Systematics 2008

Programme and Abstracts

Göttingen 7-11 April 2008

10th Annual Meeting of the
Gesellschaft für Biologische Systematik

18th International Symposium
„Biodiversity and Evolutionary Biology“
of the German Botanical Society

Edited by S. Robbert Gradstein, Simone Klatt, Felix Normann,
Patrick Weigelt, Rainer Willmann and Rosemary Wilson

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Systematics 2008, Göttingen

Tuesday, 8 April	Room 010	8:30 – 12:00 **Opening and Plenary Session I** Progress in deep phylogeny	
		13:30–15:00	15:30–16:30
	Room 009	**Session 1** Insect phylogeny	**Session 4** Phylogenomics of lower Metazoa
	Room 008	**Session 2** Plant phylogeny I	**Session 5** Plant phylogeny II
	Room 007	**Session 3** Speciation	**Session 6** Reticulate evolution I
	Room 006		**Session 7** Taxonomy and classification

Wednesday, 9 April	Room 010	8:30 – 12:00 **Plenary session II** Speciation and phylogeography	
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	Room 009	**Session 8** Animal phylogeny and classification	**Session 12** Animal phylogeography
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Thursday, 10 April	Room 010	8:30 – 12:00 **Plenary session III** New trends in biological systematics	
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	Room 008	**Session 17** Structure and evolution – animals	**Session 20** Structure and evolution – plants
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and Rainer Willmann
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Volume Editors

S. Robbert Gradstein	Simone Klatt	Felix Normann
Patrick Weigelt	Rainer Willmann	Rosemary Wilson

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15.00 Meeting of curators (Room 006)

15.00 Meeting of the Young Systematists (Room 007)

18.00-22.00 Welcoming party (Mensa 2, Wilhelmsplatz)

Tuesday, 8 April

8.00-18.00 Registration (Foyer ZHG)

8.30-9.00 Welcome and opening remarks (Room 010)

Robbert Gradstein and Rainer Willmann, Congress organisers

Kurt von Figura, President Georg-August University Göttingen

Regine Jahn, President GfBS

Volker Wissemann, Chairman DBG – Section Biodiversity and Evolutionary Biology

9.00-12.00 Plenary session I: Progress in deep phylogeny (Room 010)

Chair: Gerhard Haszprunar

9.00 Wolfgang Wägele: Deep metazoan phylogeny: on the relevance of data quality

9.30 Thomas Bartolomaeus: Deep metazoan phylogeny – the morphological perspective

10.00-10.30 Coffee break

10.30 Hans-Peter Schultze: Interrelationships of lower vertebrates: current agreements and controversies

11.00 Harald Schneider: Untangling the deep nodes of the land plant phylogeny

11.30 Mark W. Chase: The angiosperm tree of life – morphology-rich but still poorly understood

12.00-13.30 Lunch break

13.30-15.00 Session 1: Insect phylogeny (Room 009)

Chair: Ulrike Aspöck

13.30 Hans Pohl, Rolf G. Beutel: The phylogeny and evolution of Strepsiptera (Hexapoda)

13.45 *Volker Lohrmann, Christoph Bleidorn, Lars Podsiadlowski & Michael Ohl: Molecular phylogeny of Apoidea (Hymenoptera) with special emphasis on sphecid wasps

14.00 *Bastian Fromm, Steffen Roth, Reinhard Predel: A proteomic approach for studying insect phylogeny: - identification of Capa-peptides in cockroaches

14.15 *Regina Jäckel: Phylogeny of the flea beetle genus *Altica* (Chrysomelidae, Alticinae) and the impact of endoparasites on population structure, isolation and speciation

14.30 *Frank Hünefeld, Niels P. Kristensen: The evolution of the female postabdomen and genitalia in primitive moths (Insecta: Lepidoptera)

14.45 Thomas Buckley, Sven Bradler: Extreme convergence in stick insect evolution: phylogenetic placement of the rarest insect of the world (Insecta: Phasmatodea)

15.00-15.30 Coffee break

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13.30-15.00 Session 2: Plant phylogeny I (Room 008)

Chair: Frank Hellwig

13.30 Andreas Worberg, Dietmar Quandt, Nadja Korotkova, Thomas Borsch: Phylogenetic analysis of Rosids using fast evolving and non-coding chloroplast markers

13.45 Ulrike Brunken, Clemens Bayer: Floral structure and phylogeny of Malvaceae-Grewioideae

14.00 Galina Degtjareva, Dmitry Sokoloff, Tagir Samigullin, Carmen Valiejo-Roman: Molecular phylogeny of the genus *Anthyllis* (Leguminosae: Loteae): evidence for long-branch attraction in parsimony analysis of nrITS data

14.15 Mike Thiv, Michael Barfuß, Gerald Schneeweiss: Evolving to the peaks: phylogeny and habitat evolution in the European endemic Phyteuma (Campanulaceae)

14.30 *Stefan Kattari, Christian Bräuchler: Phylogeny and biogeography of Teucrium and allies

14.45 *Andreas Fleischmann, Harald Meimberg, Günther Heubl: Phylogeny of the genus *Heliamphora* (Sarraceniaceae), with special focus on biogeography and character evolution

15.00-15.30 Coffee break

13.30-15.00 Session 3: Speciation (Room 007)

Chair: Marcus Koch

13.30 Karol Marhold, Jaromír Kučera, Judita Lihová: *Cardamine maritima* (Brassicaeae) and related species - speciation in the Balkan and Apennine Peninsulas

13.45 *Corinna Laschke, Lückmann K., Hurka H., Neuffer B.: Evolution within the genus *Diplotaxis* (Brassicaceae) – the SI-System

14.00 Aniuska Kazandjian: The *Indigofera pratensis* complex (Fabaceae): morphological and molecular approaches

14.15 Uraiwan Arunyawat, Wolfgang Stephan, Thomas Städler: Population genetic approach to speciation in two closely related wild tomato species (*Solanum peruvianum* and *S. chilense*)

14.30 *Jennifer Hohagen, Stefan Koenemann: Genetic variability in sympatric species of the genus *Niphargus* (Crustacea, Amphipoda)

14.45 *Michael Braun, Michael Wink: Speciation Events in Australasian Parrots (Psittaciformes)

15.00-15.30 Coffee break

15.30-16.30 Session 4: Phylogenomics of lower Metazoa (Room 009)

Chair: Gert Wörheide

15.30 *Kerstin Pick, Fabian Schreiber, Burkhard Morgenstern, Gert Wörheide: Phylogenomics of sponges (Phylum Porifera)

15.45 Christoph Bleidorn, S. Hartmann, T.H. Struck, I. Eeckhaut, M.C. Milinkovitch, J. Selbig, R. Tiedemann: Myzostomid phylogenomics: on congruence and incongruence of gene partitions

16.00 *Martin Helmkampf, Torsten H. Struck, Iris Bruchhaus, Bernhard Hausdorf: Phylogenomic analyses firmly place lophophorates within Lophotrochozoa

16.15 *Fabian Kilpert, Lars Podsiadlowski: Genome morphology of mitochondria and the phylogeny of Isopods

16.30-18.00 Poster session I (Foyer ZHG)

15.30-16.30 Session 5: Plant phylogeny II (Room 008)

Chair: Hartmut Hilger

15.30 Saleh A. Khan, Sylvain G. Razafimandimbison, Birgitta Bremer, Sigrid Liede-Schumann: Phylogenetic relationships within Sabiceeae s.l. (Rubiaceae)

15.45 *Inge Groeninckx, De Block P., Smets E. and S. Dessein: Origin and evolution of the Malagasy Spermacoceae *s.lat.* (Rubiaceae)

16.00 *Maia Gurushidze: Evolution, diversification and biogeographic patterns in *Allium*

16.15 Nikolai Friesen: Place of origin of the genus *Allium*: Key study of the subgenus *Amerallium*

16.30-18.00 Poster session I (Foyer ZHG)

15.30-16.30 Session 6: Reticulate evolution I (Room 007)

Chair: Frank Blattner

15.30 Ovidiu Paun, Michael F. Fay, Mark W. Chase: Genetic and epigenetic consequences of allopolyploidization in *Dactylorhiza* (Orchidaceae)

15.45 *Karol Krak, Judith Fehrer, Jindřich Chrtek: Reticulation, speciation and patterns of molecular evolution in *Hieracium* (Asteraceae)

16.00 *Cordula Blöch, Hanna Weiss-Schneeweiss, Michael Barfuss, Carolin Rebernig, Josè Luis Villaseñor, Tod Stuessy: Phylogeny of the genus *Melampodium* and the development of the x = 10 chromosomal line

16.15 *Neela Enke, Birgit Gemeinholzer: Mechanisms of speciation: hybridisation and karyotype evolution in *Crepis* (Cichorieae, Compositae)

16.30-18.00 Poster session I (Foyer ZHG)

15.30-16.30 Session 7: Taxonomy and classification (Room 006)

Chair: Thomas Hörnschemeyer

15.30 Lars Vogt: On historical kinds

15.45 Galina Degtjareva, Tatiana Kramina, Tagir Samigullin, Dmitry Sokoloff, Carmen Valiejo-Roman: Taxonomy of the genus *Lotus* (Leguminosae-Loteae): evidence from molecular and morphological data

16.00 E. Rastegar Pouyani, S. Kazemi Noureini, U. Joger and M. Wink: Molecular phylogeny and intraspecific differentiation of the *Eremias velox* complex of the Iranian Plateau and Central Asia (Reptilia, Lacertidae)

16.15 Ulrich Joger, Svetlana Kalyabina-Hauf, Nikolaus Stümpel, Alexander Zinenko: Systematics of the *Vipera berus* group – a riddle

16.30-18.00 Poster session I (Foyer ZHG)

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Wednesday, 9 April

8.30-12.00 Plenary session II: Speciation and phylogeography (Room 010)

Chair: Tod Stuessy

8.30 Joachim W. Kadereit: Plant speciation in the Quaternary

9.00 Frank R. Blattner: Hybridization and polyploid formation – evolutionary accidents or driving forces of biodiversity

9.30 Peter Linder: Radiation, diversity and history

10.00-10.30 Coffee break

10.30 Axel Meyer: The origin of adaptive radiations: patterns and processes of speciation and phenotypic diversification in cichlid fishes

11.00 Heike Feldhaar: Influence of host-identity vs. host-distribution on the radiation of obligately plant-associated ants

11.30 Alfried P. Vogler: DNA profiling of insect communities: what can be learned about species and speciation?

12.00-13.30 Lunch break

13.30-15.00 Session 8: Animal phylogeny and classification (Room 009)

Chair: Andreas Schmidt-Rhaesa

13.30 Alexander Fürst von Lieven, Marcel Humar: A cladistic reexamination of Aristotle's classification of animals

13.45 *Juliane Zantke, Gerhard Steiner: Homeoboxes in tardigrades: a PCR-based survey of *Milnesium tardigradum*

14.00 *Alexander Kieneke, Wilko H. Ahlrichs: A fresh look at Gastrotricha phylogeny revealed by a new set of morphological characters

14.15 *Jana Hoffmann, Carsten Lüter: Molecular phylogeny of the Thecideoidea (Brachiopoda)

14.30 Günter Purschke, Verena Wilkens: Ultrastructure of pigmented cerebral eyes in the polychaete *Scoloplos armiger* (Orbiniidae, Annelida) – implications for annelid phylogeny and evolution

14.45 *Martin Osterholz, Lutz Walter, Christian Roos: A retroposon based phylogeny of the order Primates

15.00-15.30 Coffee break

13.30-15.00 Session 9: Plant phylogeography I (Room 008)

Chair: Joachim W. Kadereit

13.30 *Gertrud Schorr, Norbert Holstein, Antoine Guisan: The origin of species in *Primula* sect. *Auricula* – a combined species distribution modelling (SDM) and phylogeographical approach

13.45 *Patrick Teege, Alexander Köhl, Gudrun Kadereit: Multiple origin and wide dispersal of northwest European *Salicornia* "species"

14.00 *Katharina Bardy, Peter Schönswetter, Dirk C. Albach: Phylogeography on the Balkan Peninsula – examples from *Veronica* (Plantaginaceae)

14.15 Matthias Kropf: Peripheral populations: the case of *Anthyllis montana* ssp. *jacquinii* (Fabaceae) at its northern distribution limit

14.30 Péter Szövényi, Zsófia Hock, A. Jonathan Shaw, Helena Korpelainen: Nucleotide polymorphism and selective sweeps in natural populations of the bryophyte *Sphagnum fimbriatum*

14.45 *Christiane Kiefer, Christoph Dobes, Marcus Koch: The independence of genetic and species diversity in *Boechera* is revealed by a continental wide phylogeographic study

15.00-15.30 Coffee break

13.30-15.00 Session 10: Radiation (Room 007)

Chair: Volker Wissemann

13.30 Heike Wägele, Yvonne Grzymbowski: Photosynthesis in Sacoglossa (Opisthobranchia, Gastropoda)

13.45 *Korinna Esfeld, Mike Thiv, Marcus Koch: The use of nuclear coding genes for phylogenetic reconstructions in an adaptive radiation

14.00 Arno Wörz, Heike Diekmann: Classification and evolution of the genus *Eryngium* (Apiaceae-Saniculoideae): results of morphological and fruit anatomical studies

14.15 Matthias H. Hoffmann, Martin Röser: Taxon recruitment of the arctic flora

14.30 *Jana Deppermann, Martin Husemann: Phylogeny and bioacoustic evolution in the genus *Sphingonotus*

14.45 *Thekla Pleines: Gene expression analyses reveal differences in stress tolerance in three closely related *Hordeum* species (Poaceae)

15.00-15.30 Coffee break

13.30-15.00 Session 11: Taxonomy and barcoding (Room 006)

Chair: Regine Jahn

13.30 Swen C. Renner, Merijn M. Bos, Christoph L. Häuser: Towards a Global Assessment of Taxonomic Needs and Capacities: what taxonomists do we need where?

13.45 Malte Elbrächter, Marc Gottschling, Tania Hildebrand-Habel, Helmut Keupp, Rolf Kohring, Jane Lewis, K.J. Sebastian Meier, Marina Montresor, Michael Streng, Gerard J.M. Versteegh, Helmut Willems, Karin Zonneveld: Agenda for Calcareous Dinoflagellate Research (Thoracosphaeraceae, Dinophyceae)

14.00 Judith Fehrer, Štěpánka Slavíková-Bayerová, Alan Orange: Large genetic divergence of new, morphologically similar species of sterile lichens from Europe (*Lepraria*, Stereocaulaceae, Ascomycota): concordance of DNA sequence data with secondary metabolites

14.15 Ulrike Lohwasser, Anke Dittbrenner, Hans-Peter Mock, Andreas Börner: Intraspecific classification of poppy (*Papaver somniferum*) useful as detection of drug distribution?

14.30 *Jonas Zimmermann, Birgit Gemeinholzer, Michael Kube, Richard Reinhardt, Regine Jahn: Diatoms as bioindicators: watermonitoring via DNA barcoding

14.45 *Katharina Händeler, Heike Wägele, Mareike Rüdinger, Ute Wahrmund, Volker Knoop: Molecular identification of the algal origins of Sacoglossan kleptoplasts (Opisthobranchia, Gastropoda) by bar coding

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15.30-16.30 Session 12: Animal phylogeography (Room 009)

Chair: Heike Wägele

15.30 Axel Hochkirch, Yvonne Görzig: Diversification in the Mediterranean: A phylogeographic analysis of the grasshopper genus *Oedipoda*

15.45 Michael J. Raupach, Christoph Mayer, Johann-Wolfgang Wägele: Molecular studies on bizarre deep-sea Asellota (Crustacea: Isopoda): phylogeny and genetic variability of selected taxa

16.00 *André Koch, Fabian Herder, Bernhard Misof, Evy Ayu Arida, Wolfgang Böhme: Phylogeography and systematics of Sulawesi water monitors (Squamata: *Varanus salvator* Complex

16.15 *Evy Arida, Sri Sulandari, M. Syamsul Arifin Zein, Tim Jessop, Claudio Ciofi, Wolfgang Böhme: Genetic divergence and gene flow among Komodo dragons: measuring genetic drift for small island populations of a large, endangered reptile

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Chair: Dirk Albach

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15.45 *Enoch G. Achigan-Dako: Phylogenetic and phylogeographic analyses of *Momordica charantia* (Cucurbitaceae) from West Africa using AFLPs

16.00 *Paul G. Nevill, Gerd Bossinger, Peter K. Ades: Phylogeography and refugia of disjunct populations of *Eucalyptus regnans* in south-eastern Australia

16.15 *Christina Fey-Wagner, Tim Kröger-Kilian, Daniela Guicking, Brigitte Fiala, Frank R. Blattner, Kurt Weising: Genetic diversity and population structure of *Macaranga hypoleuca* (Euphorbiaceae), an important pioneer tree species of Southeast Asian lowland rainforest

16.30-18.30 Poster session II (Foyer ZHG)

15.30-15.45 Session 14: Reticulate evolution II (Room 007)

Chair: Volker Wissemann

15.30 Ivan Schanzer, Vera Voilokova, Alina Vagina, Natalya Kutlunina: Intraspecific polymorphism, hybridization and reticulate evolution in roses: how to tell the difference?

15.45 Walter Bleeker: *Rorippa* contact zones exemplify a series of stages in hybrid speciation

16.00 *Markus Ackermann, Michaela Achatz, Joana Schulz & Maximilian Weigend: Experimental "hybrid speciation" in *Caiophora* (Loasaceae subfam. Loasoideae) – reproductive isolation through nectar characters?

16.15 Olaf Werner, Rosa María Ros: Lazarus species or hybrid: the case of *Tortula mucronifolia* (Pottiaceae, Musci)

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15.30-16.30 Session 15: Palaeontology (Room 006)

Chair: Dorte Janussen

15.30 Christopher Castellani, Carolin Haug, Joachim T. Haug, Yu Liu, Andreas Maas, Dieter Waloszek: The Pentastomida story continued – new data about the ontogeny of Cambrian representatives

15.45 *Gabriele Oltmann, Jes Rust: *Vachonisia rogeri* – a Marrellomorpha from the Lower Devonian Hunsrück Slate (Germany) and the Phylogeny of the Cambrian to Devonian Marrellomorpha (Arthropoda)

16.00 Mike Reich: The early evolution and diversification of sea cucumbers (Echinodermata: Eleutherozoa))

16.15 Sonja Wedmann, David K. Yeates: Eocene records of bee flies: palaeobiogeographic implications and remarks on the evolutionary history of Bombyliidae

16.30-18.30 Poster session II (Foyer ZHG)

16.30-18.30 Poster session II (Foyer ZHG)

19.00 Reception by the mayor of Göttingen (Altes Rathaus, Marktplatz)

Mayor: Wilhelm Gerhardy

20.00 Congress dinner (Rathskeller, Marktplatz)

Thursday, 10 April

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Chair: Susanne Renner

8.30 Rolf G. Beutel, Frank Friedrich: Entomological enigmas and new approach in insect morphology

9.00 Ernst A. Wimmer: Evolutionary conservation of developmental processes to infer phylogenetic relationships

9.30 Günter Theißen, Hannelore Simon, Susanne Nolden, Mariana Mondragón-Palomino: MADS about tulips, orchids and grasses: evolutionary developmental genetics of floral organ identity in monocots

10.00-10.30 Coffee break

10.30 Christian Brochmann: Some recent advances in plant phylogeography

11.00 Thomas Friedl: Identification and phylogeny of algae dominating biofilms: a challenge for algal systematics

11.30 Dorte Janussen: Evolutionary ecology of basic metazoans from a historical viewpoint: palaeontological evidence of sponges

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13.30-15.00 Session 16: Biogeography and evolution I (Room 009)

Chair: H. Peter Linder

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13.45 *Rosa Maria Lo Presti, Christoph Oberprieler: Evolutionary history, biogeography and eco-climatological differentiation of the genus *Anthemis* L. (Compositae-Anthemideae) in the Circum-Mediterranean area

14.00 *Berit Gehrke, Peter Linder: Is habitat heterogeneity driving speciation in the Afrotemperate regions?

14.15 Nigel P. Barker, Robert J. McKenzie: The phylogeny and biogeography of the Annual *Arctotis* clade (Asteraceae): an insight into speciation in the Namakwaland region of South Africa

14.30 *Ingrid Jordon-Thaden, Marcus Koch: Global diversity patterns and migration in the genus *Draba*

14.45 Khatere Emadzade, Elvira Hörandl, Carlos Lehnebach, Peter Lockhart: Molecular phylogeny, biogeographical history and a revised classification of *Ranunculus* s.l. (Ranunculaceae)

15.00-15.30 Coffee break

13.30-15.00 Session 17: Structure and evolution - animals (Room 008)

Chair: Wolfgang Wägele

13.30 Andreas Schmidt-Rhaesa, Birgen Holger Rothe: Nervous system evolution in the Nemathelminthes

13.45 *Sid Staubach: The nervous connection - Opisthobranch cephalic sensory organs and their evolution

14.00 *Philipp Kremer, Dieter Fiege, Volker Storch & Thomas Wehe: Investigations on the ultrastructure of *Hypania invalida* (Polychaeta: Ampharetidae), an adventive species in the River Rhine, Germany, with special emphasis on the nephridia and the spermatozoa

14.15 Yu Liu, Dieter Waloszek, Andreas Maas, Joachim T. Haug, Carolin Haug: Early evolution of Arthropoda –the fate of the second appendage-bearing body segment and the evolution of head segmentation

14.30 *Silke Mosel, Michael Ohl: Functional and phylogenetic implications of the sting apparatus of solitary wasps

14.45 Tanja Schulz-Mirbach, Bettina Reichenbacher: Hearing in the dark: Changed otolith morphology in a cave-dwelling form of *Poecilia mexicana* (Teleostei)

15.00-15.30 Coffee break

13.30-15.00 Session 18: Phylogeny of early land plants (Room 007)

Chair: Harald Schneider

13.30 *Susann Wicke, Andrea Costa, Franziska Bauer, Jèsus Muñoz, Christoph Neinhuis, Dietmar Quandt: Re-organisation(s) of the nuclear ribosomal DNA (nrDNA) in land plants and its phylogenetic implications

13.45 *Ute Wahrmund, Milena Groth-Malonek, Volker Knoop: Two spacers and a pseudogene: surprises of mitochondrial DNA evolution in the earliest land plants

14.00 *Jörn Hentschel, Matt von Konrat, Tamás Pócs, S. Robbert Gradstein, Harald Schneider, Jochen Heinrichs: Phylogeny and historical biogeography of the cosmopolitan liverwort genus Frullania (Jungermanniopsida: Porellales)

14.15 Martin Nebel, Markus Preußing, Dominik Katterfeldt, Dietmar Quandt: New insights in the evolution of Aneuracae (Metzgeriales, Marchantiophyta) based on the re-placement of the genus Verdoornia R.M. Schust.

14.30 Irina Milyutina, Elena Ignatova, Michail Ignatov, Denis Goryunov Rafael Hernández-Maqueda, Aleksey Troitsky: Narrow vs. broad species concepts in Schistidium (Grimmiaceae, Musci): nuclear ITS data analysis

14.45 *Sanna Olsson, Volker Buchbender, Sanna Huttunen, Johannes Enroth, Lars Hedenäs, Ray Tangney, Dietmar Quandt: Evolution of epiphytism in the moss family Neckeraceae

15.00-15.30 Coffee break

15.30-17.00 Session 19: Biogeography and evolution II (Room 009)

Chair: Michael Kessler

15.30 *Michael Reuscher, Dieter Fiege, Thomas Wehe: Biodiversity of terebellomorph polychaetes from hot vents and cold seeps

15.45 Kristina von Rintelen, Matthias Glaubrecht, Thomas von Rintelen: Same environment, two taxa: the search for parallel patterns in the biogeography and evolution of freshwater shrimps and snails in ancient lakes of the Indonesian island Sulawesi

16.00 *Christian Schwarzer: The "inland lomas" near Omate (Peru, Depto. Moquegua) – a recently discovered plant community

16.15 *Federico Luebert, Hartmut H. Hilger, Patricio Pliscoff: Integrating molecular phylogenetics, distribution and climatic modelling to infer evolutionary processes of *Heliotropium* sect. *Cochranea* (Heliotropiaceae) in the Atacama Desert

16.30 Michael Stech, Manuela Sim-Sim, Olaf Werner, Rosa M. Ros, M. Glória Esquível, Susana Fontinha, Juana M. Gonzalez-Mancebo, Jairo Patiño: Molecular characterisation of Macaronesian pleurocarpous mosses

16.45 Oliver Gailing, Yanti Rachmayanti, Hani Nuroniah, Nga Phi Nguyen, Cuiping Cao, Randy Villarin, Reiner Finkeldey: The use of phylogenetic and phylogeographic data for wood certification in Dipterocarpaceae

15.30-17.00 Session 20: Structure and evolution - plants (Room 008)

Chair: Sigrid Liede-Schumann

15.30 *Bart Jacobs, Suzy Huysmans, Erik Smets: Are fruit and seed characters systematically useful in the family Adoxaceae (Dipsacales)?

15.45 *Andreas Mühlhausen, Günter Theißen, Klaus Mummenhoff: Dehiscent versus indehiscent fruits – a genetic case study in the Brassicaceae

16.00 Livia Wanntorp, Louis P. Ronse De Craene: Perianth differentiation in the Santalales: what morphology can tell us about molecular phylogenetics

16.15 Louis Ronse De Craene: Floral development of *Aextoxicon punctatum* (Aextoxicaceae – Berberidopsidales) – morphological evidence for a link with *Berberidopsis*?

16.30 Regine Claßen-Bockhoff, Elke Pischtschan, Ariane Heller: The trigger mechanism in Marantaceae

16.45 Helmut Freitag, Antonia Butnik: Cotyledons in Chenopodiaceae as evolutionary markers?

15.30-17.00 Session 21: Molecular evolution (Room 007)

Chair: Kurt Weising

15.30 *Natalie Cusimano, Susanne Renner: Reevaluation of the cox1 Group I Intron in Araceae and Angiosperms indicates a history dominated by loss rather than horizontal transfer

15.45 Michael F Fay, Ilia J. Leitch, Jeremy M. Beaulieu, Kwok Cheung, Lynda Hanson, Martin A. Lysak: Punctuated genome size evolution in Liliaceae

16.00 Benjamin Kilian, H. Özkan, A. Walther, J. Kohl, T. Dagan, F. Salamini, W. Martin: Molecular diversity at 18 loci in 321 wild and 92 domesticate lines reveal no reduction of nucleotide diversity during *Triticum monococcum* (einkorn) domestication: Implications for the origin of agriculture

16.15 Ignacio G. Bravo, Alexandros Stamakis, Ingo Nindl, Marc Gottschling: Multiple driving forces of papillomavirus evolution

16.30 Jan Ole Kriegs, Gennady Churakov, Maren Möller-Krull, Jürgen Schmitz: Jumping genes the key to mammalian evolutionary history

16.45 Torsten H. Struck: Salamander phylogeny and paedomorphosis - how to detect conflict between partition?

17.15-18.15 Meeting GfBS (Room 007)

18.15-18.45 Meeting DBG (Room 006)

20.30-22.00 Awards and Public Lecture (Aula, Wilhelmsplatz)

Tod Stuessy: The role of biological systematics in a modernizing world

Music: "Dumky Trio" (selected parts) by Anton Dvorak played by the Zara Trio: *Jan Gispen – Violin*, *Robbert Gradstein – Violoncello*, *Wout van Veen – Piano*

Friday, 11 April

9.00-16.00 Excursion: Spring flora and forests in the surroundings of Göttingen

Led by Erwin Bergmeier

Bus leaves from Institute of Zoology, Berliner Str. (see map). Be prepared for walks on unsurfaced roads and slippery paths in moderately steep terrain. Bring your lunch. Costs (transport by bus) 15 €.

8.15-12.00 Workshop I: Phylogeny and Biogeography of Poales (Room 007)

8.15 Georg Zizka: Introduction

Ia: Systematics, biogeography and evolution of Poaceae

Chair: Katharina Schulte

8.20 Michael D. Pirie: Phylogeny and biogeography of Danthonioideae (Poaceae)

8.35 Aelys M. Humphreys, H. Peter Linder: Clades, lemmas and awns in *Rytidosperma* s.l. (Danthonioideae: Poaceae)

8.50 Julia Schneider, Elke Döring, Martin Röser: Phylogeny, classification and morphological evolution in the grass subfamily Pooideae

9.05 Václav Mahelka, Judith Fehrer, František Krahulec: Allopolyploid origin and hybridization in an allohexaploid grass *Elytrigia intermedia* (Poaceae, Triticeae)

9.20 B. Kilian, H. Özkan, O. Deusch, S. Effgen, A. Brandolini, J. Kohl, W. Martin, F. Salamini: Independent wheat B and G genome origins in outcrossing *Aegilops* progenitor haplotypes

9.35 Marco Schmidt, Thomas Janssen, Konstantin König, Georg Zizka: Diversity patterns of grasses (Poaceae) in Burkina Faso

9.50-10.20 Coffee break

Ib: Systematics, biogeography and evolution of Bromeliaceae

Chair: Kurt Weising

10.20 Michael H. J. Barfuss, Walter Till, Rosabelle Samuel: The backbone problem: hunting for informative characters in DNA sequences of Tillandsioideae (Bromeliaceae) for reconstructing a well-resolved phylogeny

10.35 Nicole Schütz, Natascha Wagner, Kurt Weising, Georg Zizka: Taxonomy and phylogeny of the genus *Deuterocohnia* Mez (Bromeliaceae)

10.50 Martina Rex, Katharina Schulte, Georg Zizka, Jule Peters, Pierre L. Ibisch & Kurt Weising: Molecular phylogeny of *Fosterella* (Pitcairnioideae, Bromeliaceae) based on four chloroplast DNA regions

11.05 Jule Peters, Christoph Nowicki, Martina Rex, Katharina Schulte, Kurt Weising, Georg Zizka, Pierre L. Ibisch: Biogeography of the genus *Fosterella* (Bromeliaceae)

11.20 Katharina Schulte, Nicole Haußner, Elke Kiehlmann, Marco Schmidt, Konstantin König, Patricio Novoa, Georg Zizka: Systematics and biogeography of Chilean *Puya* species (Bromeliaceae)

11.35 Perspectives, discussion of cooperation

9.00-12.00 Workshop II: Biodiversity Informatics (Room 009)

Organisers: Anton Guentsch, Jörg Holetschek

IIa: Networking

Jörg Holetschek: Publishing specimen and observation records using BioCASe technology

Patricia Kelbert, Anton Güntsch, Niels Hoffmann, Walter G. Berendsohn: Checklist-driven access to European collection and observational data

Wolf-Henning Kusber, Elke Zippel, Anton Güntsch, Walter G. Berendsohn: Data portals for biological systematics

Gabriele Dröge, Holger Zetzsche, Anton Güntsch, Birgit Gemeinholzer: The DNA bank network in Germany

Coffee break

IIb: EDIT

Andreas Kohlbecker, Markus Döring: Developing the EDIT platform for cybertaxonomy

Pepé Ciardelli: The EDIT desktop taxonomic editor

Anton Güntsch, Walter G. Berendsohn: Biodiversity research leaks data. Create the biodiversity data archives!

13.00-16.00 Workshop III: Piperales, an integrative multidisciplinary approach (Room 006)

13.00 Stefan Wanke: Introduction

IIIa: Piperaceae

Chair: Marie-Stéphanie Samain

13.05 James F. Smith, Angela C. Stevens, Chris Davidson: Placing the origin of two species-rich genera in the late Cretaceous with later species divergence in the Tertiary: A phylogenetic, biogeographic and molecular dating

13.25 Lars Symmank, Marie-Stéphanie Samain, Paul Goetghebeur, Guido Mathieu, Christoph Neinhuis, Stefan Wanke: Independent evolution of different terrestrial life forms in the genus *Peperomia* (Piperaceae) and implications for biogeography of the tuberous species

13.40 Harry T. Horner, Stefan Wanke, Marie-Stéphanie Samain: Leaf calcium oxalate crystal macropatterns and their role in plant systematics and phylogeny: with special emphasis on *Peperomia* (Piperaceae)

13.55-14.25 Coffee break, poster session

IIIb: Aristolochiaceae

Chair: Christoph Neinhuis

14.25 O.V. Nakonechnaya, O.G. Koren, V.S. Sidorenko, Yu.N. Zhuravlev: Tropical species in nothern latitudes: why has the ancient relict plant *Aristolochia manshuriensis* survived?

14.40 Michael Heinrich, Jennifer Chan, Monique S.J. Simmonds: Local uses and chemistry of *Aristolochia* species – a global assessment based on bibliographic sources and chemical analysis

15.00-15.20 Coffee break, poster session

15.20 M. Alejandra Jaramillo: The role of B-class gene homologs in the evolution of petaloidy in Aristolochiaceae

15.40 Claude W. dePamphilis, Barbara J. Bliss, Stefan Wanke, Jill Duarte, P. Kerr Wall, Ali Barakat, Siela N. Maximova, Lena Landherr, Yi Hu, Jim L. Leebens-Mack, Hong Ma: Genomic and functional resources for Aristolochia fimbriata, an emerging basal angiosperm model species

16.00 Stefan Wanke: Outlook and closing remarks

13.00-16.00 Workshop IV: DNA sequence alignment for phylogenetic analysis - current approaches and future prospects (Room 008)

Kai Müller: Introduction

David Morrison: When is homology important in alignment, and how do we use it?

Claude W. dePamphilis: The impact of multiple sequence alignment on phylogenetic estimation

Frank Kauff: A recursive alignment algorithm using a profile alignment with information about alignable and non-alignable regions

Dietmar Quandt: Alignment in the presence of microstructural changes

Gerhard Steger: Non-coding RNAs: alignment and structure prediction

Harald Letsch: RNAsalsa - alignment based on structure and sequence information

Patrick Kück: Aliscore - identifying random similarity within sequence alignments

Kay Hamacher: From the genome to the proteome: how phylogenetic relationships can be inferred from genomic data without the need for sequence alignment

9.00-16.00 Workshop V: Pixel-Voxel-Morphology – Introduction to working with µCT-data (Room 005)

9.00: Thomas Hörnschemeyer: Pixel-Voxel-Morphology - Introduction to working with µCT-data

10.00: Thomas Kleinteich: From segmentation to animation: combining the advantages of different 3D software packages

11.00: Martin Heß: Fish eye 3D

12.00-13.00 Lunch break

13.00: Software demonstration (Zoological Institute)

Abstracts - Talks

Session 13

Phylogenetic and phylogeographic analyses of *Momordica charantia* (Cucurbitaceae) from West Africa using AFLPs

*Enoch G. Achigan-Dako

Leibniz-Institute of Plant Genetics and Crop Research, 06466 Gatersleben, Germany, and Faculty of Agronomic Sciences, University of Abomey-Calvi BP. 526 Cotonou, Benin

Momordica charantia is a paleotropical species used as vegetable or medicinal resource in Africa. A morphometric analysis recently suggested the occurrence of two subspecies of *M. charantia* in West Africa based on leaf characters. Although no clear correlation of these leaf characters with ecological factors was found it is still unclear if the morphologically circumscribed subspecies represent also phylogenetic entities, particularly as sequences of the rDNA internal transcribed spacer region revealed no differences between both types.

To clarify the taxonomic status of *M. charantia* subsp. *charantia* and subsp. *macroloba* we analysed 85 accessions from four major phytogeographic regions in West Africa (the evergreen and semi-deciduous forest zone, the forest/savannah mosaic in the Dahomey gap, the Sudano-Guinean zone, and the Sudanian zone) by amplified fragment length polymorphisms (AFLP). Six primers combinations produced 386 unambiguously reproducible bands, which were scored as binary characters and analysed with phylogenetic and phylogeographic methods.

Neighbour-joining clustering confirmed the existence of subsp. *macroloba*, which forms a monophyletic group within subsp. *charantia*, and indicated low amounts of ongoing geneflow between both types where they occur in close vicinity. Within subsp. *charantia* all populations collected in the dry Sudanian zone are monophyletic. The analysis indicates also the existence of a forest ecotype, as all individuals collected in this habitat cluster together, while populations from savannah and semi deciduous forests are widespread all over the tree. Subspecies *macroloba* seems to have originated from the forest ecotype.

Phylogeographic analysis reveals clear intraspecific structures within *M. charantia*, which are related to geographic regions, habitat types, and taxonomic units.

Session 14

Experimental "hybrid speciation" in *Caiophora* (Loasaceae subfam. Loasoideae) – reproductive isolation through nectar characters?

*Markus Ackermann, Michaela Achatz, Joana Schulz, Maximilian Weigend

Institut für Biologie der Freien Universität Berlin, Systematische Botanik und Pflanzengeographie, Altensteinstraße 6, 14195 Berlin

Extensive studies on the nectar production and composition of Loasaceae subfam. Loasoideae in the past few years showed a strong correlation between floral morphology, nectar characters and flower visitors (Ackermann & Weigend 2006, Annals of Botany 98: 503–514). The divergent functional types found in the subfamily are correlated with a wide range of different flower visitors/pollinators and hence reflect a premating reproductive isolation between species and species groups. The data also showed, that nectar characters evolve rapidly.

The present study investigated one possible way for the diversification of nectar characters. Our own observations and literature data document at least 11 natural interspecific hybrids between divergent species groups of *Caiophora*. Experimental crossings were carried out in order to understand the potential role of hybridization in the evolution of nectar characters. 37 interspecific crossing experiments with seven Peruvian species were carried out, representing morphologically divergent taxa and three different pollination syndromes. The F1 generation of five different interspecific combinations has been investigated. Their nectar characters were roughly intermediate between the parental taxa. Three interspecific combinations of the F2 generation showed, that nectar characters diverged dramatically. Nectar volumes, concentrations and total sugar production often exceeded the parental values. In a few cases a total loss of nectar production could be observed. This indicates that novel functional traits can arise through hybridization, i.e., that individual plants of the F2 generation may attract different pollinators than their parental taxa. In the case of the hybrid *Caiophora deserticola* x *C. carduifolia* (both parents have 50-70µl nectar with ca. 50% sugar), the F1 was very similar in nectar production to *C. deserticola* (but morphologically intermediate). F2-hybrids of this combination produced a wide range of morphologically different individuals. Their nectar production varied from 0—85 µl nectar/flower and concentration from 17—59%. To verify the stability of these novel nectar characters, the divergent F2 individuals of the latter interspecific combination were successfully selfed This F3 individuals had very similar nectar (and morphological) characters to their corresponding F2 parent, showing that both morphological and functional traits were stabilized.

Session 12

Genetic divergence and gene flow among Komodo dragons: measuring genetic drift for small island populations of a large, endangered reptile

*Evy Arida[1,2], Sri Sulandari[1], M. Syamsul Arifin Zein[1], Tim Jessop[3], Claudio Ciofi[4], Wolfgang Böhme [2]

[1]Museum Zoologicum Bogoriense (MZB), Jalan Raya Bogor km46, Cibinong 16911, Indonesia, [2] Zoologisches Forschungsmuseum Alexander König (ZFMK), Adenauerallee 160, Bonn 53113, Germany, [3]Department of Wildlife Conservation and Science, Zoo's Victoria, Parkville, Victoria 3052, Australia, [4]Dipartimento di Biologia Animale e Genetica, Universita di Firenze,Via Romana 17, Firenze 50125, Italy

The effect of genetic drift on small isolated populations is of particular concern for species viability, particularly when it involves an endangered and charismatic giant reptile such as the Komodo monitor *Varanus komodoensis*. The Komodo monitor is endemic to five islands in southeast Indonesia. The island of Komodo harbours a genetically distinct population, while Rinca and Flores show relative low levels of genetic differentiation. The smallest islands of Gili Motang and Nusa Kode, of less than 100 individuals each, appear to have quite different rates of migration to and from the larger islands, probably due to distinct biogeographical settings. In this study, we analyse levels of gene flow and assess effective population size based on genetic data obtained across temporally distinct sampling sessions for the islands of Gili Motang and Nusa Kode. Using a novel set of species-specific microsatellite markers, we compare levels of inbreeding to effective population size and provide recommendation to help devising small island populations management and conservation initiatives.

Session 3

Population genetic approach to speciation in two closely related wild tomato species (*Solanum peruvianum* and *S. chilense*)

Uraiwan Arunyawat[1], Wolfgang Stephan, Thomas Städler

Department Biologie II, Abteilung Evolutionsbiologie, University of Munich (LMU), 82152 Planegg-Martinsried, Germany, [1]Current address: Department of Genetics, Kasetsart University, Bangkhen campus, Bangkok, 10900, Thailand, uraiwan.a@ku.ac.th

We employed a multilocus approach to examine patterns of polymorphism and divergence in two closely related wild tomato species (*Solanum peruvianum* and *S. chilense*), using sequence data for eight unlinked nuclear loci from populations across much of the species' range. Both species exhibit substantial levels of nucleotide variation. The species-wide level of silent nucleotide diversity is 18% higher in *S. peruvianum* than in *S. chilense*. One of the loci deviates from neutral expectations, showing a clinal pattern of nucleotide diversity and haplotype structure in *S. chilense*. Furthermore, we used the analytical framework of divergence population genetics in evaluating the utility of the "isolation" model of speciation to explain observed patterns of polymorphism and divergence. Whereas the isolation model is not rejected by goodness-of-fit criteria established via coalescent simulations, patterns of intragenic linkage disequilibrium provide evidence for postdivergence gene flow. These results suggest that speciation occurred under residual gene flow, implying natural selection as one of the evolutionary forces driving the divergence of these tomato species.

Session 9

Phylogeography on the Balkan Peninsula - examples from *Veronica* (Plantaginaceae)

*Katharina Bardy[1], Peter Schönswetter[1], Dirk C. Albach[2]

[1]Department of Biogeography and Botanical Garden, Faculty Centre Botany, University of Vienna, Rennweg 14, 1030 Wien, Austria, [2]Institute for Special Botany, Johannes Gutenberg-Universität Mainz, Bentzelweg 9, 55099 Mainz, Germany

The Balkan Peninsula is one of the hotspots of biodiversity in Europe; presumingly because of its role as a refugial area during the Pleistocene ice ages. Additionally, the Balkan Peninsula was a place for further diversification and formation of new species further enhancing its richness in endemic species.

