magnitudes of inbreeding depression. The highest magnitudes of inbreeding depression were found in diploid progeny and lowest inbreeding depression in invasive tetraploids, respectively. Since tetraploids were generally more resistant against inbreeding depression than diploids, we conclude that this may contribute to explain the described cytotype shift. The results further suggest the occuence of purging in founder populations of tetraploids which might enhance the colonization ability of the invasive tetraploids in North America for secondary invasion.

14:45

Spontaneous hybrid formation in dogroses: implications for the evolutionary dynamics in a polyploid species complex and its morphology based taxonomy

—

Christiane M. Ritz · Veit Herklotz
Senckenberg Museum of Natural History Görlitz, Am Museum 1,
02826 Görlitz, Germany

—

Hybridization in combination with an increase in ploidy level (allopolyploidy) is considered as a major evolutionary driving force in angiosperm evolution (Soltis & Soltis 2009). The evolution of the polyploidy dogroses (*Rosa* L. sect. *Caninae* (DC.) Ser.) has been remarkably influenced by hybridization because the entire section originated by multiple hybridization events (Ritz et al. 2005) and current species diversity has been attributed to hybrid speciation (Ritz & Wissemann 2011). An intriguing outcome of hybridization in dogroses is their unique reproductive system controlled by the canina-meiosis enabling the mostly odd-ploid plants ($2n = 5 \times = 35$) to reproduce sexually. As a consequence of the imbalanced meiosis, tetraploid egg cells fuse with haploid sperm cells restoring the pentaploid somatic level resulting in strong matrocliny of the offspring. Interspecific hybrids originated apparently between members of subsect. *Rubigineae* and subsect. *Caninae* as shown for the rare hybridogenic species *R. micrantha* and *R. agrestis* (Ritz & Wissemann 2011; Herklotz 2012). We investigate, if these hybrids have been recurrently formed from the respective parental species at each study site or, if the hybrids can be deduced from a few ancestors which subsequently spread throughout the area. Genetic data from microsatellites and ploidy level estimations as well as morphological data revealed that some but not all samples of *R. micrantha* and *R. agrestis* were hybrids. Thus, under the current morphology-based species descriptions individuals of different evolutionary origin are summarized. Hybridogenic individuals originated independently from parental species in mixed stands but their establishment in the populations was strongly correlated with an increase of ploidy level. In contrast to the pentaploid parental species, we observed mostly hexaploid ($2n = 6 \times = 42$) hybrids, which must have originated by a merger of unreduced gametes. We assume that unreduced gametes are essential for stable hybrid formation because correct pairing of chromosomes during canina meiosis is strongly facilitated, if the newly formed hybrid contains at least two very similar chromosome sets.

References

Herklotz V. 2012: Populationsgenetik und Hybridisierung von Hundsrosen auf dem Strohmberg (Oberlausitz/Sachsen). Internationales Hochschulinstitut Zittau.

Ritz C.M., Schmuths H., Wissemann V. 2005: Evolution by reticulation: European dogroses originated by multiple hybridization across the genus *Rosa*. Journal of Heredity **96**: 4 – 14.

Ritz C.M., Wissemann V. 2011: Microsatellite analyses of artificial and spontaneous dogrose hybrids reveal the hybridogenic origin of *Rosa micrantha* by the contribution of unreduced gametes. Journal of Heredity **102**: 217 – 227.

Soltis P.S., Soltis D.E., 2009: The role of hybridization in plant speciation. Annual Review of Plant Biology **60**: 561 – 588.

15:00

Parallel homoploid and polyploid hybrid speciation in *Sempervivum tectorum* × *S. calcareum* (Crassulaceae)

—

Joachim W. Kadereit · Johannes Klein
Institut für Spezielle Botanik und Botanischer Garten,
Johannes Gutenberg-Universität Mainz, 55099 Mainz, Germany

—

Hybrid speciation can take place without (homoploid) or with (polyploid) changes in ploidy level. Whereas polyploid hybrid speciation has been documented for a large number of taxa and represents a speciation process accounting for up to 15% of speciation events in flowering plants, homoploid hybrid speciation has been convincingly demonstrated in fewer than 20 instances. It has been discussed that homoploid and polyploid hybrid speciation may be related to the genetic distance between the parental species, with small distances resulting in homoploid and large distances resulting in polyploid hybrid species.

Using nrITS and IGS and plastid DNA sequences (*atp*I-*atp*H, *rps*16-intron, *trn*Q-*rps*16) we demonstrate that hybridization between the widespread *S. tectorum* and *S. calcareum* from the southwest Alps resulted in both a homoploid and a polyploid hybrid derivative which should be recognized as species. The homoploid hybrid species is distributed in the Rhine Gorge area (Upper Middle Rhine, Mosel, Nahe and Ahr valleys, Germany), and the polyploid hybrid species in the Massif Central (France). Our findings imply that homoploid and polyploid hybrid speciation need not be correlated with genetic distance between parental species. As both hybrid species are geographically isolated from their parents, our findings also imply that hybrid speciation, considered sympatric by definition, may require a phase of isolation by allopatry necessary for hybrid species establishment.

15:15

Melting gene pools in the *Hypericum perforatum* complex

—

Charlotte Scheriau · Nicolai M. Nürk · Marcus A. Koch
Centre for Organismal Studies (COS) Heidelberg, Biodiversity and Plant Systematics,
University of Heidelberg, Germany

—

The modern central European flora has been drastically shaped by Pleistocene glaciations, geographically and genetically. Extensive environmental changes, the opening and closing of migration routes, the emergence, persistence and extinction of refuge areas, as well as varying dispersal abilities highly have influenced the present flora. Plant lineages confronted with these Pleistocene conditions either went extinct, or underwent range shifts, survived in refuge areas with potential allopatric speciation, and recolonized with possible secondary contacts. This spatio-temporal scenario provides an ideal framework to study the evolutionary dynamics of diverging and hybridizing lineages. We investigate a species group comprising the *Hypericum perforatum* complex (St. John's wort, Hypericaceae) and three morphologically and ecologically distinct species: *H. maculatum, H. tetrapterum and H. undulatum*, as well as hybrids between them. The species *H. perforatum* and *H. maculatum* both have wide and overlapping distribution ranges including known glacial refuge areas. Published AFLP and cpDNA analyses, however, revealed populations to cluster in three distinct gene pools. Here we present analyses of divergence time estimations and introgression patterns based on nuclear rDNA internal transcribed spacer (ITS) sequence information. We confirm that *H. perforatum* is characterized by two ancestral and distinct gene pools, whereas *H. maculatum* populations shared a third gene pool. Hybridization between the two *H. perforatum* gene pools is more frequent as compared to the third, despite all three being in sympatry. We hypothesize that allopatric speciation within different glacial refugia formed the three gene pools, but that potential species barriers between the *H. perforatum* gene pools are too week to permit lineage divergence during secondary contact. Thus, the ongoing melting of *H. perforatum* gene pools is an example of reticulate evolution within diverging lineages that were shaped by Pleistocene climate dynamics.

15:30

ITS polymorphisms shed light on hybrid evolution in apomictic plants: a case study from the *Ranunculus auricomus* complex

—

Ladislav Hodac[1] · Armin Patrick Scheben[1] · Diego Hojsgaard[1]
Ovidiu Paun[2] · Elvira Hörandl[1]

[1] Department of Systematic Botany, University of Göttingen, Germany — [2] Department of Systematic and Evolutionary Botany, University of Vienna, Austria

—

The reconstruction of reticulate evolutionary histories in plants is still a major methodological challenge. Sequences of the ITS nrDNA are a popular marker to analyze hybrid relationships, but variation of this multicopy spacer region is affected by concerted evolution, by high intra-individual polymorphism, by shifts in mode of reproduction, and by potential changes in secondary structure. We aim to shed light on the extent of polymorphism within and between sexual species and their putative natural as well as synthetic hybrid derivatives in the *Ranunculus auricomus* complex to test morphology-based hypotheses of hybrid origin and parentage of taxa. We employed direct sequencing of ITS nrDNA from 68 specimens representing three sexuals, their synthetic hybrids and one sympatric natural apomict, cloning of ITS copies in four representative individuals, secondary structure analysis, and landmark geometric morphometry on leaves. Network analyses of ITS data indicate additivity of both synthetic and natural hybrids between the parental species, whereby the triploid synthetic hybrids are genetically much closer to their maternal progenitors, probably due to ploidy dosage effects, although exhibiting a paternal-like leaf morphology. The natural hybrids are genetically and morphologically closer to the putative paternal progenitor species. Secondary structure of ITS1, ITS2 and 5.8S was rather conserved in all taxa. The observed similarities in both phenotype and ITS polymorphisms support the hypothesis that the natural apomict *R. variabilis* is an ancient hybrid of the diploid sexual species *R. notabilis* and the sexual species *R. cassubicifolius*. The additivity pattern shared by *R. variabilis* and the synthetic hybrids supports an evolutionary and biogeographical scenario that *R. variabilis* originated from ancient hybridization. Concerted evolution of ITS copies in *R. variabilis* is incomplete, probably due to a shift to asexual reproduction. Under the condition of comprehensive inter- and intraspecific sampling, ITS polymorphisms are powerful for elucidating reticulate evolutionary histories.

The role of ecogeographic isolation in the diversification of alpine *Androsace* (Primulaceae)

15:45

—

Gerald M. Schneeweiss[1] · Peter Schönswetter[2]

[1] Department of Botany and Biodiversity Research, University of Vienna, Rennweg 14, 1030 Vienna, Austria — [2] Institute of Botany, University of Innsbruck, Sternwartestrasse 15, 6020 Innsbruck, Austria

—

Alpine habitats, i.e., habitats above the tree-line, are biodiversity hotspots. The high degree of species richness is the result of the complex origin and histories of alpine habitats, being shaped by tectonic uplift, geographic isolation, climate changes, glaciation, and strong microhabitat differentiation. This renders alpine organisms well suited systems to study biogeographic and ecological aspects of diversification and speciation. A model group for diversification in the central and southern European mountain system is the *Aretia* clade of *Androsace* (Primulaceae). Apart from a nested clade of about 10 species (pertaining to former *Douglasia* plus *A. triflora*) distributed from Arctic Russia to western North America, the two dozen remaining species of the *Aretia* clade are restricted to Europe with the highest diversity in the Alps and the Pyrenees. Although these species can readily hybridize, they are generally reproductively isolated via non-overlapping distribution areas and/or distinct habitat preferences, suggesting that ecogeographic isolation is the main force behind speciation in this group. Little is, however, known about the relative importance of geographic differentiation versus ecological (habitat) differentiation. Here, we test the hypothesis that habitat differentiation will be more frequent in cases of sympatric speciation (i.e., speciation within the same discrete geographic region) than in cases of allopatric speciation. To this end, we use a time-calibrated species phylogeny of the *Aretia* clade derived from plastid sequence data and employ a dispersal-extinction-cladogenesis model of habitat and geographic evolution allowing for founder-event speciation.

16:30 Population genetic structure in alpine willow hybrids (*Salix*, Salicaceae)

—

Susanne Gramlich[1] · Anne-Caroline Cosendai[2]
Ruth Flatscher[2] · Elvira Hörandl[1]
[1] Department of Systematic Botany, Georg August University Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany — [2] Department of Evolutionary and Systematic Botany, Faculty Centre of Biodiversity, University of Vienna, Rennweg 14, 1030 Vienna, Austria

—

Little attention has been paid to evolutionary processes facilitated by the particular colonizing dynamics and succession processes triggered by climate change. The retreat of glaciers due to climate change leaves behind devastated glacier forefields as a novel territory for colonization by pioneer species. Another effect of global warming is that lowland species start to move upwards and colonize higher elevations which had been out of their ecological niche before. When these species lack postzygotic crossing barriers to alpine species due to the previous ecological isolation by altitude, such secondary contacts may result in the formation of hybrids. In F2 or later hybrid generations, transgressional segregation can result in the formation of novel genotypes that are able to establish in extreme habitats outside the ecological optimum of the parents. This study examines these processes in two *Salix* (willow) species on the Rhône glacier forefield (Switzerland), combining population genetic data from seven SSR loci and ecological data. Results show that the hybrids mostly belong to the F2 or later generations, while F1 hybrids seem to be absent. Further, some individuals represent backcrosses with one of the parental species. Niche characterization by using Ellenberg's indicator values suggest that hybrids occupy their own characteristic ecological niche, exhibiting higher tolerance to acidic soils and drought than either of the parents. Overall, the results show that hybrids have not only successfully established a population on the Rhône glacier, but they may have also a certain potential for speciation due to selective advantages in extreme habitats.

16:45 Species boundaries in the *Fosterella micrantha* group (Bromeliaceae)

—

Natascha Wagner · Tina Wöhrmann · Kai Schubert · Kurt Weising
Institute of Biology, University of Kassel

—

The mesophytic genus *Fosterella* (31 species) belongs to the bromeliad subfamily Pitcairnioideae *s.str*. Its main distribution areas are the eastern slopes of the central Andes. Recent studies suggest that *Fosterella* originated in the mid Miocene about 10 Mya in the Andean seasonally dry tropical forests (SDTF; Wagner et al., 2013). A well resolved multilocus phylogeny of *Fosterella* based on six chloroplast DNA regions (*mat*K, *rps*16 intron, *atp*B-*rbc*L, *psb*B-*psb*H, *rpl*32-*trn*L, *rps*16-*trn*K) demonstrated the monophyly of the genus and its division into six evolutionary lineages. These findings were supported by a nuclear phylogeny based on *phy*C.

Within *Fosterella*, the so-called *micrantha-group* comprises three morphologically very similar species that show a disjunct distribution pattern, probably caused by one or more long distance dispersal events. *Fosterella micrantha* is distributed in SDTFs of Central America, whereas *F. christophii* is endemic to a small area at the “Andean knee”, and *F. villosula* occurs in a wide distributional range in the Bolivian Yungas. We used AFLP and SSR markers to study the population structure and the extent of gene flow among 21 populations from all three species. Additionally we conducted crossing experiments to study fertilization barriers within the group. Our results show that most of the populations of the Central American *F. micrantha* are genetically separated from those of the Bolivian *F. christophii* and *F. villosula*. A NeighbourNet analysis of the AFLP data indicates a geographical rather than species-specific pattern for the latter two species, separating northern and southern populations of *F. christophii* and *F. villosula*. Our crossing experiments showed that all species are able to self but can also form interspecific hybrids, indicating that reproductive barriers are low within the group.

References

Wagner, N., Silvestro, D., Brie, D., Ibisch, P.L., Zizka, G., Weising, K. and Schulte, K. 2013: Spatio-temporal evolution of *Fosterella* (Bromeliaceae) in the Central Andean biodiversity hotspot. Journal of Biogeography **40**, 869 – 880.

A first four-locus plastid phylogeny of *Pitcairnia* (Bromeliaceae)

17:00

—

Kai Schubert · Natascha Wagner · Tina Wöhrmann · Kurt Weising

Institute of Biology, University of Kassel

—

With 399 described species, *Pitcairnia* is by far the largest genus of the subfamily Pitcairnioideae (Bromeliaceae). It also shows the widest distribution range within the subfamily. The genus is distributed in South and Central America except for *Pitcairnia feliciana* that is a local endemic on a mountain range in West Africa. No extensive molecular systematic analyses have yet been undertaken in *Pitcairnia*, and infrageneric relationships remain largely unknown. Here we present a first plastid phylogeny of the genus, based on the *matK* gene, two fragments of the *ycf1* gene and the two intergenic spacers *rpl32 – trnL* and *rps16 – trnK*. Sequences were assembled for 181 accessions from 128 species, resulting in an alignment of 4,989 bp. A total of 540 characters turned out to be parsimony informative. The data set was subjected to Bayesian, maximum likelihood and maximum parsimony analyses. In the resulting trees, *Pitcairnia* is monophyletic and sister to the remainder of the subfamily. A deep basal split divides *Pitcairnia* into two large lineages. *Pitcairnia feliciana* takes a relatively early branching position in one of the two lineages. Its closest relatives are found in Venezuela. Some clades reflect the distributional pattern of the underlying species (e.g. a Brazilian clade and a Carribean clade), but no overall general geographical patterns could be discerned.

17:15

Flower color evolution within the Cichorieae (Asteraceae) – the Flavonoid-3'5'-Hydroxylase

—

Birgit Gemeinholzer[1] · Thomas Gross[1] · Volker Wissemann[1]
Stefan Martens[2]

[1] AG SystematicBotany, Justus-Liebig-Universität Giessen, Heinrich-Buff-Ring 38, 35392 Giessen, Germany — Fondazione Edmund Mach – Research and Innovation Center, Food and quality nutrition department, via E. Mach 1, 38010 S. Michele all'Adige, TN, Italy

—

The blue flower color within the Cichorieae (Asteraceae) is thought to be determined by the presence of anthocyanins.The anthocyanin biosynthetic pathway is quite well studied. Two enzymes, flavonoid 3' hydroxylase and flavonoid 3', 5' hydroxylase, determine the hydroxylation pattern of the anthocyaninswhich exhibit three classes: cyanidins (mainly in charge of redish/pink flowers), delphinidins (in charge of bluish flowers), and pelargonidins (one possibility to exhibit orange flower color).

We here investigate flower color evolution in two closely related species of two different genera of the Cichorieae featuring yellow (*Catananchelutea* L.; *Lactucaserriola* L.) and bluish (*Catananchecaerulea*L., *Lactucaperennis* L.) flowers.Whereas, the yellow flowering species *C. lutea* and *L. serriola*did notexpress *F3'5'H* it was possible to partially sequence the *F3'5'H* mRNA in *C. caerulea* and *L. perennis*. The q-RT PCR expression pattern revealed *F3'5'H*to be expressed in different levels at differ-

ent times and developmental stages during flower development of *C. caerulea* and *L. perennis*.The expression is preceding the petal coloration in the flowers. A phylogenetic analysis revealed high similarity of the bluish CichorieaeF3'5'Hwith other AsteraceaeF3'Hs and F3'5'H pinpointing to a neofunctionalization of this enzyme, to enable the Asteraceae to produce delphinidins again. In addition, the flavonoid composition was analyzed via LC-MS and HPLC. All four species contain caffeic acid, *p*-coumaric acid and 3' hydroxylated flavonoids like quercetin derivatives.Delphinidin, Pelargonidin and Cyanidin were found in *C. caerulea*, while *L. perennis* only featured Pelargonidin and Cyanidin which was also found in much lower concentrations in *L. serriola*. Missing anthocyaninsin *C. lutea* might be indicative for an inactivation of the DFRenzyme(dihydroflavonol 4-reductase) in this species which might be yellow flowered due to carotinoids. Investigating enzyme activities will be the next step to reveal flower color evolution within the Cichorieae.

Systematics of Pelliaceae (Marchantiophyta, Jungermanniopsida) and the new genus *Apopellia* stat. nov. 17:30

Nicole Schütz[1] · Dietmar Quandt[2] · Martin Nebel[1]
[1] State Museum of Natural History Stuttgart, Rosenstein 1, 70191 Stuttgart, Germany —
[2] Nees Institute for biodiversity of plants, Meckenheimer Allee 170, 53115 Bonn

Recent molecular phylogenies and classifications reveal the Pelliales to be the earliest diverging lineage within the simple thalloid liverworts (Crandall-Stotler et al. 2009). The order comprises two families: Pelliaceae with eight species of *Pellia* Raddi, and Noterocladaceae with the monotypic genus *Noteroclada* Taylor ex Hook.f. & Taylor. We conducted DNA sequence analyses of the plastid loci *rps*4 and *trn*L-F of all Pelliaceae species at hand and morphological studies of selected characters.

Within *Pellia*, a considerable split into two main clades was observed: one comprising *Pellia endiviifolia* and *P. megaspora*, the other including *P. neesiana, P. appalachiana* and *P. epiphylla*. We found several morphological characters, which supported this split: e.g. smooth calyptra vs. two-celled hairs on surface, erect vs. horizontal posture of archegonia, pluricellular vs. two-celled slimehairs. Due to the conspicuous distinctness of these two clades concerning molecular as well as morphological data, we established two different genera. The former subgenus *Apopellia* Grolle (Grolle 1983), which exhibited the single species *Pellia endiviifolia*, is now classified as genus and includes *Apopellia endiviifolia* and *A. megaspora*.

Our genetic data confirmed the distinctness of the species *Apopellia endiviifolia*, *A. megaspora*, *Pellia. neesiana* and *P. epiphylla* with high statistical support.

Sequence variation within each species was quite low. However, within *A. endiviifolia* two clades were found, of which one comprised all accessions from Japan and Korea. This "type B" sequence of *P. endiviifolia* might be related to the finding of Schuster (1981), who noted morphological differences in *P. endiviifolia* specimens from Japan.

Finally, our biogeographic studies resulted in updated distribution maps of each species.

References

Crandall-Stotler, B., Stotler, R.E. & Long, D.G. 2009: Phylogeny and classification of the Marchantiophyta. Edinburgh Journal of Botany **66**: 155 – 198.

Grolle, R. 1983: Hepatics of Europe including the Azores: an annotated list of species, with synonyms from the recent literature. Journal of Bryology **12**: 403 – 459.

Schuster, R.M. 1981: Evolution and speciation in *Pellia*, with special reference to the *Pellia megaspore-endiviifolia* complex (Metzgeriales), I. Taxonomy and distribution. Journal of Bryology **11**: 411 – 431.

17:45

Small but manifold – hidden diversity in the heterotrophic golden alga *Spumella*

Lars Grossmann[1] · Christina Bock[1] · Michael Schweikert[2]
Jens Boenigk[1]
[1] Biodiversity, University Duisburg-Essen — [2] Zoology, University Stuttgart

The so-called 'genus' *Spumella* (Chrysophyceae/Chrysomonads) comprises colourless single-cell flagellates which are major phagotrophs and feeders on bacteria in freshwater and soil food webs. The group appears as the clustered '*Spumella*-like flagellates' in applied studies (concerned with protistan biodiversity and ecology). We assume, however, that the picture drawn is inexact blurring diversity and leaving the distinct ecology unanswered. Here, we present results of gene analyses as well as morphological data showing the polyphyly of *Spumella* and calling for an altered database reference thus gaining a deeper insight into the biodiversity and ecology of the group.

Session · Plant Form & Function

09:00

Key note: A Biophysical Perspective on Evolutionary Developmental Biology

—

Karl J. Niklas[1] · Stephen H. Weiss[2]

[1] The Liberty Hyde Bailey, Professor of Plant Biology — [2] Presidential Fellow,
Department of Plant Biology, Cornell University, Ithaca, NY 14853, USA

—

Development involves the participation of generic physical laws and processes (e.g., passive diffusion, cohesion, and tensile forces) and genomic processes (e.g., transcription factors and signal transduction pathways). Over the course of evolution, the relative importance of these two components of development has changed. A review of the data indicates that organisms relied on generic laws and processes to regulated developmental patterns more in the past than they do today. This allegation is based on the observation that developmental patterns in more evolutionarily derived organisms manifest greater regulatory manipulation of physical laws and processes than more ancient organisms. Examples that support this allegation include the orientation and location of the plane of cell division in land plants and the role of cellulose microfibrils in the isotropic vs. anisotropic expansion of cell growth in size.

09:30

Insights into the inside – Anatomical studies of the explosive style movement in Marantaceae

—

Markus Jerominek · Regine Classen-Bockhoff

Institut für Spezielle Botanik, Johannes Gutenberg-Universität, Mainz

—

Fast movements in plants are known from the Venus fly trap or the sensitive plant *Mimosa*. The tropical arrowroot family (Marantaceae) presents a further example by its explosive style movement. Here, pollen is placed on the style in bud stage (secondary pollen presentation) and transferred to the insect by an irreversible style movement. Thereby, position and form of the style are changed from a stretched (unreleased) to a bended (released) state. This deformation is likely based on a rapid water transport in the style. However, the size of the style and the observed velocity of the movement suggest that turgor changes alone cannot cause the explosive style movement. Rather an elastic tension must be involved. In our histological investigation, we try to verify the water shift in the style tissue. We also aim to identify the source of elastic energy.

Based on cross and tangential sections cell dimensions were reconstructed in unreleased and released styles. A comparison of both states shows that cells in the upper epidermis are constant in volume, but significantly increase in length. Consequently, the epidermis cells are not deformed by water flux but rather by a tensile stress. We assume that the elastic energy is stored in the cell walls of the upper epidermis that are more robust that those of other cells. In contrast, lower cell layers increase in volume and length. The enormous water influx must be attributed to extracellular sources. Beside the reconstruction of water fluxes, our results help to understand the histological preconditions for fast movements on a cellular level. Fundamental principles such as resilience against mechanical forces observed in the style of Marantaceae can be transferred to bionic engineering of bending materials.

09:45

Growth form shifts in the genus *Aristolochia*

—

S T Wagner[1] · S Isnard[1] · N Rowe[2] · S Wanke[3] · C Neinhuis[3]
[1] IRD, UMR-AMAP, Laboratoire de Botanique et d' Écologie Végétale Appliquées, BPA5, 98800, Nouméa, New Caledonia — [2] Univ Montpellier 2, UMR – AMAP, Montpellier, 34000 France; CNRS, UMR AMAP, Montpellier, 34000 France — [3] Institut für Botanik, Technische Universität Dresden, 01062 Dresden, Germany

—

The genus *Aristolochia* is the species richest clade among the perianth-bearing Piperales. It is well known for its large number of climbing species, alongside with comparatively few species described as herbaceous or shrub-like. This growth form diversity favours *Aristolochia* forstudies on growth form evolution, including transitions between growth habits with different functional properties. We combine anatomical and biomechanical investigations with molecular approaches to detect trends in growth form shifts and developmental processes in the genus *Aristolochia*. Thus, we also approach more generalevolutionary questions, such as: how do plants manage to switch between different mechanical architectures; andare clades, that become specialized as climbers, able to diversify further into self-supporting growth forms? Field work at natural sites shows that the rare shrub-like *Aristolochia* species, which only occur in the subgenus *Isotrema*, are neither climbing nor fully self-supporting. They develop a more or less upright growth with their branches leaning on the surrounding vegetation. Biomechanical and anatomical investigations reveal differences

between climbing and shrub-like species, but both growth forms show several stem characters typically found in climbers, such as ray parenchyma and a thick periderm, which are known to promote flexibility. Thus, our study suggests that evolution of growth forms within *Aristolochia* might be constraint by specializations towards the climbing habit: even the shrub-like species do not develop a height, size and stability typical of self-supporting shrubs and trees. However, this case of growth form shifts documented in *Aristolochia* demonstrates that plants can achieve rather contrasting mechanical properties by relatively simple modifications in stem anatomy. The shifts between non self-supporting climbing species and more or less self-supporting shrub-like species are mainly realized by changes in tissue distribution, such as a more centralized wood cylinder in the climbing species, and the storage of lignin in the wood rays of the shrub-like species. These modifications might involve heterochronic events – changes in the timing of developmental processes.

10:00

The enigmatic development of the androecium of *Eucryphia* Cav. (Cunoniaceae)

—

Kester Bull-Hereñu [1] · Louis Ronse de Craene [2] · Fernanda Pérez [3]
[1] Escuela de Pedagogía en Biología y Ciencias, Universidad Central de Chile, Departamento de Ecología, Pontificia Universidad Católica de Chile — [2] Royal Botanic Garden Edinburgh, UK — [3] Departamento de Ecología, Pontificia Universidad Católica de Chile

—

Polyandry has evolved many times independently in angiosperms. It is possible to distinguish between two major ontogenetic patterns on the flower meristem: i. primary polyandry characterized by the generation of many stamen-primordia following a spiral or whorled phyllotaxis with a centripetal order of initiation (e.g. *Ranunculus*), and ii. secondary polyandry which is characterized by the initiation of the so-called primary primordia which subsequently subdivide into many stamen (secondary) primordia in either centripetal or centrifugal direction (e.g. *Hypericum*, Ronse de Craene 2010).

The gondwanic genus *Eucryphia* Cav. (Cunoniaceae) presents a characteristic tetramerous flower of showy white petals with polyandry of unknown origin. In this study we analyse the question of the nature of this polyandry by presenting the ontogeny of four species and one hybrid (*E. cordifolia*, *E. glutinosa*, *E. milliganii*, *E. lucida* y *E. x nymansensis*) by means of electron microscopy.

At a first glance, the development of the *Eucryphia* flower is characterized by the early differentiation of a ring primordium which becomes rapidly covered with stamen primordia of variable shape showing curiously no clear signs of an ordered direction of inception. A more detailed view of the ontogenetic sequence reveals that while the stamen primordia originate on the ring primordium, the flower meristem itself increases in size at its flanks. The most distal primordia near the gynoecial area differentiate straight into stamens while towards the flanks, the coexistence of both meristem extension and stamen fractionation promotes either the apparition of new primordia between the older ones and/or the subdivision of existing primordia into secondary primordia. The ontogeny of the polyandry in *Eucryphia* is thus characterized by a chaotic distribution of stamen-primordia of different sizes.

This uncommon pattern of secondary polyandry represents a unique evolutionary path in the genus showing a novel way to accommodate a higher number of stamens in the androecium and clearly differing from the flower Bauplan of the family and order.

References

Ronse de Craene L. 2010: Floral Diagrams. An Aid to Understanding Flower Morphology and Evolution Cambridge University Press.

10:15

Evolution of C_4 photosynthesis and diversity of C_4 and C_3 leaf anatomy in Salsoleae s. s. (Chenopodiaceae/Amaranthaceae)

—

Christina Schüssler · Helmut Freitag · Gudrun Kadereit
nstitute für Allgemeine und Spezielle Botanik,
Johannes Gutenberg-Universität Mainz, 55099 Mainz, Germany

—

As regards the evolution of the C_4 syndrome, Salsoleae s. s. are a highly interesting group because the tribe contains numerous diverse C_4 clades, several isolated species and species groups appearing as C_3 relicts and at least two C_3/C_4 intermediate species. Previous molecular analyses were inconclusive regarding the number and position of C_4 lineages and even suggested the possibility of a reversal from C_4 to C_3. By including 75 of 155 species from all 20 genera we present a comprehensive dated molecular phylogeny of Salsoleae s.s.) based on five markers (*atpB-rbcl* spacer, *ndhF-rpl32* spacer, *rpl16* intron, *trnQ-rps16* spacer and ITS) and a leaf anatomical survey of most terminals to trace C_4 evolution and leaf anatomical diversification in Salsoleae s.s.

In contrast to previous studies, resolution was clearly improved, especially at the base of the tree, revealing five C_4 lineages in Salsoleae s.s. with the oldest dating back to the early Oligocene and the youngest to the Pleistocene. Reversals to C_3 photosynthesis are ruled out. C_3 species of Salsoleae s.s. show a sympegmoid leaf type or leaf types that are identical with the C_3/C_4 intermediate leaf types of *S. arbusculiformis* and *S. divaricata* pointing to further intermediate species in the tribe. C_4 leaves in Salsoleae s.s show a salsoloid anatomy and differ in presence or absence of a hypodermis, in occurence of sclerenchyma, and in position of the peripheral bundles. According to ancestral character state reconstruction based on maximum likelihood statistics the hypodermis of C_4 species might be homologous to the outer mesophyll layer found in C_3/C_4 intermediates and in C_3 species.

11:00

Key note:
Contact Mechanics at the Insect-Plant Interface: How Do Insects Stick and How Do Plants Prevent This?

—

Stanislav Gorb

Zoological Institute, University of Kiel, Germany

—

Most of the one million insect species described so far are associated with plants. Such insects should be able to attach successfully to plant surfaces. Dealing with attachment, we have to consider a contact problem, in which two bodies are involved. In our case, these are insect attachment organs and plant substrates. Both these parts may have various geometries, mechanical and chemical properties. Moreover, insects produce and deliver a secretory fluid into a contact zone. The situation is usually even more complex, since many plant substrates bear specialised surface coverage. This paper summarises our previous structural and experimental studies on insect attachment and the effect of plant substrates on it. Contacting surfaces in many insect attachment devices are subdivided into patterns of micro- or nanostructures with a high aspect ratio. This paper provides some explanations of the adhesion enhancement effect in such systems. However, attachment abilities of insects depend on the roughness and mechanical stability of the substrate features. Wax bloom of some plant surfaces causes a strong reduction of insect attachment. Four hypotheses of anti-adhesion mechanism of plant surfaces covered with epicuticular wax crystals are proposed, and three of them are experimentally supported.

11:30

Evolution of fruit structures correlates with species richness and transition to epiphytism in *Peperomia*

—

L. Frenzke · M.-S. Samain · L. Symmank · P. Goetghebeur
C. Neinhuis [1] · S. Wanke
[1] Institut für Botanik, Technische Universität Dresden, 01062 Dresden, Germany

—

Dispersal in epiphytic plants is generally characterised by fruit morphological modifications for anemochory or endozoochory. However, this is not the case in the genus *Peperomia* (Piperaceae) where small drupes have been postulated to be epizoochorous dispersed. Both terrestrial and epiphytic species are known in *Peperomia* with epiphytism being derived. As such the evolution of dispersal mode and morphological traits in combination with life form transition represents a unique case in plants. The pantropical genus *Peperomia* belongs to the ten most species-rich genera of flowering plants, and inhabits a wide array of vegetation types. We investigate fruit morphological characters using cryo-SEM and present the broadest molecular phylogeny currently available. Data is combined using ancestral character reconstruction. Epiphytic *Peperomia* species release sticky secretions on the fruit surface or exhibit hook-shaped appendages indicative of epizoochorous dispersal. Exclusively terrestrial clades lack attachment structures. We prove the epiphytic life form to have evolved in association with fruit structures related to epizoochory, contributing to diversification. Statistical analyses reveal increased fruit character diversity in epiphytes in contrast to terrestrial lineages. Higher fruit morphological complexity is recovered in species-rich clades in comparison to species poor lineages and epiphytes are overrepresented in more diverse clades.

11:45

The nectary diversity in Brassicaceae: phylogenetic trends

—

Claudia Erbar
University of Heidelberg, COS-Biodiversity and Plant Systematics,
Im Neuenheimer Feld 345, 60120 Heidelberg, Germany

—

The insect-pollinated flowers of Brassicaceae exhibit a receptacular nectary of the mesophyllary type with nectary slits for the release of nectar. In this character the Brassicaceae fit well into the rosids in which this nectary types dominate. In Brassicaceae, the receptacular nectaries show a high diversity as regards number and position as well as shape and size. There are 1 to 8 nectaries in a flower and they are

either only in transversal (lateral) position or in in transversal and adaxial/abaxial ("diagonal") position. In addition, the nectary protrusions may be separate or confluent, extrastaminal or intrastaminal or circumstaminal.

Analyzing species from all tribes (own data and data from the literature) we can recognize 8 different main diagrams (considering only number and position of the nectaries and disregarding shapes). When we plot these diagrams onto a phylogenetic cladogram with the 49 tribes currently recognized (Koch et al. 2012) we get a very unclear picture with the diagrams distributed across the tribes. The most frequent pattern with 4 nectaries on each side of the transversal stamens is found in nearly all tribes. However, there are always nectaries in the transversal floral plane. This fact accords with the disymmetry of the flowers which is also expressed in the amount and composition of nectar in a flower (Davis et al. 1998) and the site of *CRAB CLAW* gene expression (required for nectaries; Baum et al. 2001).

We can try to trace some possible trends which occurred several times in parallel: Again and again we can find a reduction of the nectary protrusions in the median flower plane. Other trends are extrastaminal confluence, ring closure around the transversal stamens and intrastaminal dislocation in the transversal flower plane.

References

Baum, S.F., Eshed, Y., Bowman, J.L. 2001: The *Arabidopsis* nectary is an ABC-independent floral structure. Development **128**: 4657 – 4667.

Davis, A.R., Pylatuik, J.D., Paradis, J.C., Low, N.H. 1998: Nectarcarbohydrate production and composition vary in relation to nectary anatomy and location within individual flowers of several species of Brassicaceae. Planta **205**: 305 – 318.

Koch, M.A., Kiefer, M., German, D.A., Al-Shehbaz, I.A., Fanzke, A., Mummenhoff, K., Schmickl, R. 2012: BrassiBase: Tools and biological resources to study characters and traits in the Brassicaceae – version 1.1. Taxon **61**: 1001 – 1009.

Reorientation in tilted stems of papaya by differential growth

12:00

—

Andreas Kempe · Thea Lautenschläger · Christoph Neinhuis
corresponding author: Andreas Kempe
Technische Universität Dresden / Dresden University of Technology,
Institute of Botany, 01062 Dresden, Germany

—

Papayas (*Carica papaya* L.) are fast growing plants that are able to reorient quickly from a tilted position by a local growth in the basal stem region. This seems to be a necessary adaptation in the struggle for light in its natural habitat, natural forest gaps. Interestingly the stem anatomy of papaya consists exclusively of parenchymatous wood, exhibiting a substantial turgor pressure. The only reinforcing tissue is found in the bark which contains a lattice like mesh of lignified fibres. Questions were raised from this peculiar mechanism of reorientation as to the role of turgor pressure during growth and to mechanical interactions between fibre mesh and parenchyma as consequence of the unusual anatomy.

A set of mechanical measurements was conducted on tissue sections of secondary phloem and xylem comparing Young's modulus and turgor pressure of upper and lower side of re-erecting stems. Additionally microscopic analyses were applied to tissues of both sides.