Up to now, our knowledge of the phylogeographic history of plant species of the Balkan Peninsula is predominantly based on the study of trees. However, most of its species richness is due to herbaceous perennials such as the genus *Veronica*.

We focus on species from three different subgenera: subgenus *Stenocarpon* – growing in alpine habitats – subgenus *Pseudolysimachion* – occurring on grasslands – and subgenus *Chamaedrys* – mainly inhabiting forests. Using genome size estimation, AFLP fingerprints and cpDNA markers we address the following main questions: 1) Which taxa form well-defined taxonomic units? 2) Which phylogeographical patterns do these taxa exhibit on the Balkan Peninsula?

Session 6

The phylogeny and biogeography of the annual *Arctotis* clade (Asteraceae): an insight into speciation in the Namakwaland region of South Africa

Nigel P. Barker, Robert J. McKenzie

Molecular Ecology and Systematics Group, Department of Botany, Rhodes University, P.O. Box 94, Grahamstown, 6140, South Africa

The Namaqualand region of South Africa is famous for its massed flower displays in spring, of which annual Asteraceae species comprise a major component. Some of the most prolific spring-flowering species belong to the genus *Arctotis*, specifically a clade within this group which comprises approximately eight annual species, including *Arctotis fastuosa* and *A. leiocarpa*. The clade is centred in Namaqualand with outlying species occurring in savanna/grassland and fynbos. Molecular data from two non-coding cpDNA regions (psbA-trnH, trnT-trnF) and the ITS nrDNA region indicate the clade had a Succulent Karoo origin with an early divergence of the widespread savanna/grassland species *A. venusta*, whereas the fynbos species *A. hirsuta* is indicated to be of more recent origin. Among the Namaqualand taxa, variation in cypsela morphology has a strong geographical basis, but the molecular data provides evidence for either ancestral genetic polymorphism or post-speciation introgression in the *A. fastuosa* species complex. A first attempt to date diversification of Arctotidinae suggests that the Annual *Arctotis* clade diverged approximately 3.5 Mya and radiation within the clade is consistent with increasing aridification and rainfall seasonality in Namaqualand coupled with a degree of vegetation and edaphic specialisation.

Plenary session I

Deep Metazoan phylogeny – the morphological perspective

Thomas Bartolomaeus

Animal systematics and evolution, Institute for Biologoy, Freie Universtiät Berln, Königin-Luise-Str. 1-3, 14195 Berlin, tbartol@zoosyst-berlin.de

N/A

Plenary session III

Entomological enigmas and new approach in insect morphology

Rolf G. Beutel, Frank Friedrich

Institut für Spezielle Zoologie und Evolutionsbiologie, FSU Jena, 0743 Jena, Deutschland, rolf.beutel@uni-jena.de, frank.friedrich@uni-jena.de

Innovative technological developments have given new impulses to insect anatomy in the last years. Microtome sectioning has been greatly improved by the use of new embedding materials. The use of confocal laser scanning microscopy (CLSM) is very useful for the study of external and internal features of very small (or very flat) insects. The application of µ-computer tomography (µ-CT), a recent development in entomology, has several remarkable advantages. It is largely artefact free and the images are perfectly aligned. It is also non-destructive and can be applied to extremely rare species ("entomological enigmas") or type specimens. Image stacks of high quality can be obtained within hours. The maximum resolution is presently c. 1 µm. Another innovation – computer based 3D reconstruction - is closely linked with most other modern techniques. 3D models and animations are not only a qualitative improvement in the study of insect morphology but result in a new level of understanding complicated arrangements of internal structures. The use is not restricted to research but is also very useful for teaching anatomy of insects or other groups of organisms. Modern morphological techniques are highly efficient and have the potential to create a remarkable renaissance in insect morphology. In combination with comprehensive molecular data, well documented extensive morphological character sets will probably lead to important new insights in insect systematics and evolution in the near future.

Plenary session II

Hybridization and polyploid formation – evolutionary accidents or driving forces of biodiversity

Frank R. Blattner

Leibniz-Institute of Plant Genetics and Crop Research (IPK), 06466 Gatersleben, Germany, blattner@ipk-gatersleben.de

Most landplants and probably all extant angiosperms underwent at least one episode of genome duplication during their evolutionary history involving either allo- or autopolyploidy, while in animals polyploid formation is thought to be much rarer. Polyploidization should results in instantaneous reproductive isolation of cytotypes with different ploidy levels and might ultimately lead to speciation events. Estimations of speciation involving ploidy level changes arrive at 2-4% of all speciation events in angiosperms and around 7% in ferns, which depends, however, on the species concept utilized, as the biological species concept (i.e. reproductive isolation) is only rarely used by plant taxonomists.

Polyploidization has several consequences for the organism. Autopolyploids, although appearing at relatively high frequencies in populations, might suffer from multivalent forming during meiosis, resulting in reduced fertility compared to allopolyploids. This, together with the ecological similarity and therefore competition with their diploid progenitor, should result in a low number of successful establishments of autoploypoids. In contrast, although occurring at low frequencies and suffering partly from genomic incompatibilities, allopolyploids show higher fertility, and the ecological requirements are mostly quite different from their progenitor species. They, therefore, have a higher chance of successful establishment. Grasses, with their often occurring wide crosses (i.e. hybrids among distantly related genera) involving polyploid formation, are a good example for a group, which is very successful in the colonization of ecologically diverse habitats. It is, however, still unclear why some taxonomic groups are easily capable of polyploid formation, whereas polyploidy seems rare in others, and what the genetic background of ecological changes after polyploid formation is. To analyze these questions sound phylogenetic and ecological information is necessary.

Session 14

Rorippa contact zones exemplify a series of stages in hybrid speciation

Walter Bleeker

Department of Botany, University of Osnabrück, Barbarastr. 11, 49069 Osnabrück, Germany

Hybrid speciation must be initiated while the parental species are in sympatry or parapatry. Although parental genotypes necessarily serve as the source of hybrid genotypes, they may also limit the development of reproductive isolation if interbreeding among lineages is common (e.g. hybrids backcrossing to parental lineages). However, interbreeding among lineages may also result in genetic assimilation of the parental species if hybrids display a higher fitness in the local environment. Hybridization between *Rorippa amphibia* (Brassicaceae) and *R. sylvestris* and between *R. austriaca* and *R. sylvestris* is a common phenomenon along European rivers. Despite of widespread interspecific gene flow along rivers, species integrity of *R. amphibia* and *R. sylvestris* is maintained in contact zones. A more complex situation has been observed in contact zones between *R. austriaca* and *R. sylvestris*. Ecological factors and the ploidy level of hybrids have been identified as important in determining hybrid zone trajectories.

We analysed the structure of eight contact zones and hybrid populations of *R. austriaca* (diploid), *R. sylvestris* (tetraploid or hexaploid) and their hybrid *R.* ×*armoracioides* (triploid, tetraploid, or pentaploid) in Central Europe. The genetic structure of populations has been analysed using AFLP and species specific chloroplast DNA (trnL intron) length variation. Morphological variation has been analysed as an additional independent data set describing population structure. Pollen stainability and seed set have been investigated as fitness parameters. Ploidy level variation has been studied using Flow Cytometry. The genetic structure of populations zones varied. Three contact zones were composed of both parental species and mainly intermediate triploid or pentaploid F1 hybrids. One contact zone was dominated by backcross hybrids in both directions (BC *austriaca*, BC *sylvestris*). In four hybrid populations we found no pure parental individuals and mainly intermediate tetraploid putative later generation hybrids. These hybrids were apparently more successful in the local environment than the parental species. *R. sylvestris* is inferior in competing with the more vigorous tetraploid hybrids providing evidence for genetic assimilation of one parental species within contact zones.

Session 4

Myzostomid phylogenomics: on congruence and incongruence of gene partitions

Christoph Bleidorn[1], S. Hartmann[2], T.H. Struck[3], I. Eeckhaut[4], M.C. Milinkovitch[5], J. Selbig[2], R. Tiedemann[1]

[1]*Unit of Evolutionary Biology/Systematic Zoology, Institute of Biochemistry and Biology, University of Potsdam, Germany,* [2]*University of Potsdam, Unit of Bioinformatics, Germany,* [3]*University of Osnabrück, Germany,* [4] *University of Mons, Belgium,* [5] *Free University of Brussels, Belgium*

With the beginning of the genomic era, there was hope that the concatenation of a sufficient amount of genes will solve most open questions of metazoan phylogeny. Despite the availability of genomic data and large scale EST-projects for many metazoan phyla, large scale bilaterian phylogeny is still controversially discussed. One of these discussions regards the phylogenetic position of Myzostomida, a group of flat-bodied marine worms that are usually ectocommensals or parasites of echinoderms. Phylogenetic affinities of the enigmatic Myzostomida have been the source of two centuries of dispute among systematists, but a recent mitogenomic survey strongly supported the view of an annelid affinity. This view is challenged by a phylogenetic analysis of concatenated dataset of ribosomal proteins. Here we report a systematic investigation of a large molecular dataset including representatives of major metazoan taxa and newly derived EST-data of *Myzostoma cirriferum* (Myzostomida). A phylogenomic pipeline has been established to recover gene families by similarity, which were clustered in a second step using TribeMCL. Alignments (amino acids and nucleotides) of the available TribeMCL-clusters were generated. Phylogenetic analyses of single-copy genes, as well as multi-copy gene families were performed using a ML-approach for each partition separately. Supported hypothesis (e.g. annelid vs. flatworm affinities of the myzostomid) were scored for each partition and underlying patterns were investigated. Phylogenetic analyses of sets of genes which support congruent hypotheses are conducted and compared with a combined analysis including all partitions. Implications regarding the phylogenetic position of myzostomids, as wells as for phylogenomic studies in general are discussed.

Session 6

Phylogeny of the genus *Melampodium* and the development of the x = 10 chromosomal line

*Cordula Blöch[1], Hanna Weiss-Schneeweiss[1], Michael Barfuss[1], Carolin Rebernig[1], Josè Luis Villaseñor[2], Tod Stuessy[1]

[1]*Faculty Center of Botany, Department of Systematic and Evolutionary Botany, University of Vienna, Austria,* [2]*Instituto de Biología, Departamento de Botánica, Universidad Nacional, Autonóma de México, México D.F.*

Melampodium (Heliantheae, Asteraceae) comprises 39 species with a broad spectrum of basic chromosome numbers (x = 9, 10, 11, 12 and 14) and frequent polyploidy. The basic chromosome numbers have played an important role in the evolution of the genus and are important characters in current sectional classification of the genus with six sections being recognized: *Melampodium* (x = 10), *Zarabellia* (x = 9), *Serratura* (x = 12), *Bibractiaria* (x = 9), *Rhizomaria* (x = 11), and *Alcina* (x = 11). More than half of the species of *Melampodium* have a chromosome number based on x = 10. A study of the phylogenetic relationships of the genus based on plastid and nuclear DNA sequence analyses combined with cytogenetic analyses allows us (1) to test the current classification of *Melampodium*, (2) to hypothesise on modes and mechanisms of chromosome number change and its correlation to relationships among the taxa, and (3) to gain insight into the origin of polyploids. Two putative sister genera of *Melampodium*, *Acanthospermum* and *Lecocarpus*, branch from within a basal polytomy of *Melampodium* taxa. The current sectional classification is supported for four out of the six sections. Phylogenetic analyses of matK and ITS sequences reveal incongruencies between both data sets. An interesting example is *M. longipilum* (x = 10), which is sister to all other taxa based on x = 10 in the matK tree, but instead groups strongly with one of the x = 11 lines in ITS analysis. Chromosomal FISH analyses of *M. longipilum* reveal a single interstitial locus of 35S rDNA which, together with other evidence, might indicate chromosomal rearrangements involving fusion (leading from x = 11 to x = 10). Both sequence data and chromosomal analyses cannot exclude two independent origins of the x = 10 species group, possibly involving the homoploid hybrid formation of *M. longipilum*.

Session 3

Speciation events in Australasian parrots (Psittaciformes)

*Michael Braun, Michael Wink

Institute of Pharmacy and Molecular Biotechnology, Dept. Biology, Im Neuenheimer Feld 364, 69120 Heidelberg, psittaciden@yahoo.de, wink@uni-hd.de

The Indo-Australian archipelago is a hotspot of biodiversity. Diversification patterns are found in several groups of parrots (Psittaciformes) in this region. Speciation events occurred at different stages, from a relatively old group (Cacatuidae) up to recent ones (*Eclectus*, Psittacidae and *Trichoglossus*, Loriidae). Using mitochondrial DNA sequence data (cytb, 1143 bp), the phylogenies of these groups were reconstructed. Distance values between clades were used in a molecular clock model to infer an evolutionary time scale for speciation events.

Session 21

Multiple driving forces of papillomavirus evolution

Ignacio G. Bravo[1], Alexandros Stamakis[2], Ingo Nindl[3], Marc Gottschling[3]

[1] Institute for Evolution and Biodiversity, University of Muenster, [2]Swiss Federal Institute of Technology, School of Computer & Communication Sciences, Laboratory for Computational Biology and Bioinformatics (LCBB), Lausanne, Switzerland, [3]Charité – Universitätsmedizin Berlin, Klinik für Dermatologie, Venerologie und Allergologie, Hauttumorcentrum Charité, Charitéplatz 1, 101 17 Berlin, Germany

Papillomavirus (PV) infection is a prerequisite for the development of cervical cancer, affecting half a million women worldwide per year. PV research has been historically focused on human PV types 16 and 18, which have been made responsible for more than 70% of the cases of cervical cancer. The strong bias towards human medicine-oriented approaches is continuous. However, most major human infectious diseases have animal origins, but in-depth investigations of the role of co-evolutionary interactions in phylogenetic diversification of pathogens and host lineages are remarkably limited. More than 140 PV complete genomes are available at present, 100 of which originate from humans. PV diversity corresponds to a broad spectrum of warm-blooded vertebrates including birds, marsupials, and placental mammals. The availability of the increasing genomic data has triggered the research on the evolution of these viruses. A complex evolutionary scenario for PV diversification now considers multiple driving forces such as co-evolution, zoonotic transmission, and periods of adaptive radiation. In the present communication, we reconstruct the phylogeny of the entire Papillomaviridae family based on the maximum length of phylogenetically informative amino acid sequences. We have addressed the extent and plausibility of virus-host co-speciation by the comparison of viral and host phylogenies. We found reliable support for the co-speciation hypothesis only for few PV taxa in highly derived phylogenetic positions of the molecular tree. We used such co-speciation episodes as calibration points for a comprehensive time-based reconstruction of the evolutionary history of Papillomaviridae. It provides evidence for an initial period of adaptive radiation of the ancestral virus (e.g., by the constitution of new ecological niches), followed by multiplied and parallel co-speciation events with the hosts. The knowledge thus gained on the evolutionary history of PVes is the basis for a phylogeny-based, revised classification of this viral family.

Plenary session III

Some recent advances in plant phylogeography

Christian Brochmann

National Centre for Biosystematics, Natural History Museum, University of Oslo, PO Box 1172 Blindern, 0318 Oslo, Norway, christian.brochmann@nhm.uio.no

Phylogeographic inference in plants is still hampered by a lack of optimal molecular markers, although this is likely to change soon with the new ultra-high-throughput sequencing technology. High-resolution fingerprints of the nuclear genome (e.g. AFLPs) in combination with organelle markers and ploidy level estimates from flow cytometry have nevertheless provided valuable new insights into the processes that shaped current genetic patterns in plants. Here I will review some of our recent studies on arctic and alpine plants and exemplify both the necessity and the power of combining different markers, e.g. in *Vaccinium* (Eidesen et al. 2007, Molecular Ecology 16: 3902-3925) and *Cassiope* (Eidesen et al. 2007, Journal of Biogeography 34: 1559-1574). I will also address some recent advances in comparative phylogeography, both among geographic regions with very different histories (the African high mountains, the European Alps, and the Arctic; cf. Ehrich et al. 2007, Molecular Ecology 16: 2542-2559) and among circumpolar/-boreal species in their entire range (based on a new 18-species dataset). Another major challenge in plant phylogeography as well as in general global change biology is to develop genetic measures of long-distance dispersal ability. I will show how AFLP data can be used to demonstrate that the arctic flora is highly mobile, with long-distance colonization occurring at much higher rates than previously envisioned (Alsos et al. 2007, Science 316: 1606-1609).

Session 2

Floral structure and phylogeny of Malvaceae-Grewioideae

Ulrike Brunken[1, 2], Clemens Bayer[1]

[1] Palmengarten Frankfurt, Siesmayerstr. 61, 60323 Frankfurt a.M., Germany,[2] Forschungsinstitut Senckenberg, Department of Botany and Molecular Evolution, Senckenberganlage 25, 60325 Frankfurt a.M., Germany

According to previous molecular studies, Grewioideae are a well-supported clade. Together with subfamily Byttnerioideae, they represent the first branching clade at the base of Malvaceae s.l. Grewioideae comprise 25 genera, including *Corchorus*, *Sparrmannia* and *Grewia*, all of which were formerly included in Tiliaceae. Floral structure of Grewioideae is highly variable, especially with regard to their multistaminate androecium, which may consist of free stamens, fascicles or androecial tubes. In contrast to Byttnerioideae, staminodes occur only in the periphery. Androgynophors are widespread. The position of nectaries on or in front of petals, as occurring in many Grewioideae, is unique within Malvaceae. Based on phylogenetic analyses of molecular (ndhF) and morphological data, a subdivision into two tribes, Apeibeae and Grewieae, is proposed. Both tribes are circumscribed by morphological characters. Special attention was paid to a comparison of floral structures with Byttnerioideae, where a differentiation into fertile antepetalous and a sterile antesepalous sectors are frequently found, often interpreted as (ob) diplostemony. Additional analyses of floral ontogeny and anatomy were untertaken in search of an underlying common “bauplan”. The features turned out to be highly variable, and no consistent diplostemonous structure could be detected. Consequences on the terminology of floral diagrams (e.g. “secondary polyandry”) are discussed, and the influence of pollination ecology is emphasized.

Session 1

Extreme convergence in stick insect evolution (Phasmatodea): phylogenetic placement of the rarest insect of the world

Thomas Buckley[1], Sven Bradler[2]

[1] Landcare Research, Private Bagg 92170, Auckland 1142, New Zealand, buckleyt@landcareresearch.co.nz, [2] Johann-Friedrich-Blumenbach-Institut für Zoologie und Anthropologie, Berliner Straße 28, 37073 Göttingen, Germany, sbradle@gwdg.de

Similarities between species can arise in two fundamentally different ways. Either each species has retained a comparable trait from their common ancestor, or each has acquired it independently. Although the first possibility might seem far more likely, convergence is a common phenomenon. Here we present evidence for the independent origin of the "tree lobster" body design within the insect order Phasmatodea (stick and leaf insects). The tree lobsters are robust, ground-dwelling phasmatodeans from the subfamily Eurycanthinae, distributed mainly in New Guinea, New Caledonia and associated islands. Its most famous member is the Lord Howe Island stick insect *Dryococelus australis*, which was believed to become extinct in the past century but was rediscovered in 2002 and is considered to be the rarest insect of the world. To resolve the phylogenetic position of *Dryococelus*, we conducted a molecular analysis based on approximately 2.5 kb of sequence data from nuclear and mitochondrial genomes of representatives of all major phasmatodean lineages. Our molecular data unambiguously placed *Dryococelus* and the New Caledonian tree lobsters outside the New Guinean Eurycanthinae as members of the recently established Australasian clade Lanceocercata. These results suggest a convergent origin of the tree lobster body form, which has misled previous taxonomists for approximately 150 years. In light of this surprising finding we re-examined the morphology of *Dryococelus* and other tree lobster genera and obtained additional support for our hypothesis of convergent evolution. We conclude that the phenotypic traits leading to the incorrect traditional classification are obligatory adaptations to ground-living behaviour. *Dryococelus* apparently represents a longstanding separate evolutionary lineage and is a key taxon to protect with respect to phasmatodean diversity.

Session 15

The Pentastomida story continued – new data about the ontogeny of Cambrian representatives

Christopher Castellani, Carolin Haug, Joachim T. Haug, Yu Liu, Andreas Maas, Dieter Waloszek

Workgroup Biosystematic Documentation, Helmholtzstr. 20, University of Ulm, 89081 Ulm, Germany, christopher.castellani@uni-ulm.de

No one would seriously disagree that there is only one evolution and one phylogeny. Yet, the discordance between morphological-data based and molecular-data based reconstructions of the systematic affinities of animals is often striking. One example is the position of the parasitic tongue worms, the Pentastomida or Linguatulida. The positional difference between an assumed close alliance to fish lice and an origin before the Arthropoda s. str. level (i.e. before achievement of the arthropod characteristics such as sclerotised body with tergites, compound eyes, or segmented limbs with exopods) could hardly be larger. In 2004, new material of Cambrian representatives of tongue worms could be extracted from Upper Cambrian limestones collected in Västergötland, Sweden. The more than 60 specimens now at hand apparently represent different developmental stages but it is unclear whether they belong to different species. In the framework of the EU-supported PhD training programme MOLMORPH we aim to learn more about 1) the still unclear ontogeny of this group, 2) morphological details profiting from the good preservation of part of the material, and 3) the taxonomic status of all fossil taxa from the Swedish 'Orsten'. We also expect to contribute to the ongoing controversy regarding the systematic position of this enigmatic parasite group.

Plenary session I

The angiosperm tree of life – morphology-rich but still poorly understood

Mark W. Chase

Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3DS UK, m.chase@kew.org

Many groups of organisms are obviously difficult to classify. These would include things such as sponges, nematodes, and algae, as well as all the unicells. However, for many other groups, such as vertebrates and most land plants, it was expected that careful study of morphology should be adequate to construct natural classifications. When DNA studies then proceeded to turn such groups on their heads, it was first questioned if there was a conflict between morphology and molecules. It subsequently became clear that similar patterns were present in both types of data; the discrepancies between the DNA trees and previous ideas about classification had more to do with the underlying methods than the data themselves. To many, it was also clear that even if analyzed in the same methodological framework, morphological data were a poor sister to DNA data. This understanding has led to two approaches to the use of morphological in plant phylogenetic reconstruction. One assumes that there is little point in using morphological data in tree construction and advocates merely mapping it on the resulting trees; the other has resorted to more intense study of morphological characters that appear to be homoplasious so that a better assessment of homology can be accomplished. The aim of the latter approach is to include such re-considered characters in phylogeny reconstruction. In either case, it is also clear that although angiosperms are relatively morphology-rich, they were also poorly understood before the advent of DNA phylogenetics.

Session 20

The trigger mechanism in Marantaceae

Regine Claßen-Bockhoff, Elke Pischtschan, Ariane Heller

Institut für Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Germany

The Marantaceae transfer pollen by means of a rapid style movement. Its high speed points to a turgor movement similar to the reversible leaf movements in the Venus flytrap and the sensitive mimosa. However, unlike these species, the movement is irreversible providing the flower with only a single chance to get pollinated. Though the unique process of pollen transfer is known for more than 150 years, the underlying mechanism was never investigated in detail. We here summarise our results from experimental and anatomical studies and make a first attempt to explain the trigger mechanism. According to our findings, the style is hold under tension by two different forces, an external mechanical pressure set up by the enveloping but too short `hooded staminode´ and an internal physiological gradient set up by membrane potentials. The rapid style movement is released by a pollinator mechanically deforming the `trigger appendage´ at the hooded staminode. Style release experiments indicate that in some species sensitive cells on the upper side of the style appear to be directly triggered by the deformation responding the impulse with a membrane depolarisation. We conclude that the sudden break down of their turgor allows the lower cells to expand and get rid of the wrapping hooded staminode. In other species the mechanical signal seems to be transferred by an elastic deformation of the entire hooded staminode. If the hood thereby slips off the style, the longitudinal counter-pressure breaks down and the cells rapidly expand. Referring the data at hand to the phylogeny of the Marantaceae it is likely that the mechanical release mechanism going along with many stabilising staminode structures represents the ancestral state. It is hypothesised that in the course of evolution the hold of the tension has been gradually transferred to membrane potentials promoting the electrophysiological release mechanism and allowing the hooded staminode to reduce its elaborate secondary structures several times in parallel.

Session 21

Reevaluation of the cox1 group I Intron in Araceae and angiosperms indicates a history dominated by loss rather than horizontal transfer

*Natalie Cusimano, Susanne Renner

Department of Biology, Ludwig Maximilian University, 80638 Munich, Germany

The origin and modes of transmission of introns remain matters of much debate. Previous studies of the group I intron in the angiosperm cox1 gene inferred frequent angiosperm-to-angiosperm horizontal transmission of the intron from apparent incongruence between intron phylogenies and angiosperm phylogenies, patchy distribution of the intron among angiosperms, and differences between cox1 exonic coconversion tracts (the first 22 nucleotides downstream of where the intron inserted). We analyzed the cox1 gene in 179 angiosperms, 110 of them containing the intron (intron^{+}) and 69 lacking it (intron^{-}). Our taxon sampling in Araceae is especially dense to test hypotheses about vertical and horizontal intron transmission put forward by Cho and Palmer (1999). Maximum likelihood trees of Araceae cox1 introns, and also of all-angiosperm cox1 introns, are largely congruent with known phylogenetic relationships in these taxa. The exceptions can be explained by low signal in the intron and long-branch attraction among a few taxa with high mitochondrial substitution rates. Analysis of the 179 coconversion tracts reveals 20 types of tracts (11 of them only found in single species, all involving silent substitutions). The distribution of these tracts on the angiosperm phylogeny shows a common ancestral type, characterizing most intron^{+} and some intron^{-} angiosperms, and several derivative tract types arising from gradual back mutation of the coconverted nucleotides. Molecular clock dating of small intron^{+} and intron^{-} sister clades suggests that coconversion tracts have persisted for 70 million years in Araceae, whose cox1 sequences evolve comparatively slowly. Sequence similarity among the 110 introns ranges from 91% to identical, while putative homologs from fungi are highly different, but sampling in fungi is still sparse. Together, these results suggest that the cox1 intron entered angiosperms once, has since largely or entirely been transmitted vertically, and has been lost numerous times, with coconversion tract footprints providing unreliable signal of former intron presence. (Manuscript in press at Molecular Biology and Evolution.)

Session 7

Taxonomy of the genus *Lotus* (Leguminosae-Loteae): evidence from molecular and morphological data

Galina Degtjareva, Tatiana Kramina, Tagir Samigullin, Dmitry Sokoloff, Carmen Valiejo-Roman

Lomonosov Moscow State University, Moscow, 119991, Russia

The genus *Lotus* includes about 120 species widespread in Macaronesia, Europe, Africa, Asia, Australia, and on the Pacific islands. Section *Lotus* is one of the most problematic within the genus; more than 100 species have been described but the majority of them are now considered synonyms. Clearly, a new taxonomic revision of the section *Lotus* is needed. The section unites species with five-leaflet leaves, predominantly yellow petals, almost actinomorphous or slightly zygomorphous calyx, papillate stylodium, multiseeded dehiscent fruit with endocarpium without brown cells, basic chromosome number x=6. A phylogenetic study of the genus *Lotus* and related genera based on nrITS1,2 data revealed that the section *Lotus* is not monophyletic, forming a clade with members of sections *Dorycnium* and *Bonjeanea*. Similar results were obtained in a phylogenetic study of the tribe Loteae based on psbA-trnH cpDNA. An analysis of nrITS and morphological data showed the monophyly of the section Lotus (including *L. conimbricensis*). The largest group within the section, the *Lotus corniculatus* group (LC) is monophyletic based on nrITS data. A morphological study of the LC group revealed diploid and tetraploid taxa morphologically close or distant to *L. corniculatus*. Interspecific hybridization is supposed to have taken place in this group. According to the nrITS data, the *Lotus angustissimus* group (LA) is not monophyletic and some of its species are resolved in the LC group. The *Lotus pedunculatus* group possesses a combination of characters of the LC and LA groups. Relationships within and between the LC and LA groups and the taxonomic position of several species are discussed.

Session 2

Molecular phylogeny of the genus *Anthyllis* (Leguminosae: Loteae): evidence for long-branch attraction in parsimony analysis of nrITS data

Galina Degtjareva, Dmitry Sokoloff, Tagir Samigullin, Carmen Valiejo-Roman

Lomonosov Moscow State University, Moscow, Russia

Anthyllis is a genus of about 20 species in the Mediterranean region and adjacent areas. Molecular phylogeny of *Anthyllis* has been recently studied using nuclear ribosomal ITS data (Kropf et al., 2002; Allan et al., 2003; Nanni et al., 2004; Degtjareva et al., 2006; Kropf, 2006). Trees inferred from parsimony and Bayesian analyses of nrITS data set differ in position of the most widerspread species of the genus, *Anthyllis vulneraria* (e.g., Degtjareva et al., 2006). Bayesian analysis suggests close relationship between *A. vulneraria* and species of the Western Mediterranean section *Dorycnioides* (*A. tejedensis, A. ramburei, A. onobrychioides*), though *A. vulneraria* occupies a very long branch. Parsimony analysis of nrITS data does not support such a relationship. To understand possible source of this incongruence, we have produced molecular phylogenetic data on *Anthyllis* using three additional markers, all from chloroplast genome (viz. rps16 intron, psbA-trnH spacer and petB-petD region). Like nrITS, each of three new markers show monophyly of the genus *Anthyllis* (including *Hymenocarpos* and *Cornicina*, but excluding *Tripodion*). Phylogenetic trees inferred from analyses of chloroplast markers are generally similar to each other. They show that *A. vulneraria* is close to species of the section Dorycnioides, but also to *A. lagascana* (sect. Sericeae). We hypothesize that placement of *A. vulneraria* in parsimony analysis of nrITS data is an artifact due to long-branch attraction. Evolution of morphological characters will be discussed in the light of the new molecular phylogenetic data.

Session 10

Phylogeny and bioacoustic evolution in the genus *Sphingonotus*

*Jana Deppermann, Martin Husemann

University of Osnabrück, Department of Biology/Chemistry, Division of Ecology, Barbarastr. 11, 49069 Osnabrück, Germany

The Mediterranean Region is one of the European hotspots of the species diversity with a large number of endemics. The genus *Sphingonotus* FIEBER, 1852 is one of the largest grasshopper genera, containing about 130 species. One of its main areas of diversification is located in the Mediterranean. The details of phylogenetic and distributional patterns within this diverse group are still sparsely studied. Some species are known for their conspicuous songs and elaborate displays. Since the evolution of premating barriers by reinforcement or sexual selection is believed to be a major force driving speciation, the genus is of high interest for our understanding of speciation processes. We performed a phylogenetic analysis of the genus *Sphingonotus* using three gene fragments (mtDNA and nDNA) and compared the evolutionary history with data on bioacoustic differentiation and the evolution of stridulatory morphologies. Two lineages within the genus (*S. caerulans* group & *S. azurescens* group) seem to represent young species flocks. *S. rubescens* and *S. caerulans* are morphologically and genetically rather similar, but they can easily be identified due to their characteristic songs. *S. rubescens* produces a loud bird-like thrill followed by drumming with the hind legs, whereas *S. caerulans* produces a rustling sound. We found five different types of sound production in the genus. The plesiomorphic state is found in the basal lineages (Oedipodinae type: serrate intercalary vein). Groups possessing apomorphic mechanisms of sound production (*radioserratus* type: serrate radius; *Pseudosphingonotus* type: thickened cross veinlets between radius and media) turned out to be monophyletic. Additionally, some species use wing crepitation during flight or drum with their hind legs on the substrate. Our study provides evidence that the evolution of morphological innovations affects pre-mating isolation and might drive rapid speciation processes.

Session 11

Agenda for Calcareous Dinoflagellate Research (Thoracosphaeraceae, Dinophyceae)

Malte Elbrächter[1], Marc Gottschling[2], Tania Hildebrand-Habel[3], Helmut Keupp[2], Rolf Kohring[2], Jane Lewis[4], K.J. Sebastian Meier[5], Marina Montresor[6], Michael Streng[7], Gerard J.M. Versteegh[8], Helmut Willems[9], Karin Zonneveld[9]

[1] Deutsches Zentrum für Marine Diversitätsforschung, Forschungsinstitut Senckenberg, Wattenmeerstation Sylt, Hafenstraße 43, 25991 List / Sylt, Germany, [2]Freie Universität Berlin, Institut für Geologische Wissenschaften – Fachrichtung Paläontologie, Malteser Straße 74-100, 12249 Berlin, Germany, [3]University of Stavanger, Faculty of Science and Technology, 4036 Stavanger, Norway, [4] University of Westminster, School of Biosciences, 115 New Cavendish Street, London W1W 6UW, United Kingdom,[5] Universität Kiel, Institut für Geowissenschaften, Labor für Rasterelektronenmikroskopie, Ludewig-Meyn-Str. 16, 24118 Kiel, Germany, [6] Stazione Zoologica 'A. Dohrn', Villa Comunale, 80121 Napoli, Italy, [7] Uppsala University, Department of Earth Sciences – Palaeobiology, Villavägen 16, 75236 Uppsala, Sweden, [8] Universität Hamburg, Institut für Biogeochemie und Marine Chemie, Bundesstrasse 55, 20146 Hamburg, Germany, [9] Universität Bremen, Fachbereich Geowissenschaften – Historische Geologie und Paläontologie, Postfach 330 440, 28334 Bremen, Germany

Calcareous dinoflagellates are considered to be a monophyletic group of peridinoids that have the potential to produce calcitic exoskeletal structures during the life cycle, or that derive from such forms. Frequently, these calcareous bodies are excellently preserved in the fossil record and have received increased attention during the past three decades with regard to their use in biostratigraphy, climate, and environmental reconstruction. Fossil and extant taxa have been classified in various, partly concurring, systematic concepts, using character complexes of the theca, cyst wall ultrastructure, and archaeopyle / operculum morphology. The significance of such character complexes is briefly presented in the light of molecular data that have been accumulated during the past decade. Over the years, the number of published taxonomic names has increased, partly due to nomenclatural changes. We propose to unify the former segregated taxonomic units Calciodinelloideae and Thoracosphaerales, using the family name Thoracosphaeraceae for the entirety of calcareous dinoflagellates and non-calcareous relatives derived from them. We outline major subjects that are in need of (re-)investigation and -evaluation (an Agenda for Calcareous Dinoflagellate Research), including nomenclature, taxonomy (protologues and typifications), character traits, documentation of diversity, life cycle, and molecular evolution. In order to contribute to a consistent and stable nomenclature and taxonomy of calcareous dinoflagellates, we compiled 96 published generic names assigned to known calcareous dinoflagellates, including their type species and information on type locality and stratigraphy. We evaluate the validity of these names, a crucial first step for any revisionary work in the future.

Session 16

Molecular phylogeny, biogeographical history and a revised classification of *Ranunculus* s.l. (Ranunculaceae)

Khatere Emadzade[1], Elvira Hörandl[1], Carlos Lehnebach[2], Peter Lockhart[2]

[1]*Department of Systematic and Evolutionary Botany, University of Vienna, Rennweg 14, 1030 Vienna, Austria,* [2]*Massey University, Allan Wilson Center, Palmerston North, New Zealand*

Ranunculus s.l. comprises c. 600 species and is distributed in all continents. Phylo-genetic reconstruction using DNA sequences (nrITS, matK-trnK) and morphological characters were utilized to get insights into relationships and evolutionary traits of the genus. Combined molecular data of c. 200 species reveal a large core clade comprising *Ranunculus* s.str., excluding the small genera *Laccopetalum*, *Krapfia*, *Ceratocephala*, *Myosurus*, *Ficaria*, *Coptidium*, *Beckwithia*, *Cyrtorhyncha*, *Halerpestes*, *Peltocalathos*, *Callianthemoides*, and *Arcteranthis*, but including the water-buttercups and the monotypic genus *Aphanostemma.* Biogeographical analyses of *Ranunculus* s.str. suggest a strong radiation within the Mediterranean - Irano-Turanian region, supporting the existence of an ancient Tethyan area. The Himalayan species are related to arctic-circumpolar, C. Asian and N. American, and European high mountain taxa. At least two independent eastern Asian - North American disjunctions including endemic species of Hawaii, are observed. Altogether the biogeographical history of the genus is in all continents not only shaped by multiple colonization events, but also by rapid regional diversifications. Morphological analyses suggest a high adaptive potential of structures, especially in vegetative parts; they show high levels of homoplasy and are not useful for classifications. Characters of fruits and petals, but also karyological features are more conserved and support not only the circumscription of genera within Ranunculeae, but also major clades within *Ranunculus* s.str. An outline of a completely new sectional classification is presented.

Session 6

Mechanisms of speciation: hybridisation and karyotype evolution in *Crepis* (Cichorieae, Compositae)

*Neela Enke, Birgit Gemeinholzer

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

Babcock described karyotype evolution as driving force of speciation in *Crepis* L.. He defined 27 sections on grounds of chromosome number and karyotype morphology and assigned 196 *Crepis* species accordingly to them. Following his hypotheses it was mainly a change in chromosome number which led to inter-specific sterility and therefore to speciation. According to Babcock hybridisation only plays a minor role in speciation in the genus. However, recent phylogenetic studies on *Crepis* showed that the karyotype evolution in the genus might be far more complex than Babcock (1947) assumed in his monograph of the genus. Molecular results suggest that quantitative karyotype characteristics and similarities in chromosome morphology are more indicative of phylogenetic relationships in *Crepis* than chromosome number alone. Furthermore, the comparison of nuclear and chloroplast markers very strongly hints on various hybridisation events and therefore reticulate evolution in the genus. As polyploidy is not common in *Crepis* except for the North-American species of section *Psilochaenia*, hybridisation, geographic and ecological barriers seem to be the main causes for the development of new species in the genus.

Session 10

The use of nuclear coding genes for phylogenetic reconstructions in an adaptive radiation

*Korinna Esfeld[1], Mike Thiv[1], Marcus Koch[2]

[1] State Museum of Natural History Stuttgart, Rosenstein 1, 70191 Stuttgart, Germany, [2] Heidelberg Institute of Plant Science, Biodiversity and Plant Systematics, Neuenheimer Feld 345, 69120 Heidelberg, Germany

Adaptive radiations with their spectacular diversity affecting morphology and physiology have been the centre of interest for several decades. Whereas phylogenetic analyses based on non-coding DNA sequences often result in polytomies or weakly supported relationships, genes involved in the evolutionary process of speciation may draw another picture. Being under the control of different selection regimes, these genes may resolve relationships within an adaptive radiation.

Here, we use DNA sequences of nuclear coding genes to contribute to a better understanding in the evolution of the Macaronesian Crassulaceae-Sempervivoideae. This group has its centre of distribution on the Canary Islands and comprises more than 75 species in the three genera *Aeonium*, *Aichryson* and *Monanthes*. The taxa display a high level of both phenotypic diversity, e.g. in floral and inflorescence morphology, and ecological variation by colonizing different habitats at various altitudes. Jorgensen & Frydenberg (1999) as well as Mort et al. (2002) failed to reflect this variation in molecular data because of low levels of sequence divergence of ITS and cpDNA. We sequenced homologues of Apetala1, controlling the organ identity of sepals and petals and affecting the number of inflorescence branches as well as the flowering time and Apetala3 which defines the position and size of petals and stamens. In addition, sequences of PEP-carboxylase, playing an important role in the fixation of CO_2 in CAM plants, were used to consider physiological adaptations to dry habitats.

Here, we compare phylogenetic reconstructions based on Apetala1, Apetala3 and PEP-carboxylase with those inferred from standard DNA markers (nrITS, cpDNA) in the Macaronesian Sempervivoideae. Preliminary results indicate a corroboration of phylogenetic patterns but at the same time, they are better resolved and supported.

Session 21

Punctuated genome size evolution in Liliaceae

Michael F Fay[1], Ilia J. Leitch[1], Jeremy M. Beaulieu[2], Kwok Cheung[1], Lynda Hanson[1], Martin A. Lysak[3]

[1] Royal Botanic Gardens, Kew, Jodrell Laboratory, Richmond, Surrey, TW9 3AB, United Kingdom, [2] California Polytechnic State University San Luis Obispo, Biological Sciences, 1 Grand Ave, San Luis Obispo, CA, 93407, USA, [3]Masaryk University, Department of Functional Genomics and Proteomics, Kamenice 5, Building A2, Brno, 62500, Czech Republic.

Most angiosperms possess small genomes (mode 1C = 0.6 pg, median 1C = 2.9 pg). Those with truly enormous genomes (i.e., >35 pg) are phylogenetically restricted, occurring in a few families (mostly monocots), including Liliaceae. This family exhibits a wide range in genome size, with species possessing some of the largest genomes so far reported for any plant and others possessing much smaller genomes. To gain insights into when and where genome size change/expansion took place during the evolution of Liliaceae and the mode and tempo of this change, data for 78 species were superimposed onto a phylogenetic tree and analysed. Results suggest genome size in Liliaceae followed a punctuated rather than gradual mode of evolution and that most of the diversification evolved recently rather than early in the evolution of the family. We consider that the large genome sizes of Liliaceae may have emerged passively rather than as a result of selection.

Session 11

Large genetic divergence of new, morphologically similar species of sterile lichens from Europe (*Lepraria*, Stereocaulaceae, Ascomycota): concordance of DNA sequence data with secondary metabolites

Judith Fehrer[1], Štěpánka Slavíková-Bayerová[1], Alan Orange[2]

[1] *Institute of Botany, Academy of Sciences of the Czech Republic, Zámek 1, 25243 Průhonice, Czech Republic,* [2] *Department of Biodiversity and Systematic Biology, National Museum of Wales, Cardiff, CF10 3NP, U.K.*

Lichenized fungi of the genus *Lepraria* are known for a paucity of morphological characters. Species identification is therefore largely based on secondary chemistry. We investigated different chemotypes of the morphologically highly similar *L. jackii* species complex by internal transcribed spacer (ITS) sequencing. In phylogenetic analyses including all available *Lepraria* species, samples belonging to different chemotypes of the *L. jackii* agg. corresponded to four highly divergent clusters. While true *L. jackii* was genetically uniform, the other three clades represented previously unrecognized species. They originated from different major speciation events, and two of them were not closely related to any other species. Assessment of intraspecific genetic variability revealed four different patterns with respect to geographic scale. ITS sequences proved to be the most reliable and distinctive characters for species recognition in the *Lepraria jackii* complex and were in accordance with chemical and ecogeographic data. Frequent occurrence of long branches, relatively few resolved relationships despite high genetic variability, and the discovery and description of a considerable part of *Lepraria* species within the last ten years suggest that the genus is probably much larger than currently known. The diversification of this asexual group in potential absence of recombination will be discussed.