We found that Young's modulus differs significantly between tissues in both sides due to morphological adaptations. Experimental data showed that turgor pressure remained constant during cell expansion, throughout the erecting process. Thus cell growth and turgor pressure sustaining water inflow are in state of equilibrium. Microscopic analyses revealed pronounced radially directed cell growth in upper side of xylem as compared to the lower side.

We found that the stem bends by a couple effect due to local secondary growth of the xylem affecting the peculiar phloem fibre arrangement. The xylem extends by directed radial growth on the upper side of leaning stems and generates an outward pointing force. The phloem fibre mesh expands in tangential direction. As a result, the structure contracts in axial direction and eventually causes a pulling force on the upper side.

12:15

Breeding system in andromonoecious *Dorema aucheri* Boiss. (Apiaceae-Apioideae), endemic to Iran

—

Yousef Ajani · Regine Classen-Bockhoff
Institut für Spezielle Botanik und Botanischer Garten,
Johannes Gutenberg-Universität Mainz, 55099 Mainz, Germany

—

Dorema aucheri Boiss. is a perennial monocarpic species endemic to southern parts of Iran. It flowers only once after a rosette stage of four years. Traditionally, the young leaves and branches are used for medicine and food which is threatening the plant. To evaluate the conservation status of the species, field investigations were conducted from May to June 2013 at a natural locality (near the waterfall of Rayen, S Kerman province), where the plants are protected against picking. The area (ca. 3000 m^2) is covered by a large population of *D. aucheri* plants from which twenty randomly chosen individuals were investigated.

When flowering, the plants are characterized by huge yellow inflorescences frequently visited by manifold insects. Most of them are pollinators moving within and among the plants. The high degree of fruit set (67%) indicates that the plants are not suffering from pollen limitation. Inflorescences are andromonoecious with a distal hermaphrodite and a proximal male part. Flowers are protandrous and synchrononized in a duodichogamous manner, i.e. starting with the male phase of the hermaphrodite flowers (2 – 3 days), followed by their female phase (2 – 3 days) and then by the male phase of the remaining flowers (3 – 4 days). Sexual phases overlap from time to time, allowing geitonogamy at some days and demanding obligate outcrossing at other days. The high degree of andromoneocy (78%) coupled with an immense pollen surplus (P/O = 157.172), sexual asynchrony between neighboring plants and the long male flowering stage increase the rate of outcrossing.

Dorema aucheri represents a further example of an apioid species whose reproductive success depends on pollinators and population structure. If harvesting will be continued in a high rate, the individual plants will die before flowering and the population will decrease in size. Distance among plants will be larger and cross pollination by insects more rare. It is thus recommended to restrict the use of the plants to conserve the population and insect fauna.

14:00

Phylogeny, biogeography and evolution of edaphic association in the European oreophytes *Sempervivum* and *Jovibarba* (Crassulaceae)

—

Johannes Klein · Joachim W. Kadereit
Institut für Spezielle Botanik und Botanischer Garten,
Johannes Gutenberg-Universität Mainz, 55099 Mainz, Germany

—

We reconstructed the phylogeny, biogeographical history and evolution of edaphic association in *Sempervivum* and *Jovibarba* (Crassulaceae), two oreophytic genera of the mountain flora of Europe and adjacent areas. Using two nuclear (ITS and parts of IGS) and three chloroplast DNA markers (*atp*I-*atp*H, *rps*16-intron, *trn*Q-*rps*16) of 44 of the 48 species recognized, we obtained a molecular phylogenetic hypothesis on relationships between and within the two genera. This phylogeny was dated and used for the reconstruction of ancestral distribution areas and the evolution of edaphic association. Our analyses showed that *Sempervivum* and *Jovibarba* are monophyletic sister genera. Several well-supported intrageneric clades were recovered in our nuclear phylogeny which generally were not supported by our chloroplast data. This incongruence most likely results from hybridization. The split between the two genera took place c. 5-9 mya, contemporary with the major uplift of the European Alpine System. This split is best explained as a vicariance event resulting in a more westerly distributed *Sempervivum* and a more easterly distributed *Jovibarba*. Most intrageneric diversification took place within the last c. 2 my. The ancestrally European distribution area of *Sempervivum* was expanded by one long-distance dispersal event into northern Africa and three long-distance dispersal events into Southwest Asia. Our reconstruction of edaphic association revealed mainly transitions from calcifuge to calcicole. Most of these transitions took place regionally, and their timing and geographical setting suggest that they were caused by range shifts in response to Quaternary climatic oscillations. The large majority of extant species in the two genera originated in the Quaternary, and all major range shifts took place in this period. With respect to changes in edaphic association, we hypothesize that climatic changes either forced populations into edaphically unsuitable habitats or allowed populations to colonize newly available but edaphically unsuitable habitats.

14:15

Macaronesian island biogeography: inter- and intra-archipelagorelationships of laurel forests

—

Paulina Kondraskov · Nicole Schütz · Mike Thiv
State Museum of Natural History Stuttgart, Rosenstein 1, 70191 Stuttgart

—

Macaronesia has been traditionally recognised as a distinct biogeographic unit consisting of the five Atlantic volcanic archipelagos, Azores, Madeira, Salvage Islands, Canary Islands, and Cape Verde Islands. Several authors implicitly challenged the concept of Macaronesia by classifying the floras of the different archipelagos to distinct biogeographic regions.

We focused on Macoronesian laurel forest that occur only on the Azores, Madeira and the Canary Islands. The study is based on phylogenetic relationships, biogeographic analyses and molecular dating of 14 representative taxa of these forests.

The relationships among the archipelagos are heterogeneous across different taxa. However a mixture of biogeographical patterns could be identified. Inter-archipelago dispersal events appear to be relatively recent for all groups. Many colonisations of Macaronesian island groups were traced to a single event. All the same, it was detected that some taxa colonised these archipelagos independently.

The biogeographic relationships within the Canary Islands are also heterogeneous for some taxa and do not correlate with the geological island histories.

14:30

Following the track of aridification – biogeography and adaptation to drought in *Anabasis* L. (Chenopodiaceae)

—

Rüdiger Masson · Maximilian Lauterbach · Gudrun Kadereit
Institute für Allgemeine und Spezielle Botanik,
Johannes Gutenberg-Universität Mainz, 55099 Mainz, Germany

—

The genus *Anabasis* L. (Chenopodiaceae, Salsoleae) comprises 25 – 30 spp. of long-lived shrubs in steppes, semi-deserts and deserts of North Africa and West and Central Asia. *Anabasis* shows conspicuous adaptations to drought and saline conditions, such as C_4 photosynthesis, succulence and very fast seed germination. The climatic niche of the genus ranges from 5 to 370 mm precipitation per year and a mean temperature of the warmest quarter between 16.5 and 35°C. The drought tolerance of some species within the genus surpasses most other plant species resulting in monospecific stands in some areas, e.g. *Anabasis aretioides* in Moroccan deserts, or dominance in others, e.g. *A. brevifolia* in Mongolian deserts.

Our dated molecular phylogeny (based on five cp markers) and biogeographical analysis show that *Anabasis* originated during the Early Miocene in the Central Asian region east of the Caspian Sea. Diversification of the genus started during the Middle Miocene and it reached the African continent and also Mongolia during the Late Miocene. Divergence timing, tree topology and the ancestrally arid ecology suggest that *Anabasis* followed the spread of arid landscapes from the Asian interior westward to North Africa and eastward to Mongolia during the Late Miocene/Pliocene. North Africa for example was reached two times by *Anabasis*, once during the Later Miocene probably migrating via land bridges along the northern margin of the Tethys. The widespread *Anabasis articulata* (Forssk.) Moq. which belongs to this clade is probably of North African origin and subsequently spread into West Asia. North Africa was reached a second time by *A. syriaca* migrating via the Saudi Arabian Peninsula after the closure of the Tethys.

Although already ancestrally adapted to dry condition, *Anabasis* evolved further adaptions to desert environments. The molecular phylogeny revealed the multiple reduction and loss of leaves, the multiple increase in epidermis layers from 1 – 2 in the ancestor to more than four (up to 11), the increase of stomatal surface proportion with increase of epidermis layers and the multiple evolution of a cau-

dex. This likely demonstrates that *Anabasis* not only followed the spread of arid landscapes but also adapted to their increasing aridity.

14:45

Phylogeny and biogeography of the highly diverse genus *Pedicularis* (Orobanchaceae)

—

Natalia Tkach · Martin Röser · Matthias H. Hoffmann
Martin Luther University Halle-Wittenberg

—

The large hemiparasitic genus *Pedicularis* (Orobanchaceae) comprises about 800 species, which are prevailingly distributed in the northern hemisphere. The species occupy different habitats and most of them occur in the high mountains of the Himalayas, Tian Shan, Caucasus and the Alps. *Pedicularis* shows a high morphological diversity, particularly in flower and vegetative characters. The taxonomy of *Pedicularis* is complicated due the lack of a genus-wide monographic treatment and suffers from many different and barely compatible approaches to evaluate morphological characters of regionally delineated sets of species. The present study focuses on the phylogenetic relationships and biogeographical distribution of *Pedicularis* in general and the arctic species in particular. To generate a reliable phylogeny, we sampled more than 200 *Pedicularis* species from different sections worldwide and almost all arctic species. The majority of the species were analyzed for the first time. The molecular phylogeny based on nuclear ribosomal (ITS) and chloroplast (*mat*K – *trn*K) markers resolved eight major clades, which showed little agreement with traditional classifications of the genus. Most traditional groups turned out to be para- or polyphyletic. The major clades of *Pedicularis*, however, reflect general biogeographical diversification patterns of the genus. Species of the early diverging clade occur predominantly in North America and/or in East Asia. The distribution of species from six clades concentrates on the diversity hot spot of the genus, the Hengduan Mountains of south-western China and the Himalayas. About two thirds of the approximately 350 *Pedicularis* species of this area are endemic. Species of one clade are entirely absent from this region. This clade comprises species from Europe, North America, but also from northern and Central Asia, including many arctic species. The arctic taxa of *Pedicularis* evolved 12 – 14 times independently and are mostly nested in lineages that otherwise occur in the high mountains of Eurasia and North America. It appears that only three arctic lineages arose from the present-day center of diversity of the genus. In this genus, molecular phylogenetic results impressively corroborate the long-standing biogeographical and 'florogenetic' hypothesis of high mountain origin of arctic species.

15:00

Contrasting two Neotropical radiations in the Asteraceae: *Plectocephalus* (Cynareae) and the *Lucilia*-group (Gnaphalieae)

Federico Luebert[1] · Andrés Moreira-Muñoz[2] · Michael O. Dillon[3]

[1] Institut für Biologie-Botanik, Freie Universität Berlin and Nees-Institut für Biodiversität der Pflanzen, Universität Bonn, Germany — [2] Intituto de Geografía, Pontificia Universidad Católica, Santiago, Chile — [3] Botany Department, The Field Museum, Chicago, USA

We present phylogenetic analyses of two plant groups of the Asteraceae that have experienced diversification in the Neotropics: *Plectocephalus* (15 species) and the *Lucilia*-group (ca. 100 species). We carried out divergence time estimations using an uncorrelated relaxed molecular clock and an Asteraceae fossil calibration, and conducted Dispersal – Vicariance analyses to investigate their geographical origin. All Chilean *Plectocephalus* (8 species) form a well-supported monophyletic group, which is sister to *Centaurodendron*, endemic to the Juan Fernández Islands. The remaining three Neotropical species of *Plectocephalus* are sister to the former clade together with *P. varians*, an east-African species. The *Lucilia*-group was recovered as paraphyletic to any traditional circumscription, and includes at least 15 different Neotropical genera broadly distributed from southern United States to the southern Andes. Within the South American representatives of the *Lucilia*-group, at least three independent Andean subclades are recovered, one formed by the tropical Andean genera *Loricaria*, *Luciliocline* and *Mniodes*, one with *Stuckertiella* associated with *Gamochaeta*, and a third clade including the southern Andean *Belloa* and part of *Lucilia*. Extra-Andean representatives of the genera *Lucilia* and *Micropsis* are associated with *Facelis* and form a clade sister to the Andean *Belloa*-*Lucilia*. *Plectocephalus* had reached South America two times independently from North America, once from the common ancestor of all *Plectocephalus* during the late Miocene, corresponding to the Chile-Juan Fernández radiation. The second colonization from North America (*P. tweedii*, eastern South America), may have occurred during the early Pliocene from North American stock (represented today by *P. americanus* and *P. rothrockii*). North America was originally reached from Eurasian relatives. Both South American colonizations may be associated with the closing of the Central American Seaway and the rise of the Andes. All crown nodes of Andean clades from the *Lucilia*-group were estimated to be of Pliocene age, just after the rapid phase of the Andena uplift had occurred. The colonization

of South America by the *Lucilia*-group occurred once directly from a Eurasian ancestor. The high-Andean environments had been reached several times from Eastern South America or through north-south range expansion along the Andes. Funded by Dahlem Centre of Plant Sciences and Foncecyt-Chile grant 1120448.

15:15

Comparative phylogeography of eight tropical herbs and lianas (Marantaceae) in central African rainforests

—

A. C. Ley [1, 2] · G. Dauby [2] · J. Köhler [1] · C. Wypior [1] · M. Röser [1] · O. J. Hardy [2]

[1] Institut für Geobotanik und Botanischer Garten, University Halle-Wittenberg,
06108 Halle, Germany — [2] Evolutionary Biology and Ecology, CP160/12,
Faculté des Sciences, Université Libre de Bruxelles, 50 Av. F. Roosevelt,
1050 Brussels, Belgium

—

Vegetation history in tropical Africa and its impact on speciation processes are still to date largely unknown. Diversification hypotheses include speciation events driven by population fragmentation following Pleistocene climate changes and ecological speciation across abiotic gradients. Phylogeographic studies might shed new light on this matter as indicated by similar studies in temperate regions. Here we analysed phylogeographic patterns (chloroplast-DNA sequences) of eight widespread rainforest herb and liana species from four different genera of the family Marantaceae including four pairs of sister species.

Across all investigated species intraspecific patterns of rare haplotype diversity are concordant with overall species diversity, displaying maximal values in the hilly areas of Cameroon and Gabon. Within Cameroon and Gabon two general patterns are repeatedly being observed across species: (1) species have a single center of diversity in North-Western or North-Eastern Gabon showing traces of expansion from there across Cameroon and the Congo basin or (2) species exhibit a subdivision into three gene pools separating Cameroon, Coastal Gabon and the Congos. In both scenarios there are some concordances between localities rich in rare haplotypes and postulated Pleistocene refuges suggesting that refugial situations may have shaped these recurrent patterns. However, also additional not yet identified refugial areas seem to have played a role. The DRCongo seems to be for most species an area of expansion proposed by the low genetic diversity and distinction found in populations in this area.

The absence of an overall pattern of centers of genetic diversity within Gabon and Cameroon across all investigated species might point either to a stochas-

tic process of a species retreating to one of many available nearby refugia and/or the reflect species ecological adaptation forcing the species to retreat to different refugia. When comparing specifically sister species there is generally a lack of concordance in centers of genetic diversity suggesting the rise of these species through the fragmentation of an ancestral population in two different isolated refugia, thus allopatric speciation.

15:30

Polyploid evolution, intercontinental biogeographical relations and morphology of the newly described African oat genus *Trisetopsis* (Poaceae)

—

Alexandra Wölk · Martin Röser

Institute of Biology, Department of Systematic Botany, Martin Luther University Halle-Wittenberg, Germany

—

Genera of the traditional grass tribe Aveneae, with focus on *Helictotrichon* and the recently described genus *Trisetopsis* from tropical and subtropical Africa, were studied for their morphology and molecular phylogeny. Morphological results obtained for 34 taxa showed that *Helictotrichon* and *Trisetopsis* differ consistently from each other and all other genera with respect to the lemma apices, awn attachment, lodicule shape, and ovary pubescence. DNA sequences of the plastid *mat*K-*psb*A region, nuclear ribosomal ITS, and the nuclear single copy gene topoisomerase 6 (Topo6) spanning two introns were generated for 81 taxa and analyzed by maximum parsimony and Bayesian methods. The molecular phylogenetic results show sub-Saharan African *Trisetopis* clearly distinct from *Helictotrichon*, which is subsequently restricted to the northern hemisphere. There were two copy types of Topo6 present in *Trisetopsis* (A and B), which are strongly different from that found in the Eurasian species of *Helictotrichon*. Copy type A probably originated from South African *T. longa* or *T. rogerellisii*, which are the only African species with only type A known so far. All other species of *Trisetopsis* possess both copy types A and B. The origin of copy type B is unclear. Unexpectedly, type B occurs in New World representatives of *Calamagrostis*, *Graphephorum*, *Peyritschia*, and *Sphenopholis*, whereas it is absent from Africa apart from the *Trisetopsis* allopolyploids.

15:45

Pattern of vascular plant endemism in the Western Carpathians and its relation to geography, environmental factors and taxon traits

—

PATRIK MRÁZ[1] · DUŠAN BARABAS[2] · LUCIA LENGYELOVÁ[2] · PETER TURIS[3]
ANDRAS SCHMOTZER[4] · MONIKA JANIŠOVÁ[5] · MICHAL RONIKIER[6]
[1] Department of Botany, Charles University, Prague, Czech Republic — [2] Institute of Geography, P.J. Šafárik University, Košice, Slovakia — [3] Institute of Geography, P. J. Šafárik University, Košice, Slovakia — [4] Low Tatras National Park Administration, Banská Bystrica, Slovakia — [5] Bükk National Park Directorate, Eger, Hungary — [6] Institute of Botany, Slovak Academy of Sciences, Bratislava, Slovakia — [7] Institute of Botany, Polish Academy of Sciences, Kraków, Poland

—

The Western Carpathians covering the area of ca 66,000 km^2 on the territory of Slovakia, Poland, Hungary, the Czech Republic and Austria are the highest European mountain range north of the Alps. They have long been considered to be an important centre of endemism of vascular plants in Central Europe though overall evaluation of endemism in the whole range is still unknown. We assessed the distributional patterns of 84 Western Carpathian or Pan-Carpathian (sub)endemic species and subspecies (excluding apomictic groups) in 121 operational geomorphological units (OGUs; mountain ranges and inter-mountain basins), each of them characterized by several environmental variables (area, proportion of calcareous bedrock and forested areas, mean altitude, altitudinal range, proportion of protected and NATURA 2000 areas). In addition, we recorded taxon traits (life form, ploidy level) and ecological preferences of each endemic taxon (habitat, bedrock and altitudinal preferences; vegetation affinities; niche breadth using β diversity indices).

Statistical analyses revealed strong positive associations between endemic richness and mean altitude, altitudinal range and proportion of calcareous and forested areas. Only weak association was found with the size of OGUs' area. Majority of endemic taxa are calciphilous (65%) and occur preferentially in the rocky and other open habitats (alpine and subalpine meadows, calcareous steppes). These results thus suggest importance of competition-free and stable habitats providing heterogeneous microniches. In addition to environmental conditions, historical processes, especially in-situ evolution in the case of the Western Carpathian endemics and migration of several Pan-Carpathian taxa from the South-eastern Carpathians likely shaped the current distributional pattern of endemic vascular plants in the Western Carpathians. High proportion of polyploids (52%) indicates that polyploidization had played an important role in evolution of endemic taxa, though no significant associations between polyploidy and elevation, bedrock affinities, niche breadth or life form were found.

16:30

Evolution of edaphic association in the European high mountain genus *Adenostyles* Cass.

—

Markus S. Dillenberger · Joachim W. Kadereit

Institut für Spezielle Botanik und Botanischer Garten,

Johannes Gutenberg-Universität Mainz, 55099 Mainz, Germany

—

Heterogeneity of edaphic conditions plays a large role in driving the diversification of many plant groups. In the Alps and other European high mountains, many closely related calcicole and calcifuge plant taxa exist. In order to better understand patterns and processes of edaphic differentiation, the phylogeny of the edaphically variable genus *Adenostyles* was studied. *Adenostyles* contains three species, of which *A. alpina* has five subspecies. Each species and subspecies is largely confined to either calcareous or non-calcareous substrates.

We analysed the phylogeny of *Adenostyles* using DNA sequences of nrITS, nrETS, nuclear chalcone synthase, and three plastid markers (*rpl32*-*trn*L, *psb*A-*trn*H, *ndh*F-*rpl32*) of 45 ingroup and five outgroup samples. The phylogeny was used to reconstruct ancestral edaphic associations and distribution areas.

Within *Adenostyles* shifts of edaphic association appear three to four times. One shift of edaphic association from calcifuge to calcicole appears within *A. alliariae* in the Alps and probably one shift in the same direction in the early evolution of the genus leading to *A. alpina*. Within *A. alpina*, the shifts from calcicole to calcifuge in *A. alpina* subsp. *briquetii* (Corsica) and in a clade of *A. alpina* subsp. *macrocephala* (southernmost Italy) plus *A. alpina* subsp. *pyrenaica* (Pyrenees) coincide with dispersal events.

We conclude that colonization of areas with novel edaphic conditions via dispersal can trigger shifts of edaphic association. Accordingly, edaphic niche shifts can result from chance events.

16:45

Evolution of the Arctic Flora

—

Matthias H. Hoffmann · Sebastian Gebauer · Martin Röser

Natalia Tkach

Martin-Luther-Universität Halle-Wittenberg

—

During the last years many data accumulated on the evolution and taxon recruitment of the Arctic flora giving a first glance into the dynamics of a biome assembly. The Arctic is a large, but young biome and provides an excellent geographical setting for studying, for example, range shifts, speciation, polyploidy. Altogether, c. 2,800 vascular plant species and subspecies presently occur in the Arctic, and are thus considered “arctic” species. Arctic plants may have evolved *in situ* or immigrated from the adjacent ecosystems. Frequently, arctic species have disjunctive distributions between the Arctic and high mountain systems of the temperate zone. This pattern may result from long distance dispersal or from glacial plant migrations and extinctions of intermediate populations. Using extensive taxon samplings, the origins of arctic species of species-rich genera of the Arctic were studied in a molecular phylogenetic framework (e.g. *Artemisia*, *Carex*, *Micranthes*, *Pedicularis*, *Poa*, *Ranunculus*, *Saxifraga*). Rapid diversifications, i.e. radiations in the Arctic appear to be rare, however, in *Carex* a case of replicate adaptive radiation with ecologically replacing species in boreal to arctic habitats has been observed. A general pattern emerging from these studies is that arctic species mostly originated independently and parallel. However, the geographical and ecological background from which the arctic taxa have evolved differ largely. Main sources of the arctic flora were wetlands, but also dry and cold steppes and high mountain ecosystems. Morphological changes affiliated with the occupation of the northern-most areas appear to be more the exception than the rule. For most of the studied character states an overlapping expression has been observed. This makes an inference of traits responsible for the occupation of arctic environments difficult. Molecular clock approaches revealed that arctic species appeared throughout the last million years. Some species seems to have evolved already before the appearance of arctic environments in geological times and may have simply immigrated. Other species appeared much later, probably since the glacial cycles. Low levels of molecular and morphological differentiation of the arctic species with respect to their non-arctic congeners suggest that they are rather young and the result of ongoing speciation.

17:00

A molecular phylogeny and biogeographic analysis of the *Euodia* alliance (Rutaceae) reveals key innovations for species richness

—

Marc S. Appelhans [1,2] · Jun Wen [2] · Warren L. Wagner [2]

[1] Department of Systematic Botany, Albrecht-von-Haller Institute for Plant Sciences, University of Goettingen, Untere Karspuele 2, 37073 Goettingen, Germany — [2] Department of Botany, Smithsonian Institution, PO Box 37012, Washington, DC 20013-7012, USA

—

Because of their wide distributions, which range from SE Asia, the Malesian region, Australia, to Pacific islands (and Madagascar in *Melicope*), the genera *Acronychia*, *Euodia* and *Melicope* (Rutaceae) are ideal examples to study Asian and Pacific biogeography. The center of species richness and endemicity of all three genera is New Guinea but the three genera differ greatly in terms of species richness (*Acronychia*: 48 spp., *Euodia*: 7 spp. and *Melicope*: about 230 spp.).

Our molecular phylogenetic studies show that *Melicope* and *Acronychia* are closely related and that *Euodia* is sister to both. A number of monotypic or small genera mainly from New Caledonia and New Guinea need to be included in *Melicope* (*Comptonella, Platydesma, Picrella,* and *Sarcomelicope*), while others are closely related to *Euodia* (*Brombya*, *Perryodendron*, and *Pitaviaster*).

Our molecular dating analyses suggest that the *Acronychia* – *Melicope* clade and the *Euodia* clade might have originated in the late Oligocene to early Miocene. Considering the similar age of the clades, the differences in species richness are striking and may be explained by differences in seed coat anatomy that enabled dispersal by endozoochory in *Acronychia* and *Melicope*. In this way, *Melicope* reached distant regions such as Madagascar, Hawai´i and the Marquesas Islands while *Euodia* remained restricted to New Guinea, Northern Australia and nearby archipelagos.

Phylogeographyofthetree fern genus *Sphaeropteris* (Cyatheaceae) 17:15

—

M. Lehnert · S. Noben · A. Weigand · M. Krug · D. Quandt
Nees Institut für Biodiversität der Pflanzen, Universität Bonn,
Meckenheimer Allee 170, 53115 Bonn, Germany

—

The genus *Sphaeropteris* belongs to the pantropically distributed scaly tree ferns (Cyatheaceae; ca. 600 spp.) and comprises the tallest extant ferns,with trunk heights surpassing 20 m. Previous studies supported the monophyly of the genus, found a sister-group relationship to the other genera of the family (i.e. *Cyathea* s. str. *Alsophila* and *Gymnosphaera*), and retrieved four well-supported subclades that correspond with morphologically conceived subgenera and sections and have distinct centers of diversity:

The *Fourniera*-clade (ca. 10 spp.) and the *Sarcopholis*-clade (19 spp.)have their center of diversity in New Guinea and range eastward to Samoa, but only *Fourniera* is also present west of Sulawesi with 1 – 2 spp. The *Schizocaena*-clade (29 spp.), which is superficially similar to *Sarcopholis*, is vicariantly distributed to that genus, from Borneo to Vietnam. *Sphaeropteris* s. str. (46 spp.)also extends into the subtropics and southern temperate regions and is present from the Himalayas to New Zealand and many Pacific Islands. Six species of *Sphaeropteris* s. str. are the only representatives of the whole genus in the Neotropics, occurring from Mexico through the Caribbean and the Andes to eastern Brazil in distinct adjoining ranges. Previous phylogenetic studies had only a limited sampling of the whole genus, and just two of the Neotropical species. Here we present a phylogenetic analysis with an extended sampling in all subclades, including five of the six Neotropicalsepecies, with the aim to test previous hypotheses of the biogeographic history of the genus.

Our results from a Bayesian analysis of three chloroplast markers (*rpl16, trnL-F,* and*trnG-R*) support the previously recognized clades in the Cyatheaceae and the genus *Sphaeropteris*, again with the New Caledonian *Sp. albifrons* isolated as sister to (*Sphaeropteris*s.str. (*Schizocaena* + *Sarcopholis*)). The distinct New Guinean *Sp. procera* is now placed at the base of the *Schizocaena* clade instead of *Sphaeropteris*s.str. Depending on the gridapplied in the reconstructions, either the Australian region or New Caledonia is resolved as ancestral area of the whole genus. Within the Neotropicalclade, the Mexican and the Caribbean species (*Sp. horrida*+ *Sp. insignis*) are sister to a clade formed by the Mesoamerican and Andean species (*Sp. brunei* + *Sp. quindiuensis*) and the Brazilian *Sp. gardneri,* making a southward migration with subsequent speciation the most parsimonious explanation for the current distribution pattern. We discuss if the ancestral northern population reached the Americas directly from Asia (Boreotropics) or represented a relict of an originallyGondwanan distributed clade, which at some point got extinct in most of its original range and subsequently had to recuperate it again.

17:30

Transylvanian basin: novel extra-Mediterranean refuge and source of diversity for the temperate herb *Erythronium dens-canis* (Liliaceae)

—

László Bartha [1] · Gábor Sramkó [2] · Polina A. Volkova [3] · Boštjan Surina [4]
Alexander L. Ivanov [5] · Horia Banciu [6]
[1] Institute for Interdisciplinary Research in Bio-Nano Sciences, Babeş-Bolyai University, Cluj-Napoca, Romania — [2] MTA-ELTE-MTM Ecology Research Group, Budapest, Hungary — [3] Moscow South-West high school N 1543, Moscow, Russia — [4] Faculty of Mathematics, Natural Sciences and Information Technologies, University of Primorska, Koper, Slovenia — [5] Department of Botany, North Caucasian Federal University, Stavropol, Russia – [6] Faculty of Biology and Geology, Babeş-Bolyai University, Cluj-Napoca, Romania

—

Diversity and distribution of many temperate plant species in Europe is currently interpreted in the light of the southern richness – northern purity paradigm. Furthermore, in the recent past few studies provided evidence for cryptic glacial refugia of temperate plants in Central Europe. Patterns of differentiation among temperate European species are rarely considered from the viewpoint of a longitudinal (geographic) gradient. Here we examined patterns of intraspecific differentiation in the temperate herb *Erythronium dens-canis* across a western – eastern European gradient. This species has a wide range in terms of longitudes (from the Atlantic coast to the Carpathians) and a relatively narrow range in terms of latitudes (doesn't penetrate above the Alps or in southern parts of main South European peninsulas). Nucleotide variation in the rpl32-trnL and rps15-ycf1 plastid regions among 52 populations of *E. dens-canis* from most of its distribution range uncovered a striking phylogeographical structure. This relies on two, geographically non-overlapping phylogroups: a genetically more diverse Transylvanian lineage with a narrow distribution range and a genetically more homogenous 'non-Transylvanian' lineage with widespread geographic distribution. The revealed pattern conforms to a previously undocumented eastern richness – western purity phenomenon. *Erythronium caucasicum*, the Transylvanian and non-Transylvanian clades form an unresolved polytomy suggesting their island like (vicariant) isolation. Eastern and Southern Carpathians, as well as Pannonian and Ukrainian steppes most likely had the highest impact on the formation of the above structures. A molecular clock approach exploring a wide range of substitution rates (0.001-0.005 subst/site/My) provides a time frame from the Early Pliocene to the mid-late Pleistocene in which these lineages could have coalesced. This may support the status of *E. dens-canis* as an emblematic Tertiary relic of Europe. The results underline a previously underestimated role of Transylvanian Basin in generating diversity among temperate herbs and serving as glacial refuge. This work was supported by a grant of the Ministry of National Education, CNCS – UEFISCDI, project number PN-II-ID-PCE-2012-4-0595.

17:45

Veni, vidi, vici: genetic bottlenecks and clonal propagation accompanied the introduction of *Vinca minor* L. (Apocynaceae) to Central Europe

—

SINA MÖLLER[1] · BRUNO HUETTEL[2] · TINA WÖHRMANN[1] · KURT WEISING[1]
[1] Institute of Biology, University of Kassel, Germany — [2] Max Planck Institute for Plant Breeding Research, Cologne

—

The lesser periwinkle (*Vinca minor* L., Apocynaceae) is native in Southern Europe and has presumably been introduced to Central Europe along with the expansion of the Roman Empire. Extensively cultivated for ornamental, cultic and medicinal purposes over centuries, *V. minor* nowadays often occurs in the surroundings of abandoned medieval settlements as a so called "relic of cultivation". Because of its carpet-like growth and the rare observation of fruits and seeds, the species is assumed to reproduce mainly asexually via stolons in Germany. However, no molecular attempts have so far been undertaken to prove this hypothesis.

We developed seven polymorphic microsatellite markers from 454 sequences to study population genetic parameters of *V. minor* in various parts of its distributional range. Besides 545 samples that were collected from eleven Italian and 33 Central European populations, we also analyzed 18 garden cultivars. Our data show that genetic diversity is low and clonal propagation predominates in Central Europe. Two megaclones were found, each carrying identical genotypes in plants from geographically widely separated locations. Some Central European populations appear to have originated from escaped garden plants. Clonality was rare in the Italian samples, which were genetically more diverse and clearly separated from the Central European ones. Taken together, our findings support the hypothesis that *V. minor* mostly reproduces sexually in its native range, and experienced a number of bottlenecks during its expansion to Central Europe, where vegetative propagation predominates and dispersal is mainly anthropogenic.

We also established six chloroplast microsatellite markers from the 454 sequence data. Five chloroplast haplotypes were identified in *V. minor* all of which occur in Italy. Only the two most common haplotypes were also found in Central Europe, where they were each associated with phenotypically different plants. Their separation by seven mutational steps suggests that the two haplotypes were independently introduced to Germany. The implications of our molecular findings for the colonization of Central Europe by *V. minor* and its subsequent propagation will be discussed, also in the light of greenhouse experiments and field observations.

Session · Phylogenomics II

09:00

Key note: Resolving Ancient Genome Duplications Across the Angiosperm Phylogeny

—

Jim Leebens-Mack

Department of Plant Biology, University of Georgia, Athens, GA 30602-7271, USA

—

The transformative impact of polyploidization and subsequent fractionation on angiosperm genome evolution is widely acknowledged. Our knowledge of the timing of specific whole genome duplications in angiosperm history is, however, typically imprecise. Resolution of the timing of ancient polyploidy events can be achieved through genome-wide synteny analyses performed within and between species, but such analyses are limited by the availability of sequenced genomes. Further, synteny analyses of distantly related species can be hampered by divergence in genome structure. Comparative analyses of Ks plots can also elucidate the timing of paleopolyploidy events, but inferences drawn from such analyses my not be robust in the face of saturation of substitutions at synonymous sites or among-lineage variation in substitution rates. As shown in examples drawn from across the angiosperm phylogeny, these limitations of synteny and Ks analyses can be overcome through phylogenomic analyses including duplicate gene pairs anchored to syntenic blocks or Ks peaks, respectively. More generally, we demonstrate how phylogenomic analyses of genome and transcriptome data available for a growing number angiosperm lineages is yielding finer resolution of the timing of paleopolyploidy events. As a consequence we are better able to assess the impact of these events on angiosperm evolution.

09:45

454 sequencing of ITS1 in the analysis of polyploid species – Challenges, prospects and lessons

—

Dirk C. Albach · Eike Mayland-Quellhorst

Institute of biology and environmental sciences, Carl von Ossietzky-University Oldenburg,
Carl von Ossietzky-Str. 9 – 11, 26111 Oldenburg, Germany

—

Inferring the ancestry of polyploid species by sequencing different orthologs and alleles of nuclear DNA regions has been traditionally difficult and involved long searches for appropriate markers and subsequent cloning, which is expensive, time-consuming and hampered by PCR-artifacts. The most commonly used nuclear marker, the internal transcribed spacer region, has the additional problem of concerted evolution homogenizing different alleles over a short-time span to an extent that direct Sanger sequencing of the predominant parental allele is possible. However, minor polymorphisms frequently hinted at the fact that other alleles are still present in the genome. Next generation sequencing now allows simultaneous sequencing of all alleles amplifiable with a specific primer pair.

For the present study we investigated 32 individuals of two groups of *Veronica* and ran them on our 454 GS Junior with specific Multiplex Identifiers for each individual. The consensus of contigs with a coverage of 5 reads per consensus or more were exported and were subsequently used in phylogenetic analyses. The importance of coverage has been compared by comparing results using contigs of various minimum coverages. In the Junior run 63,789 reads were produced of which 47,614 reads were successfully trimmed. The number of reads varied between 55 and 1,446 per individual.

We here present results from a preliminary analysis of the ITS1 region for two groups of polyploid *Veronica* (*V. persica*, *V. gentianoides*). These highlight the potential and problems of the method. The analysis of *V. persica* of a rather small group of five diploid and three tetraploid species clearly demonstrates the presence of ITS1-alleles related to diploid *V. polita* (as demonstrated by the Sanger sequence of *V. persica*), alleles related to *V. ceratocarpa* and some recombinants. The analysis at a larger scale in *V. gentianoides*, a polyploid complex with diploid to decaploid cytotypes demonstrates that the mixture of various alleles and recombinants makes a simple inference of relationships difficult to impossible.

10:00

Insights into polyploid transcriptomics of non-model plants: An example in *Veronica* (Plantaginaceae)

—

Heidi M. Meudt [1, 2] · Eike Mayland-Quellhorst [1] · Dirk C. Albach [1]
[1] Carl von Ossietzky Universität Oldenburg, Oldenburg, Germany —
[2] Museum of New Zealand Te Papa Tongarewa (Wellington, New Zealand

—

Polyploidy is one of the most important processes that can shape plant evolution. Over the past decade, the development of new genetic and genomic tools has promoted a resurgence of research on polyploidy and this has provided new insights into the mechanisms, consequences and importance of polyploidy in plants, on both ancient and recent time scales. Evidence suggests that polyploidy has played a particularly important role in several recent plant species radiations, which comprise morphologically and ecologically distinct, but genetically similar species. As species radiations are a significant contributor to generating plant biodiversity, studying recent polyploidy species radiations may be key to understanding the importance of polyploidy in angiosperm diversification.