Plenary session II

Influence of host-identity vs. host-distribution on the radiation of obligately plant-associated ants

Heike Feldhaar

Zoologie II, Biozentrum der Universität Würzburg, Am Hubland, 97074 Würzburg, Germany,
feldhaar@biozentrum.uni-wuerzburg.de

The *Crematogaster* (subgenus *Decacrema*) – *Macaranga* (Euphorbiaceae) association in SE Asia is one of the most species-rich ant-plant associations worldwide with both groups showing considerable radiation. *Macaranga* hosts are distributed in patches in disturbed sites as well as gaps in primary forest and along river edges. Non-random association patterns of ants and plants are observed in spite of the often sympatric occurrence of several host-plant species within a patch. Thus, speciation processes in the ants may be driven either by adaptation towards alternative host species, by spatial patterns of host distribution or both factors – selection and drift- in concert.

In the talk I will present evidence that the limited dispersal ability of the ants can lead to isolation by distance on small geographic scale when hosts have a patchy distribution like in gaps of primary forest. In contrast, adaptation towards alternative hosts (in sympatry) seems less likely since a) ant queens showed no constant preference for a particular host when given the choice between two host species and b) alternative hosts did not differ significantly in amount of food or nesting space which are the most important resources offered to the ants.

Thus, combined effects of spatially heterogeneous populations of *Macaranga* hosts, the limited dispersal of the ants and different selection pressures exerted by alternative hosts in allopatric habitat patches, may enhance diversification processes within obligate plant-ant species, leading to ant populations that are highly substructured on small geographic scales.

Session 13

Genetic diversity and population structure of *Macaranga hypoleuca* (Euphorbiaceae), an important pioneer tree species of Southeast Asian lowland rainforest

*Christina Fey-Wagner[1], Tim Kröger-Kilian[1], Daniela Guicking[1], Brigitte Fiala[2], Frank R. Blattner[3], Kurt Weising[1]

[1] Plant Molecular Systematics, Dept. of Sciences, University of Kassel, Germany, [2] Animal Ecology and Tropical Biology, Biocentre, University of Würzburg, Germany, [3] Leibniz Insitute of Plant Genetics and Crop Research (IPK), Gatersleben, Germany

Two contrasting hypotheses have been postulated concerning the population structure of pioneer plants. Either pioneer plants are supposed to exhibit a clear population structure due to the usually small number of individuals which colonize new areas, or frequent local extinction and recolonization enhance gene flow and hence reduce genetic differentiation among populations. To test these hypotheses, we analysed the population structure of the dioecious, ant-associated (myrmecophytic) *Macaranga hypoleuca*, which is an abundant pioneer tree in SE Asian lowland rainforests. Originally being restricted to gaps and riversides in primary forest, this species has become a conspicuous early successional plant of disturbed habitats. We conducted a microsatellite-based study to assess the genetic diversity and population structure of *M. hypoleuca* at two geographical levels, i.e., (1) on a local scale within a 2 x 2 km area of primary forest in Danum Valley (Sabah, Borneo), intersected by forest trails, and (2) throughout the distribution area of the species (Borneo and Malay Peninsula). At both geographical levels, we found high genetic diversity within populations and small differences among populations. However, a weak signal of isolation by distance could be detected, as the extent of genetic similarity among populations decreases with geographical distance. Our results thus support the hypotheses of low population structure in pioneer species and suggest relatively high levels of gene flow in *M. hypoleuca*, indicating effective long-distance pollination and/or seed dispersal as would be expected for pioneer trees.

Session 2

Phylogeny of the genus *Heliamphora* (Sarraceniaceae), with special focus on biogeography and character evolution

*Andreas Fleischmann[1], Harald Meimberg[2], Günther Heubl[1]

[1] LMU München, Department Biologie I, Systematic Botany, Menzinger Strasse 67, 80638 Munich, Germany, [2] Department of Bioagricultural Sciences and Pest Management, Colorado State University, Plant Sciences Building, University Avenue 307, Fort Collins, CO 80523, USA

The genus *Heliamphora* is a member of the New World family Sarraceniaceae, which comprises three genera of carnivorous pitcher plants. It is restricted to the remote granitic table mountains (tepuis) of the Guayana shield of Venezuela and adjacent Guyana and Brazil. The isolated distribution of the genus is one reason for a rather poor collection history and a vague taxonomic concept. Of 14 currently accepted species, 8 have been described in the past seven years. Morphological characters used for species delimination, like the shape and size of the carnivorous pitcher leaves or the pitcher appendage (lid), vary remarkably between different species and even within a single species. Therefore, previously proposed taxonomic concepts for the genus, which are exclusively based on morphological characters, are all hampered by ambiguity of species borders. We investigated species deliminations and phylogenetic relationships of all known species of *Heliamphora* using nuclear ITS and plastidic rbcL and trnL-F sequence data and compared the results with the morphology-based taxonomic concepts proposed for the genus. Origin and species distribution were inferred, matching well the molecular data. Phylogenetic reconstruction revealed four monophyletic groups (clades) within the genus *Heliamphora*, which are supported by the morphological characters of inflorescence indumentum and anther length, and by biogeographic patterns.

Session 20

Cotyledons in Chenopodiaceae as evolutionary markers ?

Helmut Freitag[1], Antonina Butnik[2]

[1] Plant Systematics & Morphology, Institute of Biology, University of Kassel, [2] Institute of Botany, Uzbek Academy of Sciences, Tashkent 700143, Uzbekistan

Comparative studies were carried out in cotyledons and leaves of Chenopodiaceae from all subfamilies and tribes. The cotyledons are foliaceous and resemble to the leaves though during germination their function shifts from storage to photosynthesis. Structurally they differ in various degree from leaves: (1) trichomes absent, (2) sclerenchyma absent, (3) size and shape (a-smaller and narrower in broad-leaved groups, b-larger and wider in many groups with narrow leaf lamina), (4) venation pattern, (5) chlorenchyma and related types of photosynthesis. Some of these characters can be used in taxonomy, particularly in difficult groups such as *Salsola* s.l. and *Bassia* s.l. The characters (1)-(3a) seem to be cotyledon-specific because they occur in all taxa studied so far and are also known from other families.

When divergent structures were found in cotyledons and leaves of the same species, the cotyledons always show the less derived conditions, e.g., lamina flat versus semi-terete or terete, size normal versus reduced, symmetry dorsiventral versus isolateral or centric, secondary bundles lateral versus peripheral, C_3 versus C_4 anatomy. It is tempting to explain that phenomenon by the theory of recapitulation. Then the simpler cotyledon structures would represent ancestral stages of leaf evolution. While for some decades recapitulation was discredited, by the discovery of regulatory genes and their combination with the concepts of heterochrony, replication and terminal addition, it became compatible with modern genetics. Thereby, in Chenopodiaceae the cotyledons might be helpful in tracing evolutionary steps which are not represented in extant species. One problem is to explain why in some taxa the cotyledons remain in a more ancestral stage but in others not. Possible answers are, e.g.: 1 – Ancestral cotyledon structures were lost by homogenisation of gene expression when advanced leaf structures are comparatively old (e.g. *Salsola* sect. *Kali*, *Bienertia*). 2 - Ancestral cotyledon structures might be retained because they are better adapted to germination conditions in early spring than the specialised leaves which are fully effective only under the combined effects of water stress, salinity, high temperature and intense radiation.

Plenary session III

Identification and phylogeny of algae dominating biofilms: a challenge for algal systematics

Thomas Friedl

Abteilung Experimentelle Phykologie und Sammlung von Algenkulturen, Albrecht-von-Haller-Institut für Pflanzenwissenschaften, Universität Göttingen, Germany, tfriedl@uni-goettingen.de

In microalgae morphological differences are often too subtile for an identification from environmental samples, but molecular signatures allow their unambiguous and rapid detection. However, the studies presented here confirmed that identification of algae from environmental samples by sequence comparison often is still not possible because their diversity is poorly reflected in sequence databases. In sequence comparisons only names as provided with the sequence accession can be used which is a source of serious concern when the identifications associated with the sequences are not clearly referenced, e.g. to a publicly available culture strain. Biofilms dominated by cyanobacteria and diatoms covering rocks in tufa forming Karstwater creeks as well as subaerial green algal biofilms on artificial hard substrates in urban environments were investigated here. From DNA extractions of biofilm material SSU rDNAs were amplified followed by cloning and sequencing. Phylotypes, i.e. groups of highly similar sequences forming distinct clades were recovered in phylogenetic analyses of partial (comprising about one third of the variable informative sites) and full SSU rDNA sequences using all available sequences from GenBank for cyanobacteria and respective classes of microalgae for comparisons. Key player phylotypes were identified from the many similar habitats compared which were abundant at atleast two or three sites within each corresponding study and retrieved in high numbers per clone library. Compared to a culture approach, only a small fraction of the key players was recovered in the cultures. However, certain key players were retrieved only by culturing. This advocates to combine both approaches for microalga diversity assessment from environmental samples. In many cases only one of the several different sequences from a phylotype could be identified to represent a species already represented in public databases or no close neighbouring species or even genera were found. In such cases the microalgae need to be retrieved in culture and identified using traditional morphological features. However, this may be significantly hampered as the culture of microalgae may be often difficult or impossible and often they represent cryptic species which cannot satisfactorily be distinguished using morphological criteria of known taxonomic significance.

Session 5

Elucidating the origin of the genus *Allium*: a molecular phylogenetic study of the subgenus *Amerallium*

Nikolai Friesen

Botanical Garden, University of Osnabrueck. Albrechtstr. 29. 49078 Osnabrück, Germany, friesen@biologie.uni-osnabrueck.de

The genus *Allium* is currently regarded as a member of the Alliaceae, subfamily Allioideae. *Allium* is distributed almost exclusively in the northern hemisphere and ca. 85% of the species are distributed in Eurasia. Chromosome number and the fact that most of the subgenera occur in the Old World, lead to the suggestion of a Eurasian origin of the genus *Allium*. Molecular phylogeny supports this suggestion. According to Friesen et al. (2006) *Allium* is subdivided into 13 subgenera and 72 sections. Most of subgenera show only one center of diversity while subgenus *Amerallium* haze three centers, i.e., North America, Europe and East Asia. Therefore the phylogeny of subgenus *Amerallium* is important to elucidate the origin of the whole genus. The phylogenetic position of the subgenus Amerallium as sister to the Mediterranean subgenus *Nectaroscordum* and the east Asian subgenus *Microscordum* provides evidence for an Old Word (x=7, 8,9,10) [in contrast to a New Word (x=7)] origin of the subgenus *Amerallium*. Current molecular studies (ITS and cpDNA) support the monophyletic origin of the subgenus *Amerallium*, which is subdivided into two major sister clades: an American group with about 86 species and a Eurasian group with two sister alliances: Mediterranean with 25 taxa and East Asian with 6 species. The relationships of the Old World *Amerallium* species (Sections *Mollium*, *Briseis*, *Chamaeprason*, *Narcissoprason*, *Ophioscorodon* and *Bromatorrhiza*) were elucidated.

Session 1

A proteomic approach for studying insect phylogeny - identification of Capa-peptides in cockroaches

*Bastian Fromm, Steffen Roth, Reinhard Predel

Institute of Zoology, University of Jena, Erbertstrasse 1, 07743 Jena, Germany

Members of the taxon Dictyoptera, which include praying mantids, cockroaches and termites, are among the oldest pterygote insects known. The phylogenetic relationships of and within these groups are the topic of several conflicting interpretations. In order to evaluate relationships among cockroaches, we used a novel character set, viz. neuropeptides processed from the Capa-gene. Capa-peptides were identified by mass spectrometry from members of all major lineages of cockroaches (Blaberidae, Blattellidae, Blattidae, Polyphagidae, Cryptocercidae) and the termite *Mastotermes darwiniensis*. The cladograms resulting from the analysis of 63 species of Dictyoptera show a topology which is in general agreement with recent molecular and morphological phylogenetic analyses, including the positioning of Isoptera within cockroaches close to Polyphagidae and Cryptocercidae. The findings were corroborated by the analysis of mitochondrial cytochrome oxidase II genes and confirmed that neuropeptide sequences of insects are suitable for reconstruction of phylogenetic relationships. Our study represents the first comprehensive survey of insect neuropeptides for phylogenetic purposes.

Session 8

A cladistic re-examination of Aristotle's classification of animals

Alexander Fürst von Lieven, Marcel Humar

AG Evolutionsbiologie, Institut für Biologie / Zoologie, Free University of Berlin, Königin-Luise-Str. 1-3, 14195 Berlin

Historia Animalium (*HA*) of Aristotle contains an extraordinarily rich compilation of descriptions of animal anatomy, development and behaviour. It is believed that Aristotle's aim in *HA* was to describe the correlations of characters rather than to classify or define animal groups. In order to determine whether Aristotle referred to a pre-existing classification underlying his descriptions, we carried out a cladistic analysis. By disentangeling 147 species- and 44 higher taxa designations from 157 predicates in the texts, we transcribed Aristotle's descriptions of animal anatomy and development in books I-V of *HA* into a character matrix for a cladistic analysis. By analysing the distribution of characters, we obtained a non-phylogenetic dendrogram displaying 58 "monophyletic" groups, 30 of which had equivalents among Aristotle's group designations. Ten groups turned out to be "non-monophyletic" and five were inconsistent with the "monophyletic" groups. Eleven of 28 taxa without equivalents in Aristotle's works had equivalents in modern classifications. The analysis shows an almost consistent underlying classification in the zoological works of Aristotle. The peculiarities of Aristotle's character concepts are discussed and the dendrogram is compared with a current phylogenetic tree.

Session 19

The use of phylogenetic and phylogeographic data for wood certification in Dipterocarpaceae

Oliver Gailing, Yanti Rachmayanti, Hani Nuroniah, Nga Phi Nguyen, Cuiping Cao, Randy
Villarin, Reiner Finkeldey

Department of Forest Genetics and Forest Tree Breeding, Büsgen-Institute, Georg-August University Göttingen, Germany, Büsgenweg 2, 37077 Göttingen, ogailin@gwdg.de

Dipterocarpaceae is the most important forest tree family in natural and close-to-nature forests in Southeast Asia. Members of this family are dominant components of lowland tropical rainforests in evergreen and seasonal tropical climates. Due to the exploitation for their valuable timber, dipterocarp forests are heavily affected by deforestation, forest fragmentation, and non-sustainable forest management including selective logging. The development of non-manipulable tools to test the origin of wood is an urgent need within the context of forest certification. Especially for species with restricted geographic range the identification of the species allows an accurate characterization of the geographic origin and is thus highly valuable for the detection of wrongly declared wood origins. Phylogenetic analyses in dipterocarps have been based on sequence analyses of several chloroplast DNA regions, the internal transcribed spacer region and single copy genes of the nuclear genome. We extended these analyses to a large number of dipterocarp species from Indonesia, the Philippines and Vietnam. In addition we analysed the genetic variation within and among geographically distinct populations of the most common and widespread emergents of lowland dipterocarp forests in Indonesia, *Shorea leprosula* and *Shorea parvifolia*. Since no variation among geographic regions was detectable with chloroplast DNA markers, we applied universal AFLPs to identify markers with pronounced frequency differences between geographic regions in Indonesia. SCARs (Sequence Characterized Amplified Regions) markers developed from AFLP markers clearly differentiated between the islands Sumatra and Borneo. Our final goal is to develop a large and reliable set of DNA markers for the verification of the geographic origin of wood within the context of forest certification.

Session 16

Is habitat heterogeneity driving speciation in the Afrotemperate regions?

*Berit Gehrke, Peter Linder

Institute for Systematic Botany, University of Zurich, Zollikerstrasse 107, 8008 Zurich, Switzerland

High species diversity has often been linked with high habitat heterogeneity. Ecologists tend to emphasise the increased number of niches provided by structurally complex habitats, which can allow more species to occur in the same area. Evolutionary biologists in contrast tend to concentrate on historical explanations, for example emphasising the role of shifts in habitat preference at speciation. The Afrotemperate regions are restricted to the high mountains of Tropical and Southern Africa, including Madagascar. Clines in elevation and latitude are important amongst the factors resulting in a number of distinct zones and habitats found across the different mountains. The flora of the Afrotemperate have been derived from two sources: recruitment of species and in situ speciation. The amount of in situ speciation is varying between different lineages even within taxa. We have explored these differences in speciation and our results show that speciation does not seem to be explained by ecological factors, in particular habitat heterogeneity, despite their demonstrated importance in other African regions. Species richness of Afrotemperate clades is however significantly correlated with their age and distribution range.

Session 5

Origin and evolution of the Malagasy Spermacoceae s.lat. (Rubiaceae)

*Inge Groeninckx[1], Petra De Block[2], Eric Smets[1, 3], Steven Dessein[2]

[1] Laboratory of Plant Systematics, K.U.Leuven, Kasteelpark Arenberg 31, PO Box 2437, 3001 Leuven, Belgium, [2] National Botanic Garden of Belgium, Domein van Bouchout, 1860 Meise, Belgium, [3] National Herbarium of the Netherlands, Leiden University Branch, PO Box 9514, 2300 RA Leiden, The Netherlands

Madagascar has a unique and spectacularly rich flora with a very high percentage of endemism. On this hotspot island, Rubiaceae are the second largest family of flowering plants. Up until now, the geographic origin of the various Rubiaceae taxa in Madagascar has never been studied in detail. Based on phylogenies inferred from plastid DNA we investigated the origin of the Malagasy members of the Spermacoceae s.lat. In its current delimitation, the herbaceous tribe Spermacoceae s.lat. unites the former tribes Spermacoceae s.str. and Manetieae, and the *Hedyotis-Oldenlandia* group. The tribe is represented in Madagascar by c. 30 species. They are present in all terrestrial niches, from the coastal dunes in the south(west) to the high plateaus in the centre of the island. Some are local endemics of inselbergs, others are pantropical weeds.

The present study focused on the species of the *Hedyotis-Oldenlandia* group endemic to Madagascar. The phylogeny of the Spermacoceae was inferred based on atpB-rbcL, rps16, trnL-trnF and petD sequences in order to reveal the origin of these Madagascan endemics. Results support the hypothesis that at least two colonisation events gave rise to the current diversity of the *Hedyotis-Oldenlandia* group on the island. One group of species is closely related to the neotropical genus *Arcytophyllum* and the North and Central American species presently classified in the genera *Houstonia*, *Oldenlandia* and *Stenaria*. The second clade contains the endemic genera *Lathraeocarpa* and *Gomphocalyx*, and is closely related to the Afro-Madagascan genus *Phylohydrax*. Concerted studies focused on the morphological diagnosability of these clades. A morphological investigation of flowers, fruits, seeds and pollen was carried out to find character support for the new phylogenetic relationships detected.

Session 5

Evolution, diversification and biogeographic patterns in *Allium*

*Maia Gurushidze[1,2]

[1]*Leibniz Institute of Plant Genetics and Crop Research (IPK), 06466 Gatersleben, Germany,* [2]*N. Ketskhoveli Institute of Botany, Tbilisi, Georgia*

The onion genus *Allium* L. is with about 750 species probably the largest genus of the petaloid monocotyledons. The genus is naturally distributed in the Northern Hemisphere, mainly in seasonally dry regions, with two main centres of diversity: one in Southwest and Central Asian mountains and a second smaller one in North America. Molecular phylogenies radically changed our understanding of the evolution of the genus. Phylogenetic analyses of *Allium* based on the nuclear rDNA internal transcribed spacer region (ITS) proved several subgenera and sections to be non-monophyletic. While ITS is useful to circumscribe intrageneric groups and resulted in a revision and new classification of the genus, the relationships among defined clades were not resolved in the ITS trees.

In order to resolve the deeper nodes in the phylogeny, which would be necessary for dating of diversification events, we applied the plastid rbcL gene, as rbcL sequences were used earlier to estimate crown and stem node ages for most orders and families of monocots. In an attempt to determine biogeographic patterns and possible causes of diversification within *Allium* we sequenced rbcL in 100 representative taxa covering all taxonomic groups (15 subgenera) and the whole geographical distribution of the genus. Phenetic, cladistic and model-based analyses resulted in nearly identical tree topologies. A relaxed molecular clock approach using the penalized likelihood algorithm implemented in r8s was used to date the resulting phylogenetic tree. The data presented here support (i) an early Tertiary origin of the genus *Allium*, and indicate (ii) an early radiation within the genus, probably attributed to the aridification at the Eocene – Oligocene transition, as well as (iii) several younger radiations connected to climate changes during the Messinian salinity crisis in the Miocene and the ice ages in the Pleistocene.

Session 11

Molecular identification of the algal origins of Sacoglossan kleptoplasts (Opisthobranchia, Gastropoda) by bar coding

*Katharina Händeler[1], Heike Wägele[1,2], Mareike Rüdinger[3], Ute Wahrmund[3], Volker Knoop[3]

[1] Institut für Evolutionsbiologie und Ökologie, Rheinische Friedrich-Wilhelms-Universität, Bonn, Germany, [2] Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany, [3]Institut für Zelluläre und Molekulare Botanik, Bonn, Germany

Some sacoglossan sea slugs have become famous for their capability to extract and incorporate chloroplasts from their algal food (mainly Ulvophyceae) and to use the photosynthetic products of those functionally enduring kleptoplasts for months. This enables several sacoglossa to survive for long periods of time without food through the ongoing photosynthesis in the incorporated chloroplasts. The algal food spectrum is known for many sacoglossans but not for certain genera (e.g. *Thuridilla*), notably also not for several taxa with a rather long term retention of chloroplasts (e.g. *Plakobranchus ocellatus*). Exact identification of those algal species which provide the chloroplasts for long term retention is of particular importance in those taxa which feed on a variety of algal species, like *Elysia crispata* and *Elysia viridis* and establishes a fundament for future molecular studies on this enigmatic endosymbiosis. Our approach is to identify suitable chloroplast genes, which allow identification of the respective algal donor taxa by analysing total DNA (slugs and algae) extracted from whole animals. Here we present first results on the chloroplast gene tufA. Partial sequences of tufA obtained out of the slugs are analysed together with sequences obtained by collected and identified species of Ulvophyceae and other available algal sequences from the databases. We here report first results allowing algal identification at least on genus level and indicating the taxonomic range of food organisms. Problems of intraspecific variation and/or paralogous genes are discussed.

Session 4

Phylogenomic analyses firmly place lophophorates within Lophotrochozoa

*Martin Helmkampf[1], Torsten H. Struck[2], Iris Bruchhaus[3], Bernhard Hausdorf[1]

[1] Zoological Museum of the University of Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany, [2] FB 05 Biology/Chemistry, AG Zoology, University of Osnabrück, Barbarastr. 11, 49076 Osnabrück, Germany, [3] Bernhard Nocht Institute for Tropical Medicine, Molecular Parasitology, Bernhard-Nocht-Str. 74, 20359 Hamburg, Germany

The position of the three lophophorate lineages, Ectoprocta, Brachiopoda and Phoronida, is particularly conflicting when comparing molecular phylogenetic analyses with the traditional perspective. Based on embryological and morphological evidence Lophophorata was considered the sister or paraphyletic stem group of Deuterostomia. In contrast, molecular data consistently indicated that lophophorates are more closely related to trochozoan taxa (annelids, molluscs and allies), which gave rise to the Lophotrochozoa concept. However, the phylogenetic relationships within this diverse group are still largely unresolved. Here we present phylogenomic analyses based on a dataset comprising 11,445 amino acid positions derived from 79 ribosomal proteins of 39 taxa, including novel data of Brachiopoda, Phoronida and Nemertea, as well as Ectoprocta and Entoprocta. These analyses unequivocally confirm that the lophophorate lineages are allied to trochozoan rather than deuterostome phyla. In contrast, topology tests rejected all hypotheses claiming that lophophorates lineages are more closely related to Deuterostomia than to Protostomia. The monophyly of Brachiozoa including Brachiopoda and Phoronida is strongly supported. Further, Ectoprocta and Entoprocta unexpectedly form a monophyletic group at the basis of Lophotrochozoa, thus resurrecting the century-old hypothesis of Bryozoa sensu lato. The position of Nemertea remains ambiguous, as this taxon either groups with Brachiozoa or with Mollusca. Using topology tests, some alternative hypotheses concerning the relationships of these taxa could be excluded, namely the Conchozoa hypothesis, according to which Brachiozoa is the sister group of Mollusca, and the hypothesis that Entoprocta forms a clade with other trochozoan phyla instead of being the sister group of Ectoprocta. An intriguing possibility among the hypotheses that could not be rejected is the sister group relationship between Bryozoa sensu lato and Brachiozoa. Sessility, the presence of a horseshoe-shaped tentacular feeding apparatus with a coelom and a trunk coelom might be synapomorphies of these groups.

Session 18

Phylogeny and historical biogeography of the cosmopolitan liverwort genus *Frullania* (Jungermanniopsida: Porellales)

*Jörn Hentschel[1], Matt von Konrat[2], Tamás Pócs[3], S. Robbert Gradstein[1], Harald Schneider[4], Jochen Heinrichs[1]

[1] Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, [2] The Field Museum, 1400 South Lake Shore Drive, Chicago, IL 60605-2496, U.S.A., [3] Botany Department, Eszterházy College, Eger, PB. 43, 3301, Hungary, [4] Department of Botany, The Natural History Museum, London SW7 5BD, U.K.

Frullania is a large and complex liverwort genus with over 1000 validly published binomials. Yet, recent estimates of the number of species lie closer to ca. 300. *Frullania* represents the largest genus of Porellales and forms a major clade of leafy liverworts. The genus includes mostly epiphytes and represents an important component of the cryptogamic vegetation in different, especially tropical, habitats. There have been abundant changes and modifications to the infrageneric classification of *Frullania*, with up to fourteen subgenera and even more sections solely based on morphology. This has led to a complex and confusing classification. Here we present the first molecular phylogeny of *Frullania* using four markers [chloroplast DNA trnL-trnF, rbcL, and psbA sequences as well as sequences of the nuclear ribosomal ITS region (ITS1-5.8S-ITS2)] and 140 accessions from throughout the range. The molecular data provide evidence for the monophyly of several subgenera and support intercontinental ranges of these clades. The relationships of Eocene and Miocene amber fossils of *Frullania* are explored in the context of the recovered phylogenetic hypothesis. Divergence time estimates based on the fossil record and DNA sequence variation are used to explore the role of dispersal and vicariance processes in the historical biogeography of this liverwort genus.

Session 12

Diversification in the Mediterranean: a phylogeographic analysis of the grasshopper genus *Oedipoda*

Axel Hochkirch, Yvonne Görzig

University of Osnabrück, Department of Biology/Chemistry, Division of Ecology, Barbarastr. 11, 49069 Osnabrück, Germany

The Mediterranean belongs to the European hotspots of biodiversity and endemism. The grasshopper genus *Oedipoda* consists of 23 species distributed from Europe and northern Africa to Central Asia, ten of which have a Mediterranean distribution. We sequenced two mitochondrial and one nuclear gene fragment of 87 individuals from twelve species to infer a phylogeny for the West-Palaearctic species. Our results revealed a basal subdivision of the genus in two major groups (germanica-group and caerulescens-group). The resolution within the germanica-group was relatively low and the taxonomical assignment sometimes conflicted with our phylogeny. This was particularly true for *O. germanica*, *O. fuscocincta* and *O. coerulea*, indicating recent gene flow among these species. Within the caerulescens-group, *O. himalayana* and *O. fedtshonki* (both from Kashmir) represented the basal group. The two sister species *O. charpentieri* and *O. miniata* turned out to contain three distinct lineages, with *O. charpentieri* in the western Mediterranean, *O. miniata* in the eastern Mediterranean and a third lineage in the central part (Tunisia, Balearic Islands, Sardinia). A former hypothesis of hybridization on the Balearic Islands could not be confirmed. *O. canariensis* contained three separate lineages for Tenerife, La Gomera and Gran Canara/Fuerteventura. However, the genetic distances between these clades were relatively low. *O. caerulescens* had only a low degree of intraspecific differentiation. The specimens from France to Russia turned out to be genetically rather homogenous, but refugia were found on the Iberian Peninsula and in northern Africa. Our results indicate that the current taxonomy of *Oedipoda* partly conflicts with the phylogenetic relationships. The Central Mediterranean lineage of the charpentieri-miniata complex should be studied morphologically to test, whether it represents a species.

Session 8

Molecular phylogeny of the Thecideoidea (Brachiopoda)

*Jana Hoffmann, Carsten Lüter

Museum für Naturkunde der Humboldt-Universität zu Berlin, Invalidenstr. 43, 10115 Berlin, Germany, jana.hoffmann@museum.hu-berlin.de

Thecideide brachiopods live in cryptic habitats of coral reefs and volcanic islands of the tropics and subtropics. They have an extensive fossil record and are known since the Jurassic. However, there are only two known Recent families, Lacazellinae Backhaus and Thecidellininae Elliot. Whereas the diversity of species in each of the three lacazelline genera is very low, the only thecidellinine genus, *Thecidellina*, is much more speciose. There is an ongoing debate on the phylogenetic position of thecideides within brachiopods and their ingroup relationships. This is mainly due to their unusual internal shell morphology, which makes comparisons with other brachiopods very difficult. As a result, there exist several conflicting hypotheses concerning the relationship of thecideides to Recent and extinct brachiopod subgroups. Furthermore, all ingroup phylogenies - many of them unresolved - are exclusively based on morphological characters.

The present study is a first comprehensive attempt using genetic markers (16S rDNA, 18S rDNA) to evaluate morphology-based phylogenetic hypotheses of thecideide relationships. The molecular data suggest monophyly of Thecideoidea and its subfamilies Thecidellininae and Lacazellininae. Additionally, a sister group relationship between the Atlantic taxa *Lacazella* plus *Pajaudina* and the Pacific/ Indic genus *Ospreyella* is likely. Although the latter result is corroborated by biogeographical data, it is not necessarily reflected in the morphology of the respective taxa. High genetic diversity is characteristic for *Thecidellina*. This consolidates the results of our ongoing morphological studies, which revealed an unexpected (cryptic) species diversity within *Thecidellina*.

The comparison of thecideide 18S rRNA data with other available brachiopod sequences confirmed the unique status of Thecideoidea. Whereas monophyly of this group is clearly supported, it is still difficult to place the group within the brachiopods. Compared to other Recent forms, they represent a separate lineage with extraordinary long internal branches.

Session 10

Taxon recruitment in the arctic flora

Matthias H. Hoffmann, Martin Röser

Martin-Luther-University Halle-Wittenberg, Institute of Biology, Am Kirchtor 3, 06108 Halle, Germany

The Arctic is the endpoint of many climatic gradients on earth and supports only a limited number of species. It is presently occupied by about 2,200 plant species of vascular plants that can cope with the harsh environmental conditions. First glaciations of the Arctic started in the Middle Eocene (~45 Myr ago) but a significant expansion of the Greenland ice shield occurred much later (~3.2 Myr ago) and led to the rise of the treeless circumpolar arctic tundra biome that varied since then in spatial extension. We evaluated molecular phylogenetic studies available to date for 178 of 374 genera occurring in the Arctic to detect common evolutionary patterns or processes that may have led to the origin of the arctic species. Total number of species in a genus revealed a good predictor for the number of arctic species. The overwhelming majority of arctic species originated multiple times in parallel and separately in different lineages within species-rich genera. Minor radiations of arctic species occurred in only few genera and major northern-hemispheric radiations are absent. The potential extinction of radiations during past glacial-interglacial cycles and hypotheses on generally slow rates of evolutionary diversification, based on low input of solar irradiation or energy flow in the ecosystem, are examined.

Session 3

Genetic variability in sympatric species of the genus *Niphargus* (Crustacea, Amphipoda)

*Jennifer Hohagen, Stefan Koenemann

Institute for Animal Ecology and Cell Biology, University of Veterinary Medicine Hannover, Foundation

In an ongoing research project on the evolution and phylogeny of groundwater crustaceans, we investigated three species of the amphipod genus *Niphargus*. In some Central European regions, *Niphargus aquilex*, *Niphargus schellenbergi* and *Niphargus fontanus* are found to occur in sympatry. These three species are morphologically very similar, with highly variable and partly inconsistent diagnostic characters. Therefore, we conducted DNA sequence analyses based on the markers mtCO 1 and 28S rDNA. Phylogenetic analyses failed to recover any of the three species as monophyletic taxon, or reveal a pattern of geographic distribution. Since the chosen genetic markers corroborate our morphologic examinations, we assume that a separate status for each of the three species may not be valid.

Session 1

The evolution of the female postabdomen and genitalia in primitive moths (Insecta: Lepidoptera)

*Frank Hünefeld[1], Niels P. Kristensen[2]

[1]Friedrich-Schiller-Universität Jena, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Entomology Group, Erbertstr. 1, 07743 Jena, Germany, Frank.Huenefeld@uni-jena.de, [2]Natural History Museum of Denmark, University of Copenhagen, Universitetsparken 15, 2100 Copenhagen, Denmark, npkristensen@snm.ku.dk

The female postabdomina and genitalia of primitive lepidopteran families (e.g., Micropterigidae, Agathiphagidae, Heterobathmiidae, Eriocraniidae) and putatively "basal" caddisflies (Trichoptera: Rhyacophilidae: *Rhyacophila* sp.) were investigated in detail. Throughout Lepidoptera, and also Trichoptera, the presence of two pairs of postabdominal apophyses (an anterior pair derived from segment VIII, and a posterior pair arising from segment IX) is widespread. Within Lepidoptera, only Micropterigidae, which have good evidence to have arisen in the first splitting event, totally lack these apophyses and the associated muscle sets, a state that clearly represents an autapomorphy of the family (secondary loss). However, in the family Agathiphagidae, putatively arisen in the second splitting event within the order, a unique situation within Lepidoptera is found: females of *Agathiphaga* sp. display three pairs of postabdominal apophyses (two anterior pairs arising from segment VIII, and the posterior pair of segment IX) and an elaborate postabdominal muscle equipment consisting of 24 muscles (in contrast: Micropterix sp. with 8 and the probably "basal" caddisfly *Rhyacophila* sp. with 15 postabdominal muscles). Homologization of the single anterior pair of apophyses of most moths and caddisflies with either the dorsal or the ventral pair of *Agathiphaga* sp. causes serious problems, and with some possibility the single anterior apophyses in "higher lepidopterans" may be a composite formation of both. In 1996, an enigmatic caddisfly was briefly described from the Fan Si Pan mountain area in Vietnam: *Fansipangana vernalis*, Mey 1996. This caddisfly has 3 pairs of postabdominal apophyses in the female sex, and possibly may shed a new light on the evolution of the female postabdomen of primitive lepidopterans and trichopterans. A comprehensive redescription of *Fansipangana* and inclusion in data sets for phylogenetic analyses is strongly required. Besides these external features, there is a peculiarity that strongly supports a most basal position of Micropterigidae within Lepidoptera: a simple spermathecal duct (as it is found in Rhyacophilidae and other trichopterans). In all "higher" lepidopteran families, the spermathecal duct includes a "2-compartment-section" with strong differentiations of the epithelium and the intima; in *Agathiphaga* sp. at least a kind of "precursor stage" is present.

Plenary session III

Evolutionary ecology of basic metazoans from a historical viewpoint: palaeontological evidence of sponges

Dorte Janussen

Forschungsinstitut und Naturmuseum Senckenberg, Senckenberganlage 25, 60325 Frankfurt am Main, Germany, dorte.janussen@senckenberg.de

In the fossil record, and according to most phylogenetic threes, Porifera is the oldest metazoan group of Earth´s history. Although great progress has been achieved, phylogeny and systematics of the recent and fossil Porifera are still ambigous and largely unresolved. Sponge taxonomy is traditionally based on skeletal characters as main classification criteria. Many recent sponge taxa are considered to be cosmopolitan and of world-wide/bi-polar distribution. Molecular investigations help testing morphologically based taxonomic classification shemes, but in this respect, the Porifera are still a largely under-investigated. Although recent molecular studies provide evidence for a high degree of regional endemism for many sponge taxa, regional distributions have just recently in a few cases been explained by phylogeographic models. Study of fossil material is one of few methods for providing evolutionary-ecological explanations of the recent taxonomic distribution. Where molecular data are scarce or inconsistent, palaeontological data are often available, and in some cases suitable for providing, or testing, phylogenetic hypotheses. Hexactinellida is a poriferan taxon, for which only fragmental molecular data so far exist, but which possesses a good fossil record. In terms of morphology, Hexactinellida is a conservative group, whose Late Mesozoic fossils are commonly identified to genus level by comparison with recent taxa (e. g. Mehl 1992, Brückner 2006). Most extant hexactinellid genera can be traced back to the Late Cretaceous, which was a flourishing time for Hexactinellida. *Rossella*, is today largely endemic for the Antarctic/Subantarctic; fossil data however show a different palaeogeographical pattern for this group during Late Mesozoic. At that time, *Rossella* spp. was widely distributed within tethyan and boreal realms. The recent Artarctic shelf with its dense populations of hexactinellid sponges offers interesting analogy to the Late Cretaceous deep-water shelf. As we look back into the Early Palaezoic, the taxonomic resolution successively decreases. Nevertheless, fossils of siliceous sponges can be found even in Late Proterozoic sediments of Ediacaran age (about 543 MY old). From Early/Middle Cambrian, all three Poriferan classes are well documented (Mehl-Janussen 1999). As one of the latest of the groups, Carboniferous stem linneage representatives of Homosclerophorida are documented by isolated spicules, probably derived from or a tetractine-bearing demospongiaen group. Fossils can be used in systematics to help reconstructing the underlying evolutionary processes.

Session 20

Are fruit and seed characters systematically useful in the family Adoxaceae (Dipsacales)?

*Bart Jacobs[1], Suzy Huysmans[1], Erik Smets[1, 2]

[1]*Laboratory of Plant Systematics, K.U.Leuven, Kasteelpark Arenberg 31, P.O. Box 2437, 3001 Leuven, Belgium,* [2] *Nationaal Herbarium Nederland, Leiden University Branch, P.O.Box 9514, 2300 RA, Leiden, The Netherlands*

For the past fifteen years, investigations based on both molecular and morphological data have greatly improved our understanding of the intergeneric relationships within the family Adoxaceae (Dipsacales). However, several questions remain unanswered. For example, how did fruits and seeds evolve in the Adoxaceae? Which synapomorphies characterize *Sambucus*? The current study focuses on the morphology and anatomy of the fruits and seeds of *Adoxa*, *Sambucus* and *Viburnum.*

For this, both light microscopy and scanning electron microscopy were used. Phylogenetic analyses (maximum parsimony and bayesian inference), based on ITS sequence data as well as a combination of the latter supplemented with morphological data, were carried out to investigate the impact of various fruit and seed characters on the phylogenetic relationships within the Adoxaceae. The outcome of the phylogenetic analyses was used as a basis for to study of the evolution of several systematically informative characters. For the first time, a number of clear synapomorphies were identified for *Sambucus*, such as a long, slender embryo and the unique morphology of the sclereids of the endocarp. We also identified additional synapomorphies for *Adoxa* and *Viburnum.* Several characters, such as endocarp structure and seed coat anatomy, confirm the close relationship of *Adoxa* and *Sambucus. Viburnum* is separated from the latter two genera based on various, distinct characters such as endosperm anatomy, seed coat anatomy and endocarp structure. Our results confirm the systematic value of fruit and seed characters at various taxonomic levels.

Session 1

Phylogeny of the flea beetle genus *Altica* (Chrysomelidae, Alticinae) and the impact of endoparasites on population structure, isolation and speciation

*Regina Jäckel

Biozentrum Grindel, Universität Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg

We could recently show that *Altica* (Coleoptera, Chrysomelidae) species are infected with different strains of the endoparasitic, maternally inherited Wolbachia bacteria which are known for their ability to manipulate arthropod reproduction, e. g. by creating cytoplasmatic incompatibility that may be the cause of genetic differences within populations. They may therefore play a role in speciation and have effects on the phylogeny of the host species. The reconstructed phylogeny of the genus *Altica* based on parts of the mtDNA (COI/II) represents 15 species with a total of 94 individuals collected from different populations where possible. One species, *A. lythri*, is resolved as polyphyletic. Within this species, at least three groups of mtDNA-haplotypes with p-distances of up to 4.6% between individuals of the same population can be found. When taken to the lab, females bearing haplotype 1 produced all-female broods, whereas females bearing haplotype 2 produced a 1:1 sex ratio. As far as we know, females bearing haplotype 3 are able to produce male and female progeny. Each of these three groups is infected with a different strain of Wolbachia bacteria. The polyphyly of *A. lythri* could be caused by incomplete lineage sorting after the last speciation event, or by hybridization between different species, leading to introgression of mtDNA. We suggest that the polyphyly is causally linked to the fact that these beetles are infected with different strains of Wolbachia. As a consequence of the maternal transmission of both the bacteria and the mtDNA, a specific infection-type is associated with a specific mtDNA-haplotype. As an infection sweeps through a population, it carries with it the mtDNA-haplotype that was associated with the initial infection. As a result, different populations or individuals either show different or identical mtDNA-haplotypes. We hypothesize that a combination of Wolbachia-infection and hybridization can explain the polyphyly of *A. lythri*. The effects of the infection and the origin of the different haplotypes are topic of current research.