We chose the genus *Veronica* (Plantaginaceae) as our study group, as it comprises about 450 species worldwide, including polyploid species radiations in both Eurasia and New Zealand. The New Zealand species comprise a lineage with high ploidy levels that is derived from Eurasian ancestors. We developed *de novo* high-throughput Illumina transcriptome data for *Veronica* polyploids and their diploid relatives from both hemispheres to 1) discover to what extent evidence for polyploidy (and specifically allopolyploidy) is apparent in these non-model plant transcriptomes, and 2) determine whether homeologous copies that originate from different parental diploid species could be identified.

RNA was extracted from fresh or RNA-later preserved leaves from eight individuals of Veronica representing polyploid species and their diploid relatives from Europe and New Zealand, and the transcriptomes sequenced using Illumina HiSeq technology. After quality control of the resulting ~12 million 100bp paired end sequence reads per individual (>100 million total sequence reads), we used several different assembly programmes for assembling the reads within and between individuals, including CLC Genomics Workbench, Trinity and Velvet/Oases. Comparisons of these assemblies and downstream contig annotation and comparative analyses will be outlined and discussed.

10:15

Phylogenetic analysis of Hordeeae (formerly Triticeae): sequence capture of 400 single-copy genes and Illumina sequencing

—

Nadine Bernhardt[1] · Eva-Maria Willing[2] · Korbinian Schneeberger[2] · Benjamin Kilian[3] · Frank R. Blattner[3]

[1] Genebank Department, Leibniz Institute of Plant Genetics and Crop Research (IPK), Gatersleben, Germany — [2] Department of Plant Developmental Biology, Max Planck Institute for Plant Breeding Research, Cologne, Germany — [3] Genebank Department, IPK Gatersleben, Germany

—

The economically important grass tribe Hordeeae (formerly Triticeae) consists of about 360 species in 20 – 30 genera. It includes the cereals wheat (*Triticum* L.), barley (*Hordeum* L.), rye (*Secale* L.), and their wild relatives. Although increasing numbers of molecular studies aiming to resolve systematic relationships within

Hordeeae are published, the outcomes of these studies are largely contradictory. Striking incongruence in gene tree topologies implies that reticulate evolution (hybridization) probably together with small- or large-scale genome duplications creating paralogous loci might cause phylogenetic inconsistencies.

We want to detect the reasons for such contradictory results and provide a reliable species-level phylogeny of the tribe. Therefor, we intend to analyze Hordeeae taxa by comprehensive species sampling, including multiple individuals per species, and sequencing 400 loci evenly distributed over the genome by targeted enrichment and Illumina sequencing.

The design of sequence capture probes was based on multiple sequence alignments of full-length cDNA (fl-cDNA) with known chromosomal positions from *Hordeum vulgare* and fl-cDNAs from *Triticum aestivum*, two taxa belonging to lineages that diverged about 12 million years ago. Fl-cDNA sequences of *Brachypodium distachyon* were added to include sequence information from a taxonomically distant lineage. Exon/intron boundaries were identified from genomic DNA sequences of *Hordeum* and *Brachypodium*.

Sequence capture was performed for the taxa considered in probe design as well as for additional genera followed by paired-end Illumina sequencing on HiSeq and MiSeq. Sequence reads were mapped to reference sequences, and consensus sequences for diploid taxa and the different homeologous sequences extracted for polyploid taxa were combined in multiple sequence alignments for every locus under study.

The study enables us to cover a high extend of genetic diversity and thus, is applicable to at least all taxa within Hordeeae. The project will result in a unique dataset that will allow us to analyze the history of different genes and gene families, different parts of the chromosomes, species and species groups, and will result in a concise phylogeny of Hordeeae.

11:00

Supermatrix or coalescent-based phylogenies? Analysis of next-generation sequenced multilocus data in *Hordeum* (Poaceae)

—

Jonathan Brassac · Frank R. Blattner
Institute of Plant Genetics and Crop Plant Research (IPK),
06466 Gatersleben, Germany

—

Within the barley genus *Hordeum*, consisting of 33 species, approximately half of the taxa are polyploids (4x/6x), and the genus experienced a rapid radiation within the last million years concerning more than half of the species. To resolve such relationships it is necessary to include multiple nuclear loci, traditionally analyzed by cloning to separate homoeologous copies.

In this study we took advantage of the long reads of 454 sequencing together with barcoding to sequence in parallel one chloroplast and 12 nuclear single-copy loci, distributed among nearly all barley chromosomes, in 96 individuals representing all species and cytotypes of the genus *Hordeum*. The 454 reads were assembled into contigs representing the 13 loci and, for polyploids, also homoeologues. Phylogenetic analyses were conducted for all loci separately and for a concatenated data matrix (supermatrix) of all nuclear loci, each for diploid taxa only and for diploids plus polyploids. For the diploid taxa a coalescent-based, dated species tree was inferred from the nuclear gene trees. Chloroplast *mat*K was used to determine the maternal parent in allopolyploid taxa.

Supermatrix and coalescent-based methods seemingly perform differently within *Hordeum* lineages depending on genetic differentiation and amount of incomplete lineage sorting. The resulting multilocus phylogeny infers for the first time safely phylogeny and progenitor-derivative relationships of all polyploid *Hordeum* taxa within a single analysis.

Our study proves that it is possible to obtain a multilocus species-level phylogeny for di- and polyploid taxa by combining PCR with second-generation sequencing of barcoded amplicons, without cloning and without creating a heavy load of sequence data that would require specialized bioinformatics hardware, software, and knowledge.

11:15

Single-copy nuclear genes place haustorial Hydnoraceae within Piperales and reveal a Cretaceous origin of multiple parasitic angiosperm lineages

—

Julia Naumann [1] · Karsten Salomo [1] · Joshua P. Der [2] · Eric K. Wafula [2]
Jay F. Bolin [3] · Erika Maass [4] · Marie-Stéphanie Samain [5] · Christoph Neinhuis [1] · Claude W. de Pamphilis [2] · Stefan Wanke [1]

[1] Institut für Botanik, Technische Universität Dresden, 01062 Dresden, Germany — [2] Department of Biology and Institute of Molecular Evolutionary Genetics, The Pennsylvania State University, University Park, PA 16802, USA — [3] Department of Biology, Catawba College, Salisbury, NC, USA — [4] Department of Biological Sciences, University of Namibia, Windhoek, Namibia — [5] Instituto de Ecología, A.C., Centro Regional del Bajío, AvenidaLázaro Cárdenas 253, 61600 Pátzcuaro, Michoacán, Mexico

—

Extreme haustorial parasites have long captured the interest of naturalists and scientists with their greatly reduced and highly specialized morphology (Kujit 1969, Musselman & Visser 1986, Davis et al. 2007). Along with the reduction or loss of their photoautotrophic ability, the plastid genome often decays as photosynthetic genes are released from selective constraint (dePamphilis and Palmer 1990). This has made it challenging to use traditional plastid genes for parasitic plant phylogenetics, and driven the search for alternative phylogenetic and molecular evolutionary markers. Thus, evolutionary studies, such as molecular clock-based age estimates, are not yet available for all parasitic lineages. In the present study, we extracted 14 nuclear single copy genes (nSCG) from Illuminatranscriptome data from one of the "strangest plants in the world", *Hydnoravisseri* (Hydnoraceae). Reasons for this statement is the mushroom-like appearance with fleshy orange flowers characteristic for this small family (about 10 species in 2 genera: *Hydnora* and *Prosopanche*, Musselman&Visser 1986). A ~15,000 character molecular dataset, based on all three genomic compartments, shows the utility of nSCG for reconstructing phylogenetic relationships in parasitic lineages. A relaxed molecular clock approach with the same multi-locus dataset, revealed an ancient age of ~91 MYA for Hydnoraceae. We then estimated the stem ages of all independently originated parasitic angiosperm lineages using a published dataset (Barkman et al. 2007), which also revealed a Cretaceous origin for Balanophoraceae, Cynomoriaceae and Apodanthaceae. With the exception of Santalales, older parasite lineages tend to be more specialized with respect to trophic level and have lower species diversity. We thus propose the "temporal specialization hypothesis" (TSH) imple-

menting multiple independent specialization processes over time during parasitic angiosperm evolution.

References

Kuijt J (1969). The Biology of Parasitic Flowering Plants. University of California Press.

Davis CC, Latvis M, Nickrent DL, Wurdack KJ, Baum DA (2007). Floral Gigantism in Rafflesiaceae. *Science* **315**(5820): 1812.

Musselman LJ, and Visser JH (1986). The strangest plant in the world! Veld Flora **71**: 109 – 111.

dePamphilis CW, and Palmer JD (1990). Loss of photosynthetic and chlororespiratory genes from the plastid genome of a parasitic flowering plant. Nature **348**: 337 – 339.

Barkman TJ, McNeal JR, Lim SH, Coat G, Croom HB, Young ND, and dePamphilis CW (2007) Mitochondrial DNA suggests at least 11 origins of parasitism in angiosperms and reveals genomic chimerism in parasitic plants. BMC EvolBiol **7**: 248.

Physical and functional plastome reduction coincides with major shifts of substitution rates and relaxation of purifying selection in photosynthetic and nonphotosynthetic parasitic Orobanchaceae

11:30

—

SUSANN WICKE [1] · KAI MÜLLER [2] · DIETMAR QUANDT [3]
CLAUDE DE PAMPHILIS [4] · GERALD M. SCHNEEWEISS [5]

[1] Department of Systematic and Evolutionary Botany, University of Vienna, Rennweg 14, 1030 Vienna, Austria and Institute for Evolution and Biodiversity, University of Münster, Hüfferstr. 1, 48149 Münster, Germany — [2] Institute for Evolution and Biodiversity, University of Münster, Hüfferstr. 1, 48149 Münster, Germany — [3] Nees-Institute for Plant Biodiversity, Rheinische Friedrich-Wilhelms-Universität Bonn, Meckenheimer Allee 170, Bonn, 53115, Germany — [4] Department of Biology and Huck Institutes of Life Sciences, Penn State University, University Park, PA 16802, USA — [5] Department of Systematic and Evolutionary Botany, University of Vienna, Rennweg 14, 1030 Vienna, Austria

—

Parasitic plants, such as those of the broomrape family (Orobanchaceae), possess strongly reconfigured plastomes due to convergent losses of photosynthesis and housekeeping genes, making them excellent model systems for studying genome evolution under relaxed selective pressures. Phylogenomic and phylostatistical analyses of 15 complete plastomes of nonparasitic and parasitic Orobanchaceae reveal that the establishment of obligate parasitism triggers the relaxation of selective constraints. Following the loss of photosynthesis, functional genome reduction proceeds rapidly, accompanied by the accumulation of recombinogenic

factors, which foster severe genomic reconfigurations. The eventual physical plastome reduction by deletion of non-essential regions is strongly influenced by their proximity to genes under selection and the co-occurrence with those in operons. This indicates complex constraints beyond gene function that determine the evolutionary survival time of plastid regions after the loss of selective pressures. By using a Random Effects Likelihood framework we show that relaxation of purifying selection occurs in several photosynthesis and housekeeping complexes along or after the transition to an obligate heterotrophic lifestyle. Maximum Likelihood and parametric bootstrapping reveals a correlation between lifestyle changes and substitution rate heterogeneity in the Orobanchaceae. We show that bursts of gene loss and genome reconfiguration coincide with shifts in nucleotide substitution rates, most notably so in non-synonymous substitution rates. However, the vast majority of genes (incl. those for the photosynthetic ATP synthase) retained in nonphotosynthetic Orobanchaceae evolve under purifying selection, suggesting that those elements are still of some functional relevance for these parasites.

11:45

Genome evolution and speciation in polyploidcomplexes: insights from transcriptomics studies in *Ranunculus auricomus*

—

M. Appelhans[1] · D. Hojsgaard[1] · M. Pellino[2] · T. Schmutzer[2] · U. Scholz[2]
H. Vogel[3] · T. Sharbel[2] · E. Hörandl[4]
[1] Georg-August-University of Göttingen, Department of Systematic Botany, Untere Karspüle 2, 37073 Göttingen, Germany — [2] Apomixis research group, Leibniz Institute of Plant Genetics and Crop Plant Research (IPK), 06466 Gatersleben, Germany — [3] Max Planck Institute for Chemical Ecology, Department of Entomology, 07745 Jena, Germany — [4] Georg-August-University of Göttingen, Department of Systematic Botany, Untere Karspüle 2, 37073 Göttingen, Germany

—

Polyploidy is a major evolutionary trait, but the effects of whole genome duplications are often blurred by genomic signatures of hybridity and/or shifts in mode of reproduction. Saltational speciation in polyploids in combination with purifying selection via sexuality would result in low genomic divergence from the diploid progenitor, but may trigger rapid divergence of a few genes under positive selection if they are associated to adaptive traits. Apomixis, the asexual reproduction via seed, is one such trait and is expected to result in accumulation of deleterious mutations as purifying selection is less efficient (Muller's ratchet). Sexual polyploids are not expected to suffer from accumulation of mutations but will show genomic signals of whole genome duplication. Diploid species in allopatry, in contrast, would slowly diverge over many loci. We performed a SNP analysis mined from of RNAseq data from three allopatric sexual diploid and autotetraploid species, and compared to a dataset of apomictic hexaploids of the *Ranunculus auricomus* complex (Pellino et al. 2013). Analysis of non-synonymous versus synonymous substitutions between diploid/diploid and diploid/tetraploid reveals signals of diversifying selection between ploidy levels with and without asexuality. Asexuals do not show signals of mutation accumulation which is probably due to the young age of lineages and purifying selection acting on facultative asexuals. We will present new data comparing sexual autotetraploids to diploid progenitors to disentangling effects of polyploidy from hybridity and asexuality. Annotation of genes under diversifying selection gives insights into functional background of adaptive traits associated to allopatric sexual speciation, to polyploidization and to shifts in mode of reproduction.We will discuss the potentials of RNAseq analysis for understanding processes of plant evolution.

References

Pellino M., Hojsgaard D., Schmutzer T., Scholz U., Vogel H., Hörandl E., Sharbel TF. (2013). Asexual genome evolution in the apomictic *Ranunculus auricomus* complex: examining the effects of hybridization and mutation accumulation. Molec Ecol **22**: 5908 – 5921

12:00

The impact of reconstruction methods, phylogenetic uncertainty and branch lengthson inferences about dysploidy in *Melampodium* (Asteraceae)

—

Jamie McCann[1] · Gerald Schneeweiss[1] · Tod F. Stuessy[1, 2]
Hanna Weiss-Schneeweiss[1]
1 University of Vienna, Dept. of Botany and Biodiversity Research, Austria —
[2] Herbarium, Dept. of Evolution, Ecology, and Organismal Biology,
Ohio State University, USA

—

Karyotypic change plays an important role in plant diversification and speciation. Whereas polyploidy has spurred enormous research efforts in the last decades, the second major mode of chromosome number change, dysploidy (the stepwise change in chromosome number that results in a sequence of base numbers in a group of related organisms), has received considerably less attention. Recent methodological developments to investigate character evolution within a phylogenetic framework allows the directionality of dysploidy (descending versus ascending) to be tested. Little is known, however, on the impact of reconstruction methods, phylogenetic uncertainty or branch lengths on inferences about dysploidy. One well-suited group to address these questions is the genus *Melampodium* (Asteraceae), which comprises 40 species, 24 of which are exclusively diploid, with five different chromosome base numbers (*x* = 9, 10, 11, 12, 14). Herein, we study chromosome base number evolution in this genus using topologies obtained from phylogenetic analyses of both nuclear and plastid datasets, and using several analytical approaches. We used Bayesian methods for phylogeny inference (allowing phylogenetic uncertainty to be taken into account) implemented in BEAST and MrBayes, where branch lengths are proportional to time and to the amount of molecular evolution, respectively. Chromosome number reconstructions were done using two general approaches of ancestral character state reconstruction (maximum parsimony in Mesquite anda Bayesian method in BayesTraits) and a likelihood method developed specifically to infer chromosome number evolution (ChromEvol). In *Melampodium*, the outcome of the analyses in terms of the estimated number of gains and losses and thus the prevalence of ascending or descending dysploidy is strongly affected by data source and method of analysis. The probability of a chromosome number at a certain node is affected by uncertainty in tree topology and is generally more variable in the analysis using BayesTraits. The most likely ancestral chromosome base number of *Melampodium* is x = 11, supporting a combination of ascending and descending dysploidy as the mode of chromosome base number change.

14:00

The discovery of the plant geography of Chile by the German botanist Karl Reiche

—

Andrés Moreira-Muñoz
Instituto de Geografía, Pontificia Universidad Católica de Chile, Av. Vicuña Mackenna 4860,
Macul, Santiago. Fondecyt 1120448, Chile

—

Karl Reiche was born in Dresden in 1860 and gained his doctoral degree in Leipzig in 1885. In 1889 he accepted an invitation for teaching natural sciences at a remote public school in Constitución, southern Chile. Apparently he performed very well anddedicated special efforts to publish textbooks for the study of botany at school. Soon he knew the regional flora better than anyone, and seven years later he was called to drive the botanical section at the Natural History Museum in Santiago. Again, with his great capacity, he began the revision of the entire Chilean flora and also studied and published about useful and medicinal plants and invasive species, totaling more than 80 papers and books including the almost complete revision of the Chilean flora in six volumes. He was also very interested in the distribution and the spatial occupation of the flora, i.e. the vegetation: the publication where Reiche intends a synthesis of 17 years of study of the Chilean vegetation is the "*Grundzüge der Pflanzenverbreitung in Chile*" (= Principles of the Distribution of Plants in Chile), published in1907 for the famous series "*Die Vegetation der Erde*", edited by Engler and Drude. Unfortunately the work was unknown in Chile, until the late translation of G. Looser in two volumes in 1934 and 1937. This translation has been re-edited this year 2014 by the National Library, within the collection of the 100 titles that helped to build the Chilean nation. The new edition includes the original photographs and maps which remained absent in the original translation, also including an index with updated scientific namesand a tribute by Professor Hugo Gunckel on the centenary of his birth.

Reiche's legacy is immense for the Chilean botany. Most of current research is still to some extent based in his work. The detailed description of the vegetation of Chile in the early twentieth century is not just anecdotic: much of the native vegetation, especially on the coast of the Maule region where Reiche first arrived, has been replaced by forest plantations, andmany endemic species are therefore today threatened. Knowing the past aspect of our ecosystems will allow us, hopefully, better planning their land use and restoration, so to allow future generations enjoying the botanical landscape that Reiche traveled, studied and loved.

Tree diversity and stand dynamics at varying proportion of balsam fir (*Abies balsamea* L.)

14:15

—

O. T. Bouman

Dept. of Biology, Cape Breton University, Canada

—

Permanent sampling plot data collected for 30 years in 5-year cycles show to what extent the initial proportion of the short-lived ubiquitous balsam fir (*Abies balsamea*) drives tree diversity and stand development of deciduous forests in Eastern Cape Breton Island, Canada. Plots of the first inventory were divided into low balsam fir (L-BF) *versus* high balsam fir (H-BF). Dominant deciduous species comprised yellow birch (*Betula alleghenіensis*), sugar maple (*Acer saccharum*), and large-leaved beech (*Fagus grandifolia*). Tree diversity was estimated by calculating the Shannon-Wiener Index (*H*') based on abundances of trees by species (i.e., compositional diversity) and by size class (i.e., structural diversity). The ratio of actual diversity to maximum diversity indicated vegetation evenness (*J*'). The basal area ratio for year *t* over year *t-5* provided an index of resilience (*R*). Compositional diversity was significantly low in H-BF and *H*' scaled positively with number of species. The H-BF stands tended to be less evenly structured than L-BF stands albeit high *J'* values for both stand types. Total basal area of live trees remained remarkably similar for both stand types. Stand dynamics were however, structurally stratified due to low *R*-values for low–diameter trees. In H-BF, a decline of fir was largely offset by a concomitant increase of yellow birch while there were no compensatory dynamics among deciduous species in L-BF stands. Yellow birch appears important for canopy gap filling in mixed stands with high fir proportion.

14:30

Phylogeny, ploidal variation and antimicrobial activity of *Rhododendron* (Ericaceae)

—

Jennifer Nolzen[1] · Dirk C. Albach[1] · Ahmed Rezk[2]
Abhinandan Shrestha[3] Nikolai Kuhnert[3] · Hartwig Schepker[4]
Matthias S. Ullrich[2]
[1] Carl von Ossietzky-University Oldenburg, AG Plant Biodiversity and Evolution — [2] Jacobs University Bremen, Group Molecular Microbiology and Cell Biology — [3] Jacobs University Bremen, Group Chemistry — [4] Stiftung Rhododendron Park Bremen

—

Plants are creative 'chemists' that have evolved fascinating and biologically active chemical substances in response to microbial pathogens and herbivore pressure. In this context, polyploidy may increase the probability of evolutionary innovations (e.g., new substances). In our project, we test the hypothesis that anti-microbial activity of secondary compounds produced by the 1,300 currently accepted species of *Rhododendron* species has a phylogenetic component and/or whether it is related to polyploidy.

Phylogenetic analyses of 250 species using nuclear (ITS, rpb2-*i*) and plastid (*trn*L-F, *trn*K) DNA markers provide a rigorous hypothesis for relationships within *Rhododendron*. Genome size measurements demonstrate that polyploidy is almost exclusive to subgenus *Rhododendron*. Regarding antimicrobial activity, the majority of species within subgenus *Rhododendron* produce substances that significantly inhibit growth of Gram-positive bacteria, but activity to Gram-negatives is restricted to a few species in different subgenera. A novel diterpene showing the highest activity of single compounds against Gram-positive bacteria has been identified.

Based on these results we are planning to use Next Generation Sequencing (RNA-seq) to further elucidate the genetic background of secondary metabolite production. Variation in gene expression induced by tissue types (e.g., roots vs. leaves), by changing environmental conditions (e.g., summer vs. winter), and in relation to antimicrobial activity is of special interest.

14:45

Innovation in palaeobotany: the Whole-Plant concept

—

Lutz Kunzmann[1] · Martina Dolezych[1] · Volker Wilde[2] · Dieter Uhl[2]
Rainer Brocke[2] · Haytham El Atfy[2]
[1] Senckenberg Naturhistorische Sammlungen Dresden — [2] Senckenberg Forschungsinstitut und Naturmuseum Frankfurt

—

When studying plant fossils from different periods of Earth History the Whole-Plant concept, an old, but currently modernized palaeobotanical approach, is usually applied nowadays if the respective fossil material is appropriate.Whole-plant taxa are essential for research on evolution of plants through time and for estimating ancient biodiversity. Furthermore, exactly described fossil species are the base for their biological interpretation as well as for palaeoecological and palaeoclimatic studies. The better whole-plant species are defined the better their putative Next Living Relatives can be selected that provide important input data for palaeoclimate reconstructions and modeling. Whole-plant reconstruction is a vital tool for getting insights in the structure and development of ancient ecosystems.

Integrative taxonomic research on plant fossils needs collaboration between traditionally separated subdisciplines such as palynology, xylotomy and macropalaeobotany including carpology; and 'clear' definition of fossil species as whole-plant species including their nomenclature. The correct use of names of any taxon is the key which is necessary for precise communication between scientists all over the world.Under the current *International code of nomenclature for algae, fungi and plants* (Melbourne Code) naming of whole plant species is legally fixed for the first time. The principle 'each fossil plant has only one name' means that the name of a whole-plant taxon has to be selected among the existing valid and legitimate names of the individual isolated organs following the rule of priority. From 2012 on it is allowed to incorporate parts or organs of fossil plants when discovered for the first time in preexisting taxa including their diagnoses.

Several opportunities exist for reconstructing whole-plant species from the fossil record. (1) Whole fossil plants are assembled based on repeated co-occurrence of isolated plant parts or organs in the same horizons. (2) Isolated plant parts or organs can be combined based on identical anatomical characters. (3) Two or more parts or organs of fossil plants are still attached to each other. Modern techniques for the investigation of fossil plants such as fluorescence, infrared, confocal laser and scanning electron microscopy should be applied if possible and appropriate.

Session · Integrative Taxonomy; Phylogenetics, Systematics (I)

11:00

Key Note: Deep Metazoan Phylogeny: progress, doubts, and mysteries

—

J. Wolfgang Wägele
Zoologisches Forschungsmuseum Alexander Koenig,
Adenauerallee 160, 53113 Bonn, Germany

—

The German Science Foundation has financed for a period of six years a priority program with about 30 participating research groups. Major results of this program will be presented. While in the more recent literature some regions of the metazoan tree of life are generally accepted, for other groups of taxa there are strong contradictions between morphological information and phylogenetic trees based on molecular data. Also, the latter are frequently mutually incompatible. Several examples from the priority program and from the recent literature are presented, e.g. concerning the relationship between diploblastic taxa and Bilateria, the placement of annelids and arthropods or the relationship between crustaceans, insects and myriapods. Some clades that appear consistently in molecular phylogenies are not compatible with evolutionary scenarios wich integrate morphological and paleontlogical data. A possible cause for these contradictions has been found: recent computer simulations have shown that important systematic errors occurring in maximum likelihood analyses can not be avoided with the currently available software. The hope that "more data" will solve all problems must be replaced with the demand for better algorithms and for more evolutionary thinking.

11:30

Naming the crown-of-thorns seastar species in the *Acanthaster planci* complex

—

Gerhard Haszprunar[1] · Martin Spies[2]
[1] Dept. Biol. II & GeoBio-Center of LMU München, Münchhausenstr. 21,
81247 München, Germany — [2] SNSB – Zoologische Staatssammlung München,
Münchhausenstr. 21, 81247 München, Germany

—

The "crown-of-thorns starfish" (COTS) are the most significant biological threat to tropical coral reefs and can be harmful to humans, thus they are among the most researched and most cited marine organisms. For a long time they were thought to belong to a single variable species, *Acanthaster planci* (Linnaeus, 1758), but recent molecular data suggest a complex of four clades separated by significant genetic distances and congruent phylogeographic patterns in the Indo-Pacific (Vogler et al. 2008, 2012, 2013). Unfortunately, the latter results have been ignored by most reef biologists and the medico-pharmaceutical world.

In trying to correlate the COI-barcoding clades with morphological data and the nomenclaturally available Linnean names, we have faced unexpected amounts of difficulties caused by numerous errors and inconsistencies committed or uncritically followed throughout the literature of the past 250 years. Our work aims to solve the various nomenclatural problems and to establish a robust taxonomic framework for the *Acanthaster planci* species complex. As none of the relevant original type material has been recovered so far, it will be necessary to collect fresh material at the type localities (as far as the latter can be determined), and to designate neotypes based on thorough morphological characterizations as well as molecular data. The case of the COTS is a remarkable example of the need for truly integrative taxonomy, in which genotypic and phenotypic data are combined with phylogeographical and ecological information.

References

Vogler C et al. (2008) A threat to coral reefs multiplied? Four species of crown-of-thorns starfish. Biology Letters **4**: 696 – 699.

Vogler C et al. (2012) Phylogeography of the crown-of-thorns starfish in the Indian Ocean. PLoS ONE **7**(8): e43499.

Vogler C et al. (2013) Phylogeography of the crown-of-thorns starfish: genetic structure within the Pacific species. Coral Reefs **32**: 515 – 525.

11:45

Sister where are you?
The phylogenetic position of the genus *Attaphila* Wheeler, 1900 (Dictyoptera, Blattodea)

—

Ute Eulitz[1] · Klaus-D. Klass[1] · Horst Bohn[2] · Volker Nehring[3]
[1] Senckenberg Naturhistorische Sammlungen Dresden, Königsbrücker Landstr. 159, 01109 Dresden, Germany — [2] Zoologische Staatssammlung München, Münchhausenstr. 21, 81247 München, Germany — [3] Biology I, University Freiburg, Hauptstrasse 1, 79104 Freiburg

—

Attaphila Wheeler, 1900 are small wingless cockroaches that live in the nests of leaf-cutting ants of the genera *Atta* and *Acromyrmex*. Six species have been described from the Neotropical Region and the Southern United States. *Attaphila fungicola* has two hosts, while all other species are known from one host ant each; the cockroaches live in the tunnels of the fungus gardens. *Attaphila* are ovoid in shape, and covered with yellowish hairs. Tegmina and wings are vestigial in males, and completely absent in females. The legs of *Attaphila* have a large ariolum, which enables both adults and nymphs to attach themselves to their hosts during swarming. This mechanism allows the species to be widely distributed. The terminal maxillary palpomeres have a unique structure that is used to detect and follow ant trail pheromones. The phylogenetic relationships of *Attaphila* to other cckroaches are still unkown, as is the morphology of their genitalia. We present our first results from a detailed study of several character systems. The focus is on the morphology of the proventriculus, the male and female genitalia, and the leg spination. The morphology of the male genitalia suggests a placement of *Attaphila* in the Blaberoidea (including the paraphyletic Blattellidae and the Blaberidae), which apart from the Cryptocercidae-Isoptera clade is the most species-rich lineage of Blattodea.

12:00

“Comments on the morphology of a new genus of Parastenocarididae (Crustacea: Copepoda:Harpacticoida) and its phylogenetic relationships”.

—

S. Gaviria[1] · D. Defaye[2]
[1] University of Vienna & Technisches Büro für Biologie, Fred Raymondgasse 19//2/4 (address for correspondence), 1220 Vienna, Austria — [2] Muséum national d’Histoire Naturelle, Département Milieux et Peuplements aquatiques, UMR 7208, CP 53, 61 rue de Buffon, 75005 Paris, France

—

A new genus of a parastenocaridid harpacticoid *Colombocaris* n.g. Gaviria & Defaye, submitted, was recently discovered on submerged mosses of a high Andean lake of Colombia.

Analysis of 17 characters suggests that *Colombocaris* constitutes an ancient genus within Neotropical parastenocaridids, and shares some morphological features with *Murunducaris*, species of the *Parastenocaris colombiensis*-group, *Remaneicaris*, and in less extension with *Brasilibathynellocaris*. Other species from Brazil could be included into this new genus (Corgosignho, pers.com.).

Following Schminke (2010) and due to the fact that 3 "truly informative characters" of *Colombocaris* are shared with Fontinalicaridinae (on male antennula, basis of leg 4 male, genital field female) and only 2 with Parastenocaridinae (on endopod of leg 3 female, caudal rami) together with a "less revealing characters" shared with Fontinalicaridinae (beared by leg 5), it is possible to include the new genus to the subfamily Fontinalicaridinae, as proposed by Schminke for the *colombiensis*-group of Noodt (1972).

The position of other genera within these subfamilies is not clear. Although the *columbiensis*-group was allocated to the Fontinalicaridinae possibly due to the type of leg 3 of male (apophysis and spine fused), leg 4 of male (endopod like a forceps, basis with row of ornaments between endopod and exopod in 2 of the 3 species) and size of leg 5 of male and female (large), it can be noted that the type of armature of the caudal rami (no gap between lateral and dorsal setae) constitutes a character typical of Parastenocaridinae. Nevertheless, the position of the lateral setae related to the dorsal seta seems to be a symplesiomorphic trait present in members of both subfamilies. Another case related to the subfamilies is the position of the genus *Remaneicaris*. Corgosinho argued that the genus should be removed from Parastenocaridinae and placed as an independent subfamily, due to many putative synapomorphies and some unique plesiomorphies (pers. comm. to S. Gaviria).

References

Gaviria, S. & D. Defaye (submitted): Description of *Colombocaris isabellae* n.g., n.sp. (Parastenocarididae) and *Elaphoidella paramuna* n.sp. (Canthocamptidae), new harpacticoid copepods from Colombia.

Noodt, W. (1972): Drei neue *Parastenocaris* aus Kolumbien (Crustacea, Copepoda). 1. Mitteilung über kolumbianische Grundwasser-Crustaceen. Studies on Neotropical Fauna **7**(1): 101 – 112, figs. 1 – 50.

Schminke, H.K. (2010): High-level phylogenetic relationships within Parastenocarididae (Copepoda, Harpacticoida). Crustaceana **83**(3): 343 – 367.

12:15

Systematics and Evolution of Nemertea

—

Jörn von Döhren

Institut für Evolutionsbiologie und Zooökologie, University of Bonn, An der Immenburg 1, 53121 Bonn, Germany

—

Nemertea (ribbon worms) is a spiralian taxon of unsegmented, nocturnal predators that hunt their prey by means of an eversible proboscis. Recently, it has been shown that Nemertea are part of the radiation of Trochozoa. However, neither target-gene nor genomic approaches have led to a robust placement of nemerteans within Spiralia so that their sister group still remains a matter of debate. Morphological approaches to this problem have been hampered by the unclear ground pattern which is due to the unresolved ingroup-phylogeny of Nemertea. Analysis of molecular data robustly supports some traditional superspecific taxa, such as Hoplonemertea and Heteronemertea. However, this data-set does not lead to consistent resolution of a single phylogenetic hypothesis nor does it lend support to Palaeonemertea, the remaining, presumably most basally branching traditional superspecific taxon. Novel data from comparative morphological studies as well as a thorough reassessment of existing data for their usefulness for phylogenetic analyses provide an independent data set for a phylogenetic analysis based on morphological characters. The resulting phylogenetic hypothesis is utilized to discuss and evaluate the conflicting molecular hypotheses. Accordingly, a hypothetical evolutionary scenario for nemerteans is stated along with a discussion of their phylogenetic affinities within Spiralia.

Curator's Workshop · Access & Benefit Sharing and other legal aspects of material transfer

14:00
—
16:00

Legal aspects of international specimen transfer – introduction and species protection

—

Peter Giere

Museum für Naturkunde Leibniz Institute for Research on Evolution and Biodiversity,
Invalidenstraße 43, 10115 Berlin, Germany

—

Over the years, the number of regulations affecting biological basic research has increased considerably. This is especially evident when a specimen to be studied is transported from one country to another. At the border crossing, the specimen is subject to a seemingly endless list of regulations that often are ignored rather than understood by the researcher. Whereas the origins lie in local phytosanitary and veterinarian provisions to protect domestic crops and animals from incoming diseases, international agreements were first introduced for the protection of wildlife from overexploitation with the "Convention on International Trade in Endangered Species of Wild Fauna and Flora" (CITES). Despite being paraphrased in a commercial context, this international agreement also covers animals and plants used in research. Maybe due to the long time since its introduction in 1975, the general provisions of this agreement (cast into national and European legislation) are better known within the research community, whereas other relevant regulations covering veterinary or phytosanitary, dangerous goods or customs are not well known, not to speak of "Access and Benefit Sharing". This and the following presentations will try to shed some light on the current and future requirements for specimen transfer that conforms to all applicable regulations and avoids confiscation or destruction of valuable samples by border officials or other undesirable effects of incorrect specimen transfer.

Access & Benefit Sharing: The concept, its implementation and its relevance for research and collections management

—

Cornelia Löhne
Botanischer Garten und Botanisches Museum Berlin-Dahlem,
Freie Universität Berlin, Königin-Luise-Str. 6 – 8, 14195 Berlin, Germany

—

With the Convention on Biological Diversity (CBD), which was adopted at the “Earth Summit” of 1992, the United Nations agreed on three major objectives: (1) the conservation of biodiversity, (2) its sustainable use and (3) the fair and equitable sharing of the benefits arising out of the utilization of genetic resources. It was especially the third objective that caused long political debates and complex legal negotiations about the ownership on genetic resources, regulations on access to them and provisions for benefit sharing. As a result, the ‘Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization’ was adopted by the CBD parties in 2010, and it is expected to come into force in autumn 2014. The Nagoya Protocol is meant to create greater legal certainty and transparency for providers and for users of genetic resources. At the same time, an EU regulation will set out the guidelines for compliance of users of genetic resources within the EU. Thereby, the main features of the Nagoya Protocol will immediately become law within all EU member states.

What may appear as a merely political or legal matter out of touch with the ‘real’ world of science, will in fact have a strong relevance and great influence on research involving organisms and biological material as well as collections management. Therefore, it is crucial for all biodiversity researchers and holders of biological collections to become familiar with this new law and its consequences for their operational practices. The presentation will give an overview on the concept of Access and benefit-sharing (ABS) and its legal implementation at the international and, especially, the European level.

Bon Voyage ?
International exchange of scientific material – legal hurdles and other obstacles

—

Dirk Neumann

Zoologische Staatssammlung München,
Münchhausenstr. 21, 81247 München, Germany

—

Modern biodiversity research (e.g. evolutionary and conservation biology) and biocontrol is dependent on accession and exchange of specimens stored in natural history collections worldwide. Legal collecting, export and worldwide transfer and exchange of scientific samples gets increasingly obstructed by national and international laws, regulations and bureaucratic burdens, which do not only challenge research institutes and associated scientists, but may also pose a real threat and can critically endanger specimens if unawareness, ignorance and incompetence of involved parties team up and join their destructive forces.

Besides aspects dealing with legal collecting exporting and importing of specimens under valid permits, dispatch of specimens by means of international (air) transportation is confronted with a jumble of laws, regulations and restrictions ranging from veterinary and species protection legislation to dangerous good regulations, postal carrier and airline restrictions and customs provisions. Despite being mostly based on identical (harmonised) international legislation, individual interpretation of federal, public or private staff has led not only to delayed delivery but to several reported cases of damaged material due to incorrect or rough handling of packages or even unintentional loss or destruction after inspection.

Moreover, being confronted with an increasing bureaucracy associated with such biomaterials that must be met, major courier companies such as FedEx, DHL or UPS, established their own – sometimes even stricter – rules for transportation and import of such biological samples or even ban them at all to avoid time-consuming and costly delays at respective destination gateways.