Session 7

Systematics of the *Vipera berus* group – a riddle

Ulrich Joger, Svetlana Kalyabina-Hauf, Nikolaus Stümpel, Alexander Zinenko

Staatliches Naturhistorisches Museum, Pockelsstr. 10, 38106 Braunschweig, Germany

The adders of the *Vipera berus* group are the most widespread terrestrial snakes on earth. Within its enormous territory, only 3 subspecies of *Vipera berus* have been recognized, but in SE Europe and Turkey, 2 separate species – *V. nikolskii* and *V. barani*, both with melanistic coloration – have been described.

We studied the phylogeography of the mitochondrial cytochrome b gene in the *V. berus* complex. The resulting haplotype pattern contradicted the morphological pattern in several aspects. Geographical units that were indistinguishable from each other had highly different haplotypes. This was the case for the Alpine adders as compared to *V. b. berus*. In *Vipera nikolskii*, populations that were geographically close to *V. b. berus* had an typical berus haplotype, whereas peripheral populations had a different haplotype. Apparently speciation in *V. nikolskii* has not yet been completed. The results are interpreted with regard to probable glacial refugia and post-glacial range expansion. This cool-tolerant species was probably able to survive the glacials in non-Mediterranian refugia.

Session 16

Global diversity patterns and migration in the genus *Draba*

*Ingrid Jordon-Thaden, Marcus Koch

Heidelberg Institute of Plant Sciences, Biodiversity and Plant Systematics, University of Heidelberg, Im Neuenheimer Feld 345, 69120 Heidelberg, marcus.koch@urz.uni-heidelberg.de.

This presentation summarizes our current work on the comparison of the worldwide biodiversity and genetic diversity of the largest genus in the Brassicaceae, *Draba*. With over 363 species currently accepted, that are distributed globally in all types of extreme ecosystems, it is an excellent model for studying the migration of gene flow and phylogeography. Genetic and species diversity, number of lineages through time, and mutation rate data will be correlated in this study. The combination of this data will allow us to investigate the migration of *Draba* across the globe over the past 5 million years, the estimated age of the genus (Koch at al. 2002). Its migration is most likely a combination of ancestral, late-tertiary diversification events and more recently due to Quaternary glaciation and deglaciation cycles. Species biodiversity was accessed by collecting the details of Floras, checklists, and personal communication with experts of the genus. Sequence information from *Draba* was obtained for the plastidic trnLF and nuclear ITS regions for approximately 80% of the genus. One main question we seek to explore is whether the origin of species is also the area of highest biodiversity and genetic diversity. The data are being projected onto maps with ESRI ArcView 8.2 allowing for superior visualization not otherwise available. Unique species distribution patterns will be discussed. In conjunction with diversity analysis, by observing the lineages occurring over time we can determine radiation events in the evolution of the species. In our preliminary results of lineage through time plots, we have concluded there have been two major radiation events. The first occurred in between the origin of *Draba* and about 4 million years ago. The second was possibly sometime during the Pleistocene cyclic glaciation period. Calibrating the time scale for these events using various rate smoothing tests is another aspect of our research.

Plenary session II

Plant speciation in the Quaternary

Joachim W. Kadereit

Institut für Spezielle Botanik und Botanischer Garten, Johannes Gutenberg-Universität Mainz, 55099 Mainz, Germany, Kadereit@uni-mainz.de

A multitude of molecular clock-dated studies has shown that the Quaternary was a period of very active speciation. The climatic oscillations of the Quaternary have resulted in substantial and oscillating shifts of the geographical distribution of taxa. This may imply geographical (allopatric) speciation as the primary mode of species formation. However, shifts of geographical distribution always involve shifts in ecological conditions even though migrating species in general will have tracked the displacement of their habitats. The purpose of this presentation is twofold. First, I will look for evidence for ecological evolution and ecological speciation in the Quaternary. Considering the Quaternary oscillations in geographical range, I will then address the question whether the products of Quaternary diversification are stable or not.

Ecological evolution will be illustrated for *Triglochin maritima* (Juncaginaceae) where we can show that the modern coastal populations in the North Sea and Baltic Sea areas originated from inland refugial populations. Ecological speciation will be demonstrated for *Oenanthe* (Apiaceae) where adaptive differentiation of two species could be demonstrated by reciprocal transplantation experiments. In *Oenanthe* the difficulties in distinguishing allo- and sympatric speciation will be illustrated. The alpine *Primula* sect. *Auricula* (Primulaceae) will be used to illustrate Quaternary geographical and ecological diversification among a larger group of species.

The evolutionary stability of species of Quaternary origin will be investigated again in *Primula* sect. *Auricula.* In this taxon it had been hypothesized that speciation took place mainly allopatrically in geographically isolated refugia. Postglacially, however, many species have obtained overlapping distribution areas. An analysis of hybridization between *Primula auricula* and *P. hirsuta* shows that although hybridization between these two species can take place, that their hybrids are fertile and give rise to subsequent hybrid generations, hybridization is strongly selected against by habitat availability.

Session 2

Phylogeny and biogeography of *Teucrium* and allies

*Stefan Kattari[1], Christian Bräuchler[1,2]

[1] LMU München, Department Biologie I, Systematische Botanik, Menzinger Str. 67, 80638 München, Germany, [2] Botanische Staatssammlung München, Menzinger Str. 67, 80638 München,Germany

Teucrium (Ajugoideae, Lamiaceae) is a large genus (ca. 250 spp.) of annual herbs to perennial shrubs found in extratropic regions worldwide. Given its distinctive corolla architecture, the circumscription of the genus stayed more or less the same from treatment to treatment. A first infrageneric classification was established by Bentham (1836) and later expanded by Boissier (1879) and Briquet (1897). The concept, however, has not changed substantially until the work of Kästner (1989), who redefined several sections and subsections.

Molecular research so far either included only a single species of the genus or focussed on mediterranean taxa. To study inter- and infrageneric relationships in more detail and investigate the group´s biogeography at a worldwide scale, a phylogenetic anaylsis using chloroplast (ndhF, trnL-F, trnQ-rps16) and nuclear (ITS) DNA sequences was conducted. While some of Kästners (1989) subsections are supported by our data, 5 out of 6 of his sections are not. The genera *Oncinocalyx* (1 sp.), *Spartothamnella* (3 spp.) and *Teucridium* (1 sp.), all from the Australian region, turn out to be nested within Teucrium. The resulting paraphyly strongly favors their inclusion in the genus. Biogeographically there is a split in several groups, some restricted to the Mediterranean, one northern hemispheric found from Europe to Asia and North America and one alliance with taxa predominantly from the Mediterranean as well, but with two disjunct lineages in the Americas and Australia/South Africa.

Session 3

The *Indigofera pratensis* complex (Fabaceae): morphological and molecular approaches

Aniuska Kazandjian

Departamento de Biología de Organismos, Universidad Simón Bolívar, Venezuela

Indigofera pratensis is a widespread species endemic to northern Australia. Revision of herbarium specimens revealed considerable infraspecific variation. In addition, two other species *I. cinericolor* and *I. sericovexilla* were identified as closely related because of a high degree of similarity of many key morphological characters. The complex was evaluated using clustering and multidimensional methods of data obtained from herbarium specimens and individuals grown under standardised environmental conditions. Phylogenetic analysis of DNA sequence data based on the rDNA internal transcribed spacer region (ITS-1, ITS-2 and the 5.8S rDNA) and the trnL-UAA intron-trnL-F intragenic spacer were also conducted. Phenetic analysis uncovered eight distinct groups defined by a set of highly correlated characters using Principal Axes Correlation. Plants grown from seed under standardised conditions did not differ from their parental phenotype indicating that the high correlated morphological characters are not the result of different environmental conditions. Pairwise genetic distances of DNA sequences among the eight morphological groups were less than 1% using trnL and about 3% using ITS. These differences were marginally increased when sequences from members of the *I. pratensis* complex were compared with other Australian endemic *Indigofera*. No clear relationships were able to be elucidated using this molecular data among the *I. pratensis* complex, although monophyly was supported. Molecular data also support a monophyletic origin for Australian endemic *Indigofera*, but no clear relationships were found among them suggesting that the Australian endemic *Indigofera* represent a relatively recent and rapid radiation throughout Australia.

Session 5

Phylogenetic relationships within Sabiceeae s.l. (Rubiaceae)

Saleh A. Khan[1,3], Sylvain G. Razafimandimbison[2], Birgitta Bremer[2], Sigrid Liede-Schumann[1]

[1] Department of Plant Systematics, University of Bayreuth, Universitätstr. 30, 95440 Bayreuth, Germany, [2] Bergius Foundation, Royal Swedish Academy of Sciences· Department of Botany, Stockholm University, 10691 Stockholm, Sweden, [3] Department of Botany, Jahangirnagar University, Savar 1342, Dhaka, Bangladesh

Phylogenetic analyses based on ITS and trnT-F sequence data of 78 taxa have been performed to: (1) test the monophyly of competing circumscriptions of Sabiceeae and *Sabicea*; (2) assess the phylogenetic relationships within Sabiceeae; and (3) infer the biogeographical origin of *Sabicea*. *Pentaloncha* and *Temnopteryx* have been shown not to belong to Ixoroideae s.l. but to subfamily Rubioideae. A broad circumscription of Sabiceeae including *Ecpoma*, *Hekistocarpa*, *Pseudosabicea*, *Sabicea*, *Schizostigma*, *Stipularia*, *Tamridaea*, and *Virectaria* is supported. *Sabicea* sensu Wernham is not monophyletic, unless *Ecpoma*, *Pseudosabicea*, *Schizostigma*, and *Stipularia* are included so that the newly circumscribed Sabiceeae contain only *Hekistocarpa*, *Sabicea* s.l., *Tamridaea*, and *Virectaria*. Finally, our analyses indicate continental African origins for the tribe as a whole and for its largest genus *Sabicea*. Neotropical *Sabicea* is mononophyletic, indicating a single long-distance dispersal event.

Session 9

The independence of genetic and species diversity in *Boechera* is revealed by a continental wide phylogeographic study

*Christiane Kiefer, Christoph Dobes, Markus Koch

University of Heidelberg, Heidelberg Institute of Plant Science, Department I, Biodiversity and Plant Systematics, Im Neuenheimer Feld 345, 69120 Heidelberg, Germany

High species diversity may go hand in hand with a high genetic diversity; however, it does not so in *Boechera* (Brassicaceae). While most species of this genus are found in California and Nevada (USA), the centres of genetic diversity of the two evolutionary lineages containing most of the species were found to be in the Klamath/Siskiyou Forest region and the Wyoming Basin. We tried to find reasons for this incongruence and elucidated the phylogeographic history of the genus. *Boechera* as a large monophyletic group is not only a suitable model system for studying hybridisation, reproductive modes and ecology, it is also a model for evolution in the highly diverse and dynamic landscape of North America. Among the 55 taxa that we studied we found only few species-specific lineages. The most frequent haplotypes were shared among several species which demonstrates *Boechera*'s high ability for hybridisation as well as the young age of the majority of the species.

Session 8

A fresh look at Gastrotricha phylogeny revealed by a new set of morphological characters

*Alexander Kieneke[1, 2], Wilko H. Ahlrichs[2]

[1] *FI Senckenberg, DZMB, Südstrand 44, 26382 Wilhelmshaven, Germany* [2] *Molekulare Systematik, Universität Oldenburg, 26111 Oldenburg, Germany*

A cladistic analysis of Gastrotricha based on morphological characters is presented. A novelty of this analysis is the usage of species as terminal taxa instead of higher level taxa, for which monophyly is oftentimes uncertain. The analysis comprises 80 ingroup taxa and 135 binary as well as many multistate characters in total. Character coding is based on a careful assessment of original species descriptions. Characters included cover general body organisation, internal and external features as, for example, data concerning the adhesive tubes, digestive tract or sensory devices. Character systems for which it was problematic to obtain data for a large set of the included taxa were not considered, even if they were of phylogenetic information. To minimize presumptions, all characters were treated with equal weight and left unordered. Four outgroup taxa were chosen according to the current sister group hypotheses for Gastrotricha.

Both search strategies, a heuristic search using the PAUP software and a parsimony ratchet search using the PRAP program and PAUP reveal a comparable scenario. Gastrotricha split into two sister taxa. One group comprises genus *Neodasys* only, the sister group N.N.1 (Eutubulata nom. nov.) consists of all remaining Gastrotricha. Within Eutubulata, monophyletic Macrodasyida s. str. and N.N.2 (Abursata nom. nov.) are sister taxa of highest rank. Abursata consists of the "freshwater macrodasyids" *Marinellina* and *Redudasys* as sister group of monophyletic Paucitubulatina. Some traditional families are supported by this analysis. Possible key events during phylogenesis of Gastrotricha could be reconstructed.

Session 21

Molecular diversity at 18 loci in 321 wild and 92 domesticate lines reveal no reduction of nucleotide diversity during *Triticum monococcum* (einkorn) domestication: Implications for the origin of agriculture

Benjamin Kilian[1,6], H. Özkan[2], A. Walther[3], J. Kohl[4], T. Dagan[1], F. Salamini[5,6], W. Martin[1]

[1] Institute of Botany III, Heinrich-Heine-Universität Düsseldorf, Universitätsstrasse 1, 40225 Düsseldorf, Germany, kilian@mpiz-koeln.mpg.de, [2] Department of Field Crops, Faculty of Agriculture, University of Cukurova, 01330 Adana, Turkey, [3] Regional Climate Group, Earth Sciences Centre, Göteborg University, Box 460, 40530 Göteborg, Sweden, [4] Institute of Bioinformatics, Heinrich-Heine-Universität Düsseldorf, Universitätsstrasse 1, 40225 Düsseldorf, Germany, [5] Fondazione Parco Tecnologico Padano, Via Einstein – Localita Cascina Codazza, 26900 Lodi, Italy, [6] Max Planck Institute for Plant Breeding Research, Department of Plant Breeding and Genetics, Carl-von-Linné-Weg 10, 50829 Köln, Germany

Archaeological, phytogeographical, and genetic evidence indicates that western agriculture originated in the Fertile Crescent somewhat after the last ice age, in aceramic Pre-Pottery Neolithic (PPN) from about 12,000 to 9,500 years ago. The diploid einkorn wheat *Triticum monococcum* L. was among the first crops domesticated by humans in the Fertile Crescent and is thought to have been domesticated form its wild progenitor *T. boeoticum* around the volcanic Karacadag mountain range in South East Turkey. During the last 5,000 years einkorn was replaced by tetraploid and hexaploid wheats and largely forgotten. Einkorn germplasm is thus devoid of breeding bottlenecks and has therefore preserved in unfiltered form the full spectrum of genetic variation that was present during its domestication. Given the absence of breeding bottlenecks in einkorn, we reasoned that extensive sampling of genetic diversity among wild and domesticate accessions should discriminate between competing hypotheses for cereal domestication. We report nucleotide variation at 18 loci for 92 domesticate einkorn lines in comparison to 321 lines from wild populations and a genetic view of crop domestication that is unbiased by green revolution breeding. Our data reveal that wild einkorn underwent natural genetic differentiation, prior domestication. That differentiation bears heavily upon inferences concerning the domestication process because it brought forth three distinct wild einkorn races. Only one of those natural races, β, was exploited by humans for domestication. Nucleotide diversity and haplotype diversity in domesticate einkorn is higher than in its wild sister group, the β race, indicating that einkorn underwent no reduction of diversity during domestication. This is in sharp contrast to previous findings among more intensely bred crop species. Based upon combining our data with recent archaeological findings, we were able to present a new model of einkorn domestication, indicating that a specific wild einkorn race was subjected to multiple independent domestication events and later spread out of the Fertile Crescent.

Session 4

Genome morphology of mitochondria and the phylogeny of Isopods

*Fabian Kilpert, Lars Podsiadlowski

Institut für Zoologie, Freie Universität Berlin, Berlin, Germany

DNA sequencing has entered the common tool set of today's systematic researchers but often fails to provide clades with sufficient support. The mitochondrial genome of animals is known for almost invariable gene content and relative rare changes of gene order. In some cases "genome morphology" (non-sequence characters like gene order, RNA secondary structure etc.) provides valuable characters for phylogenetic inference that can easily be combined with a morphological data matrix. Isopoda provide a possible textbook example for the use of mitochondrial genome morphology in phylogenetics. Gene order is much less conserved than one would expect for crustaceans. We have compared the complete or almost complete mitochondrial DNA from several isopod taxa (Phreatoicidea, Asellota, Oniscidea, Valvifera, Cymothoidea, Sphaeromatidea). All examined species show a different arrangement of mitochondrial genes. Especially tRNA genes seem to show an increased mobility, as they differ in their locations even between closer related species. The positions of protein coding genes are more stationary, but are not invariant. All studied isopods share commonly derived gene arrangements in comparison to other malacostracan crustaceans. Further non-sequence characters provide valuable data for tree reconstruction: a reversed strand bias of nucleotide frequencies, evidence for a reversed origin of replication, was detected for the Scutocoxifera; aberrations to the usual clover-leaf tRNA structure are frequently found; linearization of the otherwise circular genome in *Armadillidium*.

Session 12

Phylogeography and systematics of Sulawesi water monitors (Squamata: *Varanus salvator* complex)

*André Koch[1], Fabian Herder[1], Bernhard Misof[1], Evy Ayu Arida[1, 2], Wolfgang Böhme[1]

[1] Zoologisches Forschungsmuseum Alexander Koenig, 53113 Bonn, Germany, [2] Museum Zoologicum Bogoriense, Cibinong, Indonesia

Sulawesi lies right in the centre of the Malay Archipelago, comprising the transitional zone between the Asian and Australian zoogeographic regions. Due to its complicated geological evolution in combination with a long geographic isolation, Sulawesi shows a high degree of faunal endemism. Moreover, Pleistocene changes in sea level resulting in temporarily fragmentations of the island and subsequent independent development of single populations had a large influence on the evolution of different taxa. These observations have led to the definition of areas of endemism (AOE) representing genetically distinct units that additionally increased the diversity of Sulawesi organisms. In contrast, colonization of Sulawesi was favoured during periods of low sea levels.

We investigated morphologically different populations of water monitor lizards (*Varanus salvator* complex) representing 14 operational taxonomic units (OTUs) that inhabit Sulawesi and its smaller off-shore islands to elucidate the taxonomic diversity and evolution of these giant reptiles. Statistical analyses were run using univariate (ANOVA) and multivariate (cluster analysis, neighbour-joining, PCA, and CVA) procedures. Additionally, AFLP methodology was used to generate DNA-fingerprintings of anonymous markers spread throughout the *Varanus* genome.

Our results strongly indicate that past sea level oscillations caused by world climate changes also affected the evolution of formerly isolated monitor lizard populations despite their well-known ability to cross marine barriers – possibly due to strong sea currents. Today, the four peninsulas of Sulawesi are populated by an equal number of differently coloured phenotypes of monitor lizards that live in parapatry. The surrounding islands are each inhabited by further endemic phenotypes which are even more distinct in colour pattern. Morphological (and genetic) analyses revealed that particularly these off-shore populations are significantly different from the Sulawesi mainland populations due to ongoing geographic isolation. Currently, only one of the recognized OTUs represents a valid taxon, viz. *V. togianus* Peters, 1872, while another Sulawesi taxon, viz. *celebensis* Schlegel, 1844, still needs to be revalidated. The remaining OTUs await their taxonomic evaluation. Finally, our results shall support future efforts to protect locally restricted and endemic taxa of Sulawesi water monitors which are exploited for the international reptile leather and pet trade.

Session 6

Reticulation, speciation and patterns of molecular evolution in *Hieracium* (Asteraceae)

*Karol Krak, Judith Fehrer, Jindřich Chrtek

Institute of Botany, Academy of Sciences of the Czech Republic, Zámek 1, 25243 Průhonice, Czech Republic

The genus *Hieracium* (≈650–8000 species, two subgenera) is notorious for its large morphological variability associated with variation in ploidal level, mode of reproduction and extensive past hybridization. Subgenus *Hieracium* comprises mostly Eurasian species, diploid sexuals as well as polyploid apomicts. For the exclusively American subgenus *Chionoracium*, only sexual or autogamic diploids were described. To resolve major phylogenetic relationships and to gain insight into the origin of polyploid taxa, we used sequences of the chloroplast trnT-trnL intergenic spacer and the ETS region of nuclear ribosomal DNA for a representative selection of taxa (80 accessions/ 70 species).

The genus is monophyletic, but both subgenera are polyphyletic. Despite relatively low interspecific variation, the ETS dataset revealed the existence of two major groups roughly corresponding to species with a Western or Eastern European origin. All *Chionoracium* species were derived from the eastern clade, multiple lineages suggesting several introductions to the New World. A few additional subclades were found within each of the major groups. Surprisingly many taxa, including diploid species, turned out to be of hybrid origin: polymorphic sites in the ETS region were additive between the two major clades or among different subclades. Further species were found to have been introgressed by species from other lineages according to chloroplast capture.

In ETS, a high level of intraindividual polymorphism occurred in both diploids and polyploids. While such a pattern was expected for allopolyploids where concerted evolution should be slow due to a lack of sexual reproduction, this was also true for diploid taxa. Persisting rDNA variants despite sexual reproduction indicate that concerted evolution does not seem to operate well in this species group. A considerable amount of intraindividual polymorphism occurred that was either independent of or additional to the additive patterns accounted for by hybrid origin. Shared intraindividual polymorphisms among closely related species suggest that this variation occurred prior to speciation events while frequent absence of one of the alternative character states could suggest a contribution of extinct taxa to the *Hieracium* diversity observed today.

Session 17

Investigations on the ultrastructure of *Hypania invalida* (Polychaeta: Ampharetidae), an adventive species in the river Rhine, Germany, with special emphasis on the nephridia and the spermatozoa

*Philipp Kremer[1], Dieter Fiege[2], Volker Storch[1], Thomas Wehe[1]

[1]Zoologisches Institut, Abt. Morphologie & Ökologie, Universität Heidelberg,Germany,
[2]Sektion Marine Evertebraten II, Forschungsinstitut & Naturmuseum Senckenberg,
Frankfurt am Main, Germany

Native to the Ponto-Caspian Basin the tube-dwelling species *Hypania invalida*, a representative of the family Ampharetidae is a recent invader of the Western European river systems. Coming from the Black Sea a slow upstream migration in the River Danube was documented until the early 1960s. However, with the opening of the Main-Danube Canal in 1992 a shortcut was opened to the River Rhine. Following this opening *Hypania invalida* rather rapidly invaded Western European rivers, including the River Rhine, and built up populations with high individual numbers. Interestingly *H. invalida* is the only freshwater polychaete reported for Germany, whereas crustaceans or mollusks of marine or brackish water origin are frequent invaders. Although the species is frequently found no information was available on the ultrastructure so far, as such observations on ampharetid polychaetes are in general scarce. Besides some early anatomic descriptions and several rather short notes on the path of invasion more recently, less is known about the ecology or invasion biology. During this ultrastructural study emphasis was placed on single organs in order to eventually find some morphological adaptations for a life in freshwater environments. By using transmission- and scanning microscopic techniques our main focus was on the examination of the metanephridial system, the gross-morphology of which was already described in 1927 by Annenkova, mentioning a differentiation and specialization of the nephridia of *H. invalida.* As assumed we found cells with structures clearly related to secretion or resorption processes. However, cells are of different types along the nephridial tubes, and several distinct regions could be examined, most probably correlating with different functions during the preparation of the urine. Of the three pairs of nephridia the third one shows much shorter tubes and very prominent nephrostomes, and is responsible for releasing the gametes. The male gametes were investigated in more detail and the spermatozoa of *H. invalida* show some peculiarities, which have not been observed before and are thus also presented.

Session 9

Peripheral populations: the case of *Anthyllis montana* ssp. *jacquinii* (Fabaceae) at its northern distribution limit

Matthias Kropf

Institute of Botany, Department of Integrative Biology, University of Natural Resources and Applied Life Sciences, Vienna, Gregor Mendel-Str.33, 1180 Vienna, Austria

Diversities are unevenly distributed throughout species distribution ranges; likewise, are individual/population numbers and densities. However, evolutionary models predict phenotypically and genotypically monomorphic populations at range peripheries. In addition, peripheral populations often show higher dynamics and stronger inter-population differentiation. Therefore, peripheral populations can be an important source for genetic novelties, and might be generally considered as Evolutionary Significant Units (ESUs).

Here, I consider a central-marginal transect towards the northern distributional edge of *Anthyllis montana* ssp. *jacquinii* (Fabaceae). There are refugial populations of this submediterranean mountain plant at the margin of the Alps including its northern-most and threatened Austrian populations. These are compared here to central (i.e. more southern) individual-rich populations from the Balkan Peninsula. Genetic structure and diversity patterns were analysed based on Amplified Fragment Length Polymorphism (AFLP) variation.

Population differentiation in an Analysis of Molecular Variance (AMOVA) was moderate (F_{ST}-value = 0.185), and the central-marginal transect investigated was characterised by an isolation-by-distance pattern. Genetic distances and Bayesian clustering revealed two groups, interestingly separating the two northern-most Austrian populations from the third Austrian (GOE) and the remaining more southern populations. All three Austrian populations showed an ordinary amount of AFLP diversity, being highest in GOE. This high diversity might be explained by the coexistence of individuals with "peripheral" (i.e. refugial) and "central" genetic constitution. In the other two smaller populations the "central gene pool", which is obviously wide-spread on the Balkan Peninsula, has been lost, likely due to genetic drift. Further evidence against local adaptation (i.e. natural selection) was provided by an outlier analysis that found only one AFLP fragment potentially indicating divergent selection. In conclusion, the specific genetic constitution of the northern-most populations probably arose from their isolation as long-standing refuge. Furthermore, some genetic characteristics have been lost due to genetic drift, in two populations due to reduced population size, but not due to peripheral location per se, as the third individual-rich population (GOE) confirmed.

Session 3

Evolution within the genus *Diplotaxis* (Brassicaceae) – the SI-system

*Corinna Laschke, K. Lückmann, H. Hurka, B. Neuffer

Department of Botany, University Osnabrück, Barbarastr.11, 49076 Osnabrück, Laschke@biologie.uni-osnabrueck.de

The genus *Diplotaxis* DC. belongs to the tribe Brassiceae in the family of the Brassicaceae and comprises about 30 species. They are native to the Mediterranean region, and central Europe, and throughout North Africa (especially in the Sahara) extending eastwards to Afghanistan and the Indian subcontinent, and reach in the West the Caper Verde Islands. Some species are weedy and colonizing. *D. tenuifolia* and *D. muralis* for instance, are neophytes in the New World, Australia, and South Africa. The genus is a polyphyletic group as molecular data reveal (data will be presented), and is one of the nearest wild relatives of the genus *Brassica*. There is a significant variation in chromosome numbers ranging from n=7 through n=8, 9, 10 and 11, to n=13. Irrespective of their chromosome numbers, all taxa are regarded as diploids, and only *D. muralis* with n=21 is as an allopolyploid species originating from a cross between *D. tenuifolia* and *D. viminea*. Many species are obligate outcrossers and are characterized by a genetically based self-incompatibility system (SI). The transition from SI to selfcompatibility (SC) occurs in several lineages, and can be an important driving force in the evolution in *Diplotaxis*. Selfing allows for uniparental reproduction and will promote colonisation. In addition, the likelihood of segregation in the progeny is reduced and combination of genes, that has proved successful, will stay together. The fixing of variants may have local adaptive advantage. Here we focus on the diploid sister species *Diplotaxis tenuifolia* (SI, n=11) and *Diplotaxis cretacea* (SC, n=11). This species pair offers the opportunity to study the molecular basis for the transition from SI to SC in natural populations and the environmental factors that promote SC. *D. tenuifolia* is strictly out-crossing, a successful coloniser and native to south and central Europe. *D. cretacea* is highly selfing and locally restricted to the Northern Ukraine and adjacent parts of Russia. The breakdown of the SI-system in *D. cretacea* might be correlated to its peripheral geographic position compared to the self-incompatible and widespread *D. tenuifolia.*

Plenary session II

Radiation, diversity and history

Peter Linder

Institute of Systematic Botany, University of Zurich, Zollikerstrasse 107, 8008 Zurich, Switzerland, plinder@systbot.uzh.ch

Radiation or diversification is a consequence of an excess of speciation over extinction. However, since both the speciation and extinction rate can vary independently, the same diversity can be the result with slow speciation and slow extinction, or of high speciation and extinction rates. Simplistically, we can distinguish two types of radiations. In "recent, rapid radiations" extinction has had little effect, and the extant diversity is largely the result of rapid speciation. Such radiation typically shows a very high diversification rate. In "mature radiations" there is almost a balance of speciation and extinction, and the extant diversity is a consequence of earlier diversification. The overall diversification rates in mature radiations appear to be low. Recent, rapid radiations and mature radiations are typical of different regions, and reflect different environmental histories. Older surfaces, where there has been little geological or climatic change during the Neogene, such as Australia and southern Africa, are characterised by mature radiations. These crown groups date back to the Oligocene or Eocene, and are often typical of large biomes. More recent environments, such as the alpine regions of the Andes or New Zealand, only have recent, rapid radiations. These areas have had massive geological or climatic perturbation during the latter part of the Neogene, and many crown groups date to the Late Miocene or Pliocene. Some very species rich areas have mixtures of mature and recent radiations. Thus the same modern species richness can be the result of very different histories.

Session 17

Early evolution of Arthropoda – the fate of the second appendage-bearing body segment and the evolution of head segmentation

Yu Liu, Dieter Waloszek, Andreas Maas, Joachim T. Haug, Carolin Haug

Workgroup Biosystematic Documentation, University of Ulm, Ulm, Germany, yu.liu@uni-ulm.de

We explore the evolution of head segmentation in the Arthropoda, with particular reference to the fate of the second appendage-bearing segment. Originally, this post-antennular, resp. first post-oral, segment bore a pair of limbs, which had the same design as all successive appendages. The second appendage-bearing segment was, likewise, as voluminous as all the others. This condition is, e.g., present in several early Cambrian arthropods, such as *Shankouia zhenghei* (Waloszek et al. 2005, Arthr. Str. Dev. 34) and euarthropods, such as the Trilobita. A similar condition can still be observed in extant euarthropods, in the early embryonic development of, e.g., *Paruroctonus mesaensis* (Scorpionida, Chelicerata) (Farley 2001, J. Morph. 250). During evolution, not only the antennulae suffer from severe modifications within different lineages of Euarthropoda, but also the second pair of appendages become significantly altered. Even more, the whole second appendage-bearing segment was affected by changes, even to the extreme of its almost complete loss in adult myriapods and insects (convergently?). Yet, traces of the segment, the intercalary segment, can be followed up in certain early embryonic stages of various tracheates. To investigate the changes of the second appendage-bearing body segment within Euarthropoda in more detail, we accumulated data from both extinct and extant species. Assuming that the situation is more conserved in the early developmental phase of an animal, we studied embryos of selected living euarthropods. Here we introduce to the first steps of our approach by presenting investigations of the embryonic development of *Latrodectus geometricus* (Araneae, Chelicerata) and *Gryllus assimilis* (Orthoptera, Insecta). Emphasis is placed on the topological situation of those segments representing the future adult head and their outgrowths (especially appendages) in different embryonic stages. This study will be flanked, in the future, by the application of different staining techniques marking the nervous system and of confocal laserscanning microscopy.

Session 16

Evolutionary history, biogeography and eco-climatological differentiation of the genus *Anthemis* (Compositae-Anthemideae) in the Circum-Mediterranena area

*Rosa Maria Lo Presti, Christoph Oberprieler

Institute of Botany, University of Regensburg, Regensburg, Germany

Anthemis L. is the second largest genus in the Compositae-Anthemideae and comprises in its traditional circumscription around 200 species. Its geographical range encompasses most of western Eurasia, the Mediterranean region, and a small part of eastern Africa. Here we present an almost complete molecular phylogeny of the genus (150 species) based on the nrDNA internal transcribed spacer (ITS) region and two cpDNA (psbA-trnH and trnC-petN) regions.

A combination of dispersal-vicariance analysis (DIVA) and molecular clock dating of a calibrated, rate-smoothed maximum-likelihood tree was used to reconstruct the biogeographical history of the genus. The reconstructions suggest that the diversification of the group temporally coincides with geological changes during the Tertiary-Miocene ("Messinian salinity crises") and that the flooding of the Mediterranean basin after its desiccation may have triggered the divergence of major lineages. We used over 4000 geo-referenced herbarium specimens of the species used in the phylogenetic analysis and global climate data to reconstruct potential climate niches of the nodes and the terminal taxa through GIS-based approaches. A comparison of the climatic niches of the species and their ancestors suggests that the climate changes occurred in the Mediterranean region since 10 Ma (progressive aridification and successive appearance of a typical mediterranean clima) have played a very important role in the diversification of the main clades.

Session 1

Molecular phylogeny of Apoidea (Hymenoptera) with special emphasis on sphecid wasps

*Volker Lohrmann[1], Christoph Bleidorn[2], Lars Podsiadlowski[3], Michael Ohl[1]

[1] Museum für Naturkunde der Humboldt-Universität zu Berlin, Invalidenstraße 43, 10115 Berlin, [2] Universität Potsdam, Institut für Biochemie & Biologie, AG Evolutionsbiologie / Spezielle Zoologie, Karl-Liebknecht-Str. 24-25, Haus 26, 14476 Golm, [3] Freie Universität Berlin, Institut für Biologie, Chemie, Pharmazie, AG Evolution und Systematik der Tiere, Königin-Luise-Str. 1-3, 14195 Berlin

Sequences from the nuclear long-wavelength-rhodopsin and the mitochondrial cytochrom-c-oxidase (subunit I) from different representatives of the Apoidea, with special emphasis on digger wasps (Sphecidae sensu lato), were analysed using maximum parsimony, maximum likelihood and Baysian inference methods. Compared with previous phylogenetic studies based on morphology, the results of the molecular analyses are controversial but correspond in the absence of support for the Sphecidae s. l. (sensu Bohart & Menke 1976). The relationships within the Sphecidae sensu stricto correspond largely with recent morphological studies. There is circumstantial evidence that the Ampulicidae and Sphecidae s. str. together form a monophyletic group, whereas the relationships within this taxon are still uncertain. Although there is no evidence for a definitive phylogenetic position of the Heterogynaidae; it can be excluded that they are the sistertaxon to all other Apoidea. Instead, they are probably a derived group within the Crabronidae. In conflict to the majority of current morphological studies, the molecular analyses provide no support for the Crabronidae and Bembicinae. Some molecular analyses imply a close relationship between Philanthinae and bees.

Session 11

Intraspecific classification of poppy (*Papaver somniferum*) useful as detection of drug distribution?

Ulrike Lohwasser, Anke Dittbrenner, Hans-Peter Mock, Andreas Börner

Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), Corrensstrasse 3, 06466 Gatersleben, Germany

Poppy (*Papaver somniferum* L., Papaveraceae) is one of the few species utilized since the Neolithic. More than 40 alkaloids can be found in this plant, the five main ones being morphine, codeine, thebaine, papaverine and noscapine. The first use of poppy alkaloids as an ingredient of tinctures for medicinal purpose dates back to Middle Ages, where it was initially called Theriak. In the 16th century, Paracelsus developed another famous tincture called Laudanum. Today, morphine is the dominating alkaloid and the strongest naturally occurring pain reliever. But beside its pharmaceutical use, the abuse as heroin plays a major role. Study of 300 accessions of the Gatersleben genebank provided insight in the morphological, molecular and phytochemical variability within the species. A few morphological characters like capsule dehiscence, shape of stigmatic lobes and colour of flowers and seeds allow for the taxonomic characterisation. Amplified fragment length polymorphism (AFLP) was used to analyse the genetic diversity and to investigate the relationship between the accessions. With high performance liquid chromatography (HPLC), composition and content of the five main alkaloids was analysed. Accessions were characterized by combination of the data, allowing for detecting drug distribution on a worldwide basis.

Session 19

Integrating molecular phylogenetics, distribution and climatic modelling to infer evolutionary processes of *Heliotropium* sect. *Cochranea* (Heliotropiaceae) in the Atacama Desert

*Federico Luebert[1], Hartmut H. Hilger[1], Patricio Pliscoff[2]

[1]Freie Universität Berlin, Institut für Biologie, Systematische Botanik und Pflanzengeographie, Altensteinstraße 6, 14195 Berlin, Germany, [2]World Wildlife Fund - Chile, Carlos Anwandter 624, Casa 4, Valdivia, Chile

Heliotropium sect. *Cochranea* is one of the most specious and geographically restricted sections among the South American *Heliotropium*. It consists of ca. 19 species, endemic to the coastal Desert of Chile and Peru. First phylogenetic results from four molecular markers have shown that the section *Cochranea* is monophyletic. An age estimate suggests that section *Cochranea* originated most likely in the middle Miocene and experienced a diversification process since the early Pliocene. This last diversification process has been interpreted as a radiation. In order to examine a possible ecologically driven evolution in the group, the geographic distribution of the species was modelled using a digital elevation model, seven climatic variables, and three methods (Bioclim, Garp and Maxent). The environmental similarity between species was calculated and the overlapping of their geographic ranges was estimated. For 11 species the results of the modelling coincide with the field records, suggesting that the distribution of the species is largely controlled by at least some of the considered climatic variables. However, for a group of eight species, the results of the modelling largely predict additional occurrence where the species are indeed absent. This suggests that the distribution of these species is also controlled by other variables, not covered by the models. The results show two predominant patterns among the species: similar environmental domains associated to parapatry and different environmental conditions associated to allopatry. With respect to the phylogenetic analyses, two main speciation processes would have been implied in the diversification of *Heliotropium* sect. *Cochranea*: 1) ecologically mediated divergence selection in isolation and 2) secondary contact followed by incidental divergence in allopatry. The first process had been dominant during the early diversification of the group, while the second one had been predominant in the later diversification. This last would be in agreement with a permanent metapopulation dynamics of the species over recent evolutionary times.

Session 3

Cardamine maritima (Brassicaeae) and related species - speciation in the Balkan and Apennine Peninsulas

Karol Marhold[1,2], Jaromír Kučera[1], Judita Lihová[1]

[1] *Institute of Botany, Slovak Academy of Sciences, Dúbravská cesta 14, 84523 Bratislava, Slovak Republic & [2] Department of Botany, Charles University, Benátská 2, 12801 Praha 2, Czech Republic*

The Balkan Peninsula is an area neglected in recent phylogenetic and phylogeogra-phic studies, despite its high floral and faunal diversity and importance as a refugium during Pleistocene glaciations. The present study aims to resolve evolution and taxonomy in *Cardamine maritima* and related taxa in the W Balkan and the Apennine Peninsula, being a case of speciation at the diploid level. The questions addressed include (1) What are the patterns of genetic variation among populations of Italian *C. monteluccii*, broadly conceived Balkan *C. maritima*, and related taxa (*C. carnosa*, *C. glauca*, *C. graeca* and *C. plumieri*)? (2) Do molecular data support currently recognized or previously described (but often not accepted) taxa? (3) Does genetic variation correlate with morphological patterns? (4) Can we recognize the impact of Pleistocene glaciations on the currently observed patterns? Clear differentiation among the currently accepted *C. maritima*, *C. monteluccii* and the four related taxa was confirmed. In addition, recognition of a few other taxa is supported: *C. fialae*, *C. serbica*, and *C. rupestris*, all three restricted to W Balkan mountain ranges. Furthermore, two or three distinct entities (new species) exist within a taxon previously considered as *C. maritima* s. str. They are supported by both morphological and molecular data and occupy their own non-overlapping distribution areas. The evidence from AFLP data, nrDNA and cpDNA sequences suggests rapid radiation within the *C. maritima* lineage that most probably predated glaciation events. Apparently, these taxa experienced only small-scale Pleistocene altitudinal distributional shifts and remained localized within small mountain ranges.

Plenary session II

The origin of adaptive radiations: patterns and processes of speciation and phenotypic diversification in cichlid fishes

Axel Meyer

Lehrstuhl für Zoologie und Evolutionsbiologie, Universität Konstanz, Universitätsstr. 10, 78457 Konstanz, Germany, axel.meyer@uni-konstanz.de

During the last two decades the phylogenetic patterns within and among the adaptive radiations of cichlid fishes in the large East African Lakes has become established due to molecular phylogenetic approaches. The topology of their phylogenetic tree revealed that parallelisms and convergences are abundant both in and across species flocks. That evolution repeated itself raises interesting questions regarding the underlying molecular and developmental mechanisms of these parallelisms. I will present results of recent work on the molecular basis of morphological differences and re-evolved similarities and work on the genetics of speciation and species differences among closely related species of cichlid fishes.

Session 18

Narrow vs. broad species concepts in *Schistidium* (Grimmiaceae, Musci): nuclear ITS data analysis.

Irina Milyutina[1], Elena Ignatova[2], Michail Ignatov[3], Denis Goryunov[3], Rafael Hernández-Maqueda[4], Aleksey Troitsky[1]

[1] A.N.Belozersky Institute of Physicochemical Biology, M.V.Lomonosov Moscow State University, Leninskie Gory. Moscow, 119991, Russia, bobr@genebee.msu.su, [2] Biological Department, M.V.Lomonosov Moscow State University, Leninskie Gory. Moscow, 119991, Russia. [3] Main Botanical Garden of RAS, Botanicheskaya str. 4, Moscow, 127276, Russia. [4] Real Jardin Botanico, Plaza de Murillo 2, Madrid, 28014, Spain.