To avoid potential issues, researches worldwide transferring samples over national or international borders must improve documentation of shipped specimens by: i) detailing fixation and preservation of included samples clearly excluding potential risk of disease (veterinary legislation), ii) referring to relevant chemicals interfering with the international dangerous goods regulations of the International Civil Aviation Organization (ICAO), the International Air Transport Association (IATA) and the Universal Postal Union (UPU), and iii) providing relevant information needed to allow customs clearance and import of samples (indication of a declared value of included non-commercial research samples < 50 U$ and the

harmonised HS-Code 9705.00). Basic reading and comprehensive information was provided by Renner et. al. (2011), however needs to be compared in detail for consistency because of recent amendments and updates of specific regulations.

References

Renner S.C., D. Neumann, M. Burkart, U. Feit, P. Giere, A. Gröger, A. Paulsch, C. Paulsch, M. Sterz & K. Vohland. 2012. Import and export of biological samples from tropical countries–considerations and guidelines for research teams. Organisms, Diversity, Evolution **12**: 81 – 98.

Session · Phylogenomics I

16:30

Key Note:

Anchored Phylogenomics: Rapidly Expanding Across the Tree of Life

—

Alan R. Lemmon · Emily Moriarty Lemmon
Department of Scientific Computing, Florida State University

—

The field of phylogenomics is undergoing a revolution, enabled by new methods of data collection that leverage both genomic resources and recent advances in DNA sequencing. We developed a cost-efficient and rapid approach to obtaining data from 100s to 1000s of loci and individuals for deep and shallow phylogenetic studies. Specifically, we designed probes for target hybrid enrichment of 100s of loci in moderately conserved anchor regions of genomes (flanked by less conserved regions). We enriched genomic DNA libraries for these anchor regions, and sequenced these targets using high-throughput sequencing. The resulting data sets contain 100s of loci with low levels of missing data and high levels of phylogenetic information across taxonomic scales and produce phylogenies with high levels of resolution. This approach is expediting resolution of deep-scale portions of the Tree of Life and greatly accelerating resolution of the large number of shallow clades that remain unresolved. The combination of low cost (~ 1% of the cost of traditional Sanger sequencing and ~ 3.5% of the cost of high-throughput amplicon sequencing for projects on the scale of 500 loci × 100 individuals) and rapid data

collection (~ 2 weeks of laboratory time) make this approach tractable even for researchers working on systems with limited genomic resources. Here, I present new work from vertebrates and unpublished data from Angiosperms and several Metazoan phyla, including multiple insect orders. I also discuss future directions and new applications.

17:00

Key Note:
Phylogenomics sheds new light on the evolutionary history of insects – Results from the international 1KITE project

—

Oliver Niehuis
Zoologisches Forschungsmuseum Alexander Koenig, Sektion Biodiversitätsgenomik
und Molekularlabor, Adenauerallee 160, 53113 Bonn, Germany

—

Insects (Hexapoda) are one of the most species-rich and abundant lineages of multicellular animals. They conquered the air, colonized and shaped terrestrial and limnic ecosystems, and affected all other forms of life, including humans. Detailed knowledge of the insects' early diversification could shed light on how the appearance of different ecosystems and organisms, such as gymno- and angiosperms, forged the spectacular insect diversity seen today. However, inferring the phylogenetic relationships and origin of the major extant insect groups has proven notoriously difficult. We therefore decided to sequence transcriptomes of more than 1,000 insect species with the ambitious aim to infer the evolutionary history of insects and to provide reliable geological time estimates for the appearance of the major extant insect lineages. In my talk, I will present our results from inferring the phylogenetic relationships and geological appearance of the extant insect orders after studying more than 1,450 different protein-coding genes in app. 150 representative insect species. I will outline what kind of methodological approaches we developed and applied to overcome well-known problems of tree-inference, such as sparsely populated data matrices, the comparison of non-orthologous nucleotide or amino acid sequences, and deviations from underlying assumptions of nucleotide or amino acid substitution models. Finally, I will provide an outlook of how the 1KITE data can be further exploited for studying the evolution of genes of interest and for designing baits for target DNA enrichment.

17:30

Illuminating the base of the annelid tree using transcriptomics

—

Anne Weigert[1] · Günter Purschke[2] · Kenneth M. Halanych[3]
Torsten H. Struck[4] · Christoph Bleidorn[1]
[1] Molecular Evolution and Animal Systematics, University of Leipzig, Talstr. 33, 04103 Leipzig Germany — [2] Department of Zoology and Developmental Biology, University of Osnabrueck, Barbarsastr. 11, 49069 Osnabrueck Germany — [3] Molette Biology Laboratory for Environmental and Climate Change Studies, University of Auburn, 101 Rouse Life, AL 36849 USA — [4] Zoological Research Museum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany

—

Annelida is a highly diverse animal taxon with still unresolved phylogenetic background. Traditionally grouped into Clitellata and Polychaeta, phylogenetic relationships of the approximately 125 families varied between analyses depending on molecular or morphological markers. Increasing the amount of molecular data stabilized the annelid tree comprising most of the annelid biodiversity into two major groups: Errantia and Sedentaria. However, basal relationships within the annelid tree lacked resolution in part due to their age. Resolving these basal relationships is crucial for our understanding of annelid evolution and for major transitions in animal evolution such as the origin of segmentation, evolution of the nervous system or larval types like the trochophore larvae.

Hence, we generated 22 Illuminatranscriptomic libraries covering numerous annelid families and potential basal branching annelids, covering 79 species. Our analyses, based on 68,750 – 170,497 amino acid sites from 305 – 622 proteins, strongly support monophyletic Annelida and a basal radiation comprising Chaetopteridae, Amphinomidae, Sipuncula, Oweniidae, and Magelonidae. Our results reflect a hypothesis made by Rieger in 1988 were he suggested that members of Oweniidae closely resemble the annelid stem species and should be placed near the base of the annelid tree. Oweniidae possess certain morphological characters, which were considered as plesiomorphic rather than derived, since they were absent in the majority of the annelid radiation. Here we evaluate these characters in the light of the new annelids phylogeny and discuss its impact on the *annelid ground pattern*.

17:45

Phylogenomic analyses of *Wolbachia* supergroup relationships

MICHAEL GERTH[1] · MARIE-THERES GANSAUGE[2] · ANNE WEIGERT[1]
CHRISTOPH BLEIDORN[1, 3]

[1] Leipzig University, Institute for Biology, Molecular Evolution & Systematics of Animals, Talstrasse 33, 04103 Leipzig — [2] Max-Planck Institute for Evolutionary Anthropology, Department for Evolutionary Genetics, Advanced DNA Sequencing Techniques Group, Deutscher Platz 6, 04103 Leipzig — [3] German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig, Deutscher Platz 5e, 04103 Leipzig)

The nominal bacterial species *Wolbachia pipientis* comprises various genetically distinct strains ("supergroups"). All of these strains are obligate intracellular symbionts of ecdysozoans, yet their ecology shows marked differences: *Wolbachia* of supergroups A and B infect terrestrial arthropods, whereas C and D *Wolbachia* are found only within filarial nematodes. Furthermore, in arthropods *Wolbachia* act mostly opportunistic and horizontal transmissions are common. In contrast, filarial *Wolbachia* are mutualists that coevolve with a single host over evolutionary timescales. Interestingly, supergroup F *Wolbachia* can infect both, nematodes or arthropods.

As a prerequisite to address questions such as the ecology of the last common ancestor of all *Wolbachia* strains and the number of nematode-arthropod host switches (or vice versa) in *Wolbachia*'s evolutionary history, a well-supported phylogenetic hypothesis is needed. So far, phylogenetic reconstructions were hampered by insufficient data and the lack of suitable outgroups.

With a phylogenomic approach we attempted to clarify the phylogenetic relationships within *Wolbachia*. To this end, we performed Illumina whole genome shotgun sequencing of highly host specific *Wolbachia* strains from supergroups E and H as well as from supergroup F. We thereby generated the first genomic data for these supergroups. We compiled a multigene dataset of 90 loci from these data and already published *Wolbachia* genomes (supergroups A, B, C & D).

We present a robust phylogenetic hypothesis of *Wolbachia* supergroup-level relationships that provides a foundation for evolutionary research on this ubiquitous endosymbiont.

18:00

The embryonic transcriptome of the damselfly *Ischnura elegans*

—

SABRINA SIMON[1] · MERCER R BRUGLER[1] · HEIKE HADRYS[2] · ROB DESALLE[1]
[1] Sackler Institute for Comparative Genomics, American Museum of Natural History, New York, NY 10024, USA — [2] ITZ, Ecology & Evolution, Stiftung Tierärztliche Hochschule Hannover, 30559 Hannover, Germany

—

To understand insect development, e.g. how the segmental body plan is patterned and how the timing of segmentation has diverged during insect evolution (Davis and Patel, 2002), the full genomic complement of genes, their structures, and the patterns of gene expression during development is needed. Transcriptomics have been applied to a wide array of developmental biology problems in insects. For example, recent studies have already demonstrated the use of *de novo* assembled transcriptomes spanning various developmental stages to identify developmental genes and members of signaling pathways and to explore genome-level questions (Ewen-Campen et al., 2011; Zeng et al., 2013). However, transcriptomic data across developmental stages are still mainly available for derived holometabolous insects, especially drosophilid dipteran species.

Here, we fill in an important gap for future comparative gene expression analyses by analyzing and comparing transcriptomic data across the whole embryonic development of the damselfly *Ischnura elegans*. Roche 454-multiplexed transcriptomic data was generated for four time-periods (day 1 – 3, 4 – 5, 6 – 7, 8 – 9) spanning the entire embryonic lifespan. In addition, based on a protocol for ultra-low input library preparation and transcriptome profiling, modified Nextera libraries of single embryos for each of the nine embryonic days have been generated and sequenced on the Illumina HiSeq 2500 platform, resulting in over 250M PE reads after quality control.

This *de novo* assembled transcriptome and comparative analyses between the different embryonic stages will provide the first insights in the temporal gene expression changes during early damselfly development. In addition, this new genomic information of a non-model organism will not only provide resources to quantify variability in gene expression across developmental stages within a species, it will also help to study in detail an essential large scale developmental paradigm in developmental biology – the molecular signatures of embryonic developmental constraints.

References

Davis, G.K., Patel, N.H., 2002. Short, long, and beyond: molecular and embryological approaches to insect segmentation. Annu Rev Entomol **47**, 669 – 699.

Ewen-Campen, B., Shaner, N., Panfilio, K.A., Suzuki, Y., Roth, S., Extavour, C.G., 2011. The maternal and early embryonic transcriptome of the milkweed bug Oncopeltus fasciatus. BMC Genomics **12**, 61.

Zeng, V., Ewen-Campen, B., Horch, H.W., Roth, S., Mito, T., Extavour, C.G., 2013. Developmental gene discovery in a hemimetabolous insect: de novo assembly and annotation of a transcriptome for the cricket Gryllus bimaculatus. Plos One 8, e61479.

S.Si. was supported by a fellowship within the Postdoc-Program of the German Academic Exchange Service (DAAD).

Session · Morphology, Development & Evolution

09:00

Key Note: The mouth, the anus and the blastopore: Open Questions about questionable Openings

—

Andreas Hejnol
Sars International Centre for Marine Molecular Biology, Thormøhlensgt. 55,
5008 Bergen, Norway

—

Over 100 years ago Karl Grobben subdivided all bilateralsymmetric animals into Protostomia and Deuterostomia using embryological characters. While recent molecular phylogenies support this grouping, a closer examination of the embryology indicates that this subdivision is made based on highly variable characters. All deuterostomes form the mouth separate from the blastopore, but protostomes show variability in the fate of the blastopore. I will provide new developmental data from different protostome taxa that suggest that deuterostomy is ancestral for the protostomes and thus for all Bilateria.

09:30

Key Note: Evolutionary developmental biology of Myxozoa

—

Alexander Gruhl
Natural History Museum, Department of Life Sciences, Cromwell Road,
London SW7 5BD, United Kingdom

—

Myxozoa are a completely endoparasitic subtaxon of Cnidaria that has undergone an immense radiation, with more than 2100 species currently described, exploiting mainly annelids and bryozoans as primary hosts, and marine and freshwater fish as secondary hosts. Compared to their free-living relatives, myxozoans show drastic modifications of both their body-plan and life-cycle features. This includes on the one hand the reduction of many fundamental metazoan features like the intestinal tract, nervous system, gametes, gonads, body axes or even epithelial organisation, but on the other hand an increase in complexity of certain other morphological traits, like transmissive spores, or in the diversity of life cycle stages. In this talk I will synopsise the knowledge on the developmental biology of this bizarre and little known group contrasting it to known patterns in cnidarians. I will demonstrate in a few case studies how recent advances in microscopic and molecular biological methods can help to elucidate in non-model species how changes in developmental patterns can lead to major morphological changes. In more general terms this talk will emphasise the value of studying neglected branches of the tree of life for gaining insights into patterns of morphological evolution.

10:00

Molluscan evodevo: ancestral states and phylogenetic implications

—

Andreas Wanninger [1] · Maik Scherholz [1] · Emanuel Redl [1]
Christiane Todt [2] · Tim Wollesen [1]

[1] University of Vienna, Dept. of Integrative Zoology, Althanstrasse 14, 1090 Vienna, Austria — [2] University Museum of Bergen, The Natural History Collections P.O Box 7800, 5020 Bergen, Norway

—

As particularly speciose phylum, second only to Hexapoda, Mollusca is represented by a wide spectrum of bodyplan morphologies, unparalleled by any other metazoan phylum. However, despite considerable interest in their morphology, development, and phylogenetic inter- and intrarelationships, little is known concerning their early evolution. Recent phylogenomic analyses have revived the old idea of a monophyletic assemblage that includes the eight-shelled polyplacophorans (chitons) as well as the shell-less, worm-like aplacophorans (comprising the caudofoveates or chaetodermomorphs and the solenogasters or neomeniomorphs). This Aculifera-concept has been corroborated by morphogenetic analyses and has resulted in a suggested scenario of a last common aculiferan ancestor that bore a number of polyplacophoran-like features. This talk will review the state-of-the-art of molluscan comparative evolutionary developmental biology and will highlight current research efforts, recent progress, open questions, and competing phylogenetic and evolutionary concepts revolving around one of the most diverse and fascinating phyla on the planet: the Mollusca.

10:15

Longevity of plastids in sacoglossan sea slugs – what counts in this unique association?

—

Heike Wägele [1] · Valerie Schmitt [1] · William F Martin [2] · Gregor Christa [1]

[1] Zoologisches Forschungsmuseum Alexander Koenig, Adenauer Allee 160, 53113 Bonn, Germany — [2] Institut für Molekulare Evolution, Heinrich-Heine-Universität, Universitätsstraße 1, 40225 Düsseldorf, Germany — Christa Gregor, Zoologisches Forschungsmuseum Alexander Koenig, Adenauer Allee 160, 53113 Bonn, Germany

—

Several members of the sea slug group Sacoglossa are known to survive starvation periods of many months. This ability is ascribed to the sequestration of intact chloroplasts from their preferred food, usually ulvophycean algae, and their maintenance for long periods of time within the digestive tract. Recent publications have shown that the longevity of the plastids is not based on a long assumed lateral gene transfer of algal nuclear genes into the slugs' genomes. Therefore, factors intrinsic to the algae and factors intrinsic to the slugs have to be investigated to explain the long maintenance and photosynthetic performance of chloroplasts in the slug's digestive system. We will present new results on the slugs that further elucidate this – within Metazoa – unique phenomenon. However we will also show new puzzles resulting from our experiments.

11:00

Oral innervation in a velvet worm provides insights into the evolution of the ecdysozoan brain

—

Christine Martin · Georg Mayer

Animal Evolution & Development, Institute of Biology, University of Leipzig, Talstraße 33, 04103 Leipzig, Germany

—

As one of the closest relatives of arthropods, Onychophora plays an important role in understanding the evolution of arthropod body plans. Currently there is controversy surrounding the evolution of the brain among the ecdysozoan clades, which shows a collar-shaped, circumoral organisation in cycloneuralians but a ganglionic architecture in panarthropods. Based on the innervation pattern of lip papillae surrounding the mouth, the onychophoran brain has been interpreted as a circumoral ring, suggesting that this organisation is an ancestral feature of Ecdysozoa. However, this interpretation is inconsistent with other published data. To explore the evolutionary origin of the onychophoran mouth and to shed light on the evolution

of the ecdysozoan brains, we analysed the innervation pattern and morphogenesis of the oral lip papillae in the onychophoran *Euperipatoides rowelli* using DNA labelling, immunocytochemistry and neuronal tracing techniques. Our morphogenetic data revealed that the seven paired and one unpaired oral lip papillae arise from three anterior-most body segments. Retrograde fills show that only the first and the third nerves supplying the lip papillae are associated with cell bodies within the brain, whereas the second nerve exclusively receives fibres from somata of peripheral neurons located in the lip papillae. According to our anterograde fills and immunocytochemical data, the first nerve supplies the anterior-most pair of lip papillae, whereas the second and the third nerves are associated with the second to fifth and second to eighth lip papillae, respectively. These data suggest that the lip papillae of *E. rowelli* are mainly innervated by the proto- and deutocerebrum, whereas there are only a few additional cell bodies situated posterior to the brain. According to these findings, the overall innervation pattern of the oral lip papillae in *E. rowelli* is incompatible with the interpretation of the onychophoran brain as a modified circumoral ring.

11:15

On the evolutionary changes in the integument of the onychophoran *Plicatoperipatus jamaicensis* (Peripatidae)

—

Ivo de Sena Oliveira [1] · Carsten Lüter [2] · Klaus W. Wolf [3]
Georg Mayer [1]

[1] Animal Evolution and Development, Institute of Biology, University of Leipzig, Talstraße 33, 04103 Leipzig, Germany — [2] Museum für Naturkunde, Leibniz-Institute for Research on Evolution and Biodiversity, Invalidenstrasse 43, 10115 Berlin, Germany — [3] Electron Microscopy Unit, University of the West Indies (Mona), Kingston 7, Jamaica

—

The dorsal integument of nearly all species of Peripatidae – one of the two major subgroups of Onychophora (velvet worms) – typically exhibits 12 annuli (=plicae) per segment. The only exception occurs in *Plicatoperipatus jamaicensis*, from which 24 plicae per segment have been reported. This would suggest that the number of plicae has been duplicated in this species. However, if this assumption is correct, one would expect that the structure of the duplicated plicae would resemble that of the original plicae and that the structures commonly associated with the plicae, such as crater-shaped papillae and hyaline organs, would also have been duplicated. To clarify whether there was indeed such duplication, we compared the structure of the integument in embryos and adults of *Plicatoperipatus jamaicensis* (with the putative number of 24 plicae per segment) and *Principapillatus hitoyensis* (with the

common number of 12 plicae per segment). Our scanning electron microscopic data revealed that the embryos of the two species have 12 plicae per segment. While this number persists in adults of *Principapillatus hitoyensis*, 12 additional rows of papillae occur in the dorsal integument in adults of *Plicatoperipatus jamaicensis*. These additional rows differ from the original plicae in that they are not equipped with primary papillae and are situated in furrows between the plicae, as evidenced by the position of hyaline organs and crater-shaped papillae. Furthermore, our data show that the number of the ventro-lateral plicae, crater-shaped papillae and hyaline organs is similar in the two species studied. These findings suggest that the plicae have not been duplicated in the integument of *Plicatoperipatus jamaicensis*, but rather additional rows of papillae have been inserted between the 12 original plicae. These additional rows might have lead to a denser package of dermal papillae in the dorsal integument of *Plicatoperipatus jamaicensis*, but the functional significance of this evolutionary change is unknown.

11:30

Evolution of life habits in silverfish (Insecta, Zygentoma)

—

Markus Koch
Biozentrum Grindel und Zoologisches Museum, Universität Hamburg, Germany

—

Silverfish show remarkably variable life habits and thus form an interesting case study for inferring general patterns of adaptive radiations in soil arthropods. New astonishing records of rare subterranean and myrmecophilous species from the Neotropics and Australian fauna are reported and form the background for presenting first approaches to unravel the evolution of the various life habits in silverfish. Current conclusions are based on hypotheses on the phylogeny of the Zygentoma inferred from characters of the external morphology and internal anatomy. Insights obtained thus far favour repeated radiations and convergent adaptations to subterranean life as well as to troglophily, myrmecophily, and psammophily in various silverfish lineages. Specific anatomical transformations correlated with these life habits are demonstrated, including current support for an exceptional case of predacious life habits in arid environments characterizing the few extant species of the Maindroniidae. The hypothesis is discussed whether silverfish are originally bark-dwellers in rotten woods.

11:45

Functional morphology of the genitalia of *Anania hortulata* (Lepidoptera: Crambidae)

Francesca Vegliante · Matthias Nuss
Senckenberg Naturhistorische Sammlungen Dresden, Königsbrücker Landstraße 159,
01109 Dresden, Germany

Based on observations on *Anania hortulata* (Linnaeus, 1758), we describe in detail the specializations of the external genitalia proposed by Leraut (2005) as autapomorphies of the genus *Anania* Hübner, 1823, and illustrate their role during copulation.

In females, a deep invagination (sinus vaginalis) opens ventrally between the 7th and 8th abdominal segments; the anterior end of this pocket is evaginated forming a finger-like protuberance, which bears the copulatory opening (ostium bursae). At rest, the finger-like protuberance is entirely located within the sinus vaginalis, and the ostium bursae appears closed. The male intromittent organ (phallus) bears a strong, distally directed spine at approximately half of its length; in *A. hortulata*, this spine is bifurcated and it reaches posterior to the apex of the phallic body, where the genital opening is located. Additional to the autapomorphies of the genus *Anania*, *A. hortulata* shares further specializations with a limited number of congeneric species. In the male, both appendages of the 9th abdominal segment (valvae) bear a ventral spine (pollex); a strong, hook-shaped spine is borne on the juxta (a sclerite just ventral to the phallus). In the female, the floor of the sinus vaginalis is at rest partially overlapped by a movable sclerite (lamella antevaginalis).

In copula, the male uses its uncus (10th abdominal tergite), valvae, and juxta to grasp the female abdomen dorsally, laterally, and ventrally respectively. The pollices compress so strongly the pleural membranes of the female's 7th abdominal segment that, at their level, the female's body can be reduced to ¼ of its original width. The sinus vaginalis is partially evaginated, exposing the tip of the finger-like protuberance; the dorsal and ventral arm of the phallic spine slide along the sides of the finger-like protuberance, acting as a guide for the tip of the phallic body, which penetrates the ostium bursae. The lamella antevaginalis of the female is rotated by 165° towards the male, and the spine of the juxta becomes engaged in the transverse fold thus generated between the anterior border of the lamella antevaginalis and the female's 7th abdominal sternite.

References

Leraut P. 2005: Contribution à l'étude de quelques genres et espèces de Pyraustinae (Lepidoptera, Crambidae). Nouvelle Revue d'Entomologie (N. S.) **22**(2): 123 – 139.

12:00

Coevolution of plumage pattern and migratory behaviour with range in swifts (Aves: Apodini)

—

DIETER THOMAS TIETZE[1] · MARTIN PÄCKERT[2]

[1] Institut für Ökologie, Evolution und Diversität, Goethe-Universität Frankfurt am Main, Max-von-Laue-Straße 13, 60439 Frankfurt am Main, Germany — [2] Senckenberg Naturhistorische Sammlungen Dresden, Museum fürTierkunde, Königsbrücker Landstraße 159, 01109 Dresden, Germany

—

Old-World Apodini swifts (Aves: Apodiformes) serve as an example for a recent radiation on an intercontinental scale on the one hand and for the interplay of trait and range evolution with speciation, extinction and trait transition rates on a low taxonomic level on the other hand. Hugall & Stuart-Fox (2012) investigated polymorphic plumage in several higher-level taxa of birds. In their larger data sets, polymorphism was a rarely expressed trait that significantly increased speciation rates and rates of losing polymorphism were significantly higher than rates of gaining it. Swifts are well adapted to a permanent life in the air and long-distance movements. Their colouration is generally dull, but lighter patches of chin and rump stand out. Only few of the 23 extant taxa breed outside the tropics; they are the only species in the study group that migrate long distances to wintering grounds. We dated our molecular phylogeny (Päckert et al. 2012) using fossil constraints. Several methods were used for reconstruction of historical biogeography. Two models were used to trace character evolution along the phylogeny. We finally correlated trait expression with geographic state. The differentiation of the Apodini took place in less than 9 Ma. Their ancestral range comprised vast parts of the Old-World tropics, although the majority of extant taxa breed in the Afrotropic and the closest relatives occur in the Indomalayan. The expression of all three investigated traits increased speciation rates and they were more likely lost than gained. Chin patches are found in almost all species so that no association with phylogeny or range could be found. Rump patches showed a phylogenetic signal. Apodini swifts have performed long-distance migration whenever they expanded their range to temperate latitudes. The study was funded by Sächsisches Staatsministerium für Wissenschaft und Kunst, AZ4-7531.50-02-621-08/1 and Deutsche Forschungsgemeinschaft (Ti 679/2-1).

References

Hugall A. F., Stuart-Fox D. (2012): Accelerated speciation in colour-polymorphic birds. Nature **485**: 631 – 635.

Päckert M., Martens J., Wink M., Feigl A., Tietze, D. T. (2012): Molecular Phylogeny of Old World swifts (Aves: Apodiformes, Apodidae, *Apus* and *Tachymarptis*) based on mitochondrial and nuclear markers. Molecular Phylogenetics and Evolution **63**: 606 – 616.

Session · Integrative Taxonomy; Phylogenetics, Systematics (II)

Key Note: Integrative taxonomy and the nature of species 14:00

—

George Sangster

Department of Bioinformatics and Genetics, Swedish Museum of Natural History,
P.O. Box 50007, SE-104 05 Stockholm, Sweden. E-mail: george.sangster@nrm.se

—

Species are the basic currency in biodiversity studies but what constitutes a species has long been controversial. A major breakthrough in the late 1990s was the insight that most systematists agree that species are lineages, and that there are multiple valid ways to document such species in practice. Building on this insight, it was proposed that multiple lines of evidence should be employed and integrated, a procedure called integrative taxonomy. I use examples of integrative taxonomic studies of birds and meta-analyses of species properties to illustrate the power of this method. My studies document dramatic differences in species properties even among closely related species and demonstrate that no single line of evidence can identify all species. I discuss the importance of integrative taxonomy for biodiversity studies and how integrative taxonomy can provide new insights into the nature of species and even the speciation process.

Phylogeny and expression of Pax genes in the onychophoran *Euperipatoides rowelli* 14:30

—

Franziska A. Franke · Isabell Schumann · Georg Mayer

Animal Evolution & Development, Institute of Biology, University of Leipzig,
Talstraße 33, 04103 Leipzig, Germany

—

The genes of the Pax family encode a class of transcription factors that regulate a number of developmental processes in various metazoans, including body segmentation, neural patterning, and eye formation. Thus, the study of expression patterns of these genes in Onychophora (velvet worms) – one of the closest relatives of arthropods – might provide insights into the evolution of these processes in Panarthropoda (Onychophora + Tardigrada + Arthropoda). We therefore searched for homologs of all Pax genes in the embryonic transcriptomes of the onychophoran *Euperipatoides rowelli* and performed a phylogenetic analysis to clarify their phylogenetic relationship and orthology across metazoans. Our data revealed homologs of all six major Pax subfamilies in the onychophoran transcriptome, including *pax2/5/8* (*shaven*), *pax6*, *pox-neuro*, *pox-meso* (*pax1/9*) and *pax3/7*. Moreover, we identified an additional, new member, which does not fall into any other known subfamily of Pax genes. Our ongoing expression study of all Pax orthologs revealed repeated *pax3/7* domains in every segment in embryos of *E. rowelli*, suggesting that *pax3/7* acts as a segment polarity gene in the onychophoran development. This contrasts with the situation in arthropods, in which *pax3/7* orthologs have two different functions. While they exclusively act as segment polarity genes in myriapods and chelicerates, they initially show a pair-rule function (double-segment periodicity) in crustaceans and insects, which changes to a segment polarity function during development. These findings suggest that *pax3/7* had a role as a segment polarity gene in the last common ancestor of Onychophora and Arthropoda.

14:45

Slime protein profiling: A non-invasive tool for species identification in Onychophora

—

Alexander Baer · Ivo de Sena Oliveira · Georg Mayer
Animal Evolution and Development, Institute of Biology, University of Leipzig,
Talstraße 33, 04103 Leipzig, Germany

—

Onychophorans (velvet worms) use an adhesive, protein-based slime secretion for prey capture and defence. The glue-like slime is ejected via a pair of modified limbs and the sticky threads entangle their victim. In this study, we analysed the protein composition of slime in twelve species of Onychophora from different parts of the world, including two species of Peripatidae from Costa Ricaand Brazil, and ten species of Peripatopsidae from Australia, using sodium dodecyl sulphate polyacrylamide gel electrophoresis. Our results revealed high intraspecific conservationin protein composition of slime among the species studied. In contrast, the protein profiles differ considerably between the species in both number and position of bands. We observed the highest number of differences (in 20 out of 33 considered band positions)between a peripatid and a peripatopsid species, whereas the lowest number of differences (in 4 band positions) occurs between two closely related egg-laying species. The reconstructed Maximum Parsimony cladogram, based on the electrophoretic characters, largely reflects the phylogenetic relationships of the species studied, suggesting that the slime protein profiles contain useful phylogenetic information. Based on these findings, we suggest that slime protein profiling is a valuable, non-invasive method for speciesidentification, which will help to discover potentially new species. This will be of particular interest for the upcoming systematic and taxonomical work, as the < 200 described species of Onychophora most likely underrepresent the actual diversity of the group.

15:00

New insights into spinicaudatan diversity (Crustacea: Branchiopoda) – identification and differentiation of several undescribed *Eocyzicus* species

—

Lisa Tippelt · Martin Schwentner · Stefan Richter
Universität Rostock, Allgemeine und Spezielle Zoologie, Universitätsplatz 2,
18055 Rostock, Germany

—

Spinicaudata live in temporary water bodies all over the world except Antarctica. The taxonomy, particularly the morphological identification of spinicaudatan species is difficult because of great morphological differences between individuals of the same species (intraspecific variability) and small morphological differences between various species (interspecific variation). Thus, unambiguously delimiting new species is often impeded by the inability to clearly differentiate variability from variation, potentially resulting in inaccurately drawn species boundaries. In our study we have focused on species of the genus *Eocyzicus* from Australia. All individuals were genetically analyzed prior to their morphological assessment. In addition to the two described species *Eocyzicus parooensis* Richter & Timms, 2005 and *E. argillaquus* Timms & Richter, 2009, eight new species were identified by molecular analyses. These findings were the starting point for morphological examinations to unambiguously differentiate intra- from interspecific differences. Our analysis revealed a very high intraspecific morphological variability. The majority of studied characters scored with the aid of the taxonomic software DELTA exhibit many different states and these often overlapped with those observed in other species. This applies to characters with defined states as well as numerical ones. Hence, several studied characters do not allow a clear differentiation of species, suggesting that morphological polymorphisms are retained over long evolutionary times and independent of speciation events. All results were viewed in the light of different species concepts to highlight potential differences in species delimitation based on morphological and molecular data.

15:15

Discovery of a species complex in the *Leucinodes* genus group damaging Solanaceae fruits in Sub-Saharan Africa and moving in trade (Insecta: Lepidoptera)

—

Richard Mally[1] · Anastasia Korycinska[2] · David Agassiz[3]
Jennifer Hodgetts[2] · Matthias Nuss[4]
[1] University Museum of Bergen, NO — [2] Food and environment research agency, Sand Hutton, UK — [3] Weston-super-Mare, Somerset, England, UK — [4] Senckenberg Natural History Collections Dresden, D

—

Leucinodes Guenée, 1854 and *Sceliodes*Guenée, 1854 areclosely related genera of snout moths (Pyraloidea) in the Old World tropics. The larvae are feeding in the fruits of a variety of Solanaceae, thus causing significant economic damage. We redefine the genera*Leucinodes*and *Sceliodes*based on homologies in wing pattern and morphology of genitalia and larvae. The generic redefinition excludes five of the 6 previously recognized African species from *Leucinodes*. The sixth species, *L. orbonalis*, is not found in this region. Instead, integrative taxonomy using DNA data and morphology show that Sub-Saharan Africa harbors a complex of at least four cryptic *Leucinodes* species and two additional *Sceliodes* species, which we describe as new to science. One of these cryptic species has been imported frequently to Europe during the last 50 years, but remained undiscovered as misidentification of *L. orbonalis*.

15:30

Phylogeography and systematics of Himalayan and Chinese birds – multiple lines of evidence

—

Martin Päckert[1] · Jochen Martens[2] · Yue-Hua Sun[3]
[1] Senckenberg Natural History Collections Dresden, Königsbrücker Landstrasse 159, 01109 Dresden, Germany — [2] Institut für Zoologie, Johannes Gutenberg-Universität, 55099 Mainz, Germany — [3] Key Laboratory of Animal Ecology and Conservation, Institute of Zoology, Chinese Academy of Science, Beijing 100101, China

—

Taxonomic diagnosis at the species and subspecies level has become increasingly sophisticated using a combination of multidisciplinary analyses in an integrative approach. Integrative taxonomy becomes most relevant for species groups or entire genera showing only subtle morphological variation among species. In these cases cryptic diversification might be found in other characters such as gene markers or behavior such as vocalizations of songbirds.

The mountain forest belt at the southern and the southeastern margin of the Qinghai-Tibetan Plateau (QTP) is one of the most prominent avian biodiversity hotspots of Eurasia. In species-rich genera the same phylogeographic East-West divides can be found repeatedly at different elevational levels in vertical parapatry. Among 27 leaf-warbler species (Phylloscopidae) from the QTP region only three are currently considered uniform without any internal trans-SinoHimalayan diversification. One of them, the Buff-barred warbler (*Phylloscopus pulcher*), is split into one Chinese and another Himalayan genetic lineage that correspond to different diagnostic song dialects. For the Chinese populations the subspecies name *vegetus* was recommended for revalidation.

In contrast, wren-babblers (*Pnoepyga*) comprise only two Himalayan-Chinese species pairs at different elevations. Song patterns are diagnostic for all species and intraspecific East-West differentiation was found in one high-elevation species, *Pnoepyga albiventer*. Species status for the Chinese populations of the latter was recently recommended and the name *Pnoepyga mutica* was revalidated. A third so far unnamed genetic lineage was found in Myanmar. The wren-babbler species pair of the mean and lower elevations has more simply-structured and less modulated songs that are possibly adaptive to a noisy environment in close neighborhood of torrent streams.

In the Western Palearctic far beyond their Asian breeding and wintering ranges, most Asian bird species have only been recorded as rare vagrants in the non-breeding season. However, a first breeding record of a small Asian heron species, the Chinese Bittern (*Ixobrychus sinensis*) could be reliably confirmed in coastal and river mangroves of Eastern Egypt based on an integrative analysis.

J.M. received repeated travel funding from Feldbausch Stiftung and Wagner Stiftung, both at Mainz University. The leaf-warbler study was part of a DFG-funded project PA1818/3-1.

15:45

Should we register and name all species on Earth, and if we should, how can we achieve it?

—

Michael Ohl

Museum fuer Naturkunde, Leibniz-Institut fuer Evolutions- und
Biodiversitaetsforschung, Invalidenstr. 43, 10115 Berlin, Germany

—

Numerous historical and recent studies have tried to estimate the true amount of the global species diversity. Starting in the 17th century, the magnitude of the total number of species has been constantly increasing and has reached a maximum in the late 20th century. However, even more conservative recent studies agree that at least a few million species still await discovery. Since a number of years, the rate of global species discovery is about 18,000 species per year. Depending on the estimate of the global species richness, an inventory of all species on Earth requires many decades or even centuries to be completed. At the moment, extinction rates obviously outnumber discovery rates, so that we are constantly loosing species from our global inventory. Given a limited amount of financial and personal resources, it seems highly unlikely that the rate of species discovery can be significantly increased in the frame of the current project-based funding scheme. In the moment, biodiversity discovery is aiming at selected target groups or geographic regions. However, there are many well-founded reasons why all species on Earth should be registered and named, but the current research agenda is unsuitable to reach that goal. The current cultures and practices of biodiversity discovery are ambiguous and suffer from the conflict between a tradition-based demand for completeness and insufficient methods, theories and actions to gain completeness. It has become obvious that a new global strategy for biodiversity discovery is needed. If the scientific community decides that a global inventory is not feasible or sensible, criteria are needed to decide, which group or region not to inventory. If the scientific community agrees on the goal of a complete inventory, it is obviously necessary to transform taxonomy into “big science”, which is a multinational, highly collaborative endeavor.

Session · Integrative Taxonomy; Phylogenetics, Systematics (III)

09:00

Key Note:

Modern integrative taxonomy: new methods, techniques and applications

—

Michael J. Raupach

AG Molecular Taxonomy of Marine Organisms, German Center of Marine Biodiversity Research, Senckenberg am Meer, Südstrand 44, 26382 Wilhelmshaven, Germany

—

The correct identification and classification of species is vital for most biological disciplines, for example ecology, biodiversity research and phylogeny. As consequence of the tremendous advances in molecular technologies during the last few years, new methods and approaches have become available to describe and delimitate species more precisely. Beside already established DNA sequence-based approaches, various other techniques including spectroscopic and spectrometric techniques can be used to describe and classify species more in detail. Most of these methods are routinely used for the identification and classification of bacteria and other microorganisms. However, studies analyzing non-microorganisms are still rare, but pioneering studies reveal the potential of these approaches. In addition to these new technologies, a web-based cybertaxonomy offers digital dimensions for modern taxonomy, allowing the build-up of comprehensive open-access data bases. The application and combination of these new methods, implemented in the framework of an integrative taxonomy, offers fascinating perspectives for taxonomy.

09:30

How many species of grass snakes are out there? Phylogeography, gene flow across contact zones and taxonomy of *Natrix natrix*

Carolin Kindler[1] · Wolfgang Böhme[2] · Claudia Corti[3] · Václav Gvoždík[4]
Daniel Jablonski[5] · David Jandzik[5] · Margarita Metallinou[6]
Pavel Široký[7] · Uwe Fritz[1]

[1] Senckenberg Natural History Collections Dresden – Museum of Zoology, Koenigsbruecker Landstrasse 159, 01109 Dresden, Germany — [2] Zoologisches Forschungsinstitut und Museum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany — [3] Museo di Storia Naturale dell'Università di Firenze, Sezione di Zoologia "La Specola", Via Romana 17, 50125 Firenze, Italy — [4] Department of Zoology, National Museum, Cirkusová 1740, 19300 Prague, Czech Republic — [5] Department of Zoology, Faculty of Natural Sciences, Comenius University Bratislava, Mlynská dolina B-1, 84215 Bratislava, Slovakia — [6] Institut de Biologia Evolutiva, Animal Phylogeny and Systematics, Passeig Marítim de la Barceloneta 37 – 49, 08003 Barcelona, Spain — [7] Department of Biology and Wildlife Diseases, Faculty of Veterinary Hygiene and Ecology, University of Veterinary and Pharmaceutical Sciences, Palackého 1/3, 61242 Brno, Czech Republic

Grass snakes (*Natrix natrix*) represent one of the most widely distributed snake species of the Palaearctic region. Within *N. natrix*, up to 14 distinct subspecies are regarded as valid. In addition, some authors recognize big-headed grass snakes from western Transcaucasia as a distinct species, *N. megalocephala*. Based on phylogenetic analyses of a 1984-bp-long alignment of mtDNA sequences (cyt *b*, ND4+tRNAs) of 410 grass snakes, a nearly range-wide phylogeography is presented for both species. Within *N. natrix*, 16 terminal mitochondrial clades were identified, most of which conflict with morphologically defined subspecies. Hypotheses regarding glacial refugia and postglacial range expansions are presented. Holocene range expansions led to the colonization of more northerly regions and the formation of secondary contact zones. In Central Europe, there are two contact zones of three distinct mitochondrial clades, one of these contact zones was theretofore completely unknown. In agreement with previous studies using morphological characters and allozymes, there is no evidence for the distinctiveness of *N. megalocephala*. Therefore, *N. megalocephala* is synonymized with *N. natrix*. In addition, first preliminary results of 14 tested microsatellite loci are presented as an outlook on future work.

09:45

DNA-barcode-assisted biodiversity assessment of passerine birds on the Qinghai-Tibetan Plateau

—

Patrick Strutzenberger[1] · Martin Päckert[1] · Jochen Martens[2]
Yue-Hua Sun[3]
[1] Senckenberg Natural History Collections Dresden, Königsbrücker Landstrasse 159, 01109 Dresden, Germany — [2] Institut für Zoologie, Johannes Gutenberg-Universität, 55099 Mainz, Germany — [3] Key Laboratory of Animal Ecology and Conservation, Institute of Zoology, Chinese Academy of Science, Beijing 100101, China

—

The passerine fauna on the Qinghai-Tibetan Plateau (QTP) is characterized by species that are part of several predominantly palearctic radiations. This study aims to generate barcode records for select taxa of passerines occurring on the plateau and adjacent regions, e.g.: old-world warblers, larks, redstarts, snow-finches, and thrushes. With the data generated we hope to facilitate identification of previously unrecognized genetic lineages. In addition we are taking a first step towards a biodiversity inventory for this under-investigated region. A preliminary analysis of a dataset of COI barcode sequences obtained from 371 specimens representing 155 species was performed. The barcode index number (BIN) system was adopted for delineation of barcode clusters. 140 BINs with at least two individuals were recognized. Of these 140 BINs, 103 (74%) were concordant with recognized taxonomy. The other 26% were almost exclusively comprised of cases with more than one BIN per species, i.e. cases where the BIN system has split a species into at least two clusters. This is unusual as the BIN system is known to underestimate global species numbers for birds. It is however not an unexpected finding in our dataset that includes many recently diverged species with large to very large geographic ranges. Unsurprisingly, most cases of discordance occur in taxa that are known to include very recent radiations with often-disputed taxonomy and oftentimes occupy geographic ranges on a continental scale e.g.: larks and redstarts. Taxa representing predominantly older radiations with more restricted geographic ranges like old-world-warblers (Phylloscopidae) instead exhibit almost perfect accordance of barcode clusters with recognized taxonomy. Additional mitochondrial and nuclear markers as well as morphology will be used to investigate incidents of discordant clusters. An analysis of intra- vs. interspecific pairwise genetic distances as well as a tree-based identification approach showed that all but four out of 155 species (99.97%) can be readily distinguished by DNA barcoding. This high identification success despite complex evolutionary histories could only be achieved by a representative geographic sampling. During our endeavor we were so far able to add barcode records for 48 species previously not represented in the Barcode Of

Life Datasystems (BOLD). For the QTP region itself, records for most species were completely lacking prior to commencement of this study. This study was supported by the DFG; P1818/3-1.

11:00
—
12:30

Workshop · Alle Bio-Literatur online!?
Workshop · All biology literature online!?

Alle Bio-Literatur online!?
Literaturversorgung der Biodiversitätsforschung im Wandel
//
All biology literature online!?
Supply of literature for biodiversity research in transformation

—

Judith Dähne · Gerwin Kasperek
University Library Johann Christian Senckenberg, Bockenheimer Landstr. 134 – 138,
60325 Frankfurt am Main, Germany

—

Die Universitätsbibliothek Frankfurt am Main betreut das DFG-geförderte Sondersammelgebiet Biologie mit dem Fachportal vifabio und verfügt über die größte Sammlung biologischer Literatur in Deutschland. Über Fernleihe und Dokumentlieferung versorgt sie Biologen deutschlandweit mit spezialisierter Literatur. Der starke Wandel, der durch das Internet und die Online-Verfügbarkeit von wissenschaftlichen Informationen eingetreten ist, führt auch zu neuen Herausforderungen für solche Dienstleistungen. Im Rahmen des Workshops soll mit der Fachcommunity der Tagung BioDivEvo 2014 diskutiert werden, wo aktuelle Probleme und Verbesserungsmöglichkeiten liegen und welche Rolle die Bibliothek bei der Literaturversorgung spielen sollte.

Im Workshop sollten beispielsweise Antworten auf folgende Fragen erarbeitet werden: Wo besteht Bedarf für die Neuentwicklung von innovativen Angeboten? Welche Teildisziplinen der Biologie benötigen gedruckte Literatur (heute/in den nächsten 3 – 6 Jahren), welche Teildisziplinen können auf gedruckte Literatur mittlerweile weitestgehend verzichten? Wie kann überregionale Verfügbarkeit wissenschaftsfreundlich gewährleistet werden? Welche Ressourcen/Medien, die i. d. R. nicht vor Ort vorhanden sind, wären für eine überregionale Lizenzierung relevant?

Den Wissenschaftlern wird mit dem Workshop eine Möglichkeit geboten, bei der Neugestaltung der überregionalen Angebote mitzuwirken und damit zur mittel- und langfristigen Verbesserung ihrer eigenen Literatur- und Informationsversorgung beitragen. Weitere Informationen unter: http://www.vifabio.de/about/files/news_SSGbio_2014_1_de.pdf.

//

The University Library Frankfurt am Main is in charge of the Special Collection Biology, which is co-funded by the Deutsche Forschungsgemeinschaft (DFG), and operates vifabio. The library houses the largest collection of biological literature in Germany and supplies researchers throughout Germany, and abroad, with specialised literature via inter-library loan and document delivery services. The substantial changes brought about by the Internet are leading to new challenges for this kind of services. The present workshop, held in German language, is intended to discuss these issues with the science community, in order to identify problems and prioritize improvement opportunities, and to specify the role of the library in the supply of scientific literature and information.

The workshop is expected to develop answers to questions like the following ones: Is there a need for development of innovative services? Which subdisciplines of biology are still in need of printed literature (today, 3 years from now, 6 years from now)? Which subdisciplines can do completely without printed literature? How can nation-wide availability be ensured in a way that is most beneficial for science? Which are the most relevant electronic resources for nation-wide licensing?

Via the present workshop scientists in biodiversity research are given the opportunity to help shaping future services regarding biological literature. For further information see: http://www.vifabio.de/about/files/news_SSGbio_2014_1_de.pdf.

Session · Biogeography and Molecular Clocks

14:00

Key Note:

Genes in Space and Time: The molecular Biogeography of Europe

—

Thomas Schmitt

Biogeographie, Universität Trier, Universitätsring 15,
54296 Trier, Germany

—

Due to the rich orographic structures of Europe, a large variety of different biogeographic patterns have evolved over time. In general, three major biogeographic groups can be distinguished: Mediterranean, continental and arctic/alpine species showing rather different extant and glacial distribution patterns and diverse range dynamics. These patterns well can be understood by genetic analyses. Many species survived the glacial cold stages in Mediterranean retreats where different genetic lineages have frequently evolved. After the end of the last ice age, many of these species expanded from these retreats and four major patterns of postglacial range expansion have evolved depending whether or not the Pyrenees and / or the Alps hindered the northward expansion. These expansions are often accompanied by genetic erosions and resulted in the building-up of contact zones between lineages throughout Europe, with or without hybridisation of lineages depending on orographic structures and the mode of expansion. However, the Mediterranean retreats were not homogeneous, but often show highly relevant substructures. Species with wide trans-Palearctic distributions were often named "Siberian" elements in the past and were assumed of having expanded from eastern Palearctic refugia to Europe only during postglacial times. However, recent genetic analyses have given strong evidence for the existence of extra-Mediterranean refugia north of the typical Mediterranean retreats, in many cases in climatically buffered pockets in the cold steppe biomes of Central Europe. The geographic distribution of these refugia, often with rather limited geographic extent, can be highly diverse, but areas around the Alps, in the Carpathian region and the extra-Mediterranean part of the Balkan Peninsula are of particular importance. Boreo-montane and montane-disjunct species in some cases have similar phylogeographic patterns, but sometimes might even have been continuously distributed during glacial conditions with only postglacial disjunction and differentiation. High mountain species can also have extant occurrences in the arctic. The arctic-alpine species often have the same genetic lineage in the North and in mountain systems in the South; however, endemic lineages also can be found for some mountain systems or parts of them due to glacial isolates of these species in nearby areas. However, species today being disjunctively distributed over different mountain systems in most cases show more complex phylogeographic patterns than artic-alpine species as they in general have survived in many retreats at the mountains' foothills retreating into one (or sometimes more) adjoining maintain areas with the postglacial warming.

Sulawesi – A biogeographic melting pot

14:30

—

Björn Stelbrink[1] · Mark de Bruyn[2] · Christian Albrecht[3]
Robert Hall[4] · Thomas von Rintelen[1]
[1] Museum für Naturkunde – Leibniz Institute for Research on Evolution and Biodiversity, Berlin, Germany — [2] School of Biological Sciences, Bangor University, Bangor, UK — [3] Department of Animal Ecology and Systematics, Justus Liebig University Giessen, Giessen, Germany — [4] SE Asia Research Group, Royal Holloway University of London, UK

—

Sulawesi is the largest island in Wallacea, an area of largely oceanic islands between the continental Sunda and Sahul shelves in the Indo-Australian Archipelago. The complex palaeogeographic history of the island offers a theoretical chance for a vicariant origin of Sulawesi's taxa stemming both from the west and east. The origin of animal taxa on Sulawesi is reviewed through a meta-analysis of biogeographic studies containing dated phylogenies for these taxa. The likelihood of the island's colonization by dispersal or vicariance is discussed with respect to the island's geology, particularly the past configuration and movement of terranes and distribution of land and sea.

Our analyses support the predominantly Asian origin of Sulawesi taxa as suggested by most studies. The divergence time estimates support a vicariant origin on the island for only a few taxa, particularly those from the Australian margin. Our comparative and meta-analytic approach clearly illustrates the advantage of going beyond single-taxon studies in biogeography. The scarcity of phylogenetic and phylogeographic data for many taxa, however, underlines the need for coordinated effort to overcome potential sampling biases in that outstanding hotspot of biodiversity.

14:45

Some like it cold – hybridization in Atlantic sister species of *Terebratulina* (Brachiopoda)

Carsten Lüter · Nina Ebeling
Museum für Naturkunde, Invalidenstraße 43, 10115 Berlin, Germany

The brachiopod genus *Terebratulina* in the Atlantic is represented by the sister species *T. retusa* and *T. septentrionalis*. Whereas *T. retusa* is restricted to the NW Atlantic and the Mediterranean, *T. septentrionalis* is predominantly distributed along the North American and Canadian East coasts. Molecular clock estimates date the speciation event back to the Lower Triassic (~60 mya) (Lüter & Cohen 2002) mirroring the development of the N Atlantic through tectonic separation of N America and Europe. The two species were traditionally told apart by shell ornamental characters. However, a bunch of specimens collected in the 1940s around Iceland, where both species live in sympatry, show "chimaeric" shells and have puzzled brachiopod researchers ever since. The question was whether these chimaeras represent the "missing link" between morphotypes of a single, highly plastic species or whether they are a product of hybridization events. We investigated recent samples of *Terebratulina* from the NE and SW shelfs of Iceland. Sequence information from both nuclear and mtDNA (28S, 12S, and 16S) revealed unambiguous genetic signatures for species indentification with up to 8% sequence divergence (16S rRNA) between *T. retusa* and *T. septentrionalis*. However, these clear signatures were inconsistent with traditional morphological characters resulting in nine specimens of (genetic) *T. retusa* living in a *T. septentrionalis* shell. As this may only reflect morphological plasticity, genetic chimaeras had to be detected to proof hybridization. And indeed, two specimens showed a mitochondrial (12S, 16S) genetic signature of *T. retusa*, whereas their nuclear sequence (28S) was clearly *T. septentrionalis*, thus we were looking at hybrids resulting from a fertilization event of a *T. retusa* egg and a *T. septentrionalis* sperm. With no signs of heterozygosity in the sequences, these specimens were the results of backcrossings with a parental species, in this case *T. septentrionalis*. As both species were geographically separated during Pleistocene glaciation (Curry & Endo 1991), hybridization may have started not earlier than post-glacial warming and northbound dispersal of *T. retusa*.

References

Curry GB, Endo K (1991) Migration of brachiopod species in the North Atlantic in response to Holocene climate change. Geology **19**, 1101 – 1103.

Lüter C, Cohen BL (2002) DNA sequence evidence for speciation, paraphyly and a Mesozoic dispersal of cancellothyridid articulate brachiopods. Marine Biology **141**, 65 – 74.

15:00

Ancient biogeography and evolution of dragonflies (Odonata: Anisoptera)

—

Harald Letsch[1] · Brigitte Gottsberger[1] · Jessica Ware[2]

[1] Department of Biological Sciences, Rutgers University, Newark, NJ, 07102, USA —
[2] Department für Botanik und Biodiversitätsforschung, Universität Wien, Österreich

—

From Early Triassic to Middle Jurassic, earth land masses were united in the supercontinent Pangaea. The Late Jurassic break-up of Pangaea into Laurasia (later giving rise to North America, Europe, and Asia), and Gondwana, (later South America, Africa, India, Antarctica, and Australia) led to increased diversification and the contempory vicariant distribution of plants and animals. While the congruence of tetrapod evolution and continental fragmentation has been documented by recent phylogenetic and biogeographical studies, no work has been conducted until now to explicitly reconstruct the phylogenetic relationships and biogeography of insect groups in the context of ancient continental drift in the Mesozoic. In the present study, we want to explore the potential pangaean appearance of dragonfly families (Odonata: Anisoptera) and their subsequent diversification in concordance to continental schisms. We compiled a comprehensive molecular data set, based on eight ribosomal RNA and protein coding genes, representing all major dragonfly groups. Based on this data, tree reconstruction was conducted and divergence times of the anisopteran families were estimated. We additionally reconstructed ancestral areas to retrace their historical biogeography. Our phylogenetic reconstruction proposes Aeshnoidea as the first branch in Anisoptera and Petaluroidea as sister group to Cavilabiata, the latter being subdivided into Cordulegastroidea and Libelluloidea. Divergence time estimation clearly shows a pangaean appearance and early radiation of all anisopteran superfamilies. The reconstruction of ancestral areas suggests North America as the cradle of all Anisoptera and hot spot for the early radiation of Gomphoidea and Petaluroidea. Libelluloidea probably emerged and primary radiated in Eurasia, with subsequent independent dispersal events to the southern continents. Our results suggest a persistent yet tenuous dispersal route between Eurasia and Africa in the Lower Cretaceous.

1

Development and characterization of nuclear single copy genes for phylogenetics in *Thottea* (Aristolochiaceae)

—

Claudia Paetzold[1] · Birgit Oelschlägel[1] · Karsten Salomo[1]
Tze Leong Yao[2] · Christoph Neinhuis[1] · Stefan Wanke[1]
[1] Institut für Botanik , Technische Universität Dresden, 01062 Dresden, Germany —
[2] Forest Research Institute of Malaysia, 52100 Kuala Lumpur, Wilayah Persekutuan Kuala Lumpur, Malaysia

—

The genus *Thottea* Rotböll (Aristolochiaceae) comprises 44 species occurring in two disjunct distribution areas in southern Asia; one is Southwest India with Sri Lanka and the other Southeast Asia. A molecular phylogenetic analysis based on three chloroplast regions, revealed the genus to be monophyletic but interspecific resolution and support was not fully satisfactory. A matrix of nine concatenated chloroplast regions representing all species from the Indian diversity area contained more than 10.000 characters did also not fully support relationships on species level, as only 1.5% of characters were phylogenetically informative. Therefore we aim to employ one or more nuclear single copy gene (NSCG) region.

We propose a novel strategy to develop and characterize potential NSCG marker regions using the example of *Thottea*. In three species, *T. siliquosa* and *T. sumatrana* representing the two distributional areas and *Aristolochia fimbriata* as outgroup we sequenced 5 reported NSCGs entirely, resulting in a character matrix, which contains more than 13 kb. We characterized these genes with respect to number and length of exon and intron regions and rate of variable characters. The phylogenetic informativeness was profiled for each partition of the NSCGs as well as the plastid *trnK-matK-psbA* region in comparison. We exemplarily amplified a fraction of one NSCG using 34 accessions representing 16 species, to compare phylogenetic informativeness in a larger taxon set. Finally we propose a set of marker regions consisting of various intron and exon regions of these NSCGs based on their phylogenetic informativeness profiles, the ease of amplification and alignment, as well as their potential to fully resolve and support species-level relationships in the genus *Thottea* allowing addressing evolutionary biological questions in future studies.

2

A first molecular phylogeny of *Aristolochia* subgenus *Pararistolochia* (Aristolochiaceae) with special focus on the Australasian species

Katja Buchwalder [1] · Marie-Stéphanie Samain [2] · Garry Sankowsky [3]
Christoph Neinhuis [1] · Stefan Wanke [1]
[1] Institut für Botanik , Technische Universität Dresden, 01062 Dresden, Germany —
[2] Instituto de Ecología, A.C., Centro Regional del Bajío, AvenidaLázaro Cárdenas 253,
61600 Pátzcuaro, Michoacán, Mexico — [3] Australian Tropical Herbarium,
James Cook University, Cairns Campus, P.O. Box 6811, Cairns, Queensland 4870,
Australia / P.O. Box 210, Tolga, Qld 4882 Australia

The genus *Aristolochia* is subdivided into three monophyletic groups considered as subgenera, namely *Isotrema*, *Pararistolochia*, and *Aristolochia*. *Aristolochia* subgenus *Pararistolochia* currently comprises 35 species including four subspecies, occurring in Africa and Australasia. The two disjunct distribution areas harbor 12 species in tropical central and western Africa, and 23 species in Australasia, in particular New Guinea and tropical Australia (Queensland). We present the first molecular phylogeny based on the plastid encoded *trn*K-*mat*K-*psb*A region (3000 bp). The species representing the main biogeographic entities are both monophyletic. The sampling is particularly strong with respect to the Australian taxa. All but one of the Australian species are monophyletic. *Aristolochiadeltantha* is parapyletic with a disjunct distribution in Queensland (extended the Daintree National Park versus the Girringun and the Paluma Range National Park).

3

A new set of nuclear SSR markers in *Macaranga gigantea* and *M. pearsonii* (Euphorbiaceae) derived from 454 pyrosequencing

Sarah Schüssler · Daniela Guicking · Kurt Weising
Institute of Biology, University of Kassel, Heinrich-Plett-Str. 40, 34132 Kassel, Germany

SSRs are the most popular makers in population genetic studies, but so far only few SSR markers have been reported for the palaeotropical pioneer tree genus *Macaranga* (Euphorbiaceae) by enrichment cloning (Guicking et al. 2006; Baier et al. 2009). Here we present the isolation and characterization of 20 new SSR markers by exploiting 454 pyrosequencing data from *M. gigantea* and *M. pearsonii*, both belonging to section *Pruinosae*.

A total of 956 perfect di- to hexanucleotide repeats were found in 42.700 reads of *M. gigantea*, and primer pairs could be designed for 763 loci. In *M. pearsonii*, 784 perfect di- to hexanucleotide repeats were found in 30.522 reads, and primer pairs could be designed for 607 loci. For both species, an abundance of one SSR per 8.4 kb was determined. The statistical analysis of the 454-data revealed that the $(AG)_n$ motif is less frequent in both studied species than the $(AC)_n$-motif, an observation that is uncommon in plants. The dominant SSR motifs in both *Macaranga* species consisted of AT-rich repeats.

Ten loci from each species were exemplarily chosen for further study, and six SSR markers (two from *M. pearsonii* and four from *M. gigantea*) proved to be polymorphic in two test populations from each of the two studied species. In *M. pearsonii*, allele numbers at these loci ranged from 4 – 15 and in *M. gigantea* from 2 – 9 .

Average values of observed and expected heterozygosities were 0,74 and 0,69 for *M. pearsonii* and 0,47 and 0,46 for *M. gigantea.* A reciprocal comparison showed that all six loci were more variable in *M. pearsonii* than in *M. gigantea*, indicating the absence of an ascertainment bias. The newly established SSR loci will provide a rich source for our ongoing population genetic studies of various *Macaranga* species.

Guicking D., Rana T.S., Blattner F.R., Weising K. (2006) Microsatellite markers for the palaeotropic pioneer tree genus *Macaranga* (Euphorbiaceae) and their cross-species transferability. Mol. Ecol. Notes **6**: 245 – 248.

References

Baier C., Guicking D., Prinz K., Fey-Wagner C., Wöhrmann T., Weising K., Debener T., Schie S., Blattner F. (2009) Isolation and characterization of eleven new microsatellite markers for *Macaranga* (Euphorbiaceae). Mol Ecol. Resources **9**: 1049 – 1052.

4

Phylogeographic patterns within the pioneer tree genus *Macaranga* (Euphorbiaceae) in Sumatra and Borneo, Southeast Asia

MALTE ZIRPEL · DANIELA GUICKING · KURT WEISING

Institute of Biology, University of Kassel, Heinrich-Plett-Str. 40, 34132 Kassel, Germany

The palaeotropical genus *Macaranga* (Euphorbiaceae) comprises approximately 300 species, many of which are important pioneer trees in lowland dipterocarp forests of South East Asia. About 30 species are obligate myrmecophytes. A diversity hotspot of *Macaranga* is in Sundaland (including the islands of Java, Sumatra, Borneo, and the Malay Peninsula), a region with a very complex and young palaeogeography. We are studying the phylogeography of *Macaranga* in Sundaland with particular emphasis on Sumatra and Borneo. Here we present results obtained with eleven new chloroplast simple sequence repeat (cpSSR) markers that were established from 454 pyrosequencing data of *Macaranga gigantea*. The markers proved to be highly variable, showing up to eight alleles within a single species. First results from *M. gigantea* suggest that chloroplast haplotypes differ strongly between northern Borneo, southern Borneo and the Malay Peninsula, whereas populations from Sumatra and the small island of Bangka are genetically closely related to southern Bornean populations. We are currently extending our studies to additional *Macaranga* species present in the region to find out whether this pattern is typical for *Macaranga*, or whether it varies between species.

Bromelioideae – phylogenetic relationships and evolution 5

—

Sascha Heller[1] · Elton Leme[2] · Juraj Paule[1] · Rafaela Forzza[3] · Ana Maria Benko-Iseppon[4] · Georg Zizka[1]

[1] Senckenberg Research Institute and Natural History Museum Frankfurt, Senckenberganlage 25, 60325 Frankfurt am Main, Germany · Goethe-University, Department of Ecology, Evolution and Diversity, Max-von-Laue-Str. 13, 60439 Frankfurt am Main, Germany · Biodiversity and Climate Research Centre (BiK-F), Senckenberganlage 25, 60325 Frankfurt am Main, Germany — [2] Herbarium Bradeanum, Rio de Janeiro, RJ, Brazil — [3] Botanical Garden of Rio de Janeiro, RJ, Brazil — [4] Genetics Dep., Universidade Federal de Pernambuco, Recife, PE, Brazil

—

The subfamily Bromelioideae comprises more than 900 species in 33 genera and is the second largest subfamily of Bromeliaceae (Poales). In the last years several molecular phylogenetic analyses showed that many bromeliad genera, originally defined on the basis of morphological characters, are para- or polyphyletic. Furthermore, patterns and processes behind the bromelioid biodiversity are only poorly understood. In our attempt, using taxonomically comprehensive sampling and both nuclear and plastid DNA markers, we aim to identify monophyletic groups, contribute to a new generic classification and to elucidate the evolutionary history of the Bromelioideae.

Results from our molecular analyses including nearly 400 Bromelioideae species are presented. The special focus is on the core Bromelioideae, which are represented with 350 species in the study (app. 50% of the total of 675 spp.).

6 Tillandsia usneoides – why is the species morphologically so variable?

Sascha Heller · Juraj Paule · Georg Zizka
Senckenberg Research Institute and Natural History Museum Frankfurt, Senckenberganlage 25, 60325 Frankfurt am Main, Germany — Goethe-University, Department of Ecology, Evolution and Diversity, Max-von-Laue-Str. 13, 60439 Frankfurt am Main, Germany — Biodiversity and Climate Research Centre (BiK-F), Senckenberganlage 25, 60325 Frankfurt am Main, Germany

Tillandsia usneoides is the most widely distributed species of the family Bromeliaceae (Poales). It ranges from the southeastern United States to Argentina and Chile. Tillandsia usneoides grows epiphytic and is dispersed by seeds as well as by fragments of the plant. Within the species striking morphological differences can be observed as far as size characters are concerned. Morphotypes have shown to be stable in cultivation while growing under the same conditions. To investigate possible reasons for the variation we measured the relative genome size of 75 specimens covering the whole distribution range and combined this information with morphological, distribution and climate data.

7 Molecular phylogenetic structure of grass subfamily Pooideae based on a nuclear single copy gene

Anne Blaner · Julia Schneider · Martin Röser
Institute of Biology, Department of Systematic Botany, Martin Luther University Halle-Wittenberg, Neuwerk 21, 06108 Halle (Saale), Germany

The grass subfamily Pooideae was studied using newly obtained DNA sequence information from the nuclear single copy gene region topoisomerase VI (Topo6) exon 8 – 13 in a sample of 44 taxa covering all of its tribes. *Fargesia nitida* and *Pleioblastus fortunei* from subfamily Bambusoideae were used as outgroup. Phylogenetic analyses using MrBayes v.3.1.2 (Bayesian inference), raxmlGUI (Maximum Likelihood) and PAUP* 4.0b10 (Maximum Parsimony) all yielded the same tree topology with several well-supported lineages. *Brachyelytrum* (Brachyelytreae) formed the earliest diverging lineage of subfamily Pooideae, followed by tribe Nardeae (with subtribes Lygeinae and Nardinae) as sister to the remaining species. The other taxa divided into three groups: (1) the genera of tribe Duthieeae with some of the *Trikeraia pappiformis* and *Ampelodesmos mauritanicus* clone sequences; (2) *Diarrhena* plus tribes Meliceae (with Brylkiniinae and Melicinae), Phaenospermatae, and Stipeae (including the remaining clone sequences of *A. mauritanicus* and *T. pappiformis*); and (3) the Aveneae/Poeae tribe complex, tribes Hordeeae (with Brominae, Hordeinae and Littledaleinae), Brachypodieae, and *Neomolinia*. The tribes and subtribes are generally highly supported, in accordance with previous investigations based on chloroplast and repetitive nuclear ITS DNA sequences (cf. Schneider et al. 2009, 2011). The most interesting results were the divergent positions of some clone sequences of the stipoid taxa *Ampelodesmos mauritanicus* and *Trikeraia pappiformis*. *Ampelodesmos mauritanicus* was previous classified as a monotypic tribe Ampelodesmeae, under tribe Poeae or under a separate subfamily Stipoideae. This genus differs mainly from the traditional Stipeae by spikelets with several instead of single florets (cf. Schneider et al. 2009) and may appear closely related to the early diverging lineages of Pooideae. Cai and Wu (1997) already considered *Trikeraia pappiformis* closely allied with *Stephanachne* (especially *S. nigrescens* as corroborated by our results) based on morphological characters. This suggests that *A. mauritanicus* and *T. pappiformis* could have hybrid origin.

References

Cai, L.-B. & Wu, Z.-L. 1997: Studies on the biosystematic relationships and geographic distribution of *Trikeraia* Bor and *Stephanachne* Keng. Bulletin of Botanical Research (Zhiwu-yanjiu: jikan) **17**: 380 – 388.

Schneider, J., Döring, E., Hilu, K. W. & Röser, M. 2009: Phylogenetic structure of the grass subfamily Pooideae based on comparison of plastid *mat*K gene- 3'*trn*K exon and nuclear ITS sequences. Taxon **58**: 404 – 424.

Schneider, J., Winterfeld, G., Hoffmann, M. H., & Röser, M. 2011: Duthieeae, a new tribe of grasses (Poaceae) identified among the early diverging lineages of subfamily Pooideae: molecular phylogenetics, morphological delineation, cytogenetics, and biogeography. Systematics and Biodiversity **9**: 27 – 44.

8

Phylogeny and evolution of the mistletoe genus *Viscum*

—

Karola Maul[1] · Michael Krug[1] · Daniel L. Nickrent[2] · Kai F. Müller[3]
Dietmar Quandt[1] · Susann Wicke[3]
[1] Nees Institute for Biodiversity of Plants, University of Bonn, Meckenheimer Allee 170, 53115 Bonn, Germany — [2] Department of Plant Biology, Southern Illinois University, Carbondale, IL 62901-6509, USA — [3] Institute for Evolution and Biodiversity, University of Münster, Hüfferstr. 1, 48149 Münster, Germany

—

The mistletoe genus *Viscum* (Viscaceae, Santalales) comprises between 70 and 100 obligate parasitic plants in Europe, Africa, Asia, and Australia. *Viscum* species are aerial parasites, which retain the ability to photosynthesize to a greater or lesser extent while feeding on a wide range of woody hosts. The genus also includes an endoparasitic form, *V. minimum*, which infests succulent *Euphorbia* species in Southern Africa. Several classifications were proposed for *Viscum* during the past century based on morphological characters, but those different taxonomic arrangements have not been tested using a molecular phylogenetic approach so far. Here, we present the first molecular phylogeny of *Viscum* based on the nuclear ribosomal ITS regions. Our final dataset comprises a representative sampling from the major distribution areas of the genus, allowing us to reconstruct the colonization history and its approximate timing. Our results clearly show that clades are more consistent with the distribution of species they contain than with sections and subsections of previous classification systems. Using Bayesian and likelihood approaches, we find, among others, that the colonization of continental Asia has likely occurred twice from Africa, where the genus originated about 98.6 mya. Europe, Northern Africa and Australasia were probably colonized between 91.25 and 59.96 mya. Furthermore, our results show that e.g. monoecy and also the reduction of leaves up to their complete loss evolved multiple times within *Viscum*, the latter suggesting a great diversity of trophic stages with different dependencies and specializations on host plants.

Salvia s. l. on trial – reassessing the taxonomic rank of sect. *Eremosphace* Bunge

Maria Will · Regine Classen-Bockhoff
Institut für Spezielle Botanik und Botanischer Garten,
Johannes Gutenberg Universität Mainz, Germany

Large genera were repeatedly found to be non-monophyletic. This is also true for *Salvia* L., the formerly largest genus in the mint family (Lamiaceae). Its latest revision dates back to the 19th century when species were placed in a sectional system based on morphology. However, since that time many new species have been described.

Based on molecular data it is evident that almost all of these sections are highly artificial. One of the well-supported clades within *Salvia* s. l. is the *S. aegyptiaca*-group (Clade III-A). Most species nesting in this clade were traditionally placed in *Salvia* sect. *Notiosphace* Benth. and sect. *Eremosphace* Bunge.

However, molecular data, morphology, and distribution provide a good background to split this particular group from *Salvia* s. l. Fourteen species were recognized in the new genus *Eremosphace* (Bunge) M. Will & Class.-Bockh. stat. nov. They are adapted to desert-like habitats in the Saharo-Sindian region. Furthermore, they differ from other representatives of *Salvia* s. l. in a certain character syndrome: growth as dwarf shrubs, having small, often few xeromorphic leaves, and minute to small flowers.

This study also provides the so far first molecular evidence for hybridization in Old World *Salvia* s. l. and *Eremosphace*.

10

A new molecular-based classification of the pantropical Ochnaceae s. l. (Malpighiales) based on five DNA sequence regions

—

Julio V. Schneider [1,2,3] · Pulcherie Bissiengou [4,7,8]
Maria do Carmo E. Amaral [5] · Ali Tahir [1,2,3] · Michael F. Fay [6]
Marco Thines [1,2,3] · Marc S.M. Sosef [4,7] · Georg Zizka [1,2,3] · Lars W. Chatrou [7]
[1] Senckenberg Research Institute and Natural History Museum Frankfurt, Senckenberganlage 25, 60325 Frankfurt am Main, Germany — [2] Goethe-University, Department of Ecology, Evolution and Diversity, Max-von-Laue-Str. 13, 60439 Frankfurt am Main, Germany — [3] Biodiversity and Climate Research Centre (BiK-F), Senckenberganlage 25, 60325 Frankfurt am Main, Germany — [4] Naturalis Biodiversity Center (section NHN) – Wageningen branch, Wageningen University, Gen. Foulkesweg 37, NL-6703 BL Wageningen, The Netherlands — [5] Department of Plant Biology, Institute of Biology, CP 6109, University of Campinas – UNICAMP, 13083-970, Campinas, SP, Brazil — [6] Jodrell Laboratory, Royal Botanic Gardens Kew, Richmond, Surrey, TW9 3DS, United Kingdom — [7] Wageningen University, Biosystematics group, Droevendaalsesteeg 1, NL-6708 PB Wageningen, the Netherlands — [8] Herbier National du Gabon (IPHAMETRA-CENAREST), B.P. 1156 Libreville, Gabon

—

Ochnaceae (Malpighiales) are a pantropical family of 32 genera and about 550 species of trees, shrubs or, rarely, herbaceous plants. Infrafamilial classification and relationships have been controversial partially due to the lack of a robust phylogenetic framework. Including 30 genera and DNA sequence data for five DNA regions (ITS, *matK*, *ndhF*, *rbcL*, *trnL-F*), we provide for the first time a nearly complete molecular phylogenetic analysis of Ochnaceae s. l. resolving most of the family's phylogenetic backbone. In our new classification, Ochnaceae s. l. are subdivided into the pantropical Ochnoideae, the neotropical Quiinoideae and the monotypic Medusagynoideae, an endemic of the Seychelles. Our data support a monophyletic Ochneae, but Sauvagesieae in the traditional circumscription are paraphyletic because *Testulea* emerges as sister to the rest of Ochnoideae, and the next clade shows *Luxemburgia* + *Philacra* as sister group to the remaining Ochnoideae. Therefore, we classify Luxemburgieae and Testuleeae as new tribes. The African genus *Lophira* emerges as sister to all other Ochneae. Thus, endosperm-free seeds and ovules with completely, partly or for most of their length united integuments are characters that unite all members of that tribe. The relationships within its largest clade, Ochnineae (former Ochneae), are poorly resolved, but former Ochninae (*Brackenridgea*, *Ochna*) are polyphyletic. Within Sauvagesieae, the genus *Sauvagesia* in its broad circumscription is polyphyletic. Within Quiinoideae, in contrast to former phylogenetic hypotheses, *Lacunaria* and *Touroulia* form a clade sister to *Quiina*.