The taxonomy of the genus *Schistidium* (Grimmiaceae, Musci) is very complicated and there is a controversy between a traditional broad and a narrow species concepts, the later advocated by Blom (1996, 1998). A reconstruction of *Schistidium* phylogeny based on nrITS sequences for 48 specimens of 16 species from Russia and West Europe represented three of the five groups of *S. apocarpum* complex described by Blom was performed. Interspecies variability of ITS from *Schistidium* is very high and permits clear distinguishing of "narrow" species. At the same time ITS sequences are extremely conservative within species even between populations separated by the large distance like 6000 km. The combination of these two points supports the narrow species concept in *Schistidium*. The relationships between species inferred from ITS data are not in a complete agreement with division into groups proposed by Blom. His group "*Atrofuscum*" is sustained by ITS data. However *S. submuticum* from this group keeps a large deletion in ITS1 and combines by this feature with *S. subflacidum* and *S.* sp. nov. in a separate clade. *S. submuticum* ssp. *arcticum* does not differ from the type subspecies by ITS1, while *S. apocarpum* ssp. *canadense* occupies a quite remote position from ssp. apocarpum and most likely has to be considered as a distinct species. The "*Apocarpum*" group species is allocated to several clades in ITS phylogenetic trees, and most likely has to be divided too. The clades discovered in ITS1 phylogenetic tree are congruous with the distribution among accessions of synapomorphic deletions resulted in a stepwise shortening and a rearrangement of the hairpin near the 5'-end of ITS1 region. The comparing of ITS1 sequences permits inferring relationships between two morphologically similar species, *S. papillosum* and *S. boreale* and two forms of *S. papillosum* have to be considered as cryptic species.

In conclusion, although some bryologists consider that *Schistidium* has been "oversplitted" by Blom, it is probably still "undersplitted". More work is required for understanding the taxonomy of this genus.

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Session 17

Functional and phylogenetic implications of the sting apparatus of solitary wasps

*Silke Mosel[1], Michael Ohl[1]

[1]Museum of Natural History, Department of Research, Invalidenstrasse 43, 10115 Berlin, Germany

The sting apparatus of solitary wasps is one of the most prominent apomorphic characters of the Aculeates. It is of importance for an understanding of phylogenetic and evolutionary processes of the aculeate Hymenoptera. Derived from the ovipositor it serves as a tool for prey paralysis in addition to its defense function. It can be presumed that the sting apparatus has evolved in close functional association to its specific biological meaning, for example in adjustment to reproduction strategies. Apoid wasps exhibit a great diversity of foraging and parental behaviours as well as a great variation of morphological characters. Modifications of the sting apparatus may be expected to result from variation in the prey utilized and the precision of the stinging action. These modifications are particularly pronounced in the shape and structure of the stylet and lancets and may reflect a correlation with the mobility and physical strength of the prey. The presence of barbs or teeth on the distal parts of the lancets can be correlated with a less sclerotized body wall of the prey. This morphological diversity can be found on all systematic levels and is of great significance for the phylogeny of solitary wasps. A representative set of morphological characters taken from all skeletal parts of the sting apparatus of a large number of species has been examined. Based on these characters a comprehensive cladistic analysis was performed in order to investigate the relationships among apoid wasps. The results combined with the various behavioural strategies will give rise to a scenario of the evolution of the sting apparatus of solitary wasps.

Session 20

Dehiscent versus indehiscent fruits – a genetic case study in the Brassicaceae

*Andreas Mühlhausen[1], Günter Theißen[2], Klaus Mummenhoff[1]

[1] Universität Osnabrück, Botanik, Barbarastraße 11, 49069 Osnabrück, Germany, [2] Friedrich-Schiller-Universität Jena, Genetik, Philosophenweg 12, 07743 Jena, Germany

Recent developmental genetic studies on fruit dehiscence in *Arabidopsis thaliana* provided detailed information about the anatomy and the gene regulating network underlying the dehiscence (opening) of fruits. To evaluate a general pattern of fruit opening and the impact of lignification on the dehiscence process we examined the anatomy and lignification patterns of fruit valve margin cells in dehiscent and indehiscent fruits of wild Brassicaceae species. We have identified a convenient study system consisting of *Lepidium campestre* (dehiscent fruits) and *L. appelianum* (indehiscent fruits). Both species are closely related and they are diploid (2n=2x=16).

Fruit dehiscence in *Arabidopsis* is initiated by differentiation of three specialized cell types in the fruit valves, i.e., the lignified endocarp layer b, the lignified valve margin cells, and the dehiscence zones. As in *Arabidopsis* wild type fruits, well developed dehiscence zones are apparent on both sides of the replar vascular bundles in *Lepidium campestre* fruits. Furthermore, lignified valve margin cells and endocarp layer b cells are discernible. As with *Arabidopsis* mutant (indehiscent) fruits, no valve margin cells and no dehiscence zones are formed in *L. appelianum* fruits, although the replum is visible on the outside. Instead, a continuous strip of lignified cells stretches from one replar vascular bundle to the other on the opposite side of the fruit.

Thus, the anatomy of dehiscent and indehiscent *Lepidium* fruits corresponds to the *Arabidopsis* wild type (dehiscent) and mutant (indehiscent) fruit types, suggesting that orthologous genes are involved in both mutational (*Arabidopsis*) and evolutionary (*Lepidium*) indehiscence. First results indicate the presence of these orthologs in the *Lepidium* system.

Session 18

New insights in the evolution of *Aneuracae* (Metzgeriales, Marchantiophyta) based on the re-placement of the genus *Verdoornia*

Martin Nebel[1], Markus Preußing[1], Sanna Olsson[2], Dominik Katterfeldt[1], Dietmar Quandt[2]

[1]*State Museum of Natural History Stuttgart, Rosenstein 1, 70191 Stuttgart, Germany,* [2]*Dresden University of Technology, Institute of Botany, Zellescher Weg 20b, 01217 Dresden, Germany*

The monotypic thalloid liverwort genus *Verdoornia* (Aneuraceae) is endemic to New Zealand and is characterized by central placement of the gametangia. In all other Aneuraceae gametangia are marginal. Our investigations on the molecular phylogeny of Aneuraceae (based on chloroplast DNA: trnL and rps4) place *Verdoornia*, *Lobatiriccardia*, *Aneura* and *Cryptothallus* in the same clade ("Aneura-clade"), indicating that gametangial placement in this clade is variable. The Aneuracean genus *Riccardia* constitutes a sistergroup to the "Aneura-clade" which suggests that marginal gametangia may have evolved twice within the family. This conclusion is supported by differences in fungal symbiosis between the two sistergroups. In the "Aneura-clade" symbiotic fungi only inhabit parenchyma cells of the thallus and never the epidermal cells, whereas if fungal symbionts are present in *Riccardia* they mostly live in epidermic cells. Marginal placement of gametangia developed from a reduction of lateral branches, and because liverworts are slow growing plants, such a reduction saves biomass and thus increases fitness. The developement of marginal gametangia placement is comparable with the evolutionarily important change from acrocarpous to pleurocarpous bryophytes by branch reducing. In both cases a higher spore production takes place. The convergent evolution of gametangial placement is suggestive of adaptive radiation in the Aneuraceae.

Session 13

Phylogeography of the south-east Australian montane tree species *Eucalyptus regnans*

*Paul G. Nevill[1], Gerd Bossinger[2], Peter K. Ades[1]

[1]The School of Forest and Ecosystem Science, The University of Melbourne, Parkville, Victoria 3010, Australia, [2]The University of Melbourne, The School of Forest and Ecosystem Science, Water Street, Creswick, Victoria 3363, Australia

Cyclical climate oscillations during the quaternary have had a strong influence on species distributions and evolution. During the Last Glacial Maximum (LGM), south-eastern Australia was colder and more arid than present day and tree species are thought to have contracted to coastal refugia. Chloroplast DNA has been used to examine the broad scale phylogeography of selected members of the *Eucalyptus* genus with studies focusing on the predominately lowland *Eucalyptus globulus*. Less is known about the effect of past climate changes on widespread montane species. This study examines the phylogeography of the south-east Australian montane tree species *E. regnans* and infers the location of refugia during past climate oscillations. *E. regnans* is discontinuously distributed on the Australian mainland and on the large island of Tasmania. We determined the chloroplast DNA (cpDNA) haplotypes of 400 *E. regnans* individuals (40 locations) based on five chloroplast microsatellites. Among the 400 *E. regnans* individuals analysed 35 haplotypes were identified. Phylogenetic relationships were determined by maximum parsimony. Genetic structure was examined using an analysis of molecular variance (AMOVA) and a statistical parsimony network constructed showing the number of nucleotide differences between haplotypes. The statistical parsimony network and cladistic analysis show haplotypes divided into two distinct groups corresponding to continental Australia and Tasmania. The distribution of haplotypes across the range of *E. regnans* shows strong geographic patterns with many populations and even certain regions in which a particular haplotype is fixed. All samples from the central highlands of Victoria were fixed for one haplotype while all samples from the northern and central Tasmanian regions were fixed for other haplotypes. These regions are thought to have been treeless during the LGM. Many locations had unique haplotypes, particularly those in East Gippsland in Victoria, north-east Tasmania and south-east Tasmania. Higher haplotype diversity was found in putative refugia and lower haplotype diversity in areas likely to have been re colonized since the LGM. The data are consistent with the long term persistence of *E. regnans* in certain regions such as East Gippsland and the recent recolonisation of other regions, such as the central highlands of Victoria.

Session 21

Jumping genes the key to mammalian evolutionary history

Jan Ole Kriegs, Gennady Churakov, Maren Möller-Krull, Jürgen Schmitz

Institute of Experimental Pathology, University of Münster, Von-Esmarch-Str. 56, 48149 Münster, Germany

Jumping genes such as retroposons bequeath their traces of activity in the genomes of their hosts over tens to hundreds of million years. Mainly free of function, dispersed over the entire genome, and easy to recognize, they offer a perfect marker-system to elucidate phylogenetic coherences. Their interpretation is rather simple and requires no complex statistic: informative retroposons are present in one taxon and absent at the orthologous genomic loci of the sister group. The only tricky point is to identify the informative ones. This talk will present an introduction to bioinformatics search strategies and interpretations of retroposon presence/absence patterns exemplified by such diverse mammalian orders as primates, rodents, and xenarthrans. The recently published, conclusive placement of a previously misplaced living rodent fossil species indicates the easy expansion of preexisting retroposon phylogenies by the inclusion of additional species. The tracing of ancient retroposed elements, from the tips back to the base of the mammalian phylogenetic tree, indicate their broad range of application.

Session 18

Evolution of epiphytism in the moss family Neckeraceae

*Sanna Olsson[1,2] Volker Buchbender[1], Sanna Huttunen[2,3], Johannes Enroth[2], Lars Hedenäs[3], Ray Tangney[4], Dietmar Quandt[1]

[1] Institute of Botany, Technical University of Dresden, 01062 Dresden, Germany, [2] Botanical Museum and Department of Biological and Environmental Sciences, University of Helsinki, P.O. Box 7, 00014 Helsinki, Finland, [3] Department of Cryptogamic Botany, Swedish Museum of Natural History, Box 50007, 10405 Stockholm, [4] Department of Biodiversity and Systematic Biology, National Museum and Gallery, Cardiff, CF10 3NP, UK

Currently, little agreement exists concerning the family relationships among pleurocarpous mosses. One of the few significantly supported sister group relationships are the Lembophyllaceae and Neckeraceae (including the Thamnobryaceae). Whereas the Neckeraceae have a wide geographic distribution consisting of largely tropical as well as predominantly temperate genera, members of the Lembophyllaceae are mainly found in temperate areas. Although a close relationship is highly supported in all previous analyses, recent phylogenetic analyses challenge the monophyly as well as the current circumscription of both families. In order to shed light on the radiation and character evolution in this fascinating group we analysed a representative taxon sampling of both families and potentially closely related taxa, based on two plastid (rps4-trnF & rpl16) regions, the mitochondrial nad5 and the nuclear encoded ITS1 & 2.

Phylogenetic analyses indicate that current generic delimitations need to be refined. Moreover, morphological characters such as peristome structure and seta length, previously used as diagnostic characters, evolved independently in different lineages and seem to correlate with a habitat shift from terrestrial to epiphytic.

Session 15

Vachonisia rogeri – a Marrellomorpha species (Arthropoda) from the Lower Devonian Hunsrück slate (Germany)

*Gabriele Oltmann

Institute of Palaeontology, Nussallee 8 in 53115 Bonn, Germany, goltmann@uni-bonn.de

Vachonisia rogeri Lehmann, 1955, is redescribed based on 5 known and 15 new specimens. The species exhibit a dorsal shield, which covers the full length of the body. The limbs are arranged in two tagmata: a head and a trunk region. The head region possesses a hypostome, one pair of short and stout antennae and four additional limb pairs. Each of the first three post-antennal pairs of appendages has an endopod and an exopod. The endopods of the first and second post-antennal limb pair have a terminal chela. Ontogenetically advanced individuals developed between 50 and 80 biramous trunk appendages. The exopodial axis consists of numerous rather short podomeres, each bearing an endite and a flattened seta with strengthened margins. The new material includes an ontogenetic series with three stages identified in the available material. Opposite to the advanced ontogenetic stages, the dorsal shield of the earliest ontogenetic stage has a rounded outline. Some characters, like the chelate condition of two endites in the head are taken as indicators for a similar mode of life like *Limulus*. *V. rogeri* was obviously able to capture and chop up also larger food particles. The trunk appendages and the shape of the shield of *V. rogeri* indicate at least a temporarily swimming locomotion.

Session 8

A retroposon based phylogeny of the order Primates

*Martin Osterholz, Lutz Walter, Christian Roos

Primate Genetics, German Primate Center, Kellnerweg 4, 37077 Göttingen

With at least 70 genera and about 350 species, the order Primates is one of the most diverse mammalian orders. Even though the phylogenetic relationships among major lineages are elucidated, those within families are still disputed and part of lively debates. Knowledge about the phylogenetic relationships is of prime importance for comparative research fields and forms a reliable fundament, because it could reveal the development, formation and coherences of different social systems, phenotypes or diseases. Retroposons offer a tremendous informative source of genome diversity and are mainly involved in shaping genomes. The integration of a retroposon into the genome is generally thought to be unidirectional and precise excision, homoplasy or character conflicts are highly unlikely. Due to these features, combined with their high abundance, retroposons represent probably the most powerful molecular tool to reconstruct phylogenetic relationships in mammals and have helped to elucidate many important evolutionary issues. For example retroposons support evidence for the position of whales within even-toed ungulates or shed more light into eutherian evolution. To study the phylogeny of primates we used mainly primate-specific retroposons belonging to the SINEs (Short INterspersed Elements) and are so called Alu elements (with an approximate length of 300 bp). They comprise at least 11 % of the human genome and are increasingly used as informative phylogenetic markers in primates. Both attributes, the absence of homoplasies and the clear polarity, lead to a nearly noise free molecular Hennigian synapomorphy. A common ancestry of two taxa can be determined by a shared orthologues insertion. Although there are already some studies on primate phylogeny based on Alu elements, all lack information of several important primate genera, most likely due to their endangered status. Based on our comprehensive DNA bank (Gene Bank of Primates), we first focussed on the colobine monkeys. There are still many controversial views, e.g. whether the Asian and African clades or the odd-nosed monkeys form monophyletic groups. First results indicate that the African colobines probably don't form a monophyletic group. Furthermore, we focused on New World monkey and strepsirrhine phylogenies.

Session 6

Genetic and epigenetic consequences of allopolyploidization in *Dactylorhiza* (Orchidaceae)

Ovidiu Paun[1], Michael F. Fay[2], Mark W. Chase[1]

[1] Molecular Systematics Section, Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3DS, UK, o.paun@kew.org, m.chase@kew.org, [2] Genetics Section, Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey, TW9 3DS, U.K., m.fay@kew.org

Hybridization and polyploidization are now recognized as major phenomena in the evolution of plants, promoting genetic diversity, adaptive radiation and speciation. Modern molecular techniques have recently provided evidence that allopolyploidy can induce several types of genetic and epigenetic events that are of critical importance for the evolutionary success of hybrids: (1) chromosomal rearrangements within one or both parental genomes; (2) demethylation and activation of dormant transposable elements; (3) rapid and reproducible loss of low copy DNA sequence; and (4) organ-specific up- or down-regulation of one of the duplicated genes, resulting in unequal expression or silencing of one copy. All these alterations have the potential, while stabilizing allopolyploid genomes, to produce novel expression patterns and new phenotypes, which together with increased heterozygosity and gene redundancy might confer on hybrids an elevated evolutionary potential, with effects at scales ranging from the molecular to the ecological. An important feature of hybridization is its potential to occur repeatedly between different populations of the same parental taxa, leading to arrays of allopolyploids that subsequently interbreed. We are analyzing the allotetraploid pair *Dactylorhiza traunsteineri* and *D. majalis* s.s., which both resulted from hybridization of *D. fuchsii* and *D. incarnata*, to further our understanding of the consequences of hybridization and polyploidy on natural evolution of genomes and adaptation to the environment. Despite similar genetic background, this allotetraploid pair shows marked difference in evolutionary history, distribution and ecology. A genome-wide survey of the transcriptome using cDNA amplified fragment length polymorphism (cDNA-AFLP) and of the epigenetic variation using methylation sensitive AFLP (MSAP) allows us to discuss the functional relevance of gene expression alterations, nature of the diploidization process, and molecular mechanisms that result in adaptation to different ecological conditions/habitats leading to reproductive isolation.

Session 4

Phylogenomics of sponges (Phylum Porifera)

*Kerstin Pick

Courant Research Center Geobiology, Geoscience Center Göttingen, Georg-August-Universität Göttingen Goldschmidtstr. 3, 37077 Göttingen, Germany

The phylum Porifera is one of the most ancient metazoan lineages on our planet. The first sponge body-fossils were found in the early Precambrium about 580 million years ago. Sponges are sessile, aquatic filter-feeders without complex tissues. While morphological studies support the monophyly of sponges and its three extant classes Hexactinellida, Calcarea, and Demospongiae, several molecular systematic datasets suggested sponge paraphyly, albeit with low support. Existing 18S rDNA, 28S rDNA and protein-coding single gene analyses were not yet able to unequivocally refute or confirm the monophyly of phylum Porifera. While "Classes" Calcarea and Hexactinellida have been shown to be monophyletic, classically recognized Demospongiae were not, as the placement of the order Homoscleromorpha is currently under discussion. Here, a phylogenomic approach was implemented with the aim to contribute to solving the conundrum of the relationships of the major sponge lineages. Embedded in the DFG Priority Program "Deep Metazoan Phylogeny" (http://www.deep-phylogeny.org/). Together with our national and international collaborators we sequenced over 23,000 sponge ESTs from eleven sponge taxa from the main sponge lineages, including 3 Hexactinellida, 2 Calcarea, 4 Demospongiae and 2 Homoscleromorpha. A bioinformatics pipeline was developed for downstream sequence processing, annotation, and alignment. Ribosomal protein and multiple protein-coding gene alignments were analysed phylogentically. First results of this phylogenomic approach will be presented.

Session 10

Gene expression analyses reveal differences in stress tolerance in three closely related *Hordeum* species (Poaceae)

*Thekla Pleines

Leibniz Institute of Plant Genetics and Crop Research (IPK), 06466 Gatersleben, Germany

The genus *Hordeum* (Poaceae, Triticeae) underwent rapid radiation in non-tropical South America. In the course of this process, different climatic regions as well as different ecological habitats were colonized. Three South American species are particularly interesting with respect to the study of possible ecological speciation mechanisms, since they are closest relatives and have overlapping distribution areas, but inhabit different ecological niches. One species, *H. comosum*, occurs only in very dry parts of the Patagonian steppe, whereas the other two species, *H. patagonicum* and *H. pubiflorum*, are restricted to moister, but often highly salt-influenced habitats. The latter species is restricted to lowland areas, while the other taxa occur from sea level to high Andean habitats. We assume that this situation is the result of divergent evolution of stress tolerance. In this study, gene expression analyses using a barley (*H. vulgare*) cDNA array and greenhouse experiments were performed to evaluate the response of all three species to salt, osmotic and cold stress. First results of a comparison between the species show that there are indeed regulatory differences in stress response. For example, *H. comosum* reacts differently to osmotic stress compared to the other two species, as could be expected from its occurrence in often very dry habitats. However, *H. comosum* is less salt tolerant than *H. patagonicum* and *H. pubiflorum*, thus showing pronounced differences in gene expression patterns for both stress factors. The differences in gene regulatory pathways evolved probably within a relatively short time, during or after the formation of these species. Our study shows that gene expression analyses can provide useful information in studies of speciation and ecological adaptation of non-model species.

Session 1

The phylogeny and evolution of Strepsiptera (Hexapoda)

Hans Pohl, Rolf G. Beutel

Entomology Group, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Friedrich-Schiller-Universität Jena, Erbertstrasse 1, 07743 Jena

An evolutionary scenario for the enigmatic group Strepsiptera is provided, based on the results of a comprehensive cladistic analysis of characters of all life stages. †*Protoxenos janzeni* – the most archaic strepsipteran, sheds new light on the early evolution of the group and reduces the "morphological gap" between Strepsiptera and other insects. It weakens both current hypotheses – Coleoptera + Strepsiptera and Diptera + Strepsiptera (= "Halteria"). The splitting event into †*Protoxenos* and the remaining Strepsiptera was linked with a distinct size reduction and many morphological changes. Unlike males of extant strepsipteran species †*Protoxenos* was still able to process food. Mengeidae (†Mengea), with two small species, is the sister-group of extant Strepsiptera. A unique characteristic of extant males (Strepsiptera s. str.) is the mouthfield sclerite. It is part of an air-uptake apparatus, which belongs to an extremely modified air-filled "balloon-gut". Besides this, male strepsipterans possess specialised antennae and compound eyes, a strongly developed flight apparatus, large testes, and a sperm pump. Males are designed to find females within few hours and to copulate. The change to pterygote hosts and the permanent endoparasitism of the females are evolutionary novelties acquired by Stylopidia, and linked with far reaching morphological transformations, e.g. the presence of unique brood organs. Hairy tarsal adhesive devices are present in males and guarantee efficient attachment to the host during copulation. A well-founded clade within Stylopidia is Stylopiformia, which are characterised by a unique fissure-shaped birth opening. The evolutionary development towards the most specialised and successful forms (parasites of aculeate Hymenoptera) is a stepwise process. The presented evolutionary scenario comprises a complex network of functionally correlated morphological changes in primary larvae, secondary larvae, females and males.

Session 8

Ultrastructure of pigmented cerebral eyes in the polychaete *Scoloplos armiger* (Orbiniidae, Annelida) – implications for annelid phylogeny and evolution

Günter Purschke, Verena Wilkens

Zoologie, Fachbereich Biologie/Chemie, Universität Osnabrück, 49069 Osnabrück, Germany

The phylogeny and evolution of Annelida is far from being resolved. Conflicting hypotheses concern the in-group relationships as well as their position within Lophotrochozoa. Debating the evolution of Annelida one has to keep in mind that most likely annelids have a biphasic life cycle with a planktonic larva and a benthic adult, both of which have different plans of organization. With respect to cerebral eyes, the trochophore larva is characterized by a pair of simple ocelli composed of one or two rhabdomeric sensory cells and a pigmented supportive cell forming a pigment cup with inverse design of photoreceptors. These ocelli are either replaced by complex multicellular adult eyes or persist in the adults. Additional ocelli of the same type may be added in the latter case. Multicellular cerebral eyes have only been found in the parapodia-bearing Aciculata whereas the remaining taxa, i.e. the sedentary polychaetes as a rule possess simple ocelli. Depending on the phylogenetic tree suggested different scenarios for eye evolution have to be proposed. Molecular analyses could neither recover a basal clade Scolecida found in morphological analyses characterized by absence of appendages nor a monophyletic Aciculata. Instead one subgroup of the former, Orbiniidae, usually falls inside Aciculata. Since a taxon Scolecida has been questioned repeatedly on molecular and morphological evidence, the proof of a cerebral eye of the Aciculata-type in Orbiniidae would give additional evidence for a wrong placement and support trees found in molecular analyses. Although equipped with small eyes it was not known whether they in fact represent persisting larval eyes or miniaturized adult eyes. The ultrastructural analysis of the eyes in *Scoloplos armiger* showed that they comprise an additional cell type, a corneal cell and an additional sensory cell and thus with a high degree of probability they actually represent miniaturized adult eyes. Thus, a different placement of Orbiniidae is supported by these additional morphological data and the validity of a taxon Scolecida is seriously questioned. Very likely this grouping is artificial due to common character losses which have a high potential of convergence and which often remain undetected in morphological cladistic analyses.

Session 7

Molecular phylogeny and intraspecific differentiation of the *Eremias velox* complex of the Iranian Plateau and Central Asia (Reptilia, Lacertidae)

Eskandar Rastegar Pouyani[1,3], S. Kazemi Noureini[1], U. Joger[2], M. Wink[3]

[1] Department of Biology, Teacher Training University of Sabzevar, Sabzevar, P.O.Box 397, Iran Eskandar.Rastegar-Pouyani@urz.uni-Heidelberg.de, e-rastegar@sttu.ac.ir, [2] State Natural History Museum, Pockelsstr. 10, 38106 Braunschweig, Germany, [3] Institute for Pharmacy and Molecular Biotechnology, Department of Biology, University of Heidelberg, Im Neuenheimer Feld 364, 69120 Heidelberg, Germany

The rapid fringe-toed lizard, *Eremias velox,* is a widely distributed species of the Eurasian genus *Eremias*. Within its vast distribution range in the Iranian plateau and Central Asia, specimens from 13 geographically distant populations were available. Here we compare sequences of the mitochondrial marker genes, cytochrome b and 12S rRNA, and genomic ISSR-PCR fingerprints from 13 geographically distant localities in Iran and Central Asia. Separate phylogenetic analyses of the sequence datset and ISSR-PCR fingerprints were highly concordant and both successfully recovered six major clades within the *E. velox* complex with moderate or high support values. The calibrated molecular clock suggests that the north Iranian clade diverged first some 11-12 mya and that the Central Asian lineages diverged from the northeast Iranian lineage some 6 mya caused by uplifting of the Kopet-Dagh mutations. In addition, high degree of interclade genetic distances among the Iranian lineages on one hand and high degree of homogeneity among the Central Asian units, despite their vast area of distribution, on the other, indicated that the *E. velox* clade well originated in the Iranian plateau. In addition, the data molecular data provide strong evidence for a fundamental revision of the taxonomic status within the complex. At least four distinct species and three well-supported subspecies can be distinguished within the traditional *E. velox* clade in its vast area of distribution.

Session 12

Molecular studies on bizarre deep-sea Asellota (Crustacea: Isopoda): phylogeny and genetic variability of selected taxa

Michael J. Raupach[1], Christoph Mayer[2], Johann-Wolfgang Wägele[1]

[1] Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160, 53113 Bonn, [2] Lehrstuhl für Evolutionsökologie und Biodiversität der Tiere, Fakultät für Biologie und Biotechnologie, Ruhr-Universität Bochum, Universitätsstrasse 150, 44801 Bochum

Isopod crustaceans are an adaptable and varied group that have species in many terrestrial as well as aquatic environments. However, it is in the deep sea that they show their most impressive radiation, and where they are found at all depths down to the deepest trench. Asellote isopods are the best–known of Peracarida from great depths, with more species described (about 900 species) than any other crustacean group inhabiting this environment. The detritus-feeding habit of asellotes is thought to suit them to life on the deep-sea bottom, allowing a great variety of bizarre and extravagant range of body forms, which include long elongated animals (Ischnomesidae), burrowing dozer-like forms (Janirellidae), spinose species (Mesosignidae) and even some secondarily highly modified swimmers within the Munnopsidae. Although deep-sea Asellota are ecologically important and biogeographically interesting, we have is only limited knowledge about their biology, and there are only a few phylogenetic studies based on morphology and focused on single families.

Our first extensive molecular study of more than 110 species of deep-sea Asellota using the complete 18S rRNA and partial 28S rRNA gene gives evidence for a multiple colonization of the deep sea and the munnopsoid radiation, including many typical deep-sea families. In addition to this, molecular studies based on mitochondrial and nuclear genes, give evidence for the existence of complex species flocks within so-called cosmopolitan or widespread species, supporting the patch-work theory of closely related but distinct populations in the deep sea.

Session 13

Polyploidization and phylogeography in the three varieties of *Melampodium cinereum* (Heliantheae, Asteraceae)

*Carolin A. Rebernig[1], Gudrun Kohl[1], Hanna Weiss-Schneeweiss, Cordula Blöch[1], Renate Obermayer[1], Jose L. Villaseñor[2], Tod F. Stuessy[1]

[1] Faculty Center of Botany, Department of Systematic and Evolutionary Botany, University of Vienna, Rennweg 14, 1030 Vienna, Austria, [2] Instituto de Biologia, Departament de Botanica, Universidad Nacional Autonoma de Mexico, Mexico D.F.

The genus *Melampodium* (Heliantheae, Asteraceae) comprises 39 species, which are distributed throughout Mexico, Central America and the southwestern US All species have yellow rays, except for three species with white rays that are distributed on the northern most edge of the distributional range. These three shrubby, xerophytic taxa (*M. leucanthum, M. cinereum*, *M. argophyllum*) form the so-called white-rayed complex of the genus. These species vary in their distribution as well as in their ploidy level. *M. leucanthum* and *M. cinereum* have diploid and tetraploid cyto-races, whereas *M. argophyllum* possesses a hexaploid cytotype. In this study we focus on the intraspecific relationships of *M. cinereum*, which based on morphological characters was divided into three varieties: var. *cinereum*, var. *hirtellum* and var. *ramosissimum*. Intraspecific relationships were studied using AFLP fingerprinting data, chloroplast haplotype analysis and ploidy level estimations based on flow cytometry. The purpose of this study is: (1) to test if the current taxonomic grouping is correlates with genetic entities; (2) to investigate the origin of the polyploids (allo- or autopolyploidy); and (3) to determine whether polyploidization took place one or multiple times during the evolution of this species. AFLP data clearly supports the separation of the varieties into different genetic entities, even though they do not fully reflect the previous taxonomic concepts based on morphological characters. *M. cinereum* var. *hirtellum* is divided into an eastern and a western group, with the former clustering with *M. cinereum* var. *cinereum* and the latter forming a clade with *M. cinereum* var. *ramosissimum*.

Session 15

The early evolution and diversification of sea cucumbers (Echinodermata: Eleutherozoa)

Mike Reich

Geowissenschaftliches Zentrum der Universität Göttingen, Museum, Sammlungen & Geopark, Göttingen, Germany

Compared to their modern counterparts, the palaeobiology and early evolutionary history of holothurians are poorly understood. Currently, there are only nearly 800 fossil holothuroid paraspecies and species, ranging from the Early Palaeozoic to the Quaternary, in comparison to more than 1,400 Recent species. In part, this is due to their disjunct endoskeleton with ossicles and calcareous ring elements, which are released following decomposition of the surrounding tissue. However, under favourable conditions, holothurians may be preserved completely in various fossillagerstaetten. The combination of micro- and macropalaeontological methods makes new findings and views within the research on fossil sea cucumbers possible. The early evolution and diversification of the sea cucumbers have been reviewed and reinterpreted, including new records of Ordovician, Silurian, and Devonian material. Holothuroids have a Phanerozoic history extending back more than 464 Ma, ranging from the early Middle Ordovician to the present time. The maximum level of morphological diversification was apparently reached in the Mesozoic, in all likelihood due to a lack of research in other strata. A revised hypothesis of Early Palaeozoic higher-level relationships within the Holothuroidea and Eleutherozoa is presented.

Session 11

Towards a global assessment of taxonomic needs and capacities: what taxonomists do we need where?

Swen C. Renner, Merijn M. Bos, Christoph L. Häuser

State Museum of Natural History, Rosenstein 1, 70191 Stuttgart, Germany

The Global Taxonomic Initiative (GTI) is a cross-cutting theme of the UN Convention on Biological Diversity (CBD), and has asked in 2002 for national, regional and global assessments of taxonomic needs and capacities (UNEP/CBD/COP6/Decision VI/8). Whereas several national and regional assessments of taxonomic needs and capacities have already been compiled (see www.cbd.int), a global assessment is still pending. As an important contribution for a global assessment, information about the current state of knowledge of national biodiversity and available taxonomic capacities is being compiled.

The German GTI National Focal Point contributes to the global assessment by analyzing numbers of existing vs. needed taxonomists, and by assessing the species numbers per taxonomic group and country, with a focus on species inventories of protected areas on a global scale. The preliminary results indicate, not surprisingly, that existing taxonomic knowledge and resources are distributed unequally among countries and taxonomic groups. Whereas numbers of taxonomists and the relative states of knowledge about their countries' biodiversity are positively correlated, numbers of taxonomists negatively correlate with the known or estimated species richness per country. Especially tropical regions of Africa urgently need more taxonomic expertise, as well as many parts of SE Asia. Moreover, the state of knowledge of certain "unpopular" and not especially prominent groups such as micro-organisms, algae, fungi, and several invertebrate groups is regionally as well as globally poor.

Session 19

Biodiversity of terebellomorph polychaetes from hot vents and cold seeps

*Michael Reuscher[1,2], Dieter Fiege[1], Thomas Wehe[1,2]

[1]Forschungsinstitut Senckenberg, Sektion Marine Evertebraten II, Senckenberganlage 25, 60325, Frankfurt/M, Germany. [2]Institut für Zoologie, Ruprecht Karls Universität Heidelberg, Im Neuenheimer Feld 230, 69120 Heidelberg, Germany

The discovery of the ecosystems at hot vents in the late 70s and cold seeps in the early 80s in the last century, has been one of the greatest sensations in marine biology. Many new species and higher taxa were found and described, among them also polychaetous annelids. Though many efforts have been undertaken since then in order to examine these extraordinary habitats, our knowledge of the biodiversity of these ecosystems is still incomplete, especially as regards Polychaeta. Some groups, for instance polynoid scale worms or the vestimentiferan tubeworms, which are now considered as belonging to polychaetes are quite well known. Within the group of Terebellomorpha the same is true for the Alvinellidae or "Pompeji worms", exclusively occurring at hot vents, which have been subject to diverse physiological studies. However, not much is known about the diversity of the remaining terebellomorph polychaetes belonging to Ampharetidae, Pectinariidae, Terebellidae and Trichobranchidae. Non or only a few species belonging to these families have so far been described from vent and seep sites. Therefore a study was undertaken focusing on the examination of terebellomorph specimens collected by the German research vessels *Meteor* and *Sonne* from the Mid-Atlantic and NE-, SE- and W-Pacific in the last 10 years. During this ongoing study several new species and new records were found, currently awaiting publication. About 20 different species are recorded belonging to 4 of the respective families. Among these records so far 5 species are newly described. All records of Terebellidae from hot vents are new to science, since so far no species have been described from these habitats. New species and records will be presented and a main focus will be given to aspects of larval development, dispersal and biogeography. The widely distributed genus *Amphisamytha* will be used to exemplify problems of species identification, taxonomy and resulting distribution patterns. Morphological evidence from larval development will be presented in order to demonstrate, that the widely distributed *A. galapagensis* is most probably not a deep sea cosmopolitic species, as it has already been suggested on the base of molecular studies.

Session 20

Floral development of *Aextoxicon punctatum* (Aextoxicaceae – Berberidopsidales) – morphological evidence for a link with *Berberidopsis*?

Louis Ronse De Craene

Royal Botanic Garden Edinburgh, 20A Inverleith Row, Edinburgh EH3 5LR, U.K.

The monotypic genus *Aextoxicon* Ruíz & Pavón is an evergreen, dioecious tree of southern Chile and adjacent Argentina. In recent molecular studies (e.g. Soltis et al. 2003, Am. J. Bot. 93: 461-470) *Aextoxicon* has been associated with Berberidopsidaceae in an order Berberidopsidales at the base of the core eudicots. Ronse De Craene (2004, Ann. Bot. 94:741-751) hypothesized that the spiral flowers of Berberidopsis with undifferentiated perianth represent a prototype for floral evolution in the core eudicots. *Aextoxicon* has pentamerous flowers with a differentiation of sepals and petals and it was suggested that the flower of *Aextoxicon* is derived from a *Berberidopsis*-like ancestor by a progressive differentiation of the perianth.

Floral development was carried out to understand the flower structure of *Aextoxicon* in the context of the Berberidopsidales. The flowers are enclosed in a calyptra formed by two bracteoles and are subtended by a bract. The floral development is highly variable, either spiral or unidirectional; the sequence does not follow a regular 2/5 pattern as is common for pentamerous flowers. The perianth and stamens arise sequentially and there is no difference between sepals and petals in early stages of development. About five-seven stamens or staminodes are initiated and are followed by a single carpel. The gynoecium encloses two pendulous ovules. Nectaries arise as broadly winged platforms in alternation with the stamens in preanthetic buds.

Development shows that the perianth parts of *Aextoxicon* are homologous, with petals being little differentiated from the sepals. Pentamery appears to be superposed on a dimerous or trimerous Bauplan. The species shares a number of characters with *Berberidopsis*, including the spiral sequence of all organs, the presence of two bracteoles associated with the flower, and the broad nectary. *Aextoxicon* is morphologically strongly isolated.

Session 14

Intraspecific polymorphism, hybridization and reticulate evolution in roses: how to tell the difference?

Ivan Schanzer, Vera Voilokova, Alina Vagina, Natalya Kutlunina

Main Botanical Garden RAS, Botanicheskaya 4, 127276 Moscow, Russia

Taxonomy of *Rosa* is notoriously difficult due to intraspecific polymorphism, hybridization and reticulate evolution in the past. Attempts to reconstruct the phylogeny of the genus are often hampered by inability to discern between these cases, especially when hybridogenous species of the Caninae section are mixed up with recent interspecific hybrids erroneously regarded as separate species. Extensive rose populations sampling over European part of Russia with subsequent analyses of patterns of variability of morphological and ISSR markers in natural populations enabled us to make such a distinction. Diploid and polyploid species of the section Cinnanomeae appeared to be highly polymorphic, both morphologically and genetically. *R. glabrifolia, R. gorinkensis* and *R. pratorum* are not separate species but intraspecific forms of *R. majalis*. Heterogamous species of the section Caninae are much less polymorphic, however producing a bewildering diversity of morphotypes via hybridization with each other and *R. majalis* of the Cinnamomeae section. So far we can state that *R. caesia*-like plants in European Russia comprise the F1 of *R. canina* x *R. majalis* hybridization; *R. dimorpha, R. podolica, R. subpomifera* are all various products of *R. canina* x *R. villosa* hybridization. Further research to unravel such hybrids and cases of intraspecific polymorphism are needed. We suppose that more firm establishing of species limits and exclusion of recent hybrids and products of introgression from the analyses may be a necessary prerequisite to reconstruction of the *Rosa* phylogeny in future.

Session 17

Nervous system evolution in the Nemathelminthes

Andreas Schmidt-Rhaesa[1], Birgen Holger Rothe[2]

[1] *Zoological Museum and Institute, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany, a.schmidt-rhaesa@uni-hamburg.de,* [2] *Evolutionary Biology, University Bielefeld, Morgenbreede 45, 33615 Bielefeld, Germany*

Complex organ system such as the nervous system can be visualized by fluorochrome-labelled immunocytochemical markers of particular neurogenic substances such as transmitters or tubulin. Analysis with the confocal laser scanning microscope gives three-dimensional information on the entire architecture of the nervous system. The results often result in a better understanding of nervous systems than is possible by e.g. ultrastructural investigations. We present data from several taxa among the Nemathelminthes: Gastrotricha, Kinorhyncha, Priapulida and Nematomorpha. The latter three taxa form, together with Nematoda and Loricifera, the monophyletic taxon Cycloneuralia, this is supported by a ring-like brain and a characteristic arrangement of nuclei anterior and posterior of the brain neuropil. Characters such as segmental patterns in the nervous system, the formation of ganglia and fusion of nerve cords are discussed. The Gastrotricha are hypothesized as the sister group of Cycloneuralia on the basis of morphological characters, but this is not supported by molecular data. The nervous system of Gastrotricha is particular in having a brain with a strong dorsal and a very fine ventral commissure. The nuclei of the brain are in a lateral position. The possibility is discussed that this architecture is close to an ancestral bilaterian condition. Furthermore, the ring-like cycloneuralian brain may be derived from a gastrotrich-like brain.

Plenary session I

Untangling the deep nodes of the land plant phylogeny

Harald Schneider

Department of Botany, Natural History Museum, London SW7 5BD, UK, h.schneider@nhm.ac.uk

The origin and early diversification of land plants are among the most puzzling events in the history of life. This successful colonization of terrestrial habitats resulted not only in the establishment of the four major lineages of land plants but also in dramatic changes of the physical environment at a global scale and transformation of the prospects for other organisms living in terrestrial habitats such as animals and fungi. The hypothesis of plants as key protagonists of global change in the Palaeozoic still requires further investigation because several aspects of the correlations between early land plant diversification and global change of the physical environment as well as correlated evolution between plants and other organisms are poorly understood. Two major obstacles are currently hindering progress. The first obstacle is the still problematic untangling of the relationships among the four extant major lineages of land plants – hornworts, liverworts, mosses, and tracheophytes – but also the relationships of fossil taxa from Ordovician to mid Devonian times. The second obstacle, the lack of robust estimates of divergence times for the early divergences in the phylogeny of land plants, has to be resolved as part of our ongoing research on the untangling the deep nodes of the green branch of the tree of life. In this review, I will discuss our current understanding of these relationships, especially focusing on the "bryophyte grade" hypothesis in which the liverworts, mosses and hornworts form are steps in a grade leading to the tracheophytes. To overcome current obstacles, I will outline a palaeogenomic research approach that integrates genomic and fossil evidence. The successful employment of this approach will relay on progress in analytical procedures as well as recovering additional evidence. However, this approach promises an ultimate answer to most key questions.

Session 9

The origin of species in *Primula* sect. *Auricula* – a combined species distribution modeling (SDM) and phylogeographical approach

*Gertrud Schorr[1], Norbert Holstein[2], Antoine Guisan[3]

[1] Insitut für Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Germany, [2]Systematische Botanik, Ludwig-Maximilians-Universität München, Germany, [3] Department of Ecology and Evolution, University of Lausanne, Switzerland

Most speciation events in one of two clades of the *Primula* sect. *Auricula* took place during Quaternary glacials, presumably in geographically isolated refugia on the edge of the ice shield, as implied by previous studies of the phylogeny and the temporal course of diversification. To further support this hypothesis our main aim is to locate the refugial areas of sister species where speciation from a common ancestor occurred. Therefore we combine phylogeographical analyses using AFLPs with a modeling approach to predict species distribution in the last glacial maximum (LGM), 20.000 years ago, based on current ecological requirements of the species and palaeoclimate. For the AFLP analyses we selected two pairs of sister species (*Primula hirsuta* & *P. daonensis, P. marginata* & *P. latifolia*) and sampled populations along gradients from potential refugial areas (according to Schönswetter et al., 2005) into post-glacially recolonized areas. Our first results do not provide simple answers for the first species pair (*P. hirsuta* and *P. daonensis*) investigated. Mainly two things can be shown. First, patterns of genetic diversity suggest multiple refugia in both species, located close to described potential refugial areas at the periphery of the ice shield but also well within the ice shield. Second, in both species genetically distinct populations are found on the southern edge of their distribution ranges and close to the southern border of the last glacial maximum ice shield. These populations did not serve as source populations for recolonization and therefore are interpreted as 'relic' populations. They presumably diverged in their isolated peripheral refugia and so illustrate that also speciation could have taken place in peripheral refugial areas.