11

Stachys gaziantepensis (Lamiaceae), a new species from South Anatolia, Turkey

—

Muhittin Dinç · Süleyman Doğu
Necmettin Erbakan University, Faculty of Education, Department of Biology, 42090 Meram, Konya, Turkey

—

Stachys gaziantepensis M.Dinç & S.Doğu sp. nov. is described and illustrated. It exhibits general features of sect. *Infrarosularis*. However, it differs from the other members of the section from Turkey by its slender appearance. In addition, while the other species of the section grow on limestone or serpentine rocks, the new species grows on marble rocks. Diagnostic characters of *Stachys gaziantepensis* from sect. *Infrarosularis* species, especially from its closest relative *S. pumila* and *S. choruhensis* with extreme distribution, are discussed. The accompanying taxa within its habitat are given. The conservation status of the new species is also evaluated based on population density and possible threats within presently known locality.

12

Some taxonomic notes on *Genista Sessilifolia* Complex (Fabaceaw) in Turkey

—

Muhittin Dinç · Yavuz Bagci[2] · Ahmet Duran[1]
[1] Dept. of Biology, Faculty of Education, Selçuk Univ., Meram, 42090 Konya, Turkey —
[2] Dept. of Biology, Faculty of Science, Selçuk Univ., Campus, 42031 Konya, Turkey

—

A morphological study on populations of *Genista sessilifolia* DC and G. *aucheri* Boiss. from *Genista* sect. *Spartocarpus* Spach in Turkey has been undertaken, based on herbarium specimens and field observations. We conclude that *G. aucheri* should be treated as a synonym of *G. sessilifolia*. However, a new subspecies of *G. sessilifolia*, *G. sessilifolia* subsp. *unalii* M. Dinç & Y. Bağcı, is described and illustrated. The new subspecies differs from *G. sessilifolia* subsp. *sessilifolia* by having short, 1-2-flowered or sterile stems ending in leafy shoots (not long and many flowered ending in an inflorescence), leaves with densely hairy upper surfaces (not glabrous or sparsely hairy). The two taxa also have allopatric distributions, with *G. sessilifolia* subsp. *sessilifolia* distributed in the central and northern parts of east Anatolia, whereas *G. sessilifolia* subsp. *unalii* is restricted to the transition zone of central and South Anatolia.

13

Sodium nitroprusside (SNP): an effective protectant on antioxidant activity in maize roots subjected to polyethylene glycol-induced osmotic stress

Evren Yildiztugay[1] · Ceyda Ozfidan-Konakci[2] · Mustafa Kucukoduk[1]
Seyit Ahmet Tekis[1]

[1] Selcuk University, Faculty of Science, Department of Biology, 42250 Selcuklu, Konya, Turkey — [2] Necmettin Erbakan University, Faculty of Science, Department of Molecular Biology and Genetics, 42090, Meram, Konya, Turkey

The present study was design to examine whether exogenous sodium nitroprusside (SNP) supplementation has any ameliorating action against PEG-induced osmotic stress in Zea mays L. cv FRB73 roots. 20% and 40% polyethylene glycol (PEG6000; – 0.5 MPa and – 1.76 MPa, respectively) treatment alone or in combination with 150 and 300 µM SNP was given to hydroponically grown maize roots for 72 h (hours). Although only catalase (CAT) activity increased when maize roots are exposed to PEG-induced osmotic stress, induction of this antioxidant enzyme was inadequate to detoxify extreme levels of reactive oxygen species (ROS), as evident by growth, water content, superoxide anion radical ($O_2^{\cdot -}$), hydroxyl radical ($OH^{\cdot}$) scavenging activity and TBARS content. However, supplementation of SNP with PEG significantly could alleviate stress-induced damage through effectively water management and enhancing levels of antioxidant defense markers including the enzymatic/non-enzymatic systems. Exogenously applied SNP under stress resulted in an up-regulation of activities of glutathione peroxidase (GPX), glutathione S-transferase (GST), and ascorbate peroxidase (APX), glutathione reductase (GR), total ascorbate and glutathione contents involved in ascorbate-glutathione cycle. On the other hand, growth rate, osmotic potential, CAT, APX, GR, GPX increased in maize roots exposed to both concentrations of SNP alone, but activities of monodehydroascorbate reductase (MDHAR) and dehydroascorbate reductase (DHAR) decreased. Based on the above results, an exogenous supply of both 150 and 300 µM SNP to maize roots protected from PEG-induced toxicity. The present study provides new insights into the mechanisms of SNP (NO donor) amelioration of PEG-induced osmotic stress damages in hydroponically grown maize roots.

Exogenously applied gallic acid in the total antioxidant capacity: Ameliorating effects in leaves of Oryza sativa versus deleterious effects of salt and osmotic stresses

CEYDA OZFIDAN-KONAKCI [1] · EVREN YILDIZTUGAY [2] · MUSTAFA KUCUKODUK [2]

[1] Necmettin Erbakan University, Faculty of Science, Department of Molecular Biology and Genetics, 42090, Meram, Konya, Turkey — [2] Selcuk University, Faculty of Science, Department of Biology, 42250, Selcuklu, Konya, Turkey

The aim of our study was to examine whether exogenously applied with gallic acid (GA) enhances the tolerance of two rice cultivars to polyethylene glycol(PEG)-induced osmotic stress or salt (NaCl) stress. After two Oryza sativa cultivars, a salt and drought-tolerant cultivar Pokkali and a sensitive cultivar IR-28, were hydroponically grown for three weeks, seedlings were treated with GA (0.75 and 1.5mM), 120mM NaCl and 20% PEG-6000 producing the same osmotic potential(-0.5MPa) or without GA and stress (control) for 72 hours(h). Salt and PEG decreased the maximum photochemical efficiency(F_v/F_m), the photochemical quenching coefficient(qP) and the actual quantum yield(Φ_{PSII}), even more pronounced at NaCl in IR-28, thereby inhibiting photosynthetic activity. PEG had greater reduction in growth rate(RGR) and relative water content(RWC) than at NaCl in both cultivars. Also, the most notable increase in lipid peroxidation(TBARS) and hydrogen peroxide(H_2O_2) content was observed with PEG compared with that under NaCl. Activities of superoxide dismutase(SOD), ascorbate peroxidase(APX) and glutathione reductase(GR) in Pokkali and catalase(CAT) and peroxidase(POX) in IR-28 were induced to a greater extent by PEG. The sensitivity of plants to stress was higher in IR-28 than in Pokkali. Also, comparing the injury between the NaCl and PEG stresses, it was greater under PEG-mediated osmotic stress than NaCl. However, compared with the stress-treated plants alone, in NaCl-stressed leaves of Pokkali, added GA significantly decreased H_2O_2 and TBARS content, and enhanced the activities of SOD, CAT, POX and APX as well as increasing of RGR, osmotic potential(Ψ_P), F_v/F_m and proline (Pro). GA strongly suppressed H_2O_2 and TBARS content, up-regulated SOD and APX activities and increased RGR, RWC and Ψ_P in PEG-treated IR-28 cultivars. It could be concluded that the both GA concentrations alleviate NaCl and PEG toxicity not at the level of antioxidant defense by mitigating stress toxicity, but by efficient use of water management in Pokkali and IR-28, respectively.

15

Effects of nitric oxide (as sodium nitroprusside) on the osmotic stress tolerance associated with photosynthetic capacity and water management in hydroponically grown maize leaves

Yagmur Duran[1] · Mustafa Kucukoduk[1] · Evren Yildiztugay[1] · Ceyda Ozfidan-Konakci[2]

[1] Selcuk University, Faculty of Science, Department of Biology, 42250, Selcuklu, Konya, Turkey — [2] Necmettin Erbakan University, Faculty of Science, Department of Biology, 42090, Meram, Konya, Turkey

The present study was design to examine whether exogenous sodium nitroprusside (SNP) supplementation had any ameliorating action against PEG-induced osmotic stress in Zea mays L. cv FRB73 leaves. 20% and 40% polyethylene glycol (PEG6000; – 0.5 MPa and – 1.76 MPa, respectively) treatment alone or in combination with 150 and 300 µM SNP was given to hydroponically grown maize leaves for 72 h (hours). PEG stress decreased growth (fresh and dry weight and length of maize shoots), relative growth rate (RGR), water content (RWC), leaf osmotic potential (Y_{Π}) and the maximum photochemical efficiency(F_v/F_m), the photochemical quenching coefficient(qP) and the actual quantum yield(Φ_{PSII}), and more suppressed them at 40% PEG. Also, stress caused a greater induction in proline content (Pro) at 40% PEG (19 fold) than at 20% PEG (7 fold). However, supplementation of SNP with PEG significantly could alleviate stress-induced damage through effectively water management and enhancing growth and photosynthetic efficiency. Exogenously applied SNP under stress resulted an increase in RGR, RWC, Y_{Π}, F_v/F_m, qP and Φ_{PSII}. On the other hand, RGR, RWC, Y_{Π}, Pro and F_v/F_m did not change in maize leaves exposed to both concentrations of SNP alone. Based on the above results, an exogenous supply of both 150 and 300 µM SNP to maize leaves protected from PEG-induced toxicity, especially in 150 µM SNP-treated plants under low PEG concentration. The present study provides new insights into the mechanisms of SNP amelioration of PEG-induced osmotic stress damages in hydroponically grown maize leaves.

16

Reproductive strategies of the alpine apomictic plant *Ranunculus kuepferi* under different ecological conditions

Christoph Carl-Friedrich Schinkel [1] · Stefan Dullinger [2] · Simone Klatt [1] · Bernhard Kirchheimer [2] · Elvira Hörandl [1]
[1] University of Goettingen, Albrecht-von-Haller Institute for Plant Sciences, Department of Systematic Botany — [2] University of Vienna, Faculty Centre of Biodiversity, Department of Conservation Biology

In marginal habitats such as higher latitudes and altitudes asexual organisms have a larger distribution range than their sexual relatives, known as geographical parthenogenesis (GP). It is assumed that asexuals have an increased colonizing ability due to uniparental reproduction. The frozen niche variation (FNV) model predicts broader niches of asexual populations, as niche specialization of different genotypes, inherited from the sexual progenitors, enable a more efficient exploitation of the available resource space. Effects of the colder climate in the northern part of the Alps may also have a direct influence on unreduced gamete formation and the quantitative expression of apomixis.

Empirical studies on alpine plants are largely missing. We test hypotheses for GP in the alpine plant species *Ranunculus kuepferi*. To provide some insights into the variation in reproductive modes and the facultative expression of apomixis in wild populations, we conducted a quantitative study on frequencies of apomixis with Flow Cytometric Seed Screening.

First results show, that tetraploids are more widespread than diploids, despite a overall lower reproductive fitness (seed set). An observed high amount of facultative sexuality in tetraploid apomicts may maintain high levels of genetic variation within polyploid populations, thus allowing for a better adaptation and a higher flexibility in the reproduction system. Some tetraploids, however, are sexual. Furthermore, also some diploid individuals show apomictic seed formation, while ploidy levels remain stable. This indicates multiple pathways of shifts to apomixis, and a high flexibility in reproductive strategies.

In the future, rigorous testing of the influence of temperature in climate chambers compared to controls will be conducted to test direct environmental influence on the quantitative expression of apomixis and alternative meiotic development.

Combined with a niche modeling study based on comprehensive ecological data collected in the field, results will enable us to develop a comprehensive and predictive ecological model for GP.

17

Foliar plasticity and nutrient contents of beech (*Fagus sylvatica* L.) in advance regeneration on strongly acidic soils with chronic N deposition

O. T. Bouman

Dept. of Biology, Cape Breton University, Canada

The ontogenetic capacity of plant species to adjust their morphology and physiology, often referred to as plasticity, enables them to grow and survive in a changing environment. The deciduous beech (*Fagus sylvatica* L.) is well known for its ability to persist at the sapling stage for many years in deep shade until canopy openings allow for recruitment into the tree stratum. The persistence has often been ascribed to morphological plasticity most notably horizontal spreading of the sapling crown and the differentiation of sun and shade leaves. There is also a long standing notion in the plant ecological literature that fertile soils enhance sapling survival in shade. Experimental evidence of coordinated responses by morphological and physiological leaf traits to changing light exposure and soil condition is still limited. In a non-destructive field experiment, advance regeneration of beech was tested for morphological parameters, total chlorophyll concentration, and foliar nutrients in southern Saarland, Germany. Three sapling height classes were sampled beneath tall deciduous canopy of three stands on Triassic sandstone with strongly acidified soils and chronic N deposition and a fourth stand on Triassic limestone was included for contrasting biogeochemical site conditions. Within a limited size range of beech saplings, the experiment revealed allometric ontogeny gradually changing shoot morphology; significant effects of crown position on leaf traits; linear relationship between structural and chemical determinants of photosynthetic capacity; and, no discernible effects of a distinct biogeochemical contrast on foliar concentration of nitrogen and magnesium irrespective of sapling size.

18

Morphology and vasculature of inflorescence tips in Potamogetonaceae (Alismatales)

Ingrid E. Lock · Dmitry D. Sokoloff · Margarita V. Remizowa

Moscow State University, Moscow, Russia

Recent studies found morphogenetic plasticity of inflorescence tips in several basal monocots, including Potamogetonaceae. Spikes of Potamogeton spontaneously produce terminal flower-like structures with unstable morphology that sometimes can be interpreted as pseudanthia. This phenomenon has been explored in two species with small flower-subtending bracts. We increased taxon sampling to investigate variations of inflorescence tip morphology and vascular anatomy in different genera of Potamogetonaceae (Potamogeton, Stuckenia, Groenlandia). In Potamogeton, we studied species with different flower number per inflorescence and with flower-subtending bracts either present or absent. In Potamogeton and Stuckenia, certain plants produce a terminal flower-like structure at the inflorescence tips while terminal structures were not found in Groenlandia. Our study shows presence of conspicuous wide flower-subtending bracts in Stuckenia pectinata, though they consist of two cell layers and lack vascular supply like the small bracts in Potamogeton. In S. pectinata, when terminal flower-like structure is absent, inflorescences always develop a tubular structure with serrate edges (a fusion product of uppermost bracts that do not subtend flowers). We found differences in vasculature of inflorescence axis between many-flowered and few-flowered species of Potamogetonaceae. In many-flowered Potamogeton praelongus, inflorescence axis contains 4-8 vascular bundles. Below a node, each bundle divides into three bundles: central bundle supplies a lateral flower and two bundles fuse with similar lateral braches of adjacent bundles. Terminal flower or flower-like structure is usually supplied by several (rather than one) bundles derived the bundles of the inflorescence axis. In few-flowered species (Potamogeton crispus and Groenlandia densa), bundles of inflorescence axis divide several times and form a ring from which organs of the uppermost (or the only two) flowers are supplied individually. In the absence of a single vascular trace, the lateral flowers of the few-flowered species resemble the terminal flowers (or flower-like structures) of the many-flowered species. Stuckenia has a more reduced vascular system in the inflorescence axis. It consists of a concentric vascular strand with 1 – 2 xylem elements in the centre. Lateral flowers are supplied by direct radial branches of this strand. In inflorescence vasculature, Stuckenia resembles Ruppia (Ruppiaceae). Patterns of inflorescence vasculature do not depend on presence or absence and size of flower-subtending bracts.

The work is supported by RFBR, project № 14-04-31271.

19

When ploidy meets nuclear gene data: a textbook example of allotetraploidy in the genus *Hepatica* (Ranunculaceae)

—

Kunigunda Macalik[1] · László Bartha[2] · Lujza Keresztes[1]

[1] Hungarian Department of Biology and Ecology, Babeş-Bolyai University, Cluj-Napoca, Romania — [2] Institute for Interdisciplinary Research in Bio-Nano Sciences, Babeş-Bolyai University, Cluj-Napoca, Romania

—

Despite its low species number the genus *Hepatica* presents an interesting geographic distribution characterised by intercontinental and deep inner continental disjunctions. Taxonomic status of several *Hepatica* species is still under dispute. They are, however, well characterised as far as their ploidy level and morphological circumscription is considered. Traditionally two morphological groups were recognised within the genus: the one with entirely lobed leaves and the other with crenate leaves. The crenate leaved tetraploid (2n = 28) species *Hepatica transsilvanica* Fuss., *Hepatica yamatutae* Nakai and *Hepatica henryi* Steward were traditionally regarded as hybrids of the *Hepatica nobilis* Schreb. (2n = 14, leaves entirely lobed) and *Hepatica falconeri* Steward (2n = 14, crenate leaved). Their allopolyploid origin, however, has never been tested using adequate methods (e.g. ones implying low-copy nuclear gene analysis). We here tested the hybrid origin of the Romanian (Carpathian) endemic *H. transsilvanica* by sequencing a region of the low-copy nuclear gene At103 in *H. nobilis*, *H. transsilvanica* and a recently collected Kirghizian sample of *H. falconeri*. Direct sequencing of the applied marker was straightforward and showed no length polymorphism between taxa. Sequence of *H. transsilvanica* contained six unambiguous double peaks (codified as R-Y-R-Y-S-Y) out of which four resulted from the combination of the corresponding nucleotides from *H. nobilis* and *H. falconeri* At103 sequences. Allotetraploid origin of *H. transsilvanica* is thus evidenced here for the first time using molecular methods. Furthermore, we provide a platform on which the hybrid origin of the rest of polyploid species can be tested. This work was supported by a grant of the Ministry of National Education, CNCS – UEFISCDI, project number PN-II-ID-PCE-2012-4-0595.

Niche conservatism and potential future expansion of *Eulophia graminea*

—

Marta Kolanowska
University of Gdańsk, ul. Wita Stwosza 59, 80-308 Gdańsk, Poland

—

Eulophia graminea Lindl. is an Asian orchid recently naturalized in Florida, Australia and South Africa. The native populations of this terrestrial herb occupy coast beach vegetation, grassland and open areas at low elevations from Sri Lanka and India to China, Japanese Ryuku Islands, and throughout most of Southeast Asia. In the non-native range the species was find in pine rocklands, mulch and disturbed sites (O'Connor et al. 2006; Pemberton et al. 2013). The aim of the research was to evaluate the niches similarity between native and invasive populations of *E. graminea* in the light of the recent studies on the phylogenetic niche conservatism of expansive plants.

The maximum entropy niche modeling was used to create niche distribution models based on Asian and non-native populations occurrence records. As an input data 19 climatic variables (Hijmans et al. 2005) and the digital elevation model were used. The relative contributions of the environmental factors to the MaxEnt models were calculated. The differences between the niches occupied by the native and invasive populations were evaluated using the niche identity test indexes: Schoener's D and I statistic (Warren et al. 2010). To estimate the future changes in the distribution of *E. graminea* the future climatic projections related to a hypothetical climate change with three various scenarios (A1b, A2a and B2a) were used in MaxEnt analysis (Ramirez & Jarvis 2010).

The tests indicated relatively high similarity between the niches currently occupied by native and invasive populations (I = 0.898, D = 0.706), however, different bioclimatic factors limit their occurrence. While Asian range is determined mainly by the lowest temperature in the coldest month, the non-native distribution of *E. graminea* is altitude-related. The future climatic changes will not change significantly the potential distribution of *E. graminea* neither in its native nor invasive range.

References

Hijmans R. J., Cameron S. E., Parra J. L., Jones P.G., Jarvis A. 2005: Very high resolution interpolated climate surfaces for global land areas. International Journal of Climatology **25**: 1965 – 1978.

O'Connor M., Govender T., Jolliffe K. 2006: *Eulophia graminea* – the ET orchid. Orchids South Africa **37**: 86 – 90.

Pemberton R. W. 2013: Rapid geographic spread of the alien orchid *Eulophia graminea* in Florida. Selbyana **31**(1): 47 – 51.

Ramirez J., Jarvis A. 2010: Disaggregation of Global Circulation Model Outputs. International Center for Tropical Agriculture (CIAT); CGIAR Research Program on Climate Change, Agriculture and Food Security (CCAFS). Cali, Colombia.

Warren D. L., Glor R. E., Turelli M. 2010: ENMTools: a tool box for comparative studies of environmental niche models. Ecography **33**: 607 – 611.

21

Population genetics and conservation of *Sideroxylon canariense* (Sapotaceae) on the Canary Islands

—

Philip Testroet [1] · Dietmar Quandt [1] · Arnoldo Santos-Guerra [2]
Kai Müller [3] · Wolfram Lobin [4]

[1] Nees Institute for Biodiversity of Plants, Rheinische Friedrich-Wilhelms-Universität Bonn, MeckenheimerAllee 170, 53115 Bonn, Germany — [2] Unidad de Botánica Aplicada, InstitutoCanario de InvestigacionesAgrarias, Jardín de Aclimatación de La Orotava, Spain — [3] Institut für Evolution und Biodiversität, Universität Münster, Hüfferstr. 1, 48149 Münster — [4] Botanische Gärten der Universität Bonn, Meckenheimer Allee 170, 53115 Bonn, Germany

—

Genetic diversity patterns of different populations were studied in *Sideroxylon canariense*, a Canary Island endemic of conservation concern. The species range is composed of a number of very small and isolated populations. Genetic variation of these populations was analyzed using: (1) inter simple sequence repeats (ISSR), a common fingerprinting method in plant population genetics, and (2) nucleotide sequence analyses of the nuclear ITS region.

While no intraspecific variation was detected among the ITS sequences, the ISSR data showed a very low degree of intraspecific genetic diversity among *S. canariense* populations on the Canaries, with very few genotypes. We believe that many of the populations consist of a single individual that propagates asexually. Action is urgently required to protect and propagate the highly endangered populations.

Biogeographic and phylogenetic analysis of the tree fern family Dicksoniaceae (Cyatheales) based on four chloroplast markers (*rpl16, trnL-F, trnG-R* and *matK*)

—

S. Noben [1, 2] · A. Weigand [1] · M. Krug [1] · D. Quandt [1] · M. Lehnert [1]

1 Nees Institut für Biodiversität der Pflanzen, Universität Bonn, Meckenheimer Allee 170, 53115 Bonn, Germany — [2] Institut für Systematische Botanik, Universität Zürich, Zollikerstrasse 107, 8008 Zürich, Schweiz

—

Tree ferns of the family Dicksoniaceae (Cyatheales) are among the most impressing ferns in forests of the Southern Hemisphere. Species are quite easy to identify in the field as only few species occur sympatrically. However, they may be very difficult to differentiate in cultivation because several species originating from different continents exhibit nearly the same morphology. Although, this genus has attracted the interest of hobby gardeners and conservationists because of their primitive appearance, old age and relict distribution, surprisingly it has never been in the focus of an exhaustive phylogenetic and taxonomic analysis. Thus we performed a global phylogeny of all morphologically distinguishable taxa to clarify species limits, to outline character evolution and to investigate the migration pattern of the species, with the scope to better understand the evolution of this economically and historically important genus.

Our results using four plastid markers (*rpl16 G2, trnL-F G1* & *IGS, trnG-R G2* and xy-*matK IGS*) support the monophyly of the Dicksoniaceae as well as the morphological recognized genera *Dicksonia* (distributed in the southern hemisphere), *Lophosoria* (exclusively distributed in the Neotropics) and *Calochlaena* (exclusively distributed in the Palaeotropics). The genus *Lophosoria,* previously included in its own family (Lophosoriaceae), is nested inside the Dicksoniaceae as sister to *Dicksonia.* Together they form the sister group to the genus *Calochlaena.* Within *Dicksonia* three monophyletic groups can be recognized. Based on a SDiva analysis, it is likely that the current distribution of these groups reflect their origin from single tectonic units of the former continent Gondwana: the "Pacific" clade includes species from New Caledonia, New Zealand and the Fijis; the "Antarctic" clade contains species from the Neotropics as well as Australia and New Zealand and the "Palaeotropic" clade includes species from tropical Australia, Malesia and New Guinea. These clades are supported by certain morphologic characters, such as leaf dimorphism, spore shape or lamina outline. Fossil records from Tasmania and western Antarctica are assignable to single clades. Due to the unique spore morphology of *Lophosoria*, the split between *Dicksonia* and *Lophosoria* can be confidently dated back to 100 Mya via BEAST analysis. However, the morphologically recognizable species of *Lophosoria* were impossible to distinguish due to low sequence variation.

23

Icy toes and salty kisses – How *Rosa spinosissima*tries to deal with hyperosmotic salinity, separation and displacement at German coasts

—

Jens Föller[1] · Hans-Werner Koyro[2] · Christoph-Martin Geilfus[3] · Karl Hermann Mühling[4] · Volker Wissemann[1]

[1] Systematic Botany, Justus-Liebig-University Gießen, Heinrich-Buff-Ring 38, 35392 Gießen, Germany — [2] Plant Ecology, Justus-Liebig-University Gießen, Heinrich-Buff-Ring 26, 35392 Gießen, Germany — [3] Institute of Plant Nutrition and Soil Science, Christian-Albrechts-University, Herrmann-Rodewaldstr. 2, 24118 Kiel, Germany — [4] Institute of Plant Nutrition and Soil Science, Christian-Albrechts-University, Herrmann-Rodewaldstr. 2, 24118 Kiel, Germany

—

It is suspected that during the last ice age, while Europe was more or less covered by an ice shield,the population of *Rosa spinosissima*L.was split into subpopulations. Some moved southwards into southern refugiawhile others rested on nunataks in the ice shield of the northern part. As a result two different morpho- and/or ecotypes may have been established, today known as an inland and a coastal variant, phenotypical different in size. *R. spinosissima*as a species cannot be considered as a very competitive species. The coastal ecotypeof the German coasthas a limited range of habitats and is furthermore threatened by displacement of the foreign and invasive*Rosarugosa*Thunb..The aim of this work was to study the differences in salt resistance of of*R. spinosissima*(both ecotypes) and *R. rugosa*. Therefore we cultured the roses at six levels(between 0 and 30% seawater salinity) of artificial sea water in a quick check system.

Both ecotypes of *R. spinosissima* suffered even at moderate concentrations, whereas the inland variety surprisingly tolerated higher salt concentrations than the coastal type.*R. rugosa*showed a considerable higher competitive capacity at saline conditions as *R. spinosissima*. Apart from reproductive biology patterns, one explanation for thereplacement at those salty conditions in coastal areas aredisproportionatelyhigh salt accumulation rates of *R. spinosissima*(includer type) in comparison to the excluding *R. rugosa*.Using diverse methods of investigation in morphology and physiology we found additional marked and relevant alterations between the species and also inbetween the ecotypes. In conclusion not a single parameter but a network of mechanismsfinally leadsto a higher salt resistance and the establishment of *Rugosa*-roses in coastal areas.

24

Island hopping and Sex on the Island — Different reproductive and dispersal strategy of two sympatric Asteraceae species

—

Christina M. Müller · Volker Wissemann · Birgit Gemeinholzer
Justus Liebig University, Systematic Botany, Heinrich-Buff-Ring 38,
35392 Gießen, Germany

—

Intensive large-scale agriculture leads to habitat loss and fragmentation of natural habitats. Plant populations hereby get isolated on island like patches with influences upon population genetic structures. In this study, we test the effects of habitat fragmentation and isolation in an agriculture dominated landscape. Our study site is along a desert-Mediterranean transition zone in the Southern Judaean Lowlands in Israel. By applying AFLP we investigated the population genetic structure of the annual *Geropogon hybridus* (Asteraceae) and *Catananche lutea* (Asteraceae) (Gemeinholzer et al. 2012). For both species, we screened 12 island populations in total in 3 different land-units with differences in geographic distance to each other. We detected high levels of genetic differentiation among populations but genetic structures only in part reflected spatial patterns. Patch area did not correlate to genetic diversity, neither for *G. hybridus,* nor for *C. lutea* (Gemeinholzer et al. 2012). The Structure analysis for both species resulted in a distinct modal maximum of ΔK at $K = 3$ per species, but the genetic patterns did not unambiguously reflect land-unit affiliation. By neighbor joining the *C. lutea* individuals mostly formed distinct groups according to their population affiliation and often group in clusters which are typical for their land-unit association with more or less distinct population structures. This genetic pattern is indicative for restricted gene flow between the populations of the investigation area, most likely due to pollination and/or seed-dispersal limitations. The pattern retrieved by the analyzed *G. hybridus* individuals did not reflect anything alike. The *G. hybridus* individuals featured strong genetic admixture with strong allele exchange between the individuals of different populations and land-units, pointing to a meta-population dynamics with high pollination- and/or seed dispersal capacities. Overall, *G. hybridus* seems to be better adapted to dispersal across fragmented habitats (“Island hopping”), while *C. lutea* – even featuring very similar morphological and ecological structures – seems to prefer “Sex on the island”.

References

Gemeinholzer B, May F, Ristow M, Batsch C, Lauterbach D (2012) Strong genetic differentiation on a fragmentation gradient among populations of the heterocarpic annual *Catananche lutea* L. (Asteraceae). Plant Syst Evol, **298**(8): 1585 – 1596

25

Reticulate Evolution of *Crepis* L. section *Barkhausia* (Asteraceae)

—

Ghalia Esklual · Volker Wissemann · Birgit Gemeinholzer
Justus Liebig University, Systematic Botany, Heinrich-Buff-Ring 38,
35392 Gießen, Germany

—

Background: Within the Asteraceae, Crepis L. section Barkhausia comprises twelve species. Molecular analysis of the nuclear ribosomal internal transcribed spacer (nrITS) pointed towards a monophyletic origin of the section. However, chloroplast data predicted at least three independent lineages. These discrepancies between molecular markers of different origins evoke the evolutionary picture of a hybridogenic origin of Barkhausia, potentially across different evolutionary lineages.

Objectives: In our study we1) investigate additional nuclear markers to identify species which may have contributed to the hybrid derivative lineage within Barkhausia.

2) We aim to reconstruct the phylogenetic relations of the species which recombination events led to the difference between nuclear and chloroplast phylogenies of section Barkhausia.

Methods: DNA was extracted from the leaves. gsh1 &rps 16 regions were amplified by PCR using specific markers and sequenced. The sequences were edited in ChromasLite2000 and aligned manually by using BioEdit. The phylogenetic trees were reconstructed using MEGA (Molecular Evolutionary Genetics Analysis).

Results: Maximum Parsimony trees of twelve species of section Barkhausia were reconstructed using Hispidella hispanica L. as outgroup. The single copy nuclear gsh1 region revealed 523 characters, of which 163 were parsimony informative.The phylogeny was compared to the nrITS and chloroplast matK1 &rps 16 phylogenetic trees. All analyses and marker systems revealed Barkhausia to be monophyletic. At least five different alleles of gsh1were obtained.

Conclusion: The results are preliminary, for full resolution of the hybridogenic lineage evolution,we further try to analyze the missing alleles in the section.

Spatio-temporal evolution of the subfamily Pitcairnioideae s. str. (Bromeliaceae)

—

Natascha Wagner[1] · Nicole Schütz[2] · Florian Krapp[1] · Tina Wöhrmann[1] · Kai Schubert[1] · Kurt Weising[1]

[1] Institute of Biology, University of Kassel, Heinrich-Plett-Str. 40, 34132 Kassel, Germany — [2] Natural History Museum Stuttgart, Botany Department, Rosenstein 1, 70191 Stuttgart, Germany

—

According to the revised intrafamilial classification of Bromeliaceae by Givnish et al. (2007), subfamily Pitcairnioideae s. str. includes five genera: *Pitcairnia*, *Fosterella*, *Deuterocohnia* (including *Abromeitiella*), *Dyckia* and *Encholirium*. The present study aims to scrutinize the phylogenetic relationships within Pitcairnioideae and to elucidate spatio-temporal evolutionary patterns within the subfamily. To achieve this, we sequenced three chloroplast DNA (cpDNA) loci from up to 30 accessions per genus covering the whole distribution area. The large genus *Pitcairnia* (~ 400 species, including *Pepinia*) is deeply split into two lineages that take a basal position in the subfamily. The mesophytic genus *Fosterella* (31 species) is monophyletic and sister to a well-supported xeromorphic clade consisting of *Deuterocohnia* (18 species), *Dyckia* (158 species) and *Encholirium* (25 species). Our recent studies suggest that *Fosterella* originated in the mid Miocene about 10 Mya in the Andean seasonally dry tropical forests (SDTFs; Wagner et al., 2013). The likewise Andean genus *Deuterocohnia* is clearly paraphyletic in the cpDNA tree. Whereas *Dyckia* comes out as monophyletic, the status of *Encholirium* is still ambiguous due to insufficient sampling. Our data suggest that the ancestors of *Encholirium* and *Dyckia* arrived in NE Brazil about 4.5 Mya, maybe via long distance dispersal. From here, one lineage of *Dyckia* apparently migrated to southern Brazil from where a rapid and recent radiation of suitable habitats in the Campos Rupestres took place that began about 2.5 Mya.

References

Givnish, T. J., Millam, K. C., Berry, P. E. and Sytsma K. J. 2007: Phylogeny, adaptive radiation and historical biogeography of Bromeliaceae inferred from *ndh*F sequence data. Aliso **23**: 3 – 26

Wagner, N., Silvestro, D., Brie, D., Ibisch, P.L., Zizka, G., Weising, K. and Schulte, K. 2013: Spatio-temporal evolution of *Fosterella* (Bromeliaceae) in the Central Andean biodiversity hotspot. Journal of Biogeography **40**, 869 – 880.

27

Multiple gains and losses of leaf succulence – tracing the diversification of *Zygophyllum* s. l. in arid regions of the Old World using highly variable cp markers detected in a plastid genome scan.

—

Maximilian Lauterbach[1] · Dirk U. Bellstedt[2] · Michael D. Pirie[1,2] · Pieter de Wet van der Merwe[2] · Lisa Wernet[1] · Gudrun Kadereit[1]
[1] Institut für Allgemeine und Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Germany — [2] Department of Biochemistry, University of Stellenbosch, South Africa

—

Despite recent work on the phylogeny of Zygophyllaceae subfamily Zygophylloideae, relationships within the group and particularly between species representing its four originally described genera, *Augea* Thunb. (one species), *Fagonia* L. (ca. 30 species), *Tetraena* Maxim. (one species), and *Zygophyllum* L. (ca. 150 species) remain unclear. We scanned the whole plastid genomes (cpDNA) of three *Zygophyllum* species, *Augea capensis* Thunb., *Fagonia luntii* Baker and outgroup *Tribulus terrestris* L. (Tribuloideae) to find markers adequate to address the lack of phylogenetic resolution within this group. Two of 14 candidate non-coding cpDNA regions were selected based on assessment of variability, length and reliability of sequencing: the *atpI-atpH* spacer and *trnG* intron. They compare reasonably to the *trnL-trnF* spacer, which has shown relatively high variability within Zygophylloideae in previous studies. These markers were analysed for a large sampling representing all subgroups, with particular focus on the preliminary named genera *Roepera*, *Tetraena*, and *Zygophyllum* s.s. This study was able to show that subfamily Zygophylloideae consists of the five well-supported groups: 1) *Augea* / *Zygophyllum orbiculatum*, 2) *Fagonia* / *Melocarpum*, 3) *Roepera*, 4) *Tetraena*, and 5) *Zygophyllum* s. s. Relationships within these groups are better resolved than in previous studies (Beier et al. 2003; Bellstedt et al. 2008). A leaf anatomical survey revealed a high flexibility of leaf anatomy, especially with regard to leaf succulence showing the character states non-succulent, all cell succulence and storage succulence. All cell succulent leaves revealed to be the ancestral character state in *Roepera* and as many as six losses of leaf succulence are very likely. *Zygophyllum* s.s. includes more non-succulent species, and compared to *Roepera*, the ancestral character state of clade *Zygophyllum* s.s. seems to be non-succulent and at least two independent character shifts to storage succulence took place. Whereas all but two observed *Tetraena* species showed storage succulence. The name 'Tetraena' and the respective nomenclatural changes in ca. 35 species of *Zygophyllum* (proposed by Beier et al. 2003) need further clarification, because the phylogenetic position of *Tetraena mongolica*, which is eponymous for this genus sensu Beier et al. (2003), is unclear.

References

Beier et al. 2003: Plant Systematics and Evolution **240**: 11 – 39.

Bellstedt et al. 2008. Molecular Phylogenetics and Evolution **47**: 932 – 949.

Explosive radiation in high Andean *Hypericum*

28

—

Nicolai M. Nürk[1] · Charlotte Scheriau[1] · Santiago Madriñán[2]

[1] Centre for Organismal Studies (COS) Heidelberg, Biodiversity and Plant Systematics, University of Heidelberg, Germany — [2] Laboratorio de Botánica y Sistemática, Departamento de Ciencias Biológicas, Universidad de los Andes, Bogota DC, Colombia

—

The páramos, high-elevation Andean grasslands ranging from ca. 2800 m to the snow line, harbor one of the fastest evolving biomes worldwide since their appearance in the northern Andes 3–5 million years ago (Ma). *Hypericum* (St. John's wort, Hypericaceae), with over 65% of its Neotropical species, has a center of diversity in these high Mountain ecosystems. Using nuclear rDNA internal transcribed spacer (ITS) sequences of a broad sample of New World *Hypericum* species we investigate phylogenetic patterns, estimate divergence times, and provide the first insights into diversification rates within the genus in the Neotropics. Two lineages appear to have independently dispersed into South America around 3.5 Ma, one of which has radiated in the páramos (*Brathys*). We find strong support for the polyphyly of section *Trigynobrathys*, several species of which group within *Brathys*, while others are found in temperate lowland South America (*Trigynobrathys* s. str.). All páramo species of *Hypericum* group in one clade. Within these páramo *Hypericum* species enormous phenotypic evolution has taken place – life forms from arborescent to prostrate shrubs – evidently in a short time frame. We hypothesize multiple mechanisms to be responsible for the low differentiation in the ITS region contrary to the high morphological diversity found in *Hypericum* in the páramos. Amongst these may be ongoing hybridization and incomplete lineage sorting, as well as the putative adaptive radiation, which can explain the contrast between phenotypic diversity and the close phylogenetic relationships.