The molecular data alone thus failed to clearly identify the hypothesized geographically isolated refugial areas where speciation took place and from which re-colonization started. The combination of these phylogeographical results with the results of the modeling approach promises to complete the picture. It will be discussed how phylogeography and modeling can complement each other to understand Quaternary speciation in *Primula* sect. *Auricula.*

Plenary session I

Interrelationships of lower vertebrates: current agreements and controversies

Hans-Peter Schultze

University of Kansas, Natural History Museum and Biodiversity Research Center, 1345 Jayhawk Blvd., Lawrence, Kansas 66045-7561, USA, hp1937@ku.edu

Fossil lower vertebrates outnumber the extant representatives, so that it is important to have data sets for the fossil representatives comparable to those of extant forms. In the 1920s, Stensiö introduced the serial section method to study fossil lower vertebrates; today we use Catscan and acid preparation to attain comparable study objects for fossil and extant forms. Based on new discoveries and new methods, our phylogenetic understanding of lower vertebrate phylogeny has changed and is changing. The earliest craniates are known as soft bodied forms from deposits of 525 million years ago. Fossil representatives of the soft bodied craniate hagfish and the vertebrate lamprey are known from 310 and 370 million years ago, respectively. The monorhinen osteostracans are currently considered closer related to gnathostomes than the diplorhinen heterostracans. Bone is a primitive feature within gnathostomes including placoderms and chondrichthyans. Braincases are well ossified in many primitive Devonian fishes (416-360 million years ago), e.g., chondrichthyan braincases show fissures, which are considered "typical" for osteichthyans. An eye stalk occurs in osteichthyans, chondrichthyans and placoderms. These discoveries show features that although present in primitive representatives, are lost in advanced, extant representatives. Discoveries of new forms and new characters, in combination with new techniques, may impact current concepts of interrelationships, e.g., the "reappearance" of the Holostei within the actinopterygians due to molecular evidence and to new morphological characters present in fossil forms. New discoveries in the Early Devonian of China are permanently changing our concept of interrelationships of sarcopterygians, except for the early tetrapods. There is a very dense record on the transition from piscine to tetrapod sarcopterygians in the Late Devonian, which gives the opportunity to study in detail the character acquisitions, transformations and losses thoughout time.

Session 17

Hearing in the dark: changed otolith morphology in a cave-dwelling form of *Poecilia mexicana* (Teleostei)

Tanja Schulz-Mirbach, Bettina Reichenbacher

Ludwig-Maximilians-University, Department of Earth and Environmental Sciences, Section Palaeontology & GeoBioCenter, Richard-Wagner-Str. 10, 80333 Munich, Germany, t.schulz-mirbach@lrz.uni.muenchen.de, b.reichenbacher@lrz.uni.muenchen.de

Otoliths are involved in the sense of hearing, however, the relationship between hearing physiology and otolith morphology is still poorly understood. The sulfuric Cueva del Azufre in Southern Mexico, colonized by the cyprinodontiform *Poecilia mexicana*, provided an excellent opportunity to study whether adaptation appears in otolith morphology as a result of darkness and requirement of better hearing, respectively. We studied left otoliths (N = 67) in order to investigate (i) whether sulcus morphology from the cave fish has changed along with adaptation to darkness and (ii) whether otolith contours reflect a morphological gradient from the cave outflow to the inmost cave chamber. Sulcus morphology was analyzed using scanning electron microscopy and otolith contours were quantified by Fourier shape analysis. We observed differences in sulcus morphology (sulcus depth) and otolith weight between surface- and cave-dwelling fish that suggest an improved hearing capability in the cave form. We conclude that the deepening of the sulcus is a result of increased attachment of material on the inner face of the otolith. Otolith contours show a morphological gradient that concurs with the morphocline of other traits, such as eye size. Our results show for the first time that cave-dwelling forms of a single species display a changed otolith morphology that may indicate improved hearing capabilities due to adaptation to darkness.

Session 19

The "inland lomas" near Omate (Peru, Depto. Moquegua) – a recently discovered plant community

*Christian Schwarzer

Freie Universität Berlin, Institut für Biologie, Systematische Botanik und Pflanzengeographie, Altensteinstr. 6, 14195 Berlin, Germany, schwarzer.one@web.de

During a field trip to South Peru in 2006 an area with an unusual floristic composition was encountered in the vicinity of Omate (Depto. Moquegua). The area is located near Rio Tambo and characterized by a thick layer of pumice soil. Despite its elevation between 1500 and 2500 m and a distance of about 120 km to the coast, the area described here shows floristic elements typical for the coastal loma formations. These elements include several species that have never been observed outside the lomas and which were thought to be restricted to elevations lower than 1000 m.

A complete vegetational survey of this area was undertaken which revealed that its vegetation can be divided into four groups: 1) endemic species of the coastal loma formations; 2) widespread species, which frequently occur in the coastal lomas; 3) West-Andean elements of Peruvian origin and 4) Chilean-Argentinian elements which are reported the first time for Peru. A similarity analyses showed moderate similarity between the investigated area and the lomas of Tacna, located 170 km southwards. For both, climate data show a remarkable temperature homogeneity over the year and limited water resources for a short period of time. In contrast to the fog dependent coastal loma vegetation which develops in winter, the vegetation in the studied area develops during a very short period of rainfall in summer. Thus, the establishment of the mainly ephemeral vegetation in the investigated area seems to be connected to the high water retention capacity of its substrate, a pumice soil. An unusual adaptation observed in several ephemeral species is the development of thickened roots. These are interpreted as a reservoir used to extend the growing season over a period that exceeds the rainy season by months.

Session 17

The nervous connection - Opisthobranch cephalic sensory organs and their evolution

*Sid Staubach

Institute for Ecology, Evolution and Diversity – Phylogeny and Systematics, J. W. Goethe-University, Siesmayerstraße 70, 60054 Frankfurt am Main, Germany, Staubach@bio.uni-frankfurt.de

The term cephalic sensory organ (CSO) is used for specialised structures in the head region of adult Opisthobranchia. These sensory organs show a high diversity in form and function, and the gross morphology of these organs differs considerably among taxa. They can be identified as cephalic shields, oral veils, Hancock's organs, lip organs, rhinophores or oral tentacles. Because of this extremely high diversity, the homology and the evolution of these organs have not been clarified yet. Our intention was to use neuroanatomical data sets in order to find putative homologous CSOs. Here I will present data about immunohistological and axonal tracing patterns and their applicability as morphological characters for the homologisation of structures. We confirmed earlier investigations that neurotransmitter content is often related to function. In contrast, axonal tracing patterns can be used to homologise nerves. Overall the aim of this study was to reconstruct the evolution of the CSOs of the Opisthobranchia, by projecting our neuroanatomical data sets onto a molecular phylogeny. Additionally I will show the utility of independent data sets, apart from classical morphology or molecular data, to clarify evolutionary questions in a phylogenetic context. These approaches will include immunhistochemistry, ontogeny, neuroanatomy, neurophylogeny and neuronal transcriptomes. Strengths and weaknesses of these methods will be discussed. Finally I will give an outlook about the utility of neurobiological methods in a broader sense.

Session 19

Molecular characterisation of Macaronesian pleurocarpous mosses

Michael Stech[1], Manuela Sim-Sim[2], Olaf Werner[3], Rosa M. Ros[3], M. Glória Esquível[4], Susana Fontinha[5], Juana M. Gonzalez-Mancebo[6], Jairo Patiño[6]

[1] Nationaal Herbarium Nederland, Universiteit Leiden branch, P.O. Box 9514, 2300 RA Leiden, The Netherlands, [2] Universidade de Lisboa, Faculdade de Ciências de Lisboa, DBV, Centro de Ecologia e Biologia Vegetal, C2, Campo Grande, 1749-016 Lisboa, Portugal, [3] Universidad de Murcia, Facultad de Biología, Departamento de Biología Vegetal, Botánica, 30100 Murcia, Spain, [4] Centro de Botânica Aplicada à Agricultura, ISA, 1349-017 Lisboa, Portugal, [5] Centro de Estudos da Macaronésia, Serviço do Parque Natural da Madeira, Quinta do Bom Sucesso, 9050-251 Funchal, Madeira, Portugal, [6] Universidad de La Laguna, Dpto. Biología Vegetal, Botánica, Astrofísico Francisco Sánchez, 38071 La Laguna, Tenerife, Islas Canarias, Spain

The Lauri-Macaronesian archipelagos (Azores, Canary Is., Madeira), situated in the Atlantic Ocean as a point of intersection between the tropics, North America and Europe, are well known for their remarkable biodiversity, including considerable numbers of endemic species. Within the pleurocarpous mosses of the order Hypnales, species endemic to Macaronesia are found, e.g., in *Echinodium* (*E. prolixum, E. renauldii, E. spinosum*), *Leucodon* (*L. canariensis, L. treleasei*), Thamnobryum (*T. fernandesii, T. rudolphianum*) and formerly also Platyhypnidium (*P. torrenticola*, recently synonymised with the widespread *P. riparioides*). In Macaronesia these genera are generally associated with the characteristic laurel forest (Laurisilva), however, they have different ecological preferences. *Echinodium* and *Leucodon* can be epiphytic or saxicolous; the former genus is largely confined to humid, shaded valleys or slopes, whereas the latter is more widespread and tolerates drier conditions. In contrast, *Platyhypnidium* and *Thamnobryum* are confined to aquatic habitats. In the present study, phylogenetic analyses in these four genera, based on DNA sequences (chloroplast regions and nuclear ribosomal ITS) and partly also AFLP (amplified fragment length polymorphism) fingerprinting, are compared. Results from the molecular analyses are discussed with respect to the taxonomic status, systematic relationships and phytogeographic affinities of the endemics and further species occurring on the Macaronesian archipelagos. Furthermore, molecular divergences are compared with the morphological variation and different ecological preferences of these taxa.

Session 21

Salamander phylogeny and paedomorphosis - How to detect conflict between partition?

Torsten H. Struck

Department of Zoology, Faculty of Biology, University of Osnabrück, Germany

The retention of ancestral juvenile characters by adult stages of descendants is called paedomorphosis. However, this process can mislead phylogenetic analyses based on morphological data, even in combination with molecular data, because the assessment if a character is primary absent or secondary lost is difficult. Thus, the detection of incongruence between morphological and molecular data is necessary to investigate the reliability of simultaneous analyses. Different methods have been proposed to detect data congruence or incongruence. Five of them (PABA, PBS, NDI, LILD, DRI) were used to assess incongruence between morphological and molecular data in a case study addressing salamander phylogeny, which comprises several supposedly paedomorphic taxa. Therefore, previously published data sets were compiled. Furthermore, two strategies ameliorating effects of paedomorphosis on phylogenetic studies were tested using a statistical rigor. Additionally, efficiency of the different methods to assess incongruence was analyzed using this empirical data set. Finally, a test statistic is presented for all these methods except DRI.

The addition of morphological data to molecular data results in both different positions of three of the four paedomorphic taxa and strong incongruence, but treating the morphological data using different strategies ameliorating the negative impact of paedomorphosis revokes these changes and minimizes the conflict. Of these strategies the strategy to just exclude paedomorphic character traits seem to be most beneficial. Of the three molecular partitions analyzed the RAG1 partition seems to be the most suitable to resolve deep salamander phylogeny. The rRNA and mtDNA partitions are either too conserved or too variable, respectively. The exploration of different methods to detect incongruence is preferable. However, of the different methods to detect incongruence the NDI and PABA approaches are more conservative in the indication of incongruence than LILD and PBS and NDI is computational less extensive than PABA.

Public lecture, Thursday

The importance of systematic biology in a modernizing world

Tod F. Stuessy

Department of Systematic and Evolutionary Botany, Institute of Botany, University of Vienna, Rennweg 14, 1030 Vienna, Austria, tod.stuessy@univie.ac.at

Systematics is fundamental for all aspects of human life. Contributions include the production of classifications, understanding of processes of evolution at the populational level, and the revealing of long-term phylogenetic trends. These play important roles, such as in the formation of storage and retrieval systems of information about organisms and our ability to predict unseen aspects about them, the understanding of dynamics of evolutionary change for improvement of domestic plants and animals, and the portrayal of long-term evolutionary change that provides a more informed world view and suggests routes for better management of biological resources. Human culture is modernizing rapidly through increased generation of knowledge, more rapid electronic processing of all information, worldwide communication including instantaneous sharing of international news, increase in number of multinational businesses, a more precise spatial awareness due to satellite geographic positioning systems, emergence of English as an international language, and the accumulation of immense global wealth. Regional conflicts, poverty, and disease, however, continue to subtract from the positive gains of modernization. To provide classifications, understanding of processes of evolution, and reconstructions of phylogeny for all life, the systematic biology community must first finish an inventory using all available means. To speed monographic and nomenclatural work, we need digitization of all types world-wide, plus online registration for all newly published names and combinations. We need to give back to society more precise means for identifying taxa, which is our major service function. We also need to offer more information about organisms and their relationships on the Internet, such as presently advocated by the *Encyclopedia of Life* project. In the face of an ever-increasing human population and its associated activities, immediate attention to these priorities must be given. Large-scale "Big Systematics" projects are urgently needed.

Session 9

Nucleotide polymorphism and selective sweeps in natural populations of the bryophyte *Sphagnum fimbriatum*

Péter Szövényi[1], Zsófia Hock[2], A. Jonathan Shaw[3], Helena Korpelainen[4]

[1] Biology Department, Duke University, Durham, North-Carolina, USA, 27708, [2] Department of Plant Systematics and Ecology, Eötvös Loránd University, 1117 Budapest, Hungary, [3] Institute of Systematic Botany, University of Zurich, Zurich, 8008, Switzerland, [4] Department of Applied Biology, University of Helsinki, Helsinki, Box 27, Finland

Peat mosses represent an ancient group of mosses and serve as a model system for evolutionary (speciation, hybridization, polyploidization), ecological and systematic research in bryophytes. The focal species of this study, *Sphagnum fimbriatum*, is a monoicous peat moss species with frequent sporophyte production over its range. Interestingly, although both experimental and theoretical considerations support the existence of efficient spore dispersal in peat mosses previous findings based on molecular data appear to contradict these observations in *S. fimbriatum*. The species's genetic variability appears to show strong geographic structuring. Genetic clades based on chloroplast sequence data are only slightly overlapping and largely correspond to the natural discontinuity in the distribution of the species. To understand how the unexpectedly strong geographic structuring of genotypes is maintained in spite of presumably efficient spore dispersal contribution of other factors in particular breeding system, natural selection and demography on the genome evolution of the species need to be resolved. To achieve this, we studied the population structure of *Sphagnum fimbriatum* using microsatellite and nucleotide polymorphism data along a North-South gradient in Europe for the first time in details.

To test whether natural selection can explain this contradictory pattern of genetic variation we used parameter estimates based on 14 microsatellite markers, nucleotide polymorphisms of two loci (GapC and Rpb2) and conducted coalescent simulations. Our data give solid evidence that within-population nucleotide diversity of the species is relatively high which is maintained by the cooccurrence but very rare cross fertilization among genetically diverged lineages in natural populations. Most importantly, we show that the polymorphism of the GapC gene has been shaped by a selective sweep which may explain the paradoxical pattern of strong genetic population structure in spite of effective among-population migration rates. These observations indicate effective gametophytic selection in haploids and point to the fact that phylogeographic history may be strongly dependent on the loci under consideration. Selective sweeps during the colonization of newly available environments may be especially important in organisms like bryophytes, many of which have numerous spores and good colonization ability. Our study suggests that in spite of previous predictions, non-random assortment of genotypes may exist even in the presence of effective migration in haploid organisms.

Session 9

Multiple origin and wide dispersal of northwest European *Salicornia* "species"

*Patrick Teege, Alexander Köhl, Gudrun Kadereit

Institut für Spezielle Botanik und Botanischer Garten, Johannes Gutenberg-Universität, 55099 Mainz, Germany

Along the coasts of NW Europe two different tetraploid "species" of *Salicornia* are currently recognized. These are the two lower marsh species *S. procumbens* Sm. and *S. stricta* Dumort. They grow in sympatry but are sorted along a gradient of inundation time, albeit with overlapping ranges. Morphological differentiation between *S. procumbens* and *S. stricta* is difficult due to the paucity of clear diagnostic characters. They are mainly distinguished by habit and inflorescence length. External and Internal Transscribed Spacer (ETS and ITS) sequences show no sequence differentiation between the two "species".

A reciprocal transplantation experiment in the inundation gradient revealed that both "species" retain their morphological characteristics and show adaptive differentiation with best performance in their respective native habitats.

AFLP and microsatellite analyses of 40 samples from the North Sea coasts of Germany and Great Britain and the Atlantic coast of France did neither resolve *S. procumbens* and *S. stricta* as homogenous clusters nor did they reveal any clear geographical pattern. Instead, these results show that the two "species" are scattered across several genetic clusters and that genetic clusters are widely distributed. From this we conclude that *S. procumbens* and *S. stricta* in NW Europe are best interpreted as ecotypes which originated repeatedly in adaptation to similar environmental conditions and which disperse easily and widely. Identity of sympatrically growing ecotypes is secured by their reproductive biology. Very high levels of inbreeding and low levels of outcrossing are demonstrated by observational (homogamy, low vitality of pollen when exposed to air), experimental (bagging) and microsatellite (progeny analysis) evidence.

Plenary session III

MADS about tulips, orchids and grasses: evolutionary developmental genetics of floral organ identity in monocots

Günter Theißen, Hannelore Simon, Susanne Nolden, Mariana Mondragón-Palomino

Lehrstuhl für Genetik, Friedrich-Schiller-Universität Jena, Germany, guenter.theissen@uni-jena.de

During recent years a great deal has been learned about how the identity of floral organs is specified by homeotic selector genes in eudicotyledonous model plants such as *Antirrhinum* and *Arabidopsis*. The novel insights have been pulled together in two major hypotheses, termed the 'ABC model' and the 'floral quartet model' (Theißen and Saedler, 2001). Key players in these models are MIKC-type MADS-box genes and the transcription factors encoded by them, respectively. Here we show as to how these models are now guiding investigations that help to answer long-standing questions about the diversification of the angiosperm flower. Studies in grasses such as maize (*Zea*) and rice (*Oryza*) revealed that at least some classes of floral homeotic genes have been highly conserved throughout evolution, even though the organs they specify have been modified dramatically during the early evolution of grasses (e.g., petaloid organs evolved into lodicules). Studies in tulips (*Tulipa*) revealed that heterotopic expression of *DEFICIENS*-like (*DEF*-like) and *GLOBOSA*-like class B floral homeotic genes conferring petaloidy to outer whorl organs contributed to the diversification of the angiosperm flower (Kanno. et al., 2003). Orchids have unique flowers involving three types of perianth organs: outer tepals, lateral inner tepals, and a lip. Gene expression studies and mutant analyses indicate that the identities of the different organs of the orchid perianth are specified by the combinatorial interaction of four different *DEF*-like MADS-box genes (Mondragón-Palomino and Theißen, 2008). Phylogeny reconstruction involving *DEF*-like MADS-box genes from diverse orchid species indicate that the four paralogous types of *DEF*-like genes were generated by two rounds of gene duplications during early orchid evolution, thus providing a rational means to reconstruct the evolutionary origin of the orchid flower. Several lines of evidence suggest that these gene duplicates underwent a complex series of sub- and neo-functionalization events that modularized the floral perianth so that the different kinds of tepals could evolve individually in response to selection, e.g. by pollinators. Our scenario suggests general molecular mechanisms by which gene duplication, sub-functionalization, modularization and neo-functionalization contribute to the evolutionary origin of morphological novelties.

Session 2

Evolving to the peaks: phylogeny and habitat evolution in the European endemic *Phyteuma* (Campanulaceae)

Mike Thiv[1], Michael Barfuß[2], Gerald Schneeweiss[3]

[1] Botany Department, Staatliches Museum für Naturkunde Stuttgart, Rosenstein 1, 70191 Stuttgart, Germany, [2] Department of Systematic and Evolutionary Botany, University of Vienna, Rennweg 14, 1030 Wien, Austria, [3] Department of Biogeography, University of Vienna, Rennweg 14, 1030 Wien, Austria

The rampions (*Phyteuma*, Campanulaceae) comprise 28 species of exclusively European distribution of which many are restricted to mountain areas of the Alps, Pyrenees, Balkan Peninsula and Carpathians. We investigated the inter-specific phylogenetic relationships of the genus using nuclear and plastid DNA sequence data of nearly all currently recognised species. *Phyteuma*, which is sister to *Physoplexis*, an endemic of the SE Alps, consists of two major clades. The first, characterised by globose inflorescences usually subtended by an involucrum (capitula), includes many alpine species (e.g., *P. hemishaericum, P. globulariifolium*), but also the widespread *P. orbiculare* group. The second clade comprises largely non-alpine taxa with mostly ovoid or cylindrical inflorescences without involucrum (spikes; e.g., *P. spicatum, P. betonicifolium*). Evolution of several traits, in particular chromosome base number (x = 10, 11, 12, 13, 14) and habitat preferences, is assessed using maximum likelihood and Bayesian methods of ancestral character state reconstruction over a set of posterior trees both under a relaxed clock model (branch lengths thus directly reflecting time) and without a clock (branch lengths reflecting evolutionary change, i.e., the product of rate and time). The biogeographic history of the genus is analysed using ancestral area reconstructions and molecular dating.

Plenary session II

DNA profiling of insect communities: what can be learned about species and speciation?

Alfried P. Vogler

Imperial College London and Natural History Museum, London, UK, a.vogler@nhm.ac.uk

Large-scale DNA sequencing of multi-species communities provides new opportunities for the study of species and speciation. These analyses show that species are recognisable in the space of sequence variation as groups of close relatives cleanly separated from other such groups. These findings have resulted in recent proposals to use threshold values of sequence divergence to distinguish intra- and inter-species variation (the 'barcoding gap'). How universal is this 'gap' and its magnitude among various groups of insects, and what are tehe evolutionary causes of this clear separation? Do these findings imply that 'all species are equal', i.e. do most species show similar features of within-species nucleotide variation, depth of coalescence, and divergence from others? Data to assess patterns of variation across species boundaries in multi-species lineages and entire local communities are now becoming available. We here use insect communities from various biogeographic regions and unrelated insect groups to establish generalities of species differentiation. We also perform comparative analysis of lineages with different dispersal strategies to infer the underlying population-level processes that generate these highly structured patterns.

Session 7

On historical kinds

Lars Vogt

Freie Universität Berlin, Institut für Biologie, Chemie, Pharmazie, Systematics and Evolution of Animals, Königin-Luise-Str. 1-3, 14195 Berlin, Germany

I will explain what a) the class of objects with a name beginning with 'A', b) the class of objects that I believe are red, c) the class of objects that are toxic, d) the class of human individuals that possess the disposition to completely metabolize alcohol, and e) the class of all human beings or the class of all copies of a single issue of a daily newspaper have in common and what distinguishes them qualitatively. I will explain why some objects may belong to all five types of classes at the same time and why this does not cause inconsistency.

I will discuss implications from a general definition of 'class', in order to point out conceptual differences between artificial, typological and natural classes. I will show that it is necessary to define 'naturalness' with respect to causality - elements of a natural class are defined by identity of their causal relations. Therewith, all natural classes possess explanatory power, since the assumption of the existence of the respective type provides an explanation for the similarity of its elements. I discuss two possible types of natural classes: On the one hand *essentialist natural kinds*, which represent 'universal cause' classes that are defined in reference to causal dispositional properties; on the other hand *historical natural kinds*, which represent 'historical cause' classes that are defined in reference to a common historical origin of their elements from a particular sequence of causal processes. Finally, I will discuss the uniqueness of phylogenetic systematics as a natural classification of historical natural kinds whose unambiguous encaptic hierarchical order is the result of its historical nature.

Session 16

Global Information System data for evolutionary research: three case studies

Klaus Bernhard von Hagen, Erik Welk

Institute of Biology / Geobotany and Botanical Garden, Martin-Luther-University of Halle-Wittenberg, 06099 Halle, Germany

Global information system data (GIS) is a major new and relatively easy to handle data source to describe macroclimatical niches of species. Three case studies are discussed where GIS data helped to solve typical problems of plant evolution. 1) The standard model of speciation mainly involves allopatric differentiation potentially partly only because other models of speciation are harder to detect. Analysing a complete phylogeny of *Carlina* (Asteraceae) and macroclimatic niches of all 29 species it was quantified which relative role allopatric or ecological niche separation have played during diversification of a mediterranean genus. 2) The genus *Halenia* (Gentianaceae) colonized South America at least five times independently from Central America via long distance dispersal. A GIS analysis was applied to study whether the climatic conditions of the five source regions and the five regions colonized resemble each other, or whether establishment in certain areas was more likely due to chance. 3) An important problem for emerging homoploid hybrid species is backcrossing to parental taxa. Known examples for this mode of origin mostly involved an extreme niche shift in the new lineage which helped to avoid genetic contact with parental species. A GIS analysis showed that this seems to be different in the putative homoploid hybrid *Scabiosa columbaria* (Dipsacaceae) and possible reasons are discussed.

Session 19

Same environment, two taxa: the search for parallel patterns in the biogeography and evolution of freshwater shrimps and snails in ancient lakes of the Indonesian island Sulawesi

Kristina von Rintelen, Matthias Glaubrecht, Thomas von Rintelen

Museum für Naturkunde, Humboldt-Universität zu Berlin, Invalidenstrasse 43, 10115 Berlin, Germany, kristina.rintelen@museum.hu-berlin.de

Lacustrine radiations can contribute greatly to the understanding of evolutionary processes, in particular the origin of species diversity. The ancient lakes of Sulawesi, the Malili lake system and Lake Poso, offer the unique possibility to study parallel evolution at several levels. Both lake systems were never connected and provide very similar extrinsic conditions, and both host species flocks of two freshwater taxa, the shrimp *Caridina* (Decapoda: Atyidae) and the gastropod *Tylomelania* (Cerithioidea: Pachychilidae). This setting allows for the comparison of evolutionary patterns e.g. within the same taxon between the two lake systems, or among the two groups both within one lake system and between the lakes. The two taxa differ considerably in their intrinsic properties, such as size and mobility.

We used molecular phylogenies based on sequences of the mitochondrial 16S rRNA and cytochrome-oxidase-I (COI) genes to investigate the origin of both taxa in the lakes as well as patterns of speciation and character evolution. Both shrimps and snails were found to have radiated independently in the two lake systems, and both colonized the five lakes of the Malili lake system at least twice. The two taxa also each show a strong degree of habitat specialization among the lacustrine species which is correlated with differences in trophic morphology, i.e. the lake species exhibit phenotype-environment correlation, a hallmark of adaptive radiation. There are also major differences between the patterns found in shrimps and snails, e.g. in species number, age of the lacustrine species, and the degree of infra-lake differentiation. In addition to these taxon-specific patterns, each group showed considerable lake-specific differences despite the very similar setting and environmental conditions of both lake systems.

The data from the natural parallel 'radiation experiment' in the Malili lakes and Lake Poso in two very different taxa indicate that (i) the occurence of common evolutionary patterns between these taxa may allow to uncover pivotal general factors in adaptive radiation in ancient lakes, while (ii) the finding of different patterns in the two lake systems even in such closely related organisms despite almost identical environmental conditions suggests a cautionary approach to generalizations from single data sets.

Session 10

Photosynthesis in Sacoglossa (Opisthobranchia, Gastropoda)

Heike Wägele, Yvonne Grzymbowski

Institut für Evolutionsbiologie, Rheinische Friedrich-Wilhelms-Universität Bonn, An der Immenburg 1, 53121 Bonn, Germany

Several sacoglossan species are known to incorporate chloroplasts from their food organisms, mainly algae of the taxon Ulvophyceae. This ability was assumed to be a key character that might have enhanced speciation within Sacoglossan. Although a green colour is very typical for most of these slugs and therefore many species have been assumed to incorporate chloroplasts, the retention of chloroplasts with exploitation of photosynthetic products could be verified only for few species.

In this talk we will present new data on chloroplast retention, as well as feeding experiments in dependence of chloroplast retention, and summarize all available data on photosynthetic activity of slugs. By projecting these data, as well as their food organisms, on available phylogenies, we will try to explain the evolution of this phenomenon within the Sacoglossa.

Plenary session I

Deep Metazoan phylogeny: On the relevance of data quality

Wolfgang Wägele

Zoologisches Forschungsmuseum Alexander Koenig und Lehrstuhl für Spezielle Zoologie, Rheinische Friedrich-Wilhelms-Universität Bonn, Germany, w.waegele.zfmk@uni-bonn.de

Many hypothesis concerning early divergence and relationships between animal lineages contradict each other, a fact that is usually attributed to incomplete species sampling and insufficient modelling of molecular evolution. Mainstream publications on animal phylogeny ignore the relevance of the quality of raw data. In addition, theoretical work on tree-independent a priori evaluation of data is scarce. A further problem is that available background knowledge is disregarded. Examples from published literature and possible solutions are presented.

Session 18

Two spacers and a pseudogene: surprises of mitochondrial DNA evolution in the earliest land plants

*Ute Wahrmund, Milena Groth-Malonek, Volker Knoop

University Bonn, IZMB, AG Molekulare Evolution, Kirschallee 1, 53115 Bonn, Germany

Contrasting the frequent rearrangements of mitochondrial DNA in angiosperms we recently found at least two ancient gene clusters conserved between charophycean algae and bryophytes: the trnA-trnT-nad7 and the nad5-nad4-nad2 gene arrangements. Tracing the molecular evolution of the former gene cluster we observe for the first time a strikingly dynamic evolution of mtDNA in liverworts which includes the insertion of pseudogene fragments, the inversion and the subsequent independent losses of trnT in the two major liverwort clades. In contrast, the nad5-nad4-nad2 gene continuity remains stable not only in liverwort mtDNA but also in mosses and hornworts. Strikingly, however, the nad4-nad2 intergenic region is of exactly 24 bp in all bryophyte clades while the nad5-nad4 spacer shows extreme size expansions in liverworts and hornworts. Finally, we find that the nad7 gene is mysteriously conserved as a non-functional degenerated pseudogene in the mitochondrial genomes of marchantiid and jungermannid liverworts. However, nad7 is a functional and expressed gene, whose mRNA experiences frequent modification through RNA editing in *Haplomitrium mnioides* in strong support for a placement of this taxon in a sister group to all other liverworts and for a secondary loss of RNA editing activity in the marchantiid taxa.

Session 20

Perianth differentiation in the Santalales: what morphology can tell us about molecular phylogenetics

Livia Wanntorp[1], Louis P. Ronse De Craene[2]

[1] Swedish Museum of Natural Sciences, Box 50007 SE-104 05 Stockholm Sweden,
[2] Royal Botanic Garden Edinburgh, 20A Inverleith Row, Edinburgh EH3 5 LR, Scotland, U.K.

Santalales is a monophyletic group that includes eight taxa among which the well-known families Opiliaceae, Loranthaceae, Santalaceae, and the paraphyletic Olacaceae can be found. The phylogenetic relationships between these taxa are yet mostly unresolved greatly hindering the understanding of the evolution of flower morphology of Santalales and the different levels of parasitism that are present in the order. Although most members of Santalales, as those of the Santalaceae, have flowers provided with a uniseriate perianth of broad valvate tepals, Olacaceae s.l. has flowers with a biseriate perianth with differentiated sepals and petals. In flowers of the Loranthaceae the outer perianth whorl is either absent or it is replaced by a narrow rim, generally called "calyculus". The calyculus is often interpreted as a reduced calyx around the petals, although the nature of this structure is still largely discussed.

Studies on ontogeny and morphology are crucial for understanding the homology of flower organs and can be used together with molecular evidence to clarify phylogenetic relationships. The scenario of perianth evolution is highly complex in the Santalales, and the origin of a biseriate perianth in the order remains problematic. We here examine the evolution of the perianth in several species of Olacaceae, Loranthaceae and Santalaceae. According to our results, the petals of Olacaceae are probably homologous with the uniseriate perianth of Loranthaceae and Santalaceae. While sepals are present in Olacaceae, they have been lost in other clades and are replaced by a secondary structure derived from bracteoles. Our data correspond with a hypothesised phylogeny of Santalales and open up several questions about the origin of the biseriate perianth in the core eudicots.

Session 15

Eocene records of bee flies: palaeobiogeographic implications and remarks on the evolutionary history of Bombyliidae

Sonja Wedmann[1], David K. Yeates[2]

[1] Forschungsinstitut Senckenberg, Forschungsstation Grube Messel, Markstraße 35, 64409 Messel, Germany, [2] Schlinger Fellow, Australian National Insect Collection, CSIRO Entomology, PO Box 1700 Canberra, ACT 2601, Australia

First fossils of the bee fly genus *Comptosia* Macquart, 1840 (Diptera: Bombyliidae) from the middle Eocene Messel Pit, Germany, and the upper Eocene of Florissant, USA, are presented. Extant species of *Comptosia* are currently found only in Australia, and closely related taxa are known from southern South America. Previously, this group of genera have been regarded as Gondwanan disjuncts, having originated in Gondwana and remained on its fragments. The Eocene fossil representatives of *Comptosia* from the Holarctic region argue against this interpretation. Probably *Comptosia* and its relatives were more widespread in both northern and southern hemispheres in the Paleogene. Consequently, their present distribution is relictual rather than disjunct.

The larvae of most bombyliid species are parasitoids or hyperparasitoids of other insects. The fossil record of bee flies indicates a major radiation of bombyliids in the Upper Cretaceous or Lower Cenozoic. This is supported by the comparatively young geological age of many bombyliid host taxa. For example, this is the case for their lepidopteran hosts (e.g. Gelechiidae, Tortricidae or Noctuidae), the bees (e.g. Anthophoridae), and the grasshoppers (Acrididae) on whose eggs several taxa prey. An important factor driving the specialization of many bombyliid larvae on ground-dwelling hosts may have been avoidance of competition with tachinid flies and parasitic hymenopterans.

Session 14

Lazarus species or hybrid: the case of *Tortula mucronifolia* (Pottiaceae, Musci)

Olaf Werner, Rosa María Ros

Universidad de Murcia, Facultad de Biología, Departamento de Biología Vegetal (Botánica), Campus de Espinardo, 30100 Murcia, Spain

One of the principles of evolutionary Biology, Dollo´s Law, claims that complex traits never re-evolve. Modern molecular systematic treatments of the moss familiy Pottiaceae challenge this assumption, because complex sporophyte characteristics like the twisted peristome of 32 filamentous spiculose teeth distal to a basal menbrane seem to have evolved up to seven times independently. One possible explanation that has recently been given, is the assumption that the Pottiaceae are a Lazarus taxon in the sense that major developmental adaptive complexes are resurfacing in evolutionary time contrary to Dollo´s Law. The proposed mechanism includes gene silencing and posterior reactivation of the silenced genes. While this mechanism seems not to pose theoretical problems during relative short times in terms of evolution (0.5 – 6 million years), longer time periods would tend to destroy the genetical information by the accumulation of mutations in the absence of evolutionary pressure to maintain it.

In the present study, we present the case of *Tortula mucronifolia*. The sporophyte characteristics and most gametophytic traits suggest that this species is closely related to *T. inermis*, *T. subulata* and some other similar species. Like *T. mucronifolia*, all these species have a well-developed sporophyte with the typical twisted peristome teeth. Nevertheless, a recent publication based on nuclear ITS sequences placed *T. mucronifolia* near *T. protobryoides*, a species (within the genus *Tortula*) only distantly related and situated by many authors in the genus Pottia and characterized by a reduced sporophyte morphology. Here we present combined nuclear ITS and chloroplast DNA sequence data that suggest that *T. mucronifolia* is the result of an ancient hybridization event of two not closely related species. The data suggest that hybrids are relatively frequent within and between *Tortula* and other related genera and that hybridization rather than an obscure mechanism of gene-silencing and reativation might be the better explanation for the resurfacing of complex evolutionary traits in the Pottiaceae.

Session 18

Re-organisation(s) of the nuclear ribosomal DNA (nrDNA) in land plants and its phylogenetic implications

*Susann Wicke [1,3], Andrea Costa [2], Franziska Bauer [1], Jèsus Muñoz [2], Christoph Neinhuis [1] Dietmar Quandt [1]

[1] Technische Universität Dresden, Germany, dietmar.quandt@tu-dresden.de [2] Real Jardìn Botànico Madrid (CSIC), Spain, [3] current address: Universität Wien, Dept. Biogeographie, Austria

Until recently, it has been generally agreed that the nuclear ribosomal DNA (nrDNA) in land plants is uniformly organized in tandem arrays with up to several hundred copies. Typically, each repeat unit (45S repeat) harbours a transcription unit containing the genes for the small ribosomal subunit (SSU), the 5.8S rRNA and the large ribosomal subunit (LSU) separated by the internal transcribed spacers (ITS). Controlling elements are situated in the intergenic spacers (IGS) that separate the transcription units. The gene encoding the 5S ribosomal RNA is located elsewhere forming a separate cluster. However, an alternative organisation of the nrDNA has been reported for a liverwort and a moss. In both cases, the 5S rDNA has been found co-localized with the 45S repeat, i.e. inserted into the IGS, similar to a number of other eukaryotic organisms such as cryptomonads, fungi and various protozoans. In the present study, representatives of all major land plant lineages were screened for a co-localisation of the 45S/5S rDNA using a PCR and sequencing approach. We could clearly show that the physical linkage of all nuclear ribosomal RNA genes is not unique to Marchantia and Funaria, but a common feature of all bryophyte as well as various fern lineages. Analyses including charophytes indicate that the co-localisation represents the ancestral state of green plants. Phylogenetic implications and different transpositioning theories are discussed based on circumstantial analyses of the structural organisation of the intergenic spacer regions of both co-localized and unlinked nrDNA.

Plenary session III

Evolutionary conservation of developmental processes to infer phylogenetic relationships

Ernst A. Wimmer

Department of Developmental Biology, Johann-Friedrich-Blumenbach-Institute of Zoology and Anthropology, Georg-August-University Göttingen, GZMB, Justus-von-Liebig-Weg 11, 37077 Göttingen, Germany, ewimmer@uni-goettingen.de

To analyze the phylogenetic conservation and divergence of head development mechanisms, we isolate and functionally characterize head specific genes of two different arthropod species, the red flour beetle Tribolium castaneum and the marine amphipod crustacean Parhyale hawaiensis. On the one hand, we isolate homologs of identified head genes, determine their expression patterns and study their functions by double stranded RNA mediated gene silencing (RNA interference). On the other hand, we have started to identify head specific genes by a transposon mutagenesis screen in Tribolium. This allows us to isolate genes independent of their identification in Drosophila. In Tribolium and Parhyale, a functional head resembling adult head structures already forms during embryogenesis. Therefore, analyzing head development in these two species is advantageous to an analysis in Drosophila, where embryogenesis ends with a phylogenetically derived acephalic larva, which obstructs the analysis of head structures and suggests that the underlying mechanisms might be of adapted character. A first comparison of head-gap-gene functions indicates that the genetic circuitry driving metamerization and segment specification in the insect head has experienced dramatic changes between Drosophila and Tribolium. A comparative functional analysis of head development processes in a series of differently related arthropod species will help us to determine which mechanisms are evolutionary conserved and which mechanisms have undergone group-specific environmental adaptations or were generated anew. Since head structures of insects and crustaceans are easily comparable, the comparative analysis will on the one hand allow us to draw conclusions on the evolution of head development over a time period of about 450 million years, and on the other hand potentially help us to clarify phylogenetic relationships.

Session 2

Phylogenetic analysis of Rosids using fast evolving and non-coding chloroplast markers

Andreas Worberg[1], Dietmar Quandt[2], Nadja Korotkova[1], Thomas Borsch[3]

[1] Rheinische Friedrich-Wilhelms-Universität Bonn, Nees-Institut für Biodiversität der Pflanzen, Meckenheimer Allee 170, Bonn, 53115, Germany, [2] Dresden University of Technology, Institute of Botany, Plant Phylogenetics & Phylogenomics Group, Dresden, 01062, Germany, [3] Institut für Biologie und Umweltwissenschaften, Universität Oldenburg, Oldenburg, 26111, Germany

The Rosid Clade comprises about 25% of flowering plant diversity with more than 70,000 species in 140 families and 14 orders. Although two major subclades within rosids, the malvids and fabids, are supported by various molecular studies, there are still many open questions regarding the phylogeny of rosids. We applied sequence data of the rapidly evolving matK gene, the group II trnK intron, the group I trnL intron and the trnL-F spacer, covering most rosid families with an outgroup of early branching eudicots. The dataset comprised ~6,000 positions of aligned sequence plus a separate binary indel matrix. Like in datasets of these markers for other major clades of angiosperms, sequence alignment was reliable when certain mutational hotspots were excluded. These mutational hotspots are located in terminal parts of stem-loop regions P6 and P8 of the group I intron and in domains I and IV of the group II intron. The trees obtained represent the so far best resolved and statistically supported hypothesis on rosid relationships. Our study yielded increased support for example for a Oxalidales plus Celastrales clade as sister to Malpighiales; for a Brassicales plus Malvales clade that is sister to Sapindales (all three form the malvids); or for a position of *Tapiscia* sister to the Brassicales-Malvales clade, and provides evidence for positioning of yet unplaced families.

Session 10

Classification and evolution of the genus *Eryngium* (Apiaceae-Saniculoideae): results of morphological and fruit anatomical studies

Arno Wörz, Heike Diekmann

Staatliches Museum für Naturkunde, Rosenstein 1, 70191 Stuttgart, Germany

Eryngium L. comprises about 250 species growing in W-Eurasia, North Africa, and North and South America. The most recent overall revision of this genus dates back nearly 100 years. In this paper, a new classification is presented based on morphological and fruit anatomical results and on chromosome numbers. The genus is divided into two great lineages: (1) an Old Wold subgenus with palmate structured basal leaves and dorsal-lateral vittae in fruit cross-section, and (2) 3-4 New World subgenera with undivided parallel to arcuate veined or pinnate basal leaves and dorsal-ventral vittae. A further group has vittae located in the ribs of the fruits. Its relationship is not finally cleared, but it probably belongs to the Old World lineage. The classification of the New World subgenera is discussed comparing classical and molecular results. The fruit anatomical results may support an earlier discussed paraphyly of the genus: The locations of the vittae in the fruits of the African genus *Alepidea* resemble those in the fruits of the New World *Eryngium* lineage, whereas the fruits of the Eurasian genera *Astrantia* and *Actinolema* are much more similar to the Old World subgenus *Eryngium*. A survey of the chromosome numbers indicates two large radiations of polyploids in the New World. Diploids dominate in the Old World and in one New World group (subg. *Foetida*). The results as a whole suggest an Old World origin of the genus, as a few basal species of the otherwise New World subgenus *Semiqauatica* occur in the Western Mediterranean. The migration to the New World probably occurred by long range dispersal followed by an intensive recent radiation.

Session 8

Homeoboxes in tardigrades: a PCR-based survey of Milnesium tardigradum

*Juliane Zantke, Gerhard Steiner

Molecular Phylogenetics, Dept. of Evolutionary Biology, University of Vienna, Althanstrasse 14, 1090 Vienna, Austria

Homeobox genes are regulatory genes that play important roles in embryonic and post-embryonic pattern formation and cell-fate specification in all animals. Their expression patterns and regulatory functions are best documented in several model systems (e.g. Caenorhabditis, *Drosophila*, *Xenopus*). Among homeotic genes, the Hox genes and their role in anterior-posterior body axis differentiation are best known.

Although homeobox genes are well characterised for many arthropod taxa, comparatively little is known about them in tardigrades, one of their potential sister groups. Within the Ecdysozoa, tardigrades are placed at the base of the arthropod clade and can be interpreted as intermediate between cycloneuralians and arthropods. Thus, the structural and functional characterisation of tardigrade homeobox genes may provide insight into how gene functions have evolved among arthropods and their close relatives. We used polymerase chain reaction to recover the homeoboxes and flanking regions of six homeobox genes of the eutardigrade *Milnesium tardigradum*. Assignment of gene orthology was based on identification of conserved peptide motifs. Four of the homeoboxes belong to Hox genes: we identified the genes labial, Hox3 / zen, deformed, and abdominal-B that are orthologous to *Drosophila* Hox genes. Further we recovered the complete sequence of the segment polarity gene *engrailed* using Race-PCR. Additionally, we recovered a fragment of the pair-rule gene ortholog *even-skipped*. The evolutionary relationships of the recovered tardigrade genes to homeobox genes of other metazoans were determined by comparison of the inferred amino acid sequences of the homeodomains. Our results show close affinities to arthropod and ecdysozoan orthologs. The phylogenetic analyses place the tardigrade genes transitional between representatives of Panarthropoda and Cycloneuralia.

Session 11

Diatoms as bioindicators: watermonitoring via DNA barcoding

*Jonas Zimmermann[1], Birgit Gemeinholzer[1], Michael Kube[2], Richard Reinhardt[2], Regine Jahn[1]

[1]Botanischer Garten and Botanisches Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Str. 12, 14195 Berlin, [2] Max Planck Institute for Molecular Genetics, Ihnestraße 63-73, 14195 Berlin, Germany

Diatoms are single-celled eucaryotes, which are responsible for at least 20% of all global carbon fixations through photosynthesis. Within the microscopical algae the diatoms represent the sole group being present in all types of water bodies, and can therefore be applied for monitoring. They are suitable indicators to detect water quality and reconstruct paleoclimatic conditions. Due to their microscopic size, the discrimination on species level is quite difficult.

Thus, we are trying to establish a rapid standardized molecular identification tool via DNA barcoding. We want 1) to elucidate if cox1, as the conventional DNA barcoding locus, is also applicable for identifying diatom taxa and 2) provide a standardized barcoding protocol for this group of microalgae. In the end, its application on natural samples and the feasibility for a faster and more convenient statement about the quality as well as the quantity of diatom diversity and taxon composition should be tested.

To test quantifiability, we created an artificial mix of DNA from identified diatom taxa, amplified the fragments in a PCR with the aid of diatom specific primers, and cloned the received PCR products. Afterwards, a specific amount of clones were picked and sequenced with the BigDye Terminator technique. The obtained sequences were compared with our database and numerically evaluated. The question to be answered will be, if the qualitative retrieval-rate of the inserted diatom taxa is sufficient, and how far it is possible to quantify the taxa composition in mixed samples. At present we are reaching retrieval-rates of up to 80 % in artificial samples but quantification turns out to be rather challenging.

Abstracts - Posters

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Seed viability as a proxy for fitness in artificial interspecific hybrids of *Caiophora* (Loasaceae subfam. Loasoideae)

Michaela Achatz, Joana Schulz, Markus Ackermann, Maximilian Weigend

Institut für Biologie der Freien Universität Berlin - Systematische Botanik und Pflanzengeographie - Altensteinstraße 6, 14195 Berlin, Germany

Interspecific crossing experiments have been variously conducted in the past to infer the relationship between taxa. Usually the degree of interfertility (crossability) correlates with the closeness of dependency. Crosses between different species generally lead to no or low seed set and probably to less fertile offspring. To investigate relationships at species level, crossing experiments were carried out in *Caiophora*, a large Andean genus with strong morphological variation, but very low sequence divergence. Surprisingly, crosses between all taxa, both between closely allied and remotely related species, resulted in much higher or equal fruit sets and germination rates as intraspecific/intrapopulation crosses. This included morphologically divergent species groups, such as the *C. chuquitensis*- and *C. carduifolia* group. Crossability was measured as seed germination rates. Three hybrid generations were investigated (F1, F2, F3). The robust and fully fertile F1 had a much higher germination rate (95 %) and crossability index (3,52), than the parental taxa *C. deserticola* and *C. carduifolia* (44%/10%). The F2-progenies were less viable than the F1-seeds, but had similar germination rates (23%) to those of the parental taxa. 2/3 of the F3 generation showed again higher germination rates (34-71%). The results indicate that there are no barriers to interspecific hybridization even between morphologically highly divergent taxa. Moreover, especially the F1- and F3-generation show a strong heterosis effect. The high crossability indices between all species of *Caiophora* tested indicate that postmating reproductive isolation is anything but absent. Hybridization is likely wherever premating isolation breaks down, e.g. via habitat alteration. Moreover, hybrid speciation is a real possibility, since the hybrid offspring is highly viable and may swamp parental populations in few generations.

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The epipelic algal flora of Topçu Pond (Yozgat)

Cengiz Akköz[1], Sibel Güler[2]

[1] Biology Department, Faculty of Art and Science, Selcuk Universty, Campus/Konya, Turkey [2] Final Private School-Yozgat, Turkey

In this research, the composition and seasonal changes in the epipelic algae of the Topçu Pond within Yozgat borders and the physical and chemical characteristics of the pond water between July 2000-June 2001 have been periodically studied. As a result of the research in the Topçu Pond the existance and dominance of the species of Bacillariophyta gorup in all seasons has been found as 50. The species of Chlorophyta, Euglenophyta, Cyanophyta, and Chrysophyta groups were determined as 11, 7, 6 and 1, respectively. Seasonal rises has been dense in the beginning of spring and summer and in autumunn. The pond water has a slightly alkali characteristics.

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Where are the forest refugia on the Balkan Peninsula? Phylogeography of *Veronica chamaedrys*

Dirk C. Albach[1], *Stefanie Förster[1], Katharina Bardy[2]

[1] *Institut für Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Germany,*
[2] *Department of biogeography, Faculty center of botany, University of Vienna, Austria*

Veronica chamaedrys and its relatives are prominent species of forest vegetation, mainly along its edges, open places and clearings in the forest. Originally considered one species, the group of *V. chamaedrys*, consists of five species and three additional intraspecific taxa. Whereas *V. chamaedrys* s. str. is a widespread tetraploid, all others are diploid, occur in southern and south-central Europe and are mostly confined to small areas that have been suggested as Pleistocene refugia. In our study we use nuclear low-copy markers and AFLP fingerprints for taxa related to *Veronica chamaedrys*. Flow cytometry demonstrates that diploid plants are more widespread on the Balkan Peninsula than previously assumed. This opens the possibility that tetraploids originated more than once, which we test using our sequence and fingerprint datasets. Furthermore, the analyses reveal phylogeographic groups that could correspond to Pleistocene refugia.

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Phylogeographical analysis of land planarians (Platyhelminthes) from Brazil

*Marta Álvarez-Presas, Julio Rozas, Marta Riutort

Dpt. de Genètica, Facultat de Biologia, Universitat de Barcelona, Spain

The Brazilian Atlantic Forest boasts one of the highest diversity of animal and plant species in the world (40 percent of which are endemic). Yet, less than 10 percent of the forest remains. For its protection and recovery, the Brazilian government is introducing biological corridors, sketched based on fauna (mostly vertebrates) and flora inventories. In this project, using molecular techniques and advanced methods of phylogeography and molecular population genetics (methods based on the coalescent theory), it is proposed to analyse the function of one of these corridors with a new model taxon, land planarians. This group have been chosen because their physiological and dispersal limitations make of them an optimum group for biogeographic and phylogeographic studies applied to conservation biology. Land planarians have also been demonstrated to be good indicators of the state of their local habitat and environmental change. Three types of genetic regions, one of them mitochondrial (COI; cytocrome c oxidase subunit I) and two nuclear (ITS region and the ribosomal gene 18S), are going to be used. The COI region is going to be used in the DNA barcoding project for a quick identification of species. All the sequences will be used to obtain a detailed phylogeny for the species of the subfamily Geoplaninae present in the Atlantic forest, and the variation of COI and ITS regions will allow the phylogeographic and population genetics analyses. The main aim of our investigation project is to determine the fragmentation level of the communities and to distinguish the origin of this fragmentation, antropomorphic or due to natural factors (geological-environmental). In this communication preliminary results on the phylogeny of the species and first estimations on the genetic variability of populations for the genes selected are going to be presented and discussed.

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Phylogeography of a critically endangered tree species from Africa, *Hagenia abyssinica*, revealed by chloroplast microsatellites

*Taye Bekele Ayele, Oliver Gailing, Reiner Finkeldey

Department of Forest Genetics and Forest Tree Breeding, Georg-August University, Buesgenweg 2, 37077 Goettingen, Germany

Hagenia abyssinica (Bruce) J.F. Gmel (Rosaceae) is a wind-pollinated and wind-dispersed broad-leaved dioecious tree species native to Africa. It is a highly valued multipurpose tree species that is critically endangered within its distribution range. We investigated genetic diversity and differentiation at chloroplast microsatellites in 25 populations from the highlands of Ethiopia. Ten consensus chloroplast microsatellite primers (CCMPs) were tested, three of which were polymorphic. We screened 9-12 samples from each population and identified 6 haplotypes from the combination of the three loci as detected by fragment analysis. Homology of the three loci to the respective regions of the chloroplast genome was confirmed by sequencing. The haplotypes are assembled under two major clusters and four groups showing a clear pattern of congruence between their geographical distribution and genealogical relationships. A very high level of genetic variation among populations ($G_{ST} = 0.90$) suggested a restricted migration of seeds among regions, which is also reflected in the observed geographic structuring of haplotypes. Existence of natural barriers (mountains and long distances) to seed dispersal and/or demographic history of the species might account for the strong phylogeographic pattern. Contrarily, weak geographic structuring ($G_{ST} = 0.18$) was observed in *Cordia africana* (Boraginaceae), an endozoochorus tree that grows at lower altitudes than *Hagenia* in Ethiopia. The information from the distribution of haplotypes will be used to identify populations for in situ and ex situ conservation in Ethiopia. Furthermore, an analysis of amplified fragment length polymorphisms (AFLPs) in *Hagenia* is underway with an ultimate objective of developing a viable conservation strategy for the species.

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A phylogenetic study of *Lycium* (Solanaceae) in Iran based on sequences of nuclear ribosomal DNA

N. Azadi[1,2], V. Nazeri[1,4], A. N. Shoushtari[1,2], S. Kazempour Osaloo[3]

[1] Department of Biology, Faculty of Sciences, Shahid Bahonar University, Kerman, Iran, [2] International center for Sciences & High Technology and environmental sciences, [3] Department of Plant Biology, Faculty of Basic Sciences, Tarbiat Modares University, Tehran, Iran, [4] Department of Botany, Faculty of Horticultural sciences, University of Tehran, Iran

In recent years, there has been much interest in the phylogenetic relationships within the tribe Lycieae (Solanaceae), specially the genus *Lycium* L.. Because of sexual dimorphism in *Lycium*, its evolution is of special interest. Phylogenetic studies have mostly been based on South and North American species and some species in the Old World. This research presents a phylogentic analysis of 7 Iranian species and 26 species of New and Old World taxa, using nrDNA ITS1 and ITS2 sequences. The dataset included 93 phylogenetically informative nucleotide sites. The strict consensus tree revealed that the Old World (and Iranian) species are not monophyletic. The hybrid origin of *Lycium* * *sangelakii* Nazeri et. Azadi is confirmed.

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Exploring the potential of native plants in restoration projects

*Imran Ullah Azhar

Chand Bagh Institute Muridkai Shekhupura Road Lahore, Pakistan,
imran_ullah_cheema@hotmail.com

Biological invasion by alien species is now recognized as one of the major threats to native species and ecosystems, yet awareness of the problem is alarmingly low. *Parthenium hysterophorus* L., an alien invasive species, is spreading through out Pakistan. Worldwide it has been designated as one of the most troublesome weeds. Ever since this weed had become a menace in different parts of the world, several methods have been recommended in containing the growth of *P. hysterophorus*. However, none of these appear to be satisfactory, as each method suffered with one or the other limitations such as inefficiency, high cost, impracticability, polluting the environment, temporary relief etc. It was noticed in the field that *Euphorbia hirta* and *Lantana camara* are replacing *P. hysterophorus* gradually in patches. *Datura strumarium* was selected on basis of its known toxicity. Aqueous extract of all test plant species in different ratios were applied to check the germination and early growth of *P. hysterophorus*. *Euphorbia hirta* and *Lantana camara* at different concentrations showed least germination of *P. hysterophorus* and a significant gradual depression in fresh biomass accumulation as compared to *Datura strumarium*. All test plant species and *P. hysterophorus* are competitive weeds of wastelands. In view of health hazards and likely threats to biodiversity due to *P. hysterophorus*, it is probably advisable to promote *Euphorbia hirta* and *Datura strumarium* growth, which are comparatively harmless native plants in Parthenium infested areas.

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Endemics of *Barbarea* (Brassicaceae, Cruciferae) taxa in Turkey

Yavuz Bağci[1], Ahmet Savran[2]

[1] Selçuk University, Faculty of Arts and Sciences, Department of Biology, Campus, 42075, Selçuklu, Konya, Turkey, [2] Niğde University, Faculty of Arts and Sciences, Department of Biology, Niğde, Turkey, ybagci@selcuk.edu.tr, ybagci66@gmail.com

The genus *Barbarea* R. Br. (Brassicaceae) is represented with 11 species and 4 varieties in Turkey, 9 of them endemics. Various problems exist due to inadequate descriptions of endemic and non-endemic species, inadequate knowledge of geographic distribution, and invalid publication (type not indicated). *Barbarea auriculata* var. *auriculata*, collected once in 1890, was listed as Extinct (EX) in the Red Data Book of the Turkish Plants. A picture of this endemic taxon from Erzincan is given. In addition, *Barbarea platycarpa*, not sampled for a long time, was also collected and its picture is given. The endemic taxa of *Barbarea* of Turkey and their endangered categories are as follows; *Barbarea trichopoda* Hausskn. ex Bornm. (LR (nt)), *Barbarea auriculata* Hausskn. ex Bornm. var. auriculata (EX), *Barbarea auriculata* Hausskn. ex Bornm. var. *paludosa* Coode & Cullen (CR), *Barbarea lutea* Cullen & Coode (EN), *Barbarea platycarpa* Hausskn. ex Bornm. (DD), *Barbarea integrifolia* DC (EN), *Barbarea minor* C. Koch var. *robusta* Cullen & Coode (LR (ıc)), *Barbarea minor* C. Koch var. *anfractuosa* Hartvig & Strid (EN), *Barbarea hedgeana* Kit Tan & Gemici (EN).

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Genetic structure in and among populations of the Southeast Asian tropical ant-plants of *Macaranga* (Euphorbiaceae)

*Christina Baier

Leibniz-Institute of Plant Genetics and Crop Research (IPK), 06466 Gatersleben, Germany

The genus *Macaranga* Thou. consists of about 300 shrub and tree species distributed from tropical West Africa to some Pacific islands in the east. Within the Southeast Asian sections of the genus a wide variety of ant-plant mutualisms exists ranging from the attraction of opportunistic ants to obligate myrmecophytism. Obligate myrmecophytes should be poor colonizers, as they always have to co-disperse with their ants, which should promote geographic isolation ultimately resulting in separate species. Three of the Southeast Asian Macaranga sections contain obligate myrmecophytes. While two of these sections show all signs of a rapid and relatively recent radiation in the myrmecophytes, in section *Winklerianae* (two species) no indications for an ongoing radiation could be found. We here compare population genetic parameters of *M. winkleri*, (obligate myrmecophyte of the non-radiating section) and *M. tanarius* (non-myrmecophyte) with myrmecophytes and non-myrmecophytes of the two radiated Macaranga sections, using chloroplast and nuclear microsatellite markers. First data from *M. tanarius* (non-myrmecophyte) and *M. winkleri* (myrmecophyte) indicate high genetic diversity within populations, but low differentiation among populations. So far, no obvious differences in population genetic parameters became apparent between these myrmecophyte and non-myrmecophytic species, which indicates that the populations of both species are effectively connected and form therefore a metapopulation. Although *M. winkleri* always has to co-disperse with their specific ants, primary forest is not a migration barrier for the species, whereas for *M. tanarius* it is. This might counterbalance the differences expected between these two species. In the next step we will compare these data with population genetic parameters of the obligate myrmecophytes of the rapidly radiating species groups. A more pronounced genetic structuring among populations of these species would indicate restricted geneflow and, thus, a much stronger isolation of remote populations, which is the first prerequisite for allopatric speciation.

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Taxonomy of the genus *Fritillaria* s.l. (Liliaceae) in Iran

Gholamreza Bakhshi Khaniki

Department of Biology, Payame Noor University, P O Box 19395-4697, Tehran, Iran, bakhshi@pnu.ac.ir

Taxonomy of *Fritillaria* in Iran is presented, including a key, synonyms, descriptions, taxonomic comments, ecology, and citation of specimens examined. The following taxa of *Fritillaria* are recognized in Iran: *F. crassifolia* Boiss. & Huet ssp. *kurdica* (Boiss. & Noë) Rix, *F. poluninii* (Rix) Bakhshi Khaniki & K. Persson, *F. reuteri* Boiss., *F. straussii* Bornm., *F. kotschyana* Herbert spp. *kotschyana*, *F. olivieri* Baker, *F. caucasica* Adams, *F. assyriaca* Baker, *F. chlororhabdota* Bakhshi Khaniki, *F. zagrica* Stapf, *F. uva-vulpis* Rix, *F. atrolineata* Bakhshi Khaniki, *F. chlorantha* Hausskn. & Bornm., *F. persica* L., *F. imperialis* L., and *F. raddeana* Regel.

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Phylogeny and origin of the genus *Aquilegia* based on ITS, matK and trnS-G sequences

*Jesus M. Bastida, R. Jaime, P.J. Rey, J.M. Alcántara

Área de Ecología, Universidad de Jaén, E-23071 Jaén, Spain, jbastida@ujaen.es

Evolution in the genus *Aquilegia* (columbines, Ranunculaceae) has been widely accepted as an example of adaptive radiation. This observation is based on studies conducted on the North American columbines where a spectacular specialization in different pollinators, coupled with a morphological differentiation in floral traits (spur length and form, flower coloration, flower orientation) is present. Columbines are spread also through Eurasia where the magnitude of taxonomical diversity is similar to North America, despite of less diversity of potential pollinators and floral morphologies. In contrast to the poor floral differentiation, Eurasian columbines exhibit considerable habitat differentiation and inhabit forest to alpine environments with many species restricted to rocky places and narrow altitudinal ranges. The phylogenetic relationships between Eurasiatic and North American columbines remains unclear, and the ancestral condition of *A.ecalcarata* (unique spurless columbine) must be tested. Here, we present a phylogenetic analysis of the genus based on ITS, matK and trnS-G. Thirty one species of *Aquilegia* and two outgroups (*Thalictrum tuberosum, Isopyrum fumarioides*) were included. The data sets were analyzed by Bayesian inference. Based on a cpDNA tree we estimated the origin of columbines in relative time units; additionally, we analysed our results in a family level framework. We used the age of a fossil (Prototinomiscium vangerowii) of Menispermaceae dated in 91 myr ago as the minimum age for the split of Menispermaceae and Ranunculaceae. Divergence time estimates and chronograms were based on nonparametric rate smoothing (NPRS). The origin of the genus *Aquilegia* was estimated at 9 myrs. We confirmed the ancestral position of *A. ecalcarata*. Two main lineages were found, an Eurasiatic and an Asian-North American one. Each lineage seems to have followed different biogeographic migration routes from Asia. We confirmed that not only North American but also European columbines have underwent radiation although the motor of radiation seems to have been different.

001

BioSyst EU: a new federation to further biological systematics in Europe

Olaf R.P. Bininda-Emonds[1], Ulrike Aspöck[2], Richard M. Bateman[3], Daniel Burckhardt[4], Daniel F. Goujet[5], Regine Jahn[6], Angelika Preisfeld[7]

[1] AG Molekulare Systematik, Institut für Biologie und Umweltwissenschaften, Carl-von-Ossietzky Universität Oldenburg, 26111 Oldenburg, Germany, [2] Entomologische Abteilung, Naturhistorisches Museum Wien, 1010 Vienna, Austria, [3] Royal Botanic Gardens Kew, Richmond, Surrey, TW9 3DS, U.K., [4] Entomologie, Naturhistorisches Museum Basel, 4001 Basel, Switzerland, [5] Muséum National d'Histoire Naturelle, Département Histoire de la Terre, Paléobiodiversité et Paléoenvironnements Équipe Systématique, Recherche Informatique et Structuration des Cladogrammes, 75005 Paris, France, [6] Botanischer Garten und Botanisches Museum Berlin-Dahlem, Freie Universität Berlin, 14195 Berlin, Germany, [7] Bergische Universität Wuppertal, Biologie und Biologiedidaktik – Zoologie – 42097 Wuppertal, Germany

The need for systematic and evolutionary biology as the framework bridging all aspects of biological research is evident. The same interconnectedness has yet to develop among European scientists who actually do systematic biology. Although several scientific societies for biological systematics exist in Europe, they lack a unified initiative to promote their goals and activities within the Union. BioSyst EU (www.biosyst.eu) was thus founded at the Natural History Museum Vienna on Oct. 3, 2006 by representatives of the Gesellschaft für Biologische Systematik (D), Société Française de Systématique (F), Swiss Systematics Society (CH), and Systematics Association (UK); the Network of Biological Systematics Austria (A) joined in 2007. BioSyst EU functions as a loose federation of its member organizations, which remain independent and retain full control over their internal and national affairs. It provides a European platform to: 1. promote research, teaching, and training in all areas of systematic biology, including phylogenetic, taxonomic, and biodiversity research; 2. encourage collaboration and interchange among researchers, both individually and through their respective societies; 3. coordinate national and international efforts without infringing on the autonomy of the member societies; 4. support and represent researchers in countries lacking formal societies; and 5. represent systematic biology in the European parliament to increase its profile and funding. The first joint meeting of all 5 Societies will take place in Leiden (NL) in August 2009.

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The swapped symbiont: molecular identification of symbiotic dinoflagellates in the nudibranch seaslug *Phyllodesmium* (Nudibranchia; Mollusca)

*Sabrina Bleidißel[1], Heike Wägele[2], Gela Preisfeld[1]

[1] *Zoologie und Biologiedidaktik, Bergische Universität Wuppertal,Germany,* [2] *Zoologisches Forschungsmuseum Alexander König, Bonn, Germany*

The genus *Phyllodesmium* comprises seaslugs with long cerata emerging at their dorsal side that mainly feed on cnidarians. Cnidarians are known to contain cnidocytes to catch prey and defend themselves from predators. Moreover, some Cnidarians, the corals, host symbiotic dinoflagellates of the genus *Symbiodinium.* Based on molecular data *Symbiodinium* is divided into eight distinct clades, which are labelled from A to H. These clades are not randomly distributed among, corals, but are thought to follow a distribution pattern. *Phyllodesmium* feeds on polyps of the octocorallian genus *Xenia.* While feeding on Xenia, Phyllodesmium not only ingests the cnidocysts from *Xenia* without suffering any damage, but also ingest their symbiotic dinoflagellates. In contrast to the cnidocysts, the *Symbiodinium* cells are not digested but incorporated into the cerata tissue. As yet, there is only little information about the assumed symbiosis between *Phyllodesmium* and *Symbiodinium.* A first approach is to identify and compare the *Symbiodinium* clade composition of various *Phyllodesmium* species and the corresponding *Xenia* species. *Phyllodesmium* ingests all of *Xenia*'s symbionts, but to date nothing is known which of these clades are retained and incorporated or by which means a selection is performed. Due to the lack of suitable morphological characters, the *Symbiodinium* clades can only be distinguished on a molecular basis. Among those genes qualified for discriminating *Symbiodinium*-clades are several nuclear and plastid encoded genes well established for phylogenetic analyses. Preliminary results show that all *Phyllodesmium* species investigated so far incorporated *Symbiodinium* clade C, which could also be determined in *Xenia.*

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Using the tree of *Hypericum* to understand hypericin and hyperforin evolution

Thomas Borsch[1], Detlev Metzing[1], Kerstin Wilhelm[1], Andrija Smelcerovic[2], Jan Košuth[3], Michael Spiteller[2], Eva Čellárová[3]

[1] Plant Biodiversity and Evolution Group and Botanical Garden, Carl von Ossietzky-Universität Oldenburg, 26111 Oldenburg, Germany, [2] Institut für Umweltforschung, Universität Dortmund, Otto-Hahn-Straße 6, 44221 Dortmund, Germany, [3] Institute of Biology and Ecology, P. J. Šafárik University, Mánesova 23, 04154 Košice, Slovakia

The genus *Hypericum* comprises an estimated 400 species with a nearly worldwide distribution. *Hypericum perforatum* is a well known medical plant for its hypericin and hyprforin compounds. Phylogenetic analysis based on chloroplast petD intron and psbA-trnH spacer data, and including a third of the species plus representatives of Clusiaceae and Podostemaceae, reveal the monophyly of *Hypericum*. Combining both markers, a well resolved and statistically supported tree was obtained. Several sections are confirmed as monophyletic (e.g. section *Hypericum*), whereas others are polyphyletic (e.g. section *Ascyreia*). The same plants included in the molecular analysis were also analysed for secondary compounds. Species belonging to the first branches of the tree of *Hypericum* (e.g. sections *Myriandra*, *Spachium*) generally lack both hypericin and hyperforin. Present data indicate that hypericin biosynthesis arose in a common ancestor of a clade comprising sections *Graveolentia, Hirtella, Hypericum, Oligostema, Taeniocarpium* etc. However, the presence of hyperforin does not show such a clear pattern among the core *Hypericum* lineages. DNA sequence data, in particular of the psbA-trnH spacer, are furthermore evaluated for their utility to identify *Hypericum* samples (using "DNA barcodes").

002

International collaboration between taxonomists in All Taxa Biodiversity Inventories

Merijn M. Bos

Staatliches Naturkundemuseum Stuttgart, Rosenstein 1, 70191 Stuttgart, Germany, bos.smns@naturkundemuseum-bw.de

"*All Taxa Biodiversity Inventories*" (ATBIs) are long term efforts by large numbers of taxonomists to identify and document the total biodiversity of a given area in the most efficient way possible. The EU-funded "European Distributed Institute of Taxonomy" (EDIT: Work Package 7 "Applying Taxonomy to Conservation") organizes such inventories as concept for international taxonomic collaboration. The principal objectives are to enhance the relation between taxonomists and other users of taxonomic information, to accelerate the processes of taxonomic science through the worldwide web, and to overall transform taxonomy into an integrative science. In 2007 the first ATBI started in the French/Italian Mercantour and Alpi Marittime natural parks and during the first 3 months over 40 scientists from six EU countries visited the parks with support from EDIT. These participating scientists documented a broad spectrum of taxonomic groups that included conspicuous organisms such as butterflies and birds, but also less conspicuous groups such as diatoms, bryophytes (mosses and liverworts), tardigrades (water bears), and parasites of the park's mammal species. First results underline the high biodiversity of the region, which is, however, locally affected by impacts from anthropogenic activities, for example, high intensity of livestock grazing. Records and specimens collected in the framework of EDIT's ATBI activities are being made available online for participating researchers and conservation management to maximize reusability of the results. For 2008, field work will be scaled up in the Mercantour / Alpi Marittime parks involving specialists from many additional European institutions. Furthermore, the EDIT ATBI concept will be promoted for implementation in nature reserves elsewhere in Europe (e.g., the Slovakian Carpathians) as well as in biodiversity rich countries outside Europe. In the Mercantour / Alpi Marittime parks, the first EDIT "Summer School in Taxonomy" will take place in 2008 to which students can subscribe for courses in biodiversity field recording and collection techniques.

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Diversity and paleobiology of Eocene stick and leaf insects (Insecta: Phasmatodea)

Sven Bradler[1], Sonja Wedmann[2]

[1] Johann-Friedrich-Blumenbach-Institut für Zoologie und Anthropologie, Berliner Straße 28, 37073 Göttingen, Germany, sbradle@gwdg.de, [2] Forschungsinstitut Senckenberg, Forschungsstation Grube Messel, Markstraße 35, 64409 Messel, Germany, sonja.wedmann@senckenberg.de

Fossils of the insect order Phasmatodea (stick and leaf insects) are extremely rare worldwide. Exquisitely preserved fossils are reported from the 47-million-year-old deposits at Messel in Germany. These fossils include both twig and leaf-imitating forms and provide insight into the poorly understood origin of phasmids, indicating the early presence of the basic phenotypic diversity of extant crown groups. Stick insects possess elaborate primary and secondary defence mechanisms to avoid predation. Components of both mechanisms were already developed in the Eocene. The main primary defence is camouflage, e.g. angiosperm mimicry, which is enhanced by a special behaviour: catalepsy or adaptive stillness at daylight. This behaviour can be inferred from the morphology of fossil fore femora, which are curved at their base to form a notch for the head when the legs are longitudinally aligned during catalepsy. Extant stick insects regularly shed and regenerate lost legs. The long and slender legs of stick insects can easily be grasped by a predator or become entangled in their old exoskeleton during moulting. To avoid predation after detection and to survive abortive moults, numerous stick insects possess a well developed autotomy mechanism that separates the leg with the help of a special autotomy muscle at the boundary between trochanter and femur. The complex architecture of the cuticula of the trochanter stump of a fossil stick insect provides direct evidence that this capability was already present in the Eocene. Recent phylogenetic studies of Phasmatodea have suggested multiple losses and possible regains of wings during stick insect evolution. The hypothesis of wing recurrence is highly debated, and the less parsimonious assumption of independent reduction events has been postulated. The evolution of legs and wings appears to be linked by resource allocation tradeoffs between leg generation and wing development. Individuals that regenerate lost legs experience negative effects on somatic growths, e.g. develop shorter wings. Our findings suggest that the advantage of regenerating legs was already present early in stick insect evolution and might have shaped macro-evolutionary patterns of phasmid phenotypes, viz. drove multiple evolutionary losses of wings.

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Reticulate evolution in *Suaeda* sect. *Brezia*

*Ronny Brandt[1], Kurt Weising[1], Helmut Freitag[1], Maria Lomonosova[2]

[1]*Plant Systematics & Morphology, Institute of Biology, University of Kassel, Germany*
[2]*Central Siberian Botanical Garden Novosibirsk, Russian Academy of Sciences, Russia*

In revising the hitherto vaguely circumscribed Eurasian *Suaeda corniculata* complex, two new species were detected (Lomonosova et al., in press): *S. kulundensis* and S. sibirica. Morphologically, *S. kulundensis* appears intermediate between *S. corniculata* (C.A. Mey.) Bunge s.str. and *S. salsa* (L.) Pall.. *Suaeda sibirica* combines characters of *S. corniculata* and *S. heteroptera* Kitag. but also shows characters of its own. Karyological investigations supported the hypothesis of a hybrid origin for both taxa, as the chromosome numbers of *S. kulundensis* ($2n = 72, 90$) appear as additions of *S. corniculata* ($2n = 36, 52$) and S. salsa ($2n = 36$). Likewise, *S. sibirica* ($2n = 72$) could have originated by alloploidy from *S. corniculata* and *S. heteroptera* ($2n = 18$). The new species are separated geographically, but are ± sympatric with their putative parents. Sequencing of the nuclear ITS region from almost all Eurasian species of sect. *Brezia* has confirmed earlier results that these species form three well-separated lineages. The two new species together with *S. salsa* and *S. heteroptera* belong to the *S. salsa/maritima* ITS clade, with *S. kulundensis* being almost indistinguishable from *S. salsa*, and *S. sibirica* placed nearer to *S. heteroptera*. *Suaeda corniculata* is placed far away as the core species of the *S. corniculata* ITS clade. Phylogenetic trees based on intergenic chloroplast sequences likewise exhibit three clades, however, with differing distribution of species. Both new species have chloroplasts of the *S. corniculata* type, whereas *S. salsa* belongs to the *S. salsa/maritima* type, and *S. heteroptera* to the *S. crassifolia/heteroptera* type. These results strongly suggest that *S. kulundensis* and *S. sibirica* have originated by hybridization between members of the rather distinct *S. salsa/maritima* and the *S. corniculata* lineages. *Suaeda kulundensis* most likely represents an alloploid hybrid between the still extant species *S. salsa* and *S. corniculata*. In contrast, from *S. sibirica* only one parental species (*S. corniculata*) still exists. In conjunction with other data, our ongoing study suggests that speciation by reticulate evolution has played a major role in the diversification of Eurasian species of genus *Suaeda*, sect. *Brezia*.

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Steps towards understanding deep-sea evolution: molecular phylogeny of Desmosomatidae (Isopoda: Asellota)

Saskia Brix[1], Torben Riehl[2]

[1] DZMB-Senckenberg, DZMB Hamburg, Biozentrum Grindel, Martin-Luther-King Platz, 20146 Hamburg, Germany, sbrix@senckenberg.de, [2] ZIM, Uni Hamburg, AG Brandt, Biozentrum Grindel, Martin-Luther-King Platz, 20146 Hamburg, Germany, t.riehl@gmx.de

Isopoda (Crustacea) are one of the most important macrofaunal groups in the deep sea. A high number of undescribed species with a low abundance is typical for abyssal plains. During the DIVA-2 expedition with RV *Meteor* (March 2005, South East Atlantic Ocean) we obtained DNA of over 300 specimens assigned to about 38 species of Desmosomatidae Sars, 1897 and further species of related asellote families, e.g. Haploniscidae Hansen, 1916, Ischnomesidae Hansen, 1916 Macrostylidae Hansen, 1916 and Munnopsidae Lilljeborg, 1864. Macrostylidae and Munnopsidae are known to be sistertaxa of Desmosomatidae from previous studies. As a result of morphological phylogenic analysis, Nannoniscidae Hansen, 1916 were included in Desmosomatidae. The aim of the present study is to compare results of a molecular analysis with the morphological tree. The molecular phylogeny is based on three markers (18 S, 16 S, CO I). Nearly all species used for molecular analysis are new to science. This combination of descriptions and sequences, especially CO I, links our research with the Marine Barcode of Life initiative (MarBOL) and the *Census of Marine Life* (CoML) project CeDAMar (Census of the Diversity of Abyssal Marine life), aimed at describing 500 deep-sea species by 2010.

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Developmental conditions for terminal flower production in apioid umbellets

*Kester Bull-Hereñu, Regine Claßen-Bockhoff

Institut für Spezielle Botanik, Johannes Gutenberg-Universität, Mainz, Germany

Developmental studies in racemous inflorescences of more than 40 species widely distributed within the Eudicotyledonae resulted in the hypothesis that the production of terminal flowers depends on the size, shape and phyllotaxis of the apical meristem (AM). The Apiaceae-Apioideae are an adequate model system to test this hypothesis as their umbellets posses or lack a terminal flower. We report on umbellet development in *Chaerophyllum bulbosum* (terminal flower present), Pastinaca sativa (terminal flower lacking) and *Daucus carota* (both types of umbellets). For each species we measured the diameter of the AMs, counted the number of opposed contact parastichies (cp) and calculated the average size of the three youngest lateral primordia (n = 3-6). In *D. carota* (5,8 cp) and *C. bulbosum* (3,5 cp) the terminal flower is born from an AM of 60-75 µm in diameter. Umbellets of *D. carota* that lack a terminal flower have smaller meristems (≤ 45 µm) and show aborting lateral flower buds at the top of the inflorescence. They are also characterized by less flowers and a reduced phyllotaxis (3,5 cp). Although the AMs of *P. sativa* are relatively large (c. 60 µm), their umbellets remain open and produce aborting flowers as in *D. carota*. However, due to the large size of their lateral primordia, its phyllotaxis is very low (2,3 cp). We found that neither the diameter of the AM nor the phyllotaxis alone determine the production of a terminal flower, but that, instead, the size ratio between the AM and the lateral flower primordia appear to be an adequate parameter (ratio > 1.5: terminal flower production; ratio < 1.5: no terminal flower). The findings support our hypothesis that as a general principle a terminal flower may be unleashed directly from the AM as soon as a certain primordia size ratio is given by the time of flower inception. If this ratio is not achieved, the meristem will remain open.

081

Diversity of crustose lichens in continental Antarctica: Morphological and molecular studies on the genus *Lecidea* (Lecideaceae, Ascomycota) from Ross Sea region

*Ulrike Carl-Ruprecht[1], H. Thorsten Lumbsch[2], Georg Brunauer[1], Armin Hager[1], Gerald Hochschartner[3], T. G. Allan Green[4], Roman Türk[1]

[1] Department of Organismic Biology, University of Salzburg, Hellbrunnerstr. 34, 5020 Salzburg, Austria, [2] Department of Botany, The Field Museum, 1400 S, Lake Shore Drive, Chicago, IL 60605, USA, [3] University of St Andrews, School of Biology, Harold Mitchell Building, St Andrews, KY16 9TH, UK, [4] Biological Sciences, Waikato University, Hamilton, New Zealand

Lecideoid lichens were collected along a north to south transect at five ecologically different locations in continental Antarctica (Cape Hallett, Taylor Valley, Granite Harbour - Botany Bay, Brown Hills - Darwin Glacier, Mt. Kyffin). Over 100 specimens were collected and classified to 17 species using microscopic, molecular and chemical methods. Included in this total were species from *Lecidea*, *Lecidella* and other Lecanoraceae. The specimens of the genus *Lecidea* (57) came from three localities (Taylor Valley, Botany Bay, Brown Hills). Phylogenetic analyses assigned these to three major groups supported by morphological and chemical characters. First, *Lecidea cancriformis* presents one well-supported group; second, *Lecidea* aff. *andersonii* splits into two separate clades; and the third strongly supported group consists of an undescribed species, provisionally named *Lecidea* UCR1.

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The `male flower´ in *Ricinus communis* – a pseudanthium?

Regine Claßen-Bockhoff, Herbert Frankenhäuser

Institut für Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Germany

Pseudanthia sensu Delpino (1889, 1892) are floral units that look like flowers but don't follow the organisation of a flower. Delpino concluded that these systems are `infiorescenze contratte´, i.e. extremely reduced inflorescences. They are thus exciting examples to study the flower-inflorescence boundary. In *Ricinus communis* (Euphorbiaceae-Acalyphoideae) the male flower is surrounded by five leaf structures and produces about 25 `stamen trees´ each bearing c.14 bithecal anthers. Ontogenetic studies reveal that five to eight primary primordia including a terminal one pass through five to six steps of synchronous subdivisions before the anthers appear. Unlike secondary polyandrous flowers, the numerous anthers in *Ricinus communis*

- Do not originate from only one subdivision of few primary primordia,
- are not produced in a centripetal, centrifugal or lateral sequence and
- are not restricted to lateral positions.

According to symmetry, position and differentiation in time they instead develop like densely aggregated and highly reduced flowers of an inflorescence. The interpretation of the male *Ricinus communis* flower as a pseudanthium is supported by the extremely reduced male flowers in the cyathia of the Euphorbiaceae-Euphorbioideae. However, it is also possible to maintain the interpretation of a flower if, then, interpreting the staminal tree as a branched cluster of microsporangia similar to known branched funiculi each bearing several to many ovules. In any case, the male flower of *Ricinus communis* does not fit easily into the actual concept of the angiosperm flower either being a pseudanthium instead of a flower or demanding a broader concept for the interpretation of the angiosperm stamen.