29

Evolution, biogeography, and taxonomy in the hemiparasitic genus *Euphrasia* L. (*Orobanchaceae*)

—

Katharina Schäper[1] · Susann Wicke[1] · Eberhard Fischer[2]
Kai F. Müller[1]
[1] Institute for Evolution and Biodiversity, University of Münster, Hüfferstr. 1,
48149 Münster, Germany — [2] Institut für Integrierte Naturwissenschaften – Biologie,
Universität Koblenz-Landau, Universitätsstr. 1, 56070 Koblenz, Germany

—

The hemiparasitic genus *Euphrasia* L. (*Orobanchaceae*) comprises about 350 species in c. 15 sections with a mainly bipolar distribution in Eurasia, Australia, New Zealand, and South America. Despite a number of taxonomic revisions of the genus based on morphological characters, ploidy level, and geographic extension in the past century, the 20 to 35 annual species of the Eurasian section *Euphrasia* form a taxonomically complex group. Species delimitation within this section is complicated because of an extraordinary high phenotypic plasticity. This plasticity may be the result of the association to different host plants, abiotic habitat conditions, climatic factors, and/or frequent interspecific hybridization events. This study intents to illuminate the evolution of the genus *Euphrasia* and mechanisms of its diversification in the arctic and alpine habitats of Europe and Western Asia. Specifically, we aim to resolve the origin and phylogenetic relationships of local endemic and relict species in low mountain ranges of Central Europe and the species-rich areas of the Alps, the Caucasus Mountains, the Giant Mts., and the Tatra Mts. One focus of our study is the evolution of the holarctic *E. wettsteinii* Gussarova (*E. frigida* Auct. non Pugsley) in Germany's mountain ranges (Harz, Eifel, Taunus, Vogelsberg, Spessart, Rhön, and Erzgebirge) in comparison to the arctic E. *wettsteinii* populations. Based on a population level sampling, we use AFLP data and the fast-evolving chloroplast DNA marker *rpl32-trnL* in combination with morphometric, environmental, and cytological data to understand species delimitations, the genetic diversity of Eurasian *Euphrasia* species and their different populations as well as their distribution range evolution. Our preliminary results indicate very little genetic diversity within the section, suggesting a rapid radiation and/or a recent origin with ongoing speciation. However, we find a clear distinction e.g. between artic and Central European populations of *E. wettsteinii*.

30

The *Sparganium emersum/angustifolium* complex in NW Germany and BeNeLux

Eike Mayland-Quellhorst[1] · Kay Fuhrmann[2] · Dirk Albach[1]
[1] Carl-von-Ossietzky University Oldenburg — [2] Von-Bodelschwingh-Str. 82, 26125 Oldenburg

Sparganium L. is a temperate-arctic genus of about 14 aquatic species. In Northern Germany *Sparganium angustifolium* Michaux is of particular interest, as it is restricted to oligotrophic waters, which are rapidly declining due to the high influx of nutrients from agriculture and the atmosphere. One important aspect of the conservation efforts for this species is the potential hybridization with the eutrophic congener *S. emersum* Rehmann and their putative hybrid, *S.* x *diversifolium* Graebner. Discrimination between all three taxa is sometimes very difficult, but is of importance for conservation purposes and ecological research. We tried to resolve the complex systematics of this group with a broad investigation of morphological and molecular data.

In this study we analyzed morphological data (26 characters) and molecular DNA sequence data (five chloroplast loci). Using descriptive analyses (PCoA, LDA) and a bootstrapped hierarchical clustering an optimal partition of the morphological data in three groups was achieved, but these groups are not congruent with the prior classification into the two species and their putative hybrid. The combined cpDNA molecular phylogeny showed a split between an *angustifolium* group and an *emersum* group, each of which also contains several x *diversifolium* individuals.

Further discrimination between the groups in this species complex with nuclear information is to date lacking. Microsatellite markers might be able to give more resolution as they are able to take putative hybridization into account.

31

Molecular systematics and evolution of the non-photosynthetic parasitic *Cistanche* (Orobanchaceae)

—

N. Ataei[1] · G. M. Schneeweiss[2] · Jesús Muñoz[3] · H. Weiss-Schneeweiss[2]
Eva Temsch[2] · M. A. García[3,4] · J. Valizadeh[5] · R. Sheik-Akbari Mehr[6]
S. Wicke[7] · K. Maul[1] · D. Quandt[1]

[1] Nees Institute for Plant Biodiversity, Rheinische Friedrich-Wilhelms-Universität Bonn, Meckenheimer Allee 170, 53115 Bonn, Germany — [2] Department of Biogeography and Botanical Garden, Institute of Botany, University of Vienna, Rennweg 14, 1030 Vienna, Austria — [3] Real Jardín Botánico, E-28014 Madrid, Spain) — [4] Department of Biology, University of Toronto at Mississauga, 3359 Mississauga, William G. Davis Building, Rm 3030, Mississauga, ON L5L 1C6, Canada — [5] Department of Biology, University of Sistan and Baluchistan, Zahedan, Iran — [6] Department of Biology, Faculty of Sciences, Qom University, Qom, IRAN — [7] Institute for Evolution and Biodiversity Westfälische Wilhelms-Universität, Hüfferstrasse 1, 48149 Münster, Germany

—

The non-photosynthetic parasitic genus *Cistanche* contains approx. 25 species and is distributed from North Africa via its biodiversity hotspot in Southwest Asia to East Asia, where they form a common element in arid habitats. Species delimitation and relationships in *Cistanche* are, however, poorly understood, hampering our understanding of biogeography or patterns of genome evolution (*Cistanche* has by far the largest genome size in holoparasitic Orobanchaceae). Therefore, a reappraisal of phylogenetic relationships and taxonomy in this genus is much needed. The aims of this are to: i) elucidate phylogenetic relationships within *Cistanche* and test whether these are reflected in current taxonomy; ii) identify evolutionary trends in genome size and chromosome number; iii) predict potential species distributions; iv) provide a revised taxonomic treatment). Phylogenetic relationships were inferred using MP, ML, BI on a data set comprising three plastid (*trnL-F, trnS-fM*, *psbA-trnH*) and one nuclear marker (ITS). Biogeographic and taxonomic investigations were undertaken on 670 accessions (fresh collections, herbarium specimens and web images). Morphometric analyses of vegetative and reproductive characters were conducted for ca. 180 specimens. Genome size estimation using Feulgen densitometry (FDM) were obtained for 53 accessions, many of which were also studied karyologically. Species distribution models (SDM) were generated for 18 species using Maxent. Molecular-phylogenetic data in combination with taxonomic revisions suggest recognition of 3 sections: i) sect. *Cistanchiella* (9 species, 4 of which are newly described); ii) sect. *Cistanche* (12 species, 4 of which newly described); iii) *Macrocalycinum* (2 species, one of which newly described). Despite high interspecific (3.72-fold) and intraspecific variation in genome size (from 1.18 up to 2.44-fold), the chromosome numbers are uniform. Nineteen accessions of *Cistanche* were diploid ($n = 20$) of which only one accession of *C. violacea* was triploid ($n = 30$). Chromosome number stability contrasts with genome size variation, suggesting mechanisms other than polyploidy for an increase in genome size, e.g., repetitive DNA, transposons.

32

Is fruit aroma an adaptation to primate seed dispersal?

Omer Nevo[1] · Eckhard W. Heymann[1] · Manfred Ayasse[2]

[1] Behavioral Ecology & Sociobiology Unit, German Primate Center, Germany & Department of Sociobiology/Anthropology, Johann-Friedrich-Blumbach Institute for Zoology and Anthropology, Georg-August University of Göttingen, Germany — [2] Institute of Experimental Ecology, University of Ulm, Germany

The majority of tropical angiosperms relies on frugivorous animals for seed dispersal and thus produces fleshy fruits to attract them. Fruit odor has long been speculated to be an adaptation for signaling ripeness similarly to color – a hypothesis that was only recently tested for bat-dispersed figs. Primates constitute a major proportion of the frugivore biomass in the tropics and are now known to possess olfactory capabilities higher than previously thought. It is thus likely that in order to attract them, fruits dispersed by primates developed olfactory signals for ripeness. The current project tests this hypothesis, which generates 3 predictions: (1) ripe primate-dispersed fruits have a strong odor which is distinguishable from unripe fruits; (2) fruits dispersed by animals less olfactory-dependent do not emit clear unique odor in ripeness; and (3) this pattern repeats in different systems, independent of phylogeny. We propose two mechanisms for this putative signaling: (a) the olfactory signal is presented in the fruit husk and can be detected without opening it; (b) the olfactory signals is presented in the pulp and requires manipulation/opening of the fruit. Using mass spectrometry, we analyzed the odor of intact and opened, ripe and unripe, fruits of four Neotropical plant species, two dispersed by saddle-back and moustached tamarins (*Saguinus nigricollis* and *S. mystax*) and two by small understory passerines. We show that primate-dispersed fruits have relatively high concentrations of complex blends of compounds that are clearly different between ripe and unripe fruits, either only in the pulp or in both pulp and husk, thus making their odor profiles suitable for reliably signaling ripeness. In contrast, bird-dispersed fruits produce trace amounts of simple profiles which are not different between ripe and unripe fruits and are thus not likely to provide any useful cue for frugivores. Given the phylogenetic structure of the model species, this cannot be the result of phylogenetic inertia. Thus, our results support the hypothesis that fruit aroma is an adaptation acquired to signal ripeness to seed dispersing primates.

33

Phylogenetic structure in organellar markers

Michael Krug[1] · Kai Müller · Thomas Borsch · Philip Testroet
Sarah Noben · Volker Knoop · Dietmar Quandt
[1] Nees Institute for biodiversity of plants, Meckenheimer Allee 170, 53115 Bonn

The initial step of any molecular phylogenetic analysis is the selection of an appropriate set of phylogenetic markers that qualify to provide sufficient resolution and support. Currently, this most critical decision is generally based upon case studies, existing data sets, personal experience, and of course depends on the group of organisms studied and the taxonomic level. In order to improve the selection procedure, a qualitative measure beyond a simple comparison of bootstrap values may serve as guidance in the selection process, maximizing efficiency by minimizing wet lab efforts, sequencing costs and computational time. As the sequenced markers usually differ in sequence length, number of aligned positions, and in how staggered alignments are (e.g. indels, repeats), we employ a randomly repeated resampling of equal numbers of aligned nucleotides in order to evaluate the phylogenetic structure per sequenced nucleotide (Rc). Mueller etal 2006 pointed out that regions underlying a neutral evolution are more effective than slowly evolving genes.Later, Barniske etal. 2012 revealed more insight into the capability of non coding regions in phylogenetic backbone analyses: spacer and intron regions clearly outperform codingregions except for the highest ranking matK open readingframe. Here we present and compare two studies concerning backbone phylogenies:

1. Multiple plastid markers with a taxon sampling comprising representatives of all major angiosperm lineages. We included three genes (*matK*, *rbcL* and *atpB*), four intergenic spacers (*IGS*, *atpB-rbcL*, *petB-D*, *rps3-rpl16* and *trnL-F*) three group II introns (*petD*, *rpl16*, *trnK*), and the sole plastid group I intron (*trnL*). (see Barniske et al. 2012)

2. A set of plastid and mitochondrial markers and a taxon sampling that contains taxa from all bryophyte lineages. We included plastid genes (*rps4*, *rbcL*, *matK*), mitochondrial genes (*nad2*, *nad4*, *nad5*), the sole plastid group I intron (*trnL*), two mitochondrial group I introns (*nad5* and *cobi420*), and one mitochondrial group II intron (*nad2*).

1

Species status of *Macropodia rostrata* and *Macropodia parva* (Crustacea, Decapoda, Majoidea)

—

Christina Wesse[1] · Olaf R. P. Bininda-Emonds[1] · Michael J. Raupach[2]
[1] Carl von Ossietzky Universität Oldenburg, Germany — [2] Senckenberg am Meer
Wilhelmshaven, Germany

—

Crustaceans of the decapod taxon Majoidea are distributed all over the world oceans. For their enormously long legs and therefore resemblance to spiders they are also commonly known as „spider crabs". The genus *Macropodia* (Leach, 1814) contains world-wide 19 species of which five species (*Macropodia rostrata, M. parva, M. linaresi, M. deflexa* and *M. tenuirostris*) are found in the shallow waters of the North Sea. In the case of *Macropodia parva* and *M. rostrata*, species can be distinguished from each other by the shape and spines of the dactylus of the last pereiopod as well as the length of the rostrum in relation to the fifth segment of the antennal segment/peduncle. However, former morphometric analyses indicated high degrees of morphological variability and plasticity in both characteristics for both species. In this context we investigated the species statuses of *Macropodia rostrata* and *M. parva* with further morphometric analyses and molecular methods. Neither the investigated morphological traits nor the molecular data legitimate the species status of *Macropodia parva*.

2

Phylogenetic Significance of the Trochozoan Nervous Systems: Annelida and Nemertea

—

Patrick Beckers
Institute for Evolutionary Biology and Zooecology, University of Bonn,
An der Immenburg 1, 53121 Bonn, Germany

—

Neuroanatomy is one of the promising fields to uncover phylogeny and the evolution of species. In recent years a lot of researches have been published investigating the nervous system of members of the Trochozoa to which the taxa Brachiopoda, Mollusca, Annelida and Nemertea are supposed to belong to (Edgecombe et al. 2011). Recent molecular studies recover Oweniidae at the base of Annelida (Zrzavý et al. 2009) and the taxon *Carinina ochracea* as a basal representative of nemerteans (Andrade et al. 2011, Beckers et al. 2013). By assuming that these taxa show primary morphological states, the anatomy of the nervous systems is compared. The conditions in derived species of annelids and nemerteans as well as the conditions found in other members of the Trochozoa are discussed.

In *Owenia fusiformis* and *Carinina ochracea* the central (or medullated) nervous system is located inside the epidermis (intraepidermal). It is composed of a central neuropil and surrounding perykaria. In *O. fusiformis* and *C. ochracea* the brain neuropil forms a simple ring with homogenously distributed neurons. From the ventral part of the ring lateral medullary cords branch of and run caudally. In *O. fusiformis* these nerve cords fuse to a single nerve cord. In *C. ochracea* the nerve cords are connected caudally by an anal commissure. There is no expansion and compartmentation of the brain. In derived nemerteans the *cns* is located inside the musculature except for the taxon Hubrechtidae where the *cns* is subepidermal (Bürger 1895, Beckers 2012). This is even true for very small taxa, e.g. Tetrastemmidae or Ototyphlonemertidae (Hoplonemertea), indicating that size is not a factor that affects the position of the nervous system inside the body wall layers in nemerteans. In derived annelids the nervous system may be located in different layers of the integument. The brain of these supposedly derived taxa of Annelida and Nemertea show a dorsal expansion and different neuron clusters are discernible. This condition is also present in *Sabellaria alveolata,* a tube dwelling polychaete, indicating that a sessile life does not necessarily lead to a simplification of the nervous system.

Intraepidermal anteriorly ring-shaped *cns* are also known from Brachiopoda and Phoronida. The nervous system of molluscs is always inside the musculature and may represent a derived state within Trochozoa.

References

Andrade S., Strand M., Schwartz M., Chen H., Kajihara H., von Döhren J., Sundberg P. 2012: Disentangling ribbon worm relationships: multilocus analysis supports traditional classification of the phylum Nemertea. Cladistics **28**: 141 – 159.

Beckers P, Loesel R, Bartolomaeus T. 2013: The Nervous Systems of basally branching Nemertea (Palaeonemertea). PloS one, **8**(6), e66137.

Beckers P. 2012: Nemertean nervous systems. A comparative analysis. PhD thesis. Math.-Nat.- Fakultät Universität Bonn. urn:nbn:de:hbz:5n-28884

Edgecombe G. D., Giribet G., Dunn C. W., Hejnol A., Kristensen R. M., Neves R. C., Sørensen M. V. 2011: Higher-level metazoan relationships: recent progress and remaining questions. Organisms Diversity & Evolution **11**: 151 – 172.

Zrzavý J., Říha P., Piálek L., Janouškovec J. 2009: Phylogeny of Annelida (Lophotrochozoa): total-evidence analysis of morphology and six genes. BMC Evolutionary Biology **9**: 189.

3

Behavioural data as character complex in phylogenetic reconstruction in a cryptic grasshopper species-group (Acrididae, Gomphocerinae, *Stenobothrodes*)

DIRK BERGER[1] · BRIGITTE GOTTSBERGER[2]

[1] Schäferstraße 33, 01067 Dresden, Germany — [2] Department of Botany and Biodiversity Research, Div. Tropical Ecology and Animal Biodiversity, University of Vienna, Rennweg 14, 1030 Vienna, Austria

The genus *Stenobothrus* Fischer, 1853 is one of the species rich genera of the Gomphocerinae in Europe. In contrast to morphology which is often cryptic, *Stenobothrus* taxa produce highly complex courtship songs that are composed of several acoustic and often peculiar optical components. As molecular studies reveal inter-specific differentiation falls often in the range of intra-specific variation in other insect taxa. That complicates the resolution of phylogenetic relationship in gomphocerine grasshoppers. One example is the subgenus *Stenobothrodes* Tarbinskij, 1948. *Stenobothrus eurasius* Zubovskii, 1898 is assumed to be the single species of the subgenus *sensu* Harz (1975). The European populations are restricted to small geographically separated populations and some of them are described as distinct subspecies. All forms are morphologically rather similar and are supposed to be one highly variable species (Ingrisch & Pavićević, 1985). To get insights in the evolutionary history of *Stenobothrodes*, a combined phylogenetic analysis of a dataset including behavioural (calling song, courtship song, corresponding leg movement pattern and visual courtship displays) and morphological characters of 24 *Stenobothrus* species of 28 populations was performed. The analysis reveals that morphological characters were useful for the resolution of species groups within the genus whereas higher resolutions were supported mainly by behavioural characteristics. The former described taxa *Crotalacris* Chopard, 1951 and *Stenobothrodes* were monophyletic and are sister groups. Furthermore, within the cryptic taxon *Stenobothrodes* two lineages were found. Lineage A contains *Stenobothrus eurasius* with the geographical forms (*S. e. bohemicus*, *S. e. slovacus* and a newly discovered population from the Smolikas Mountains in Greece). Lineage B shows substantial acoustic differences to lineage A so that *S. e. macedonicus* must be regarded as a separate species. The closest relative of *S. e. macedonicus* is *S. croaticus* that was considered to be a member of *Crotalacris* (Harz, 1975). We emphasize the high value of behavioural data in phylogenetic reconstruction of cryptic species complexes.

References

Harz, K. (1975): Die Orthopteren Europas II. Series Entomologica 11. Dr. W. Junk B.V. The Hague: **i**–**iv**, 1–939.

Ingrisch, S. & Pavićević, D. (1985): Zur Faunistik, Systematik und ökologischen Valenz der Orthopteren von Nordost-Griechenland. – Mitteilungen der Münchner entomologischen Gesellschaft **75**: 45–77.

Review of the Neotropical Ciidae (Insecta: Coleoptera) in the *Cis taurus* species-group

4

—

Ester Helena de Oliveira[1] · Heiko Stuckas[1]
Cristiano Lopes-Andrade[2], Klaus-D. Klass[1]
Ester Helena de Oliveira 1, Heiko Stuckas 1, Cristiano Lopes-Andrade 2, Klaus-D. Klass 1
[1] Senckenberg Naturhistorische Sammlungen Dresden, Königsbrücker Landstr. 159, 01129 Dresden, Germany — [2] Departamento de Biologia Animal, Universidade Federal de Viçosa, 36570-900, Viçosa, Minas Gerais, Brazil

—

Ciidae is a cosmopolitan family of minute (1–7 mm body length) fungivorous beetles with 43 genera and 650 described species. *Cis* is the most speciose ciid genus (370 species), but is likely paraphyletic, and is divided in several species groups. One of these is the Neotropical *Cis taurus* group, which includes 11 valid described species and likely dozens of undescribed species. This is likely the most abundant and speciose group of ciids in the Neotropics and thus of great ecological importance. The ongoing project is an in-depth study of the species diversity, phylogeny, phylogeography, and biology of the *Cis taurus* group, including morphological and molecular data as well as data on host fungi. As a first step, (1) in two recent publications we critically revised the taxonomy of the previously described species, including detailed morphological examination, standardized (re-)description, and photographic documentation of all available type specimens (often with lectotype designation) plus many specimens from museums and own collections. The specimens that could not be assigned to the known species were arranged in ca. 70 "morphospecies" showing that many additional species remain to be described. Current work focuses on (2) the sequencing of selected genes (COI, COII, 18S; protocol now established) over a large sample and on (3) the exploration of the exoskeleton for new taxonomically informative characters (including finer surface structures, using SEM, male and female terminalia and internal structures like the proventriculus and reproductive organs). Special topics to be discussed are (4) the sexual dimorphism (males with cephalic projections and abdominal sex patch) including the range of variation in males; host fungus specificity evolution inside the group and dispersion in the American continent.

5

Snails in the desert: Species diversification of *Theba* (Gastropoda: Helicidae) along the Atlantic coast of NW Africa

—

Carola Greve[1] · Martin Haase[2] · Rainer Hutterer[1] · Dennis Rödder[1] · Flora Ihlow[1] · Bernhard Misof[1]

[1] Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany — [2] Vogelwarte, Zoologisches Institut und Museum, Ernst-Moritz-Arndt-Universität Greifswald, Soldmannstraße 23, 17489 Greifswald, Germany

—

The spatial subdivision of species often plays a pivotal role in speciation. Across their entire range, species are rarely panmictic and crucial consequences of spatial subdivision are i) random genetic drift and ii) spatially variable selection regimes acting on different subpopulations of the same species. In the present study, we used a combination of genetic, morphological and ecological criteria to analyse the spatial differentiation between three closely related, parapatrically distributed species of the land snail genus *Theba* occurring along the Atlantic coast of South Morocco and Western Sahara. Ecological niche analyses and distribution of genetic diversity suggest that diversification among these species along the Atlantic coast was probably driven by a mixture of non-adaptive and adaptive, allopatric speciation. We hypothesize that climate oscillations during the Plio- and Pleistocene have led to repeated ecological changes in NW Africa and disruptions of habitats promoting differentiation by geographic isolation. However, the inferred evolutionary scenario does not fully explain the incongruence between the AFLP- and mtDNA-tree topologies. This incongruence might indicate past hybridization among the studied *Theba* species. The genetic differentiation among and within putative species was consistent with detailed geometric morphometric analyses of these partially cryptic forms.

6 Analyzing German seafood products, using DNA barcoding

—

Babett Günther · Thomas Knebelsberger · Michael J. Raupach
Senckenberg am Meer Molekulare Taxonomie Südstrand 44,
26382 Wilhelmshaven, Germany

—

The origin ofcommercially traded seafood products cannot always be proved as a consequence of insufficient or incorrect labeling.In this context,accurate species identificationis essential to insure consumer protection andprevent illegal fish capture in the future. In this study, we used a DNA barcoding approach for the analysis of commercially available fish products.This method is based on the amplification and sequencing of a 652 bpfragment of the cytochrome *c* oxidase I (COI) mitochondrial gene region. We tested 29 fish products from14different manufacturersand eightsamples froma fishstore.Overall, DNA barcodes from 78 samples were generated and analyzed in combination with data from already established DNA barcode reference libraries. All of the investigated products fromseafood manufacturerswere correctly labeled based on the index of fish trade names of the European Union. With one acception,a filetlabeledas*Salmon salar*was identified as *Oncorhynchusgorbuscha*(both Salmonidae). In contrast threesamples (38 %) fromthe fishstore were mislabeled. The present study showed that DNA Barcoding is ausefultool for species verification which can be applied to a wide range of commercial fish products.

7 Integrated Morphological and Molecular Genetic Taxonomy in North Sea Jellyfish

—

Sabine Holst[1] · Silke Laakmann[2]
[1] Senckenberg am Meer, German Center for Marine Biodiversity Research,
Martin-Luther-King-Platz 3, 20146 Hamburg, Germany — [2] Senckenberg am Meer,
German Center for Marine Biodiversity Research, Südstrand 44,
26382 Wilhelmshaven, Germany

—

Jellyfish are widespread and diverse representatives of the gelatinous zooplankton and thus attract attention in many ecological and taxonomic studies. However, the adequate fixation of their gelatinous bodies and the correct identification of different developmental stages are challenging tasks in jellyfish taxonomy. In our studies we combined morphological determinations of living and preserved jellyfish specimens with molecular genetic analyses (Holst & Laakmann 2014, Laakmann & Holst 2014). This integrative taxonomic approach was realized successfully for more than 30 scypho- and hydromedusaen species occurring in the German Bight, North Sea. In most cases, morphological species identifications were confirmed by molecular data (COI partial sequences) and the latter approach led to valid discrimination where morphological characters were insufficient. Based on our collection that includes morphological and DNA vouchers, mitochondrial and nuclear sequences, we are now able to identify ethanol-preserved species independently from the developmental stage and tissue type. Our results highlight the molecular approach as a powerful tool, extending the possibilities for valid species discriminations where morphological identification is difficult, for example, in jellyfish species with a similar or identical morphology, in early life stages with insufficient identifying features and in linking different generations (polyp and medusa). However, genetic analysis cannot replace morphologically based taxonomy in studies on species' population dynamics, physiology and ecology. Thus, most information is achieved by combining both methods in integrative studies using both morphological and molecular taxonomy.

References

Holst S., Laakmann S. 2014: Morphological and molecular discrimination of the two closely related jellyfish species *Cyanea capillata* and *C. lamarckii* (Cnidaria, Scyphozoa) from the northeast Atlantic. J Plankt Res **36**: 48 – 63.

Laakmann S., Holst S. 2014: Emphasizing the diversity of North Sea hydromedusae by combined morphological and molecular methods. J Plankt Res **36**: 64 – 76.

8

A morphological analysis of *Hyles* (Lepidoptera: Sphingidae) based on adult characters for integrative systematics

—

ANNA K. HUNDSDOERFER[1] · IAN J. KITCHING[2]
[1] Museum für Tierkunde, Senckenberg Naturhistorische Sammlungen Dresden, Königsbrücker Landstr. 159, D-01109 Dresden, Germany — [2] Department of Life Sciences, Natural History Museum, Cromwell Road, London SW7 5BD, U.K.

—

The genus *Hyles* (Lepidoptera: Sphingidae) is taxonomically difficult due to a combination of low structural diversity coupled with high variability in the patterns of both adults and caterpillars. Adult morphology in *Hyles* is remarkably uniform, particularly the male genitalia, which are the most usual source of characters used to identify and classify Lepidoptera at the species level. Consequently, most classifications of *Hyles* have placed heavy emphasis on characters derived from the colour patterns of adults and larvae, and only very rarely have the putative homologies of the pattern elements been critically assessed. Furthermore, these features are often variable within species and can be subject to local environmental influences, particularly in the larval stage. Sequence data from three mitochondrial genes and one nuclear gene have helped clarify the relationships from a molecular perspective, but this phylogeny has yet to be reconciled objectively with morphology. Augmenting the research on the molecular phylogeny of the genus with a matrix of morphological characters, which are coded in the nuclear genome only, will enable the incorporation of another independent data source for integrative systematics and taxonomy.

The morphological matrix presented here allows such a cladistic analysis of the adult phenotypes. We analysed characters widely used in the traditional taxonomy, such as elements of the wing pattern, as well as new ones derived from other body structures. Our main task was to determine the homologies of the wing pattern elements, so that we can then reconstruct the ancestral proto-*Hyles* wing pattern and gain insights into the complex evolution of wing patterns in this group of moths. Our critically constructed and objectively coded morphological matrix now enables us to test the utility of this data source for reconstructing the phylogeny of *Hyles*, and to investigate the genetic correlates of morphological variability and its possible genetic basis.

Phylogeography of *Dactylopodola typhle* across European coasts supports hypothesis of low dispersal capacity among marine gastrotrichs

—

Alexander Kieneke[1] · Cuong Q. Tang[2] · Diego Fontaneto[3]

[1] Senckenberg am Meer Wilhelmshaven, Deutsches Zentrum für Marine Biodiversitätsforschung, Südstrand 44, 26382 Wilhelmshaven, Germany — [2] Department of Life Sciences, Imperial College London, Ascot, Berkshire SL5 7PY, United Kingdom — [3] National Research Council, Institute of Ecosystem Study, 28922 Verbania Pallanza, Italy

—

Many species of the marine interstitial meiofauna, including the whole phylum Gastrotricha, do not develop any free swimming larvae or other dispersal stages. Juvenile gastrotrichs in the water column are only reported from high energy intertidal beaches. However, an effective distribution hereby is unlikely. Furthermore, gastrotrichs possess powerful features to avoid uncontrolled sweeping off, i.e. batteries of duo-gland adhesive tubes. Additionally, laid eggs are glued to sand grains which could at best facilitate a certain distribution via coastal-parallel sediment transport by current activity. The low dispersal capacity, if true, should strongly affect the genetic structure within and between geographic populations. We expect distinct genetic entities in geographically/oceanographically/ecologically faintly linked marine provinces.

We have sequenced a fragment of mitochondrial COI-gene plus a fragment of nuclear 18S rRNA-gene of specimens of the widespread marine gastrotrich species *Dactylopodola typhle* from several sites of the North Sea, Channel, Atlantic and Mediterranean. Mitochondrial sequence data give evidence of large genetic distances between geographic populations. Phylogenetic (ML, BI) and phylogeographic analyses (MP-networks) indeed show a strong structuring of the species into four distinct COI-lineages while the more conserved nuclear sequences confirm three major haplogroups. Tests for species delimitation seem to support this scenario. These three putative cryptic species correspond to distinct geographic/ecological regions: (a) central North Sea, (b) Channel to the Balearic Basin, and (c) Balearic Basin to the Thyrrenian Sea. Hence, the idea of low dispersal ability in marine interstitial meiofauna is supported by our results. Gene flow between geographically separated populations could be so low that independent evolution is fostered. Within-species diversity of COI of *D. typhle* has the potential for reconstructing population demography. This can help to understand if past geological events (e.g. sea level fluctuations, drying events) had any influence on population structuring and speciation.

10

The Phylogeny of the Nemopterinae (Neuroptera: Nemopteridae) based on morphological characters

—

Lukas Kirschey · Michael Ohl
Museum für Naturkunde zu Berlin

—

The Nemopterinae are a small group of lacewing with 98 species in 19 genera. They are grouped together with the Crocinae within the Nemopteridae, which belongs to the Myrmeleontiforma. The Nemopterinae are distributed in Australia, South America, southern Palearctic and mainly in southern Africa. One unique character of the Nemopterinae is the highly modified, ribbon-like hindwing, which measures between 13 and 35 millimeters in length. These hindwings are characterized by a varying number of apical or pre-apical dilations.

In the current study, we have conducted a phylogenetic analysis based on 35 morphological characters. We examined 19 species of the Nemopterinae as ingroups and 1 species of Psychopsidae and Crocinae, respectively, as outgroups. The resulting cladogram is partially congruent with a previously published cladistics hypothesis by Sole et al. (2013, Mol. Phyl. Evol. **66**: 360 – 368).

11

An undescribed Monostiliferan species (Nemertea: Hoplonemertea) from the Northwest Atlantic Coast of France

Daria Krämer · Jörn von Döhren · Thomas Bartolomaeus
Universitiy of Bonn, Institute of Evolutionary Biology and Ecology,
An der Immenburg 1, 53121 Bonn, Germany

Nemertea is a spiralian taxon of unsegmented, softbodied, vermiform animals, predominantly inhabiting marine environments. It comprises about 1280 described species of mainly epibenthic predators. Prey is captured with an eversible proboscis situated in a fluid filled coelomic cavity, the rhynchocoel. Approximately 45 % of all described nemertean species comprise Monostilifera (traditionally: suborder rank), the largest taxon within Nemertea. Their proboscis is equipped with a single stylet that is able to pierce the cuticle of small crustaceans. In general, monostiliferans are comparably small, ranging in body length from millimeters up to approximately 10 cm. Several unusually large specimens of a monostiliferous nemertean species of over 40 cm body length each, were found buried in 50 cm depth in an intertidal sand flat near Concarneau (France). Ecological data (endobenthic habitat) as well as morphological data (large body size) have led to the assumption that these nemerteans belong to a species new to science. Novel taxonomic standards recently erected by the international NemPhyl consortium, are employed to assess the systematic affinities of this undescribed species by combining both, morphological and molecular data. First results show that an assignment to existing monostiliferan genera is impossible leading to the assumption that this species represents a member of a new higher ranking taxon within Monostilifera (traditionally: family rank).

12

Molecular species identification of benthic nematodes of the North Sea

—

Philipp Vogt · Maria Miljutina · Michael J. Raupach
Senckenberg am Meer Wilhelmshaven

—

Nematodes or roundworms represent one of the most diverse and dominant taxon in marine benthic habitats. Whereas a morphological identification of many species is challenging, the application of molecular markers represents a promising approach for species discrimination and identification. In this study we used an integrative taxonomic approach, combining both molecular and morphological methods, to characterize nematodes of distinct sex and ontogenetic stages from three sampling sites in the North Sea. Morphospecies were discriminated after a first visual determination, followed by a molecular analysis of the nuclear 28S rDNA: D2-D3 marker. By linking each sequence to a morphological voucher, discordant morphological identification was subject to a so-called reverse taxonomy. Finally, molecular operational taxonomic units (MOTUs) and morphospecies were compared between each of the three sampling sites to assess concordance of methodology. In total, 32 MOTUs and 26 morphospecies were assigned, of which twelve taxa were identified down to species level. Both approaches showed high concordance in taxon assignment (84.4%) except for a cluster comprising various *Sabatieria* species. Our study revealed the high potential of the analyzed fragment as a useful molecular marker for the identification of North Sea nematodes and highlights the applicability of this combined taxonomic approach in general.

13

A phylogeographic study of the North East Atlantic Population of *Pagurus bernhardus* (Linnaeus, 1758) (Crustacea, Decapoda, Paguridae)

—

Sven Rossel [1] · Michael J. Raupach [2]
[1] Carl-von-Ossietzky-Universität Oldenburg, Carl-von-Ossietzky-Straße 9 – 11,
26129 Oldenburg, Germany — [2] Deutsches Zentrum für Marine Biodiversitätsforschung,
AG Molekulare Taxonomie, Südstrand 44, 26382 Wilhelmshaven, Germany

—

Pagurid decapods are an abundant and ecological important benthic taxon of the North Eastern Atlantic Ocean. Anyway, there is only little knowledge about their demographic history and recent population structure. Here, it is unknown if the population of the North Sea and around the British Islands is homogeneous or

descents from different lineages due to a recolonialisation after a Glacial Maximum from different refugia. In this study we analyzed the genetic variability of *Pagurus bernhardus,* the most common and abundant pagurid in this area, using mitochondrial cytochrome *c* oxidase subunit I sequences. We calculated a phylogenetic haplotype network revealing the existence of a homogeneous population in the North Eastern Atlantic Ocean. This was also supported by F_{ST}-values, pairwise mismatch distribution as well as other indices like haplotype or nucleotide diversity.

Fast and furious — Taxonomy and phylogeny of the sand wasp genus *Microbembex*

14

—

Martin Reiss · Michael Ohl

Museum für Naturkunde zu Berlin

—

The Crabronidae are – compared to the other three major clades of digger wasps (Ampulicidae, Heterogynaidae and Sphecidae) – the richest and most diverse group.

Within this clade, the sand wasp tribe Bembicini is a morphologically heterogeneous group of fast flying wasps, which consists of 16 genera. They are most diverse in the New World, whereas just one genus, *Bembix*, is the only bembicine genus on all other continents.

Microbembex is a bembicine genus of 34 described species, whose taxonomy is barely resolved. Being widely distributed in North and South America, these small sand wasps are known from all arid and semi-arid areas. In the course of the study, we could find four undescribed in addition to the 34 known species.

The aim of this study is to revise the genus *Microbembex* taxonomically. Moreover, a phylogenetic analysis of intraspecific relationships will be executed.

Starting to eliminate chaos – Phylogeny of Cirratulidae (Annelida) based on molecular data

15

—

Michael Weidhase · Judith Müller · Christoph Bleidorn

University of Leipzig, Institute of Biology, Molecular Evolution & Animal Systematics, Talstraße 33, 04103 Leipzig, Germany

—

Cirratulidae are a family of sedentary annelids with a worldwide distribution. They exhibit a difficult taxonomic history with many unresolved problems. Possible reasons for their taxonomic uncertainty are complex: Cirratulids possess a diverse reproductive biology. For instance, juveniles and smaller specimens produced by asexual reproduction were sometimes mistakenly described as different species. Furthermore, cirratulids contain presumably progenetic species, which were partially recognized as distinct genera or even classified outside cirratulids, as demonstrated for *Ctenodrilus serratus*. On the other hand, some species seem to comprise a complex of different species, as already suspected for *Cirratulus cirratus* as the most prominent example. Moreover, it is arguable, if typical morphological characters as chaetae shape or tentacle entry are always reliable for species differentiation.