024

Ecological preferences of mites (Acari) in urban microhabitats in middle-size city

*Dawid Diduszko[1], Paweł Ręk[2]

[1] Department of Animal Taxonomy and Ecology, A. Mickiewicz University, Umultowska 89, 61-614 Poznań, Poland, dawyyyid@yahoo.com, [2] Department of Behavioural Ecology A. Mickiewicz University, Umultowska 89, 61-614 Poznań, Poland, rek@amu.edu.pl

230 moss samples (33 moss species) collected in five different locations in Poznań (western Poland) during June and November 2005 contained 18500 specimens of mites in three orders (*Mesostigmata* 635, *Oribatida* 15395, *Prostigmata* 2387). Additionally, species in seven families of *Prostigmata* were identified: *Eupodidae* (142), *Penthalodidea* (61), *Penthaleidae* (498), *Tydeidae* (712), *Bdellidae* (420), *Cunaxidae* (51), *Cryptognathidae* (179), *Stigmaeidae* (324). Mite preferences in urban moss microhabitats are poorly known and up to now such complex studies have not been carried out. These microhabitats can be inhabited by many different species of mites. Anthropogenic influence and varying environmental conditions including moss composition may determine the habitat preferences of these mites. Apart of systematic distinction, all reported mites were divided into predatory and non-predatory taxa. Predatory mites from *Bdellidae, Stigmaeidae* (*Prostigmata*) and *Mesostigmata* preferred the most common mosses in a particular microhabitat; in contrast non-predatory mites (*Prostigmata, Oribatida*) did not show such a preference. Moreover no relationship was found between plagiotropic (sideways-growing) and orthotropic (upright-growing) types of mosses and mite composition. The most important factors determining the frequency of mite taxa were alimentary preferences and the frequency of a particular moss species.

062

Minute and misunderstood: the systematic position of *Cima*, *Graphis* and *Larochella* (Mollusca, Gastropoda)

*Angela Dinapoli, Annette Klussmann-Kolb

Institute for Ecology, Evolution & Diversity - Phylogeny and Systematics, J. W. Goethe-University, Frankfurt am Main, Germany, a.dinapoli@bio.uni-frankfurt.de

The Gastropoda comprise a very diverse group of Molluscs exhibiting a vast array of morphological and ecological adaptations. The systematic position of many gastropod taxa has not been clarified yet. Groups traditionally assigned to the "Prosobranchia" are now considered to be "primitive" Heterobranchia such as Valvatoidea, Rissoelloidea and Pyramidelloidea. Our interest lies in the revelation of the phylogentic relationships of the Heterobranchia. The current study focuses on the enigmatic genera *Cima, Graphis* and *Larochella* formerly either assigned to the Caenogastropoda or the lower Heterobranchia. We conducted a molecular systematic study of more than 39 taxa using four different markers (nuclear 28S rRNA + 18S rRNA and mitochondrial 16S rRNA + COI). Phylogenetic hypotheses were inferred by using maximum parsimony, maximum likelihood and Bayesian approaches. *Bathymargarites symplector* (Vetigastropoda) was used as outgroup. All analyses show a clade comprising the genera *Cima*, *Graphis* and *Larochella* at the base of the Heterobranchia with a high statistical support. Based on our molecular data we strongly support the opinion of Warén 1993 that the Cimidae belong to the basal Heterobranchia. We also suggest to exclude the genera *Graphis* and *Larochella* from Caenogastropoda and to assign them to the lower heterobranchs. However, morphological studies are warranted which could reveal potential synapomorphies of the taxa in question and other Heterobranchia.

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Comparison of ITS regions of *Jurinea* (Asteraceae) taxa from Turkey

Bekir Doğan[1], Erdoğan E. Hakki[2], Ahmet Duran[3]

[1] Selçuk University, Education Faculty, Department of Science Education, Konya, Turkey,
[2] Selcuk University, Faculty of Agriculture, Department of Field Crops, Konya, Turkey,
[3] Selçuk University, Education Faculty, Department of Biology Education, Konya, Turkey

In this study the species of *Jurinea* Cass. (Asteraceae) occuring naturally in Turkey are compared in terms of their nuclear ribosomal ITS regions. 17 SE ve 26 SE primers are used to sequence the ITS regions. Sequence analyses are evaluated with Clustal X software and similarity ratios among the taxa are revealed based on the dendrogram.

190

Determination of phylogenetic relationships among the taxa of the genus *Johrenia* (Apiaceae) from Turkey based on molecular methods

Bekir Doğan[1], Ahmet Duran[2], Yavuz Bağci[3], Muhittin Dinç[2], Esra Martin[2], Özlem Çetin[2], Meryem Öztürk[2]

[1] Selçuk University, Education Faculty, Department of Science Education, Konya, Turkey,
[2] Selçuk University, Education Faculty, Department of Biology Education, Konya, Turkey,
[3] Selçuk University, Science and Arts Faculty, Department of Biology Education, Konya, Turkey

The genus *Johrenia* DC. is represented with nine taxa in Turkey; its center of diversity is in the Amanos and the Bolkar mountains. The genus is taxonomically complicated and an attempt has been made to solve the taxonomic problems using molecular analyses. In this study, the DNAs of the species which belong to the genus *Johrenia*, growing naturally in Turkey were isolated with the Easy Nucleic Acid Isolation Kit (OMEGA) and analyzed, using the Inter-Simple Sequence Repeat (ISSR) as DNA finger printing method. Phylogenetic relationship among the taxa are revealed with dendrogams prepared by NTSYSpc 2.1 software.

079

The metals contents in some wild edible *Tricholoma* (Tricholomataceae) taxa from Turkey

Hasan Hüseyin Doğan, Murad Aydın Şanda

Selcuk University, Science and Art Faculty, Biology Department, Campus, Konya, Turkey

The concentrations of lead, cadmium, manganase, copper, nickel, silver, chromium, talium, vanadium, boron, barium, cobalt,and inidium were analysed in wild edible Tricholoma (Fr.) Staude taxa [*T. orirubenis* Quél, *T. imbricatum* (Fr.) P. Kumm, *T. columbetta* (Fr.) P. Kumm, and *T. cedretorum* (Bon) A. Riva] from Turkey by ICP-AES equipment. The highest Ag, Mn, and Zn concentrations were determined as 1.27, 113.83 and, 106.12 mg.kg^{-1} in *T. orirubenis* respectively. The highest Al, Cd, Fe, and Ni concentrations were determined as 5138, 8.88, 3215, and 5.40 mg.kg^{-1} in *T. columbetta* respectively. The highest Cr concentration was determined as 35.36 mg.kg^{-1} in *T. cedretorum*. The Tl, V, B, Ba, Co, and In concentrations were not detected in our mushroom samples.

009

Phylogeny and evolution of glass sponges (Porifera: Hexactinellida)

*Martin Dohrmann, Dorte Janussen, Joachim Reitner, Allen G. Collins, Gert Wörheide

Courant Research Center Geobiology, Georg-August-Universität Göttingen, Goldschmidtstr. 3, 37077 Göttingen, Germany

Hexactinellida, one of the three traditionally recognized classes of Porifera, constitutes important components of the sessile benthos and can provide a major fraction of the biomass, especially in deeper waters. The group is known from the late Precambrian and no major modifications of the body plan have occurred since then. Their unique syncytial tissue organization and triaxonic spicule symmetry clearly indicate that glass sponges form a monophyletic group, whereas ideas about the internal phylogeny have been largely speculative so far. Here the first molecular phylogenetic study of internal relationships of Hexactinellida is presented, based on partitioned analysis of a combined 18S, 28S, and 16S rDNA dataset. Further, the performance of different RNA secondary structure-specific substitution models is evaluated on the basis of this dataset. The inferred phylogeny is in good agreement with the traditional classification, and/or a previous phylogenetic study based on morphology. This stands in contrast to the other two sponge classes (Demospongiae, Calcarea), and likely results from the greater number and variability of spicule types in glass sponges, allowing taxonomists to more readily discern natural groups. A close relationship of Hexactinellida to Demospongiae *sensu stricto* is highly supported whereas Homoscleromorpha (traditionally assigned to Demospongiae) appears as the sister group of Calcarea. Implications of these results for understanding poriferan evolution are discussed, and it is argued that—contrary to still widespread beliefs—there is virtually no evidence in favor of an early-branching position of Hexactinellida within Porifera or Metazoa. First results from divergence time estimations using relaxed molecular clock approaches are presented and discussed in light of the comparatively good fossil record of Hexactinellida.

047

The evolution of adult head structures and the phylogeny of Adephaga (Coleoptera, Insecta)

*Carina Dressler, Rolf G. Beutel

Institut für Spezielle Zoologie und Evolutionsbiologie, FSU Jena, Erbertstr. 1, 07743, Jena, Germany

The head morphology of adult representatives of aquatic, semiaquatic (hygropetric) and terrestrial groups of Adephaga was examined, with emphasis on the recently described Aspidytidae and Meruidae, and the relict family Trachypachidae. 55 characters of the head were coded and analysed cladistically together with a comprehensive data set of 132 morphological features of adults and immature stages. The results suggest the monophyletic origin of the terrestrial groups (Geadephaga: Trachypachidae + Carabidae) and the non-monophyly of the aquatic and semiaquatic lineages ("Hydradephaga"). The highly specialised Gyrinidae are the sistergroup of all the remaining families. The monophyly of Dytiscoidea including Aspidytidae is confirmed. Aspidytidae are probably the sister group of the Amphizoidae. The placement of Meruidae is ambiguous. A sistergroup relationship with Dytiscoidea is one possible option. The condition found in Trachypachidae is probably closest to the groundplan of Adephaga. We assume that the last common ancestor of Adephaga was living in riparian habitats like extant species of *Trachypachus*, and the aquatic habits were acquired two or three times independently. Carabidae are characterised by a tendency to elongate the head capsule and mandibles and by densely pubescent antennae. A short and rounded, streamlined head and antennae devoid of longer setae or pubescence have evolved several times independently in the aquatic and semiaquatic groups.

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Systematic, morphological and karyological investigation of *Linum* (Linaceae) species of Konia and its surroundings, Turkey

Hüseyin Dural, Fatih Köylüoğlu, Tuna Uysal

Selçuk University, Faculty of Arts and Sciences, Department of Biology, Campus, 42075, Selçuklu, Konya, Turkey, hdural@selcuk.edu.tr

We present the results of a systematic, morphologic and karyologic study of the taxa of *Linum* L. collected in Konya and its surroundings in 2005 and 2006. The following taxa were collected: *Linum flavum* L. subsp. *scabrinerve* (P.H.Davis) P.H.Davis, *Linum nodiflorum* L., *Linum hirsutum* L. subsp. *anatolicum* (Boiss.) Hayek, *Linum tenuifolium* L., *Linum austriacum* L. subsp. *austriacum*, *Linum austriacum* L. subsp. *glaucescens* (Boiss.) P.H.Davis. We studied morphological characters of root, stem, leaf, flower, fruit and seed of these taxa and their general appearance in their natural habitats. In addition, the chromosome numbers were determined.

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A taxonomic study of *Rhabdosciadium* (Umbelliferae) based on morphologic and molecular data

Ahmet Duran[1], Bekir Doğan [1], Hayri Duamn[2], Esra Martin[1], *Meryem Öztürk[1], Özlem Çetin[1]

[1] *Selçuk University, Education Faculty, Department of Biology Education, Konya, Turkey,* [2] *Gazi University, Science and Arts Faculty, Department of Biology Education, Ankara, Turkey*

Rhabdosciadium Boiss. (Umbelliferae) globally comprises five species. Of these, three naturally occur in Iran and two (*Rhabdosciadium microcalycinum* Hand.-Mazz., *R. oligocarpum* (Post ex Boiss.) Hedge & J.M.Lamond) in Turkey. All of them are local endemics. Characteristics of the species are the glabrous, perennial, leafless, multi- branched and junciform habit. *R. microcalycinum* occurs in the provinces Elazığ and Bingöl, *R. oligocarpum* in Hatay province. Comprehensive morphological description of the two species, based on samples collected in Elazığ and Hatay were performed. In addition, fruit and pollen were examined by the electron microscope (SEM) and diagnostic characteristics evaluated. Using the Inter-Simple Sequence Repeat (ISSR) as DNA finger printing method, molecular relationship of the two species were examined. Also, the molecular relationships of *Rhabdosciadium*, *Echinophora, Myrrhoides, Chaerophyllum* and *Anthriscus* were studied. Phylogenetic relationships were revealed by NTSYSpc 2.1 software.

051

Are the sensory fields on the palps homologous within the Holometabola? – An approach from Trichoptera

*Oliver Eikel, Thomas Hörnschemeyer

Georg-August-University of Göttingen, Johann-Friedrich-Blumenbach-Institute of Zoology and Anthropology, Department of Morphology and Systematics, Berliner Str. 28, 37073 Göttingen, Germany, oeikel@gwdg.de

Some Holometabola show specialized sensory fields on the maxillary and labial palps or only on one of both. These fields consist of several sensillae, which stand together in a shallow or deeper depression. Because of their position on the terminal segments of the palps of the mouth parts, they are probably involved in the perception of food. Within Coleoptera, the Archostemata show such sensory fields only on the apical palpomers. While in *Priacma serrata* (Cupedidae) the sensillae stand in a shallow depression and have shallow grooves and a terminal pore (Eikel 2004), other Cupedidae, Micromalthidae or Ommatidae have a larger field or an arrangement, in which the sensillae are sunken into a deep cavity with a narrow opening (Hörnschemeyer 2005). A similar cavity with several sensillae has been found in some taxa of Neuroptera (Eisner 1953). Similar conditions are present in Hymenoptera, especially the Anaxyelidae, Blasticotomidae, Cephidae, Megalodontidae, Siricidae, Xiphydriidae and Xyelidae, which show sensory fields with multiporous sensillae standing either in a wide depression or in a deep cavity (Vilhelmsen 1996, Taschler-Tavćar 1989). Ljungberg & Hallberg (1992) have demonstrated that some Trichoptera also have grooved but poreless sensillae that stand together in a long depression. These sensillae on the palps of Trichoptera are innervated by a single cell like in *Priacma serrata* (Coleoptera) (Eikel 2004) and Hymenoptera (Taschler-Tavćar 1989). Although it is unknown if other taxa of the Holometabola like e.g. Strepsiptera have such sensory fields, the similarity of the sensillae in Coleoptera, Neuroptera, Hymenoptera and Trichoptera (e.g. the position, the shallow depression or deep cavity, the longitudinal grooves and the innervation by a single cell) indicate that these sensory fields are homologous. Further detailed studies on the palps of Trichoptera are presented to get more information on whether it can be assumed that such sensory fields represent a feature of the ground pattern of the Holometabola.

093

Molecular phylogeny and distribution patterns of southern African Cheilanthoid ferns

*Wolf L. Eiserhardt

Universität Hamburg, Biocenter Klein Flottbek, Germany,
wolf.eiserhardt@botanik.uni-hamburg.de

Unlike most other ferns, the Cheilanthoids (Pteridaceae-Cheilanthoideae) are centered in xeric and semi-xeric habitats. They are most diverse in six disjunctive regions, of which is Southern Africa (SA) is one. About half of the Cheilanthoid species occurring in SA are endemic and some of them are confined to relatively small areas. Therefore local adaptive radiation is expected. However, long distance dispersal (LDD) is common in ferns and played a significant role in the evolutionary history of Cheilanthoids. Furthermore, high morphological similarities of some SA Cheilanthoids to certain New World species have been described. This study aims at elucidating the relevance of immigration compared to local speciation among Cheilanthoids in SA. 14 of 37 SA species are integrated into a global molecular phylogeny of Cheilanthoids, inferred from chloroplast DNA sequence data (rbcL). These sequences of SA species were combined with sequences of Cheilanthoids from different regions worldwide, as far as available from GenBank. Two SA species (*Cheilanthes rawsonii* and *Pellaea rufa*) are nested in New World clades. Most probably they originate from speciation subsequent to LDD. Nine of the remaining SA species of Cheilanthes form a clade possibly resulting from a single local radiation. The local radiation might have been driven by the same factors as the evolution of the Cape Flora in Angiosperms. The results indicate that both LDD and local speciation played a role in the formation of SA Cheilanthoid diversity. However, there is no difference in distribution area size between species originating from LDD and those originating from local speciation. To test the hypothesis of adaptive radiation of SA Cheilanthoids, more species will be sampled and additional molecular, morphological and ecological data will be evaluated.

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Procopiania (Boraginaceae) – separate genus or part of *Symphytum*?

Burcu Elci[1,2], Hartmut H. Hilger[2], Sadık Erik[1]

[1] Hacettepe University, Faculty of Science, Biology Department, Botany Section 06800 Çankaya, Ankara, Turkey, [2] Freie Universität Berlin, Institut für Biologie, Systematische Botanik und Pflanzengeographie, Altensteinstr. 6, 14195 Berlin, Germany

The genus *Symphytum* L. (Boraginaceae) is a mesophytic genus of approximately 40 species, mainly distributed in the Euro-Siberian and Mediterranean regions. With 19 species, Turkey holds the largest number of species. *Procopiania* Guşul. is distributed in the Aegean archipelago, southern Greece and western Anatolia with three species. The genus was described by Guşuleac in 1928 with *P. cretica* (Willd.) Guşul., formerly belonging to *Trachystemon*. This division is based mainly on the presence or absence of bracts in the inflorescence and shape of fornices. Runemark (1967) did not agree with Guşuleac's approach, included *Procopiania* into *Symphytum* and supported his hypothesis by morphological, palynological and chromosomal investigations. Wickens (1969) in his treatment of Turkish taxa also synonymized *Procopiania* with *Symphytum*. However, Pawłowski (1971) and Stearn (1986) followed Guşuleac and treated *Procopiania* as separate genus. In Hilger et al. (2004) only one species of each genus was included. The affinities and differences of pollen structure of *Procopiania* and *Symphytum* is discussed in comparison with outgroups and compared with the findings of Harmata (1977, 1981). We examined the relationship of *Symphytum* and *Procopiania* – sistergroup or inclusion -- by adding palynological and molecular to morphological data. Species were chosen from the Boraginae and *Symphytum* in order to compare the similarities/dissimilarities between closely distributed species of both genera. In the tree yielded from the nuclear ITS 1 region. *P. circinale* and *P. creticum* cluster together. They are not sister to *Symphytum* but belong to the ingroup of *Symphytum*. Thus, the generic rank of *Procopiania* is not justified.

054

Significance of carbonic anhydrase activity (CA) in the calcification of the bivalve species *Paphia undulata*

Magdy El-Hedeny[1], Amel El-Gindy[2]

[1] Geology Department, Faculty of Science, Alexandria University, Egypt, m_elhedeny@yahoo.com, [2] Zoology Department, Faculty of Science, Alexandria University, Egypt, amelhosny@yahoo.com

This study reports and discusses the carbonic anhydrase activity (CA) in the mantle tissues of embryos, larvae and adult of the common bivalve species *Paphia undulata* (Born, 1778) and its effect on the calcification process of the shell. Specimens including different ontogenetic stages were caught from fine sand and mud bottoms in the intertidal and sublittoral, to a depth of about 20 m depth, along the Mediterranean coast of Alexandria. After measuring activity levels of the transport enzyme carbonic anhydrase and its histochemical localization in mantle tissue, comparison of CA activity in different developmental stages and X-ray pictures of biomineralization processes in embryonic and larval shells indicate that CA activity is maximal at the end of several developmental stages. The shell microstructure of *Paphia undulata* was described using light and scanning electron microscopy of thin sections. It is composed of four microstructure types: composite prismatic, crossed-lamellar, homogeneous and complex. The last two types characterize the outer part of the shell, toward the ventral margin behind the pallial line. In other parts of the shell, structure is mainly prismatic and crossed-lamellar. The ratio of shell width to maximum height and the position of maximum width of *Paphia undulata* is relatively uniform among all examined specimens.

084

Molecular genetic analyses of sediment cores from East African Rift Lakes

*Laura S. Epp[1], Martin Trauth[2], Ralph Tiedemann[1]

[1] Institute of Biochemistry and Biology, University of Potsdam, Germany [2] Institute of Geosciences, University of Potsdam, Germany

The eastern branch of the East African Rift System displays a series of shallow lakes in close proximity, yet with strikingly different hydrological and geological features. Present day lakes range in alkalinity from pH 11 (Lake Elmenteita) to pH 8 (Lake Naivasha) and in depth from less than a meter to 15 meters. Historically they have undergone a number of drastic changes in lake level (and size) and water chemistry, leading to differences in organismic assemblages and possibly to differences in connectivity between populations. Within this setting we are characterizing present-day and historical planktonic communities obtained from sediment cores in Kenyan Rift Lakes with the use of molecular genetic methods. Our focus is on diatom assemblages and the rotifer *Brachionus plicatilis*. Apart from presenting tools to assess the presence and dominance of taxa meaningful for ecological reconstruction, we are also attempting to trace the population structure and history of a single species in the course of severe environmental change.

010

Molecular and biochemical systematics of sponges (Porifera) without a mineral skeleton

Dirk Erpenbeck, Steve C. de Cook, Andreas Dietzel, Patricia Hendriks, Colleen Strickland, Merrick Ekins, Bernard M. Degnan, John N.A. Hooper, Gert Wörheide

Dept. of Geobiology, Geoscience Centre Göttingen, 37077 Göttingen, Germany, Queensland Centre for Biodiversity, Queensland Museum, PO Box 3300, South Brisbane, 4101 Qld., Australia, School of Integrative Biology, The University of Queensland, St. Lucia, Australia

Investigating the pharmaceutical potential of sponge metabolites is an important aspect in marine biotechnology, although fundamental aspects on the biology of sponges, such as their phylogeny, are still deficient. Knowledge of poriferan systematics can help target taxa with related bioactive properties and is important for the understanding the evolution of biosynthetic pathways. It facilitates the recollection of specimens containing biochemical properties of interest, and provides important insight into their biodiversity and ecology. Unfortunately traditional sponge systematics is clearly hampered by the lack of informative morphological characters for phylogenetic reconstruction. The polarity of morphological traits remains undecided. Both higher and lower taxa are frequently redefined and reshuffled. Evolutionary and ecologically important features such as phylogeography have been virtually unknown until recently because sponge generic relationships remain unresolved. A taxonomically particularly difficult group are the 'keratose' sponges (e.g. the 'bath sponge' *Spongia officinalis*), which lack a mineral skeleton but bear a structure of organic material instead, which decreased number of phylogenetically informative morphological characters dramatically. However those keratose sponges have recently received particular attention due to their bioactive secondary compounds. To address this issue, a molecular phylogeny is being reconstructed and compared with biochemical data. This multidisciplinary approach will further elucidate the use of biochemical compounds as potential phylogenetic markers. Our results will contribute fundamentally to applied research in the evolution and distribution of pharmacologically interesting bioactive compounds. With the robust phylogeny we will address the taxonomic distribution of the compounds. Can sister species have different absence-presence patterns of these compounds? The results will also contribute to the elucidation of the biosynthetical pathways of these valuable components. We will compare the distribution of keratose-typical compounds such as furano- and lacone terpenes with their phylogeny and aim to analyse the evolution of the secondary metabolite using 'keratose' sponges as a model group.

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Two new subspecies into *Cheirolepis-Pseudoseridia* complex of the genus *Centaurea* from Turkey

Kuddisi Ertuğrul, Tuna Uysal

Selçuk University, Science and Art Faculty, Biology Department, Campus, Konya, Turkey

In this study, two new subspecies, *Centaurea isaurica* subsp. *karamanica* Ertugrul & Uysal and *Centaurea cheirolepidoides* subsp. *dikenlidaghensis* Uysal & Ertugrul are described and illustrated from Central Taurus, Turkey. They are placed into *Cheirolepis-Pseudoseridia* complex of Garcia Jacas et al. (2006) based on molecular sequences analysis. *Centaurea isaurica* Hub.-Mor. and *Centaurea cheirolepidoides* Wagenitz, two closely related endemic and recently described species from Turkey, were known as locally distributed taxa. However, recent floristic studies indicated that they occur in many different localities in central Taurus Mountains. Moreover, they should be re-classified at subspecies level. The novel taxonomy is discussed and an identification key is given for the described new *Centaurea* taxa.

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Morphological and cytological diversity in *Bromus* sect. *Genea* (Poaceae) in Iran

*Fatemah Fadaie, Masoud Sheidai

Faculty of Biological Sciences, Shahid Beheshty University, Tehran, Iran,
f_fadaie@sbu.ac.ir, msheidai@yahoo.com

The genus *Bromus* L. is among the most important forage plants of Iran and is distributed widely in the country. The genus comprises several annual as well as perennial species. Among the annual species the section *Genea* Dum. poses taxonomic problems. The present study includes morphometric and cytogenetical analyses of 5 species and 4 varieties of the section *Genea* in Iran in order to try to improve their taxonomy. Morphometric analyses were performed on 28 populations, using 50 quantitative and qualitative characters. ANOVA was used to detect significant differences and cluster analysis and ordination were used to group species showing morphological similarities. Meiotic analysis revealed the presence of 2n=14(2x) and 2n=28(4x) chromosome numbers among the species and populations studied, including a new polyploidy level for *B. sericeous* Drobov. and *B. fasciculatus* Presl. In 3 Species the occurrence of B-chromosomes is reported for the first time.

025

Comparative analysis of chelicerate mitochondrial control regions

*Kathrin Fahrein, Lars Podsiadlowski

Institut für Zoologie, Freie Universität Berlin, Berlin, Germany

In most mitochondrial genomes a non-coding A+T-rich sequence is found, often designated as “control region”. In vertebrates it was demonstrated to bear signal sequences initiating H-strand synthesis in replication, as well as H- and L-strand transcription. While in vertebrates the control region lies between the genes trnP and trnF, its putative location in invertebrates shows great variation. Features often occuring in invertebrate mitochondrial control regions are inverted repeat sequences that could be folded into stable stem-loop structures. These are probably located at or near the origin of L-strand synthesis in replication. While some studies comparing the structure of insect mitochondrial control regions are published, comparative analyses of other arthropods are completely missing. In this study we compare control region sequences of several chelicerate taxa, including novel sequences from Ricinulei, Solifugae and Amblypygi. In most of the sequences stem-loop structures could be identified. These stem-loops are flanked by short conserved sequences, as known from insect taxa (some Diptera and Orthoptera): towards the 5´end a ´TATA´ motif and towards the 3´end a ´G(A)$_n$T´ motif occurs; the latter is also present in certain vertebrates and a plant (*Petunia hybrida*). Furthermore we found evidence for a reversal of the stem-loop structure and its flanking sequences in taxa exhibiting a reversed nucleotide frequency strand bias.

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Molecular phylogeny and hybridization in pondweeds (Potamogetonaceae)

Judith Fehrer, Zdeněk Kaplan

Institute of Botany, Academy of Sciences of the Czech Republic, Zámek 1, 25243 Průhonice, Czech Republic

Pondweeds are aquatic plants of worldwide distribution. Due to their reduced morphology and high plasticity, species identification and delimitation is challenging. In addition to some 80 species, about 50 hybrid taxa are distinguished, most of which are sterile and persist as vegetative clones. We present a basic molecular phylogeny of the family based on nuclear ITS and chloroplast rpl20-rps12 spacer sequences including about 150 accessions of 50 species and hybrids. A separation into three genera (*Potamogeton* (about 70 spp), *Groenlandia* (monotypic), and *Stuckenia* (7 spp)) is proposed. Within *Potamogeton*, basal clades are found consisting of the monophyletic Hybridi species group (also supported by anatomical features), a clade consisting of two subgroups of broad-leaved species (*Tricarinati* and *Colorati*), and a large clade consisting of the rest of all species. Within the broad-leaved species group (*Plantaginifolii*), some relationships correspond to taxonomic species subgroups while others do not. The linear-leaved species are very little differentiated. A more variable marker than ITS is needed for higher resolution among these very similar species. Intraspecific variation is usually lower than interspecific differences except in very closely related species. A few species are not monophyletic, partly due to the existence of cryptic lineages lacking distinctive morphological features, partly because taxon delimitation in some morphologically and genetically very similar species complexes is in need of revision. Many intrageneric hybrids occur within and between clades some of which are still undescribed. Hybrids show additive signals in nuclear genes by which their parents can be unequivocally identified in most cases, because concerted evolution seems to homogenize the multicopy loci only partly or not at all in these sterile clones. Chloroplast DNA variation is very low, but usually sufficient to identify the maternal parent in hybrids. An additional cpDNA marker will be needed to achieve better phylogenetic signal. This study is part of our ongoing research aimed at a taxonomic revision of the Potamogetonaceae.

044

Paraphyly in the *Longitarsus melanocephalus* group (Coleoptera, Chrysomelidae) - traces of peripatric speciation or introgression?

Sonja Feigele, Jan-Jacob Laux, Susanne Dobler

Universität Hamburg, Biozentrum Grindel und Zoologisches Museum, Martin-Luther-King Pl. 3, 20146 Hamburg, Germany

Phytophagous insects provide study systems that are experimentally amenable for investigating speciation ecology, and specifically the order in which ecological differentiation, reproductive isolation and genetic differentiation evolve. We here focus on ecological and genetic evidence to unravel the speciation history of two morphologically almost undistinguishable species of host specialized flea beetles, *Longitarsus melanocephalus* and *L. plantagomaritimus*. MtDNA analysis revealed these two species as a paraphyletic group with the salt marsh specialist of the North Sea coast, *L. plantagomaritimus*, being nested within the wide spread Palearctic species, *L. melanocephalus*. These data suggest that either the two species actually represent host races with ongoing gene flow or that *L. plantagomaritimus* might have arisen from *L. melanocephalus* through budding speciation in conjunction with a host switch. Food plant preference and larval performance data leave open whether *L. plantagomaritimus* might be simply a host race of *L. melanocephalus*. Nuclear gene sequences and allozyme analyses, however, support both species as separate gene pools with ample fixed genetic differences and exclude recent gene flow between them. We hypothesize that although speciation may have happened in a peripatric setting in the past, the present situation cannot be taken as a trace of budding speciation. Rather than incomplete lineage sorting, mtDNA introgression due to prolonged hybridization during the species northward expansion out of glacial refugia may account for the paraphyletic grouping in the mtDNA trees.

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Smilax, a paraphyletic group in Central America?

*Lilian Ferrufino, Birgit Gemeinholzer

Botanic Garden and Botanical Museum Berlin-Dahlem, Königin-Luise Str. 6-8, 14195 Berlin, Germany, l.ferrufino@bgbm.org

The genus *Smilax* L. comprises about 200-300 species distributed in temperate and tropical areas. Even several taxonomic studies attempt to distinguish the Neotropic species of the genus the group is still poorly understood. Morphological species delimitation is difficult due to a great phenotypic plasticity, which most likely can be explained by hybridization of formerly isolated species after the rise of the Central American land bridge between the Neoartic and Neotropical regions and subsequent immigration of fauna and flora from the north as well as from the south. However, the pattern of migration and speciation between plant and animal groups involved in the exchange across the land bridge has received little attention. A phylogenetic analysis based on sequence data from the chloroplast region psbA-trnH of Central American *Smilax* species was carried out to analyze if speciation might be due to hybridization. For this, fifteen species of *Smilax* were compared to two outgroup taxa belonging to different genera within the Smilacaceae. Molecular and morphological analyses were expected to verify the monophyly of the Mesoamerican *Smilax* species. However, the analysis revealed the genus *Smilax* to be paraphyletic in Central America. Even though the concept of paraphyly of the genus is difficult to accept for most taxonomists, molecular results clearly demand a detailed taxonomic revision of the genus. A broad molecular and morphological sampling within the genus will give valuable evidence for a new comprehensive classification of the genus *Smilax*.

050

Morphology and evolution of female genitalia of Neuropterida, with special emphasis on Neuroptera

*Verena Feuerstein

Johann Friedrich Blumenbach Institute of Zoology and Anthropology, Department of Morphology and Systematics, Berliner Str. 28, 37073 Göttingen,University of Göttingen, Germany, vfeuers@gwdg.de

The evolution of the ovipositor of Neuropterida (Insecta: Raphidioptera, Megaloptera, Neuroptera) is controversially discussed. While Raphidioptera possess a long and flexible ovipositor that of Megaloptera is rather short. Within Neuroptera the ovipositor structures are heterogeneous: The external female genitale structures of Osmylidae is reminiscent of the ovipositor of Megaloptera, whereas Chrysopidae show more reduced structures. Other Neuroptera have a long raphidiopteran-like ovipositor (e. g. Dilaridae). The overall similarity of external female genital structures of Neuropterida has already been demonstrated by Mickoleit (1973a). The main components of the ovipositor are the gonocoxites IX, which are fused with the valvulae III (gonostyli IX) – a common feature of Neuropterida. The gonocoxites VIII are generally assuned to be completely lost. However it is still unclear what happened to the valvulae I and II in Neuroptera. In Raphidioptera they form an unpaired ventral closure of the egg laying tube (valvulae I) interlocking with a sliding track (valvulae II), whereas in Megaloptera these structures are obviously absent. In female Neuroptera there are various structures on the ventral side of segment VIII and IX. A derivate of valvulae I is the "subgenitale", e.g. in Nymphidae, Chrysopidae and Hemerobiidae which interlocks with a pair of small sclerites (= valvulae II) at the inner side of the egg laying device. Other structures such as digitiform processus and/or platelike structures of segment VIII of certain Myrmeleontidae are difficult to address. According to Aspöck & Aspöck (2004) a reexpression of the gonocoxites VIII and valvulae I took place. Although study of the musculature is imperative for the homologization of female external genitalia, muscles of female genital segments of Neuroptera have not been examined in detail. Data on the musculature of female genitalia of several taxa of Neuroptera (e.g. Osmylidae) are presented for the first time.

061

The distribution, abundance and seasonality of cone snails (*vallapoo*) in the Tamilnadu Coast, India

*J. Benjamin Franklin[1], K. S. Krishnan[2]

[1] *Molecular Biophysics Unit, Indian Institute of Science, Bangalore, 560 012, India,*
[2] *National Centre for biological Sciences, TIFR, Bangalore, 560 065, India*

The diversity and distribution of the gastropod genus *Conus* (Conidae: Caenogastropoda) in the Tamilnadu coast of Indian peninsula is presented. Sixty species of the genus *Conus* were recorded, which increased the number of Indian Conidae from 77 to 81 adding four new species (*Conus imperialis, C. mitratus, C. striolatus* and *C. violaceus*) from the study area. A rich diversity of 48 species of *Conus* were observed in the Gulf of Mannar region followed by 22 species from northern, six from southern and five from the Palk Bay regions. Overall, *Conus amadis* was found to be the most abundant and diverse, followed by *Conus betulinus, C. figulinus, C. inscriptus, C. loroisii* and *C. monile*. Two seasonal periods, during which high abundance and species richness occurs, have been identified (monsoon and post-monsoon), and some species were occurred throughout the year. A regional distribution map for each species is developed for effective conservation planning for the genus.

043

Tetraphalerus (Archostemata) and the early evolution of Coleoptera - new technical approaches and new phylogenetic insights

*Frank Friedrich, Rolf Georg Beutel
Entomology Group, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Friedrich-Schiller-Universität Jena, Erbertstr. 1, 07743 Jena, Germany

Tetraphalerus bruchi is an extremely rare beetle assigned to the "archaic" beetle suborder Archostemata. The morphology of the head and thorax was examined and evaluated phylogenetically. A highly efficient reconstruction of external and internal features was made possible by the use of modern techniques, especially µ-computer tomography (µ-CT). Features found in *Tetraphalerus* were compared to conditions in other archostematan and non-archostematan beetles, including Paleozoic and Mesozoic fossils. The analysis of the data assessed for the extant taxa strongly supports a branching pattern with Archostemata as the sistergroup of all other beetle lineages and the monophyly of Myxophaga + Polyphaga. *Shikotealinia*, an enigmatic beetle with only one known female specimen from the Russian Far East, is placed within Archostemata, and *Tetraphalerus* and *Omma* (Ommatidae) are the sistergroup of the remaining suborder. *Tetraphalerus* is characterised by a mixture of highly specialised features of the head and many plesiomorphic characters of the thoracic skeleto-muscular system. The thorax of archostematan beetles includes six muscles also present in Neuropterida, but absent in all representatives of Adephaga, Myxophaga and Polyphaga. The pterothoracic skeleton of Archostemata shows also a series of plesiomorphic character states mainly linked to the coxal articulations. The analysis with the entire data set including extinct taxa shows that Archostemata as it is traditionally assigned is a "taxonomic waste basket". †Tshecardocoleidae and other fossil groups do not belong to this suborder but to the stem lineage of Coleoptera. It is noteworthy, that the inclusion of the fossils does not only influence the reconstruction of the character evolution but also the branching pattern within the recent taxa. Thus it is apparently better to analyse a full data set despite of missing entries than to place the fossils in a second step based on an informal character evaluation.

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Finding the next relatives of *Chenopodium quinoa* – insights from a plastid phylogeny of *Chenopodium*

*Susy Fuentes Bazan[1], Thomas Borsch[2]

[1] Nees-Institut für Biodiversität der Pflanzen, Universität Bonn, Germany, and Herbario Nacional de Bolivia, La Paz, Bolivia, [2] Institut für Biologie und Umweltwissenschaften and Botanical Garden, Universität Oldenburg, 26111Oldenburg, Germany

The genus *Chenopodium* L. with an estimated 150 species (Kühn et al. 1993) is one of the taxonomically most complex genera in Chenopodiaceae. Its ample morphological variability results in numerous described species and intraspecific taxa. Moreover, broad scale molecular phylogenetic analyses of Chenopodiaceae and Amaranthcaeae (Kadereit et al. 2003; Müller & Borsch 2005) suggest that the genus Chenopodium is polyphyletic. One Andean species, *Ch. quinoa* Willd. (quinoa), is an important food plant cultivated throughout the Bolivian and Peruvian highlands. There are other South American species that are also utilized, such as *Ch. berlandieri* and *Ch. pallidicaule*. These taxa have been proposed as close relatives of *Ch. quinoa* (Aellen & Just 1943; Wilson 1988) but the evolution of *Ch. quinoa* and allies is still not understood. No modern taxonomic treatment of South American *Chenopodium* species exists, resulting in severe limits for identification. To determine the position of *Ch. quinoa* and allies among the lineages of *Chenopodium*, a densely sampled phylogenetic analysis of *Chenopodium* spp. and taxa from subfamily Chenopodioideae is carried out. First trees based on plastid trnL-F and trnK/matK confirm the polyphyly of *Chenopodium* (and most of the sections currently recognized) and indicate that *Chenopodium quinoa* belongs to a clade with *Ch. pallidicaule*, *Ch. petiolare* and other Andean as well as North American species. Species like *Ch. berlandieri* appear to be polyphyletic as currently circumscribed. Analyses of nuclear ITS and fingerprint data among *Ch. quinoa* and putative relatives are underway to elucidate possible patterns of reticulate evolution.

023

Mites in rodent bodies in silos and flour factories of Tehran in Iran

*Saeedeh Gabbarpour[1], Abdolhosein Shiravi[1], Fariba Ardeshir[2], Andre Bochkov[3]

[1] Islamic Azad University of Damghan, Iran [2] Iranian Plants Protection Research Institute, Avin, Tehran, Iran, [3] Zoological Institute, Russian Academy of Sciences, Universitetskaya Emb. 1, 199034 Saint-Petersburg, Russia

We collected mite samples from the bodies of rodents during 2005 from silos and flour factories of Tehran. Three species belonging to 3 genera and 2 families, were collected and identified: Myobiidae: *Myobia murismusculi* (Schrank), *Radfordia affinis* (Poppe); Myocoptidae: *Myocoptes musculinus* (Koch). This paper is the first report of mites in the body of rodents in stored wheat in Iran.

076

The type material of *Coelodonta antiquitatis* (Mammalia: Perissodactyla: Rhinocerotidae)

*Alexander Gehler[1], Mike Reich[1], Dick Mol[2], Hans van der Plicht[3]

[1] Geoscience Centre of the University of Göttingen, Museum, Collections & Geopark, Goldschmidt-Str. 3, 37077 Göttingen, Germany, [2] The Natural History Museum of Rotterdam, The Netherlands, [3] Centre for Isotope Research, University of Groningen, Nijenborgh 4, 9747 AG Groningen, The Netherlands, also at Faculty of Archaeology, Leiden University, PO Box 9515, 2300 RA Leiden, The Netherlands

The woolly rhinoceros (*Coelodonta antiquitatis*) is one of the most remarkable members of the Pleistocene *Mammuthus-Coelodonta* faunal complex. During the Late Glacial, *Coelodonta antiquitatis* was widespread over most of Eurasia. In the final step of the last ice age *Coelodonta antiquitatis* became extinct. The last available records for Great Britain are around 15,000 years ago (e. g. Stuart 1982), for remaining Europe as late as 14,000 to 12,500 years ago (e. g. Kahlke 1994). The latest records from Western Siberia have an age around 10,800 years ago (Orlova et al. 2004). In 1799, J. F. Blumenbach (1752–1840) proposed the first scientific name (*Rhinoceros antiquitatis*) for the woolly rhinoceros in the 6th edition of his "*Handbuch der Naturgeschichte*". Blumenbach's description of the new species is based on material from the collections of the former "Royal Academic Museum" at the Georg-August University of Göttingen. This material originates from two different localities in Germany and Siberia. The largest amount was collected around 1750 at the southern margin of the Harz Mts. (Lower Saxony, Germany). Some of these fossils were sent to the University of Göttingen, where they were received by S. C. Hollmann (1696–1787). First thinking about elephant remains, he recognised them finally as such of a rhinoceros. Hollmann published his results in the "*Commentarii Societatis Regiae Scientiarum Gottingensis*" (Hollmann 1753a, 1753b). This work represents the first anatomical description of a rhinoceros in general. The material consists of pieces of bone of several adult as well as juvenile individuals, therefore the variation in AMS ^{14}C datings are very large. For example 20,000 ± 80 years BP for a femoral fragment and 40,830 ± 430/± 370 years BP for two premolars. The second part of the material, an occiput fragment and the anterior part of a skull, belongs to Western Siberia (Republic of Bashkortostan). The absolute age, based on AMS ^{14}C dating is 40,610 ± 340 years BP. This material was donated by G. T. von Asch (1729–1807) at the end of 18th century. It was mentioned for the first time by Blumenbach (1791), and