For a better understanding of cirratulid taxonomy and phylogeny we conducted an extensive molecular investigation of this group. Here we present a first contribution to cirratulid phylogeny, based on 16S and 18S rRNA as well as CO1 sequence data. Our investigations support the existence of cryptic species complexes, e.g. *Cirratulus cirratus* or *Cirriformia tentaculata*. Furthermore, the presented findings challenge the splitting of Cirratulidae in bi- and mulit-tentaculated genera, suggesting that the existence of more than one tentacle pair emerge at least two times in cirratulid evolution. Moreover, we provide conclusions concerning the paraphyly of some cirratulid genera and a framework to identify stable characters for determination and description.

16

Homology and evolution of the chaetae in Echiura

—

Thomas Bartolomaeus · Janina Lehrke · Ekin Tilic
Institute for Evolutionary Biology and Ecology, University of Bonn,
An der Immenburg 1, 53121 Bonn, Germany

—

Segmental pairs of dorsal (notopodial) and ventral (neuropodial) chaetal sacs giving rise to a single row of chaetae are an autapomorphy of the Annelida. Each chaeta arises from a chaetal follicle, the innermost cell of which once shaped the chaeta by modulating its apical microvilli during chaetogenesis. Chaetogenesis is restricted to the ventral part of the notopodial and to the dorsal part the neuropodial chaetal sac, so that the sites of chaetal formation are adjacent. Echiura, a small taxon of unsegmented spiralians, possess a pair of ventral chaetae; merely Echiurinae and Urechidae possess one or two caudal rings of chaetae in addition. Molecular data and serially repeated groups of neurons argue for including Echiura into Annelida. This gives rise to ask for the homology and evolutionary origin of the pair of ventral chaeta and the caudal chaetal rings in Echiura. If the ventral pair of chaetae was homologous to a pair of neuropodia, they should arise from two chaetal sacs and possess two laterally located formative sites, while a single chaetal sac and a single formative site would argue for a homology with a single neuropodium. If the caudal ring of chaetae represented elongated and merged rows of neuro- and notopodial chaetae, a corresponding number of chaetal sacs and formative sites should be found. In order to test these expectations we studied chaetogenesis in *Thalassema thalassemum* (Pallas, 1766) from Concarneau (Britany, France) and *Echiurus echiurus* (Pallas, 1767) from the German Bight (North Sea). Like in annelids, chaetogenesis is modulated by a single chaetoblast in both echiuran species. Each chaeta of the ventral pair arises from its own chaetal sac and possesses a lateral site of formation, evidencing that the pair of ventral chaetae in Echiurida is homologous to the pair of neuropodia in Annelida and evolved from neuropodia that fused on the ventral side, while the notopodia were reduced. The caudal ring of chaetae in *Echiurus echiurus* is composed of several chaetal sacs, each of which possess an own formative site. This finding argues against a homology of these rings of chaetae and annelids rows of chaetae. It seems likely that the caudal chaetal rings evolved in a common stem lineage of Echiurinae and Urechidae.

17

Chaetal Type Diversity increases during evolution of Eunicida (Annelida)

—

Ekin Tilic · Thomas Bartolomaeus

Institute of Evolutionary Biology and Animal Ecology, University of Bonn

—

Annelid chaetae are extracellular, chitinous structures formed within an ectodermal pouch, the chaetal follicle. The basalmost cell within the follicle, the chaetoblast, possesses apical microvilli, between which N-acetyle-glycosamine is secreted into the extracellular space where it polymerizes. The definite structure of the chaetae is caused by temporal changes of the microvilli pattern (O'Clair & Cloney 1974). Since chaetae are species and taxon-specific the spaciotemporal pattern of these microvilli must be strictly regulated. We therefore suppose that details of the formation process in addition to structural similarities of the fully differentiated chaetae are a valuable source for phylogeny inference. Hence, comparative studies of chaetogeneses allow making well supported homology hypotheses, which help unravel the sister-group relationships within the Annelida. Recent reconstructions of the annelid ground pattern indicate that early annelids merely had simple capillary chaetae (Struck 2011). It therefore must be assumed that complexity and diversity of chaetae increased during annelid evolution. Once evolved they were passed on to descendants, due to the strictly regulated, conservative modality of chaetogenesis. In order to test the idea of an increasing chaetal diversity and preservation of ancestral chaetal types, we studied chaetal pattern in Eunicida. In addition to internalized aciculae, a variety of chaetal types; i.e. jointed and unjointed hooded hooked chaetae, comb-shaped chaetae, winged capillary chatae and jointed chaetae with elongated tapering blades can be found within this group. By using a recent molecular analysis (Zanol et al. 2010)its hard jaws and its economic importance in the bait industry. Monophyly of Eunicidae has been contradicted in previous molecular and morphological phylogenetic analyses focusing on Eunicida or on its type genus, Eunice. The current study focused on the phylogeny of the family per se combining mitochondrial and nuclear genes in different analyses. It recovered well-resolved phylogenetic hypotheses supporting the monophyly of Eunicidae and Palola, the only monophyletic genus among the genera for which we tested their monophyly (Eunice, Marphysa, Palola, Lysidice and Nematonereis as backbone, we studied the chaetae of selected eunicid species using a variety of methods, such as light microscopy, confocal laser scanning microscopy, scanning and transmission electron microscopy. According to our results the chaetae of the notopodium are rudimentary internal capillary chaetae; externally visible are always the neuropodial chaetae only. Acicula, winged capillary chaetae and unjointed hooded hooked chaetae represent the primary set of chaetae in Eunicida. Within the Eunicida chaetal type diversity increases gradually from basal euncid taxa like *Lumbrineris* BLAINVILLE 1828 to more derived eunicids like *Marphysa* QUATREFAGES 1865 and allow to state that winged capillary chaetae must be evolutionarily older than comb-shaped and jointed capillary chaetae and that unjointed hooded hooks must be older than jointed chaetae.

References

O'Clair R, & Cloney R 1974. Patterns of morphogenesis mediated by dynamic microvilli: chaetogenesis in Nereis vexillosa. Cell Tissue Res. **157**.

Struck TH 2011. Direction of evolution within Annelida and the definition of Pleistoannelida. J. Zool. Syst. Evol. Res. **49**: 340 – 345.

Zanol J, Halanych KM, Struck TH, & Fauchald K 2010. Phylogeny of the bristle worm family Eunicidae (Eunicida, Annelida) and the phylogenetic utility of noncongruent 16S, COI and 18S in combined analyses. Mol. Phylogenet. Evol. **55**: 660 – 76.

Embryology of the tardigrade *Hypsibius dujardini* with a focus on neural development

—

Sandra Treffkorn · Vladimir Gross · Georg Mayer
Animal Evolution and Development, Institute of Biology, University of Leipzig,
Talstraße 33, 04103 Leipzig, Germany

—

Tardigrades are microscopic (up to 1 mm in length) invertebrates that live in permanently or temporarily wet environments. They are widely accepted as a part of the Panarthropoda (Onychophora + Arthropoda + Tardigrada), although exactly how these three groups fit together remains unresolved. To obtain insights into the embryonic development of the last common ancestor of Panarthropoda, we examined the patterns of muscle and neural development in the tardigrade *Hypsibius dujardini* Doyère, 1840. Individual, whole-mount embryos were manually dissected out of the chorion and labeled with a fluorescent marker for filamentous actin (phalloidin-rhodamine) in combination with a nuclear marker (SYBR® Green) to visualize the general organization of the early muscular and nervous systems. Our preliminary results indicate that structures of the nervous system develop in an anterior-to-posterior progression – not simultaneously as previously suggested – with the dorsal brain commissure arising first. The development of the brain is associated with inner and outer connectives and the circumoral nerve ring, followed by the ventral nerve cords and trunk ganglia. We did not find any evidence of a subpharyngeal ganglion, in contrast to previous studies. Muscle development is initiated only after the brain and ventral nerve cords have already formed, beginning with the muscles of the pharynx. However, the outline of the pharynx itself is visible much earlier, around the stage when the segmental mesodermal pouches are present and before the formation of the nervous system. Muscles arise as individual fibers from the very beginning rather than from sheets that would separate later. These results indicate that tardigrade neural development is similar to that of onychophorans and arthropods (except for long germ species), as the nervous system develops in an anterior-to-posterior progression. Consequently, this pattern of neural development was most likely present in the last common ancestor of Panarthropoda.

19

Immunolocalisation of intermediate filament proteins in tardigrades (water bears)

—

Julian Reichelt · Lars Hering · Thomas M. Magin · Georg Mayer

Animal Evolution and Development, Institute of Biology, University of Leipzig,
Talstraße 33, 04103 Leipzig, Germany

—

The presence of intermediate filaments (IFs) is a common feature of metazoan cells. The IFs can be classified into cytoplasmic and nuclear IFs, the latter also known as lamins. While lamins occur ubiquitously among metazoans, the cytoplasmic IFs are characteristic of bilaterally symmetric animals. Arthropods might be the only exception among bilaterians because no cytoplasmic IFs have been identified in these animals thus far (a recent report of isomin in a collembolan requires confirmation). Whether or not cytoplasmic IFs also occur in Tardigrada – one of the closest relatives of arthropods – is still unknown. We therefore analysed the transcriptome of the eutardigrade *Hypsibius dujardini* Doyère, 1840. Based on the identified sequences, we generated antisera against two possible homologs of the corresponding IF proteins. Immunolocalisation on cryosections of *H. dujardini* revealed that one of the putative IF proteins is localised at the nuclear envelope, whereas the other protein is restricted to the cytoplasm of the ectodermal cells. These data suggest that at least one lamin and one cytoplasmic IF protein are present in tardigrades. Our ongoing phylogenetic analyses of IF proteins across bilaterians will clarify whether the ortholog of the corresponding cytoplasmic IF protein gene was lost in the arthropod lineage or whether it evolved in tardigrades.

20

Unexpected diversity of opsin genes in the tardigrade *Hypsibius dujardini* – Insights into the photosensitive system in the last common ancestor of Panarthropoda

—

Lars Hering · Georg Mayer

Animal Evolution and Development, Institute of Biology, University of Leipzig,
Talstraße 33, 04103 Leipzig, Germany

—

To date colour vision – the discrimination of light based on its wavelength components by using multiple visual pigments (opsins) – is only known from vertebrates and arthropods (review Koyanagi & Terakita 2013). The presence of a single visual pigment in Onychophora (velvet worms) and the hypothesis (Hering et al. 2012)t of monochromatic vision in the last common ancestor of Panarthropoda (Onych-

ophora + Tardigrada + Arthropoda) raises the question of whether or not the same condition occurs in Tardigrada (water bears). To clarify this question, we identified the putative opsin genes in the transcriptome of the tardigrade *Hypsibius dujardini* Doyère, 1840 and performed a phylogenetic analysis of a large set of over 400 metazoan opsins and opsin-related genes, including the identified tardigrade sequences. Our screening revealed at least five different opsin genes in Tardigrada, only one of which forms the sister group to the onychophoran visual r-opsin (*onychopsin*) within the clade of visual pigments of Panarthropoda. Three of the five opsins cluster as the sister group to the arthropod c-opsins (*pteropsin*, *Opn3*), which are likely to play a role in the extra-ocular photoreception at least in mosquitos (Koyanagi et al. 2013). Notably, according to our phylogeny the fifth opsin gene of *H. dujardini* is an ortholog of *opsin-5* (*neuropsin*, *Opn5*) – a UV-sensitive pigment that activates the G_i-type G-proteins in the vertebrate retina and the brain (review Koyanagi & Terakita 2013). To our knowledge, the detection of this opsin in *H. dujardini* is the first record of a *neuropsin* in an invertebrate. Our findings confirm the hypothesis of monochromatic vision in the last common ancestor of Panarthropoda, while they also suggest that tardigrades have a remarkably diverse photosensitive system in addition to their visual system.

References

Hering L., et al. 2012: Opsins in Onychophora (velvet worms) suggest a single origin and subsequent diversification of visual pigments in arthropods. Mol Biol Evol. **29**: 3451 – 3458.

Koyanagi M., Takada E., Nagata T., Tsukamoto H., Terakita A. 2013: Homologs of vertebrate Opn3 potentially serve as a light sensor in nonphotoreceptive tissue. Proc Natl Acad Sci USA. **110**: 4998 – 5003.

Koyanagi M., Terakita A. 2013: Diversity of animal opsin-based pigments and their optogenetic potential. BBA-Bioenergetics. doi: 10.1016/j.bbabio.2013.09.003.

21

Two evolutionary pathways of sperm transfer within Sumo Crabs (Crustacea: Decapoda: Brachyura: Dorippoidea)

Juliane Vehof · Gerhard Scholtz · Carola Becker
Humboldt-Universität zu Berlin, Institut für Biologie, Vergleichende Zoologie,
Philippstr. 13, 10115 Berlin, Germany

Within brachyuran crabs, males have evolved highly specialized paired copulatory organs. These are formed by paired penes and two pairs of modified legs (the first and second gonopods), which interact in the transfer of spermatophores into the female sperm storage organs during copulation. The complex morphologies of male and female copulatory organs contain phylogenetic signals that can be used for the reconstruction of internal relationships of Brachyura. For instance, it is still uncertain whether the Dorippoidea are the sister group to the remaining Eubrachyura. One character complex supporting this position are the two last pairs of walking legs, which are positioned dorsally and are used for carrying camouflage-material, as it is the case in the so-called primitive crabs, the "Podotremata".

We used scanning electron microscopy to investigate the gonopods of representatives of the two dorippoid groups, Ethusidae and Dorippidae. Our results indicate two types of sperm transfer within the Dorippoidea. In all cases, the first gonopod forms a tube in which the penis and the second gonopod are inserted during copualtion. However, in Ethusidae, the long and slender second gonopod protrudes beyond the slightly curved first one. Presumably, sperm is transferred by the folded and spined tip of the second gonopod whereas the first gonopod stabilizes the position of the second one. In contrast to this, the first gonopods of the Dorippidae are mostly more stumpy and the distal lumen, referred to as ejaculatory canal, is longitudinally closed with a narrow opening at the curved tip. The second gonopod is shorter than the first one and sperm is transferred by a pumping mechanism: The second gonopod pushes sperm upwards inside the ejaculatory canal of the first gonopod where it is released from the distal opening into the sperm storage organ of the female. In dorippids, the first gonopod functions as the main sperm-carrier whereas in the Ethusidae, sperm is transferred by the second gonopod. These differences are interesting and indicate a certain evolutionary flexibility of the sperm transfer system. Nevertheless, the phylogenetic polarization of these characters is not yet clear.

22

The male copulatory system of spider crabs (Decapoda: Brachyura: Heterotremata: Majoidea)

—

Katja Jaszkowiak · Gerhard Scholtz · Carola Becker
Humboldt-Universität zu Berlin, Institut für Biologie, Vergleichende Zoologie,
Philippstr. 13, 10115 Berlin, Germany

—

The traditional classification of Eubrachyura (true crabs) into the two large taxa Heterotremata and Thoracotremata is based on the position of sexual openings (gonopore). While the Thoracotremata have been accepted as monophyletic, the Heterotremata are currently under controversial debate. It seems unlikely that they are monophyletic and the relationships among heterotreme groups are far from being resolved. We address these issues by investigating male gonopods. These are transformed legs that are no longer used for locomotion but for copulation. The external copulatory system in male brachyurans is situated under the ventrally folded pleon; it is constituted by the paired first and second gonopods and the likewise paired tube–like extensions of the gonopores, the penes, located symmetrically on each body half. They are part of a complex functional unit that allows the transfer of sperm to the female. The Majoidea is a diverse group within the heterotreme brachyurans. In this study, we investigate species of three different majoid groups (Inachidae, Majidae and Epialtidae) using scanning electron microscopy. The gross morphology as well as cuticular fine structures such as setae on the gonopod surface was compared. Both gonopods show numerous highly similar characters among the species investigated. The first gonopod is long and slender with a slightly bulbous, pointed tip that shows a sub-terminal opening surrounded by denticles. The second gonopod is always shorter than the first and has a compact, smooth shaft. The distal tip bears an appendix and an apical girdle with denticles. During copulation the distal tip of the first gonopod penetrates the female vagina. Both penis and second gonopod are inserted inside the tubular first gonopod by its basal opening. The penis releases the sperm into the base of the first gonopod. The transport of sperm into the female seminal receptacle is conducted by pumping movements of the second gonopod supported by the pleon. Further comparative studies will show whether the similarities of characters of gonopod morphology within the three different groups of majoid species are apomorphic characters that support the monophyly of Majoidea.

23

Tentorial mobility in geophilomorph centipedes (Chilopoda)

—

Johannes Schulz [1] · Gregory D. Edgecombe [2] · Markus Koch [1]
[1] Biozentrum Grindel und Zoologisches Museum, Universität Hamburg, Germany —
[2] Natural History Museum London, U.K.

—

The feeding habits of Geophilomorpha are exceptional among centipedes in being predominantly suctorial based on extraoral digestion. As in arachnids, anatomical transformations correlated with this feeding mode in geophilomorphs involve peculiarities of the foregut that forms a pharyngeal sucking pump and a pipette-shaped oesophagus, increasing exposure of the mouth to the environment under gradual reduction of a preoral chamber, and the (primary) loss of biting ability. The latter was considered thus far as the main reason for why in geophilomorphs the tentorial complex of the head, i.e. a sclerotic clasp of the head capsule that gives rise to the cuticular head endoskeleton, no longer performs "swinging" movements that in centipedes with biting mandibles form integral part of their biting mechanism. Recent comparative studies of head morphology, however, revealed that the articulation between the mandibular gnathal lobes and the tentorial complex is maintained in most geophilomorphs, and indicated that the tentorial complex is still mobile in at least the basalmost offshoot of the Geophilomorpha, the Placodesmata. In order to test this hypothesis we studied the head anatomy more thoroughly based on histological sections. Here we present anatomical 3D-reconstructions of the mandibles and tentorial complex, including their musculature, for *Dicellophilus carniolensis* (Placodesmata: Mecistocephalidae) and *Hydroschendyla submarina* (Adesmata: Schendylidae). Despite differences in the shape and arrangement of the mandibles and tentorial complex, their muscular equipment surprisingly shows marked correspondences in these species. Our results support the view that the tentorial mobility and its involvement in mandibular mechanisms is maintained not only in the Placodesmata but primarily also in the Adesmata among geophilomorphs, including an unexpected coupling of the tentorial and mandibular movements with movements of the hypopharynx.

24

Spiracles and other non-gonopodal morphological characters in the Australian genus *Pogonosternum* (Diplopoda: Polydesmida: Paradoxosomatidae)

—

Peter Decker
Senckenberg Museum für Naturkunde Görlitz, Am Museum 1, 02826 Görlitz, Germany

—

The most important characters for distinguishing, identifying and describing species in the order Polydesmida are those of the male gonopods, which replace the eighth pair of legs in mature males and are used in sperm transfer. In most families of Polydesmida, obvious non-gonopodal characters or a combination of gonopodal and non-gonopodal characters can be used to assign species to higher taxonomic levels, such as genus or subfamily. This is often not possible in the speciose family Paradoxosomatidae, where differences in obvious characters, e.g. tergite structure, are small. Previous studies on little-used taxonomic characters in Polydesmida, e.g. the structure and ultrastructure of the spiracles, male leg setae, spinnerets, prozonite cuticle and limbus, indicate that these characters can be useful at species, genus and higher taxonomic levels. In this study the spiracles, color pattern, male leg brushes and female leg coxae were studied using light microscopy and SEM in

10 species in the Australian paradoxosomatid genus *Pogonosternum*, which is native to Victoria, New South Wales and Tasmania.

The preliminary results indicate that within *Pogonosternum* several types of spiracles exist, with differences in shape of the rim, the spiracular opening and the spiracular filter. Leg brushes, which are pads of dense setae on the tarsus of the walking legs in mature males, are restricted to a limited number of anterior legs in each species, ranging in *Pogonosternum* to leg pairs seven to eleven. Further, the females of some species bear a cone-shaped process ventrally on the leg two coxa, and more or less obvious differences in the color pattern can be observed. These non-gonopodal characters are being used, together with gonopod details, to distinguish and describe or distinguish species of *Pogonosternum*.

25

Comparative biogeography of freshwater mollusks inhabiting the "Roof of the World" (Tibetan Plateau)

—

Catharina Clewing[1] · Christian Albrecht[1] · Parm Viktor von Oheimb[1] ·
Frank Riedel[2, 3] · Thomas Wilke[1]
[1] Department of Animal Ecology and Systematics, Justus Liebig University Giessen,
Heinrich-Buff-Ring 26 – 32, 35392 Giessen, Germany — [2] Institute of Geological Science,
Freie Universität Berlin, Malteserstr. 74 – 100, 12249 Berlin, Germany —
[3] Laboratory of Plateau Lake Ecology and Global Change, College of Tourism
and Geography, Yunnan Normal University, No.1 Yuhua District,
Chenggong, Kunming 650500, China

—

The Tibetan Plateau, located in Central Asia, has a mean elevation of ~ 5000 m and covers an area of around 2.5 million km², thus it is the highest and largest plateau on earth. This high-elevation area is characterized by extreme and unstable environmental conditions (e.g. prolonged frost periods), representing a great challenge especially for aquatic organisms such as freshwater mollusks. Here we use a comparative approach based on large-scale phylogenies and relative clock rates of four different freshwater mollusk taxa to analyze their phylogenetic and biogeographical histories (i.e. comparison of colonization events). Our meta-analysis supports previous studies showing comparatively high extant clade/lineage diversity within most of the taxa. Given that these Tibetan Plateau lineages do not form monophyletic groups, multiple colonization events have to be assumed. Interestingly, the two prominent pulmonate gastropod genera, *Gyraulus* and *Radix* (3 and 4 clades/lineages, respectively) comprise the comparatively oldest lineages persisting on the plateau at least since the early Pleistocene. Subsequently, *in situ* diversification took place and lead to the evolution of endemic lineages on the plateau. In contrast, the highly diverse Tibetan Plateau bivalves of the family Sphaeriidae (6 clades/lineages) are derived from comparatively recent colonizations with only a single endemic lineage known to date. We discuss the importance of the general geological history of the Tibetan Plateau as well as different dispersal and life-history strategies in order to explain the observed patterns. Finally, our study might contribute to the general knowledge of the biogeographical history of freshwater mollusks especially in high-elevation areas.

26

Molecular biogeography of the Western Palaearctic spurge hawkmoth (*Hyles euphorbiae* complex; Lepidoptera, Sphingidae) – Diverse patterns of hybridisation and the signals of a contact zone in motion

—

Michael B. Mende[1] · Heiko Stuckas[1] · Manuela Bartel[1]
Anna K. Hundsdoerfer[1, 2]
[1] Museum für Tierkunde, Senckenberg Naturhistorische Sammlungen Dresden, Königsbrücker Landstr. 159, 01109 Dresden, Germany — [2] Biodiversität und Klima Forschungszentrum (BiK-F), Senckenberganlage 25, 60325 Frankfurt am Main, Germany

—

The research on hybridization has become a major field of molecular ecology and general patterns have been discovered quite recently. For instance, the vast majority of field surveys as well as simulations showed that introgression generally leads to mito-nuclear discordance due to mitochondrial capture of the invading taxon from the local one for simple stochastic reasons. The spurge hawkmoth (*Hyles euphorbiae* complex) is a paramount system to study such molecular mechanisms of hybridisation. Previous studies on the biogeography of larval (and adult) colour patterns as well as mitochondrial lineages suggest two main lineages – the Asio-European *euphorbiae* and the Afro-Macaronesian *tithymali* – with potentially several, geographically separated areas of hybridisation and/or fusion. We nearly tripled the sampling extent of a previous survey to about 900 individual mtDNA sequences (2300bp of COI/II) from the entire distribution range and additionally genotyped 12 microsatellite loci to assess nuclear diversity.

No molecular traces of *tithymali* could be found in Galicia despite high affinities in larval colour patterns, whereas the putative hybrid population on Malta is highly admixed in both molecular markers. In contrast again, similar-looking populations in Southern Italy and Aegean Islands congruently show strong mito-nuclear discordance of *tithymali*-derived mitochondrial lineages with *euphorbiae*-

related nuclear markers. However, in contrast to the general pattern (see above), a historic DNA study showed that the *tithymali*-derived mitochondria in Italy only recently rose to their current high frequency in correlation with climate warming during the 20th Century, suggesting that mitochondria might not be selectively neutral. Additionally, statistical tests and the distribution of allele clines suggest a high expansion potential of the entire species complex and a moving hybrid area across Northern Africa to Central Italy. In conclusion, patterns of hybridisation in a wide, heterogeneous distribution range can be very complex, especially if they are potentially influenced by ongoing environmental changes such as climate oscillations.

27

The Great American Biotic Interchange: a meta-analysis of sequence data

—

SEBASTIAN KLAUS[1] · JASMIN BAIER[2] · MARTIN SCHULZE[2] · ABEL BATISTA[3]
DIETER THOMAS TIETZE[2]
[1] Chengdu Institute of Biology, Chinese Academy of Sciences, Chengdu, China;
Dept. of Ecology and Evolution, J.W. Goethe University, Frankfurt am Main, Germany —
[2] Dept. of Ecology and Evolution, J.W. Goethe University, Frankfurt am Main, Germany —
[3] Herpetology Section, Senckenberg Research Institute and Natural History Museum
Frankfurt am Main, Germany

—

The connection and interchange of previously independently evolving biotas is known to be a major driver that shaped the biodiversity as we know it today. Of these events, the Great American Biotic Interchange (GABI) after the establishment of a terrestrial connection of North and South America via the Isthmus of Panama can be regarded as the most thoroughly investigated. It is not only a model how biotic interchange operates and by which parameters it is influenced, it is also a major event used for calibrating molecular clocks for phylogenetic divergence time estimation. As the resulting substitution rates are used to calibrate phylogenies for taxa all over the world, an ever-increasing number of biogeographical and ecological studies heavily rely on the geological dating of the closure of the Panamanian Isthmus. Recent geological evidence, however, questions the traditional dating of the closure to the Pliocene at c. 3 Ma and points to a much earlier terrestrial connection of the continents during the Middle Miocene (c. 15 Ma). We decided to investigate the age of biotic interchange during GABI using a meta-analytical approach. We calculated divergence dates associated with dispersal between North and South America for seven bird and ten mammal families in BEAST using external substitution rates. Ancestral-area reconstruction was conducted under the

Geographic State Speciation and Extinction model (R package diversitree). When counting dispersal events per 1-Ma bin, we accounted for uncertainty phylogenetic reconstruction and node dating, respectively.

28

The Isthmus of Panama debate: a biological perspective

—

Carina Marek[1] · Christoph D. Schubart[2] · Thomas Wilke[1]
[1] Department of Animal Ecology & Systematics, Justus Liebig University Giessen, Heinrich-Buff-Ring 26 – 32, 35392 Giessen, Germany — [2] Biology 1, University of Regensburg, Regensburg, Germany

—

The rise of the Isthmus of Panama is one of the best studied geographic vicariant events. Recent studies challenge the widely accepted opinion that the emergence of the Isthmus and its final closure occurred during the Late Pliocene (approximately 3 million years ago) and allocate this event much earlier, around 15 million years ago (Ma). The exact age of the closure is, however, important for studies that use the time of closure as internal calibration point in molecular clock analyses. The proposed shift of the age of this closure from 3 to 15 Ma will thus not only have a considerable impact on our understanding of the historical biogeography of the American continents, but also on the timing of numerous phylogenies that used the Isthmus as calibration point for molecular dating.

Here we investigate the timing of the Isthmus emergence from a biological perspective by studying transisthmian sister species of the mangrove crab genus *Sesarma* and of the mud crab family Panopeidae. These studied species pairs have evolved as a result of the emergence of the Isthmus of Panama. Our inferred trees reveal the presence of two well supported transisthmian sister species complexes within both the genus *Sesarma* and the family Panopeidae. In order to estimate divergence times between the transisthmian sister species we employ an independent external molecular clock rate in a Bayesian phylogenetic framework. Our results are in concordance with the prevailing opinion (indicating an isthmian closure around 3 Ma) and thus do not support the recently proposed hypothesis of a middle Miocene closure around 15 Ma.

A novel target enrichment strategy for phylogenomic analyses of sphecid wasps

—

Manuela Sann[1] · Christoph Mayer[2] · Alexander Donath[2] · Ralph S. Peters[2] · Oliver Niehuis[2] · Christoph Bleidorn[3] · Michael Ohl[1]

[1] Museum für Naturkunde zu Berlin, Germany — [2] Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany — [3] University of Leipzig, Institute for Biology, Leipzig, Germany

—

Sphecid wasps are a morphologically and behaviorally heterogeneous group of aculeate Hymenoptera and comprise about 10,000 described species. Together with the species-rich bees (Anthophila), they form a well-supported monophyletic group named Apoidea. To understand the phylogeny and evolution of Apoidea, we compiled a taxonomic sampling for molecular phylogenetic analyses that includes all major extant lineages of sphecid wasps as well as selected bees and outgroup taxa.

We aim to conduct a phylogenomic analysis that is based on a target DNA enrichment approach for Illumina multiplexed Next Generation Sequencing. Annotated genomes of a set of reference species as well as 24 transcript libraries of Crabronidae and Sphecidae from the 1KITE project (www.1kite.org) were used to detect a total of 5.537 single-copy orthologous protein-coding genes. Based on the *Nasonia vitripennis* gene models, the aligned transcript sequences were spliced into 25.016 coding exons. Of these, only gap-free multiple nucleotide sequence alignments that contain a nucleotide sequence from at least one representative of the 24 sphecid wasps from the 1KITE project, were used to search for potential DNA target regions. Target regions of 240bp in length were tiled into 120-bp-long baits with a new bait every 20bp. Finally, using a clustering approach, bait-binding sequences were clustered into groups that differ less than 6 % from each other. This was used to generate artificial bait sequences that exhibit the smallest possible maximum distance to any sequence in a given sequence cluster. We designed 73,719 artificial baits to capture 486 coding exons.

Initial results based on analyzing 16 test species revealed that artificial baits highly successfully enrich the target DNA of both closely and distantly related Hymenoptera.

To shed light on the evolutionary history of sphecid wasps, we intend to study 192 of 301 currently recognized sphecid wasp genera. Due to this, it should be feasible to reconstruct the phylogenomic relationships of the major lineages within the apoid wasps.

30

Male-biased dispersal promotes gene flow on large scale in the subterranean army ant *Dorylus* (*Typhlopone*) *fulvus*

—

M. Benjamin Barth[1] · Robin F. A. Moritz[2] · Christian W. W. Pirk[3]
F. Bernhard Kraus[2]
[1] Museum of Zoology, Senckenberg Natural History Collections Dresden,
Konigsbrücker Landstr. 159, 01109 Dresden, Germany — [2] Department of Biology,
Martin-Luther-University Halle-Wittenberg, Hoher Weg 4, 06120 Halle (Saale),
Germany — [3] Department of Zoology and Entomology, University of Pretoria,
Pretoria 0002, South Africa

—

Sex-biased dispersal is a widespread phenomenon in the animal kingdom and strongly influences gene flow and population structure. Particularly army ants, which are important key-stone species in the tropics and subtropics, are prone to population fragmentation and isolation due to their extraordinary mating system: Permanently wingless queens propagate via colony fission, while only the males disperse in mating flights. Here we report on sex-biased dispersal and genetic population structuring in the subterranean African army ant *Dorylus* (*Typhlopone*) *fulvus*. By using maternally inherited mtDNA and bi-parentally inherited microsatellites we found strong biogeographical structuring of mtDNA haplotypes, in contrast to a significantly weaker pronounced microsatellite genetic population structure. Strong mtDNA and lower microsatellite genetic differentiation translated to a more than an order of magnitude larger male migration rate compared to that of queens. This reflects the low motility of queens and strong, promiscuous dispersal by the well flying males. Thus, *D. fulvus* males appear to be the sex to promote gene flow on large scale. With this study we aim to achieve a better understanding of how the evolution of sex specific dispersal patterns and mating systems shape the biogeography and population structure of species.

31

LibrAlign – A GUI library for displaying and editing multiple sequence alignments and attached data

—

Ben C. Stöver · Kai F. Müller

Institute for Evolution and Biodiversity, WWU Münster, Hüfferstr. 1,
48149 Münster, Germany

—

Several applications currently developed in our group and by our cooperators deal with multiple sequence alignments (MSA) or associated raw and meta data, and allow the user to view and edit it in a graphical user interface (GUI). Instead of implementing independent solutions for these different tasks, we decided to create a library containing powerful and reusable common GUI components. Since this library is open source (GNU GPL 3) it can be used and extended by other researchers, who are then able to focus on the core functionality of their applications, but can still provide a user-friendly GUI.

Besides components allowing the displaying and editing of MSAs, several types of data (e.g. trace files, comments, statistical sequence information, positions of tandem repeats, hairpins or inversions) can be attached either to single sequences or to the alignment as a whole. All these data views implement a common interface that makes it easy for developers to create new custom views. Several components from our library (e.g. displaying different types of data) can be connected to each other in the application they are embedded in, so that the user can scroll through one of them while all others will automatically display the data associated with the current position.

LibrAlign is fully interoperable with the BioJava API and all components are provided in a native Swing and a native SWT version (the two major GUI frameworks for Java), so that they can be integrated into any Java GUI application, including projects based on the Eclipse Rich Client Platform or Bioclipse.

Several software projects based on LibrAlign are currently in development in- and outside our group. Among those are (i) the Taxonomic Editor of the EDIT platform which is extended to support sequence and alignment associated data for the Campanula portal of EDIT, (ii) a new version of the alignment editor PhyDE, (iii) AlignmentComparator (an application to visualize differences between alternative automatic and manual alignments, which we currently use in study investigating the influence of manual alignment corrections on phylogenetic studies), and (iv) HIR-Finder (an application which locates microstructural mutations like tandem repeats possibly associated with hairpins).

LibrAlign download: http://bioinfweb.info/LibrAlign

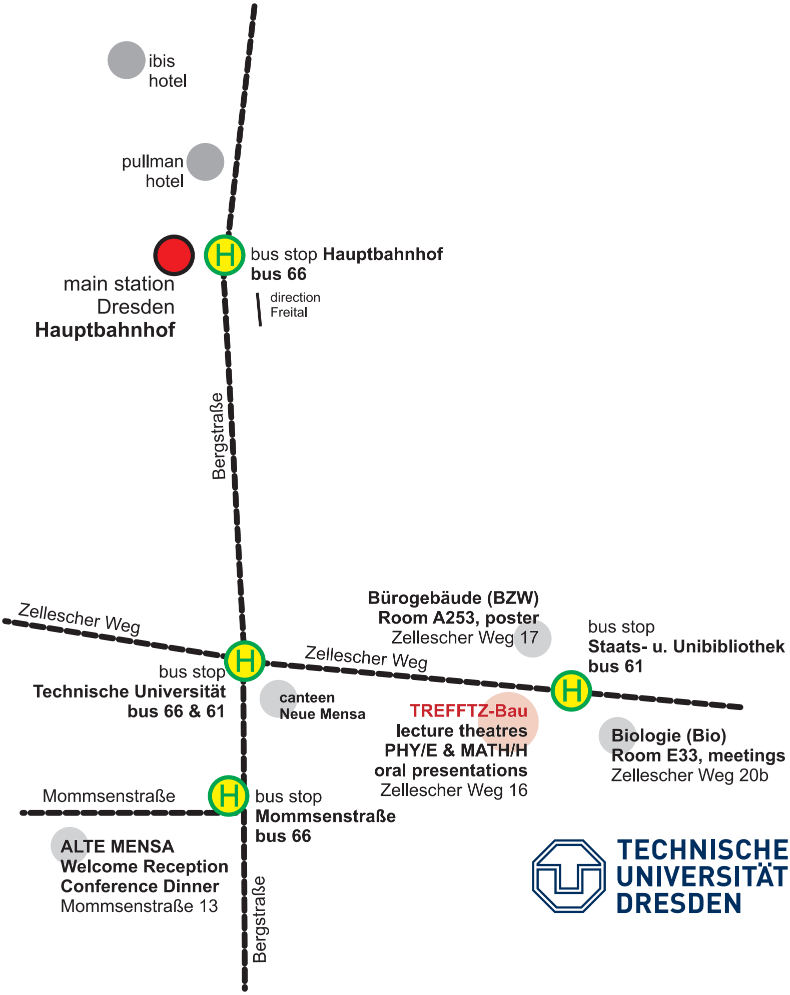
Alphabetical table of contents

Alphabetical table of contents

Alphabetical table of contents

Conference Venue

TREFFTZ-Bau · Zellescher Weg 16 · 01069 Dresden



Conference Venue

"Trefftz-Bau" · Haus A — TU Dresden
Zellescher Weg 16 · 01069 Dresden · Germany

https://navigator.tu-dresden.de/karten/dresden/geb/tre

Schweizerbart
Science Publishers

Springer
Life Sciences · www.springer.com

TECHNISCHE
UNIVERSITÄT
DRESDEN

SENCKENBERG
world of biodiversity

ISBN

978-3-910006-49-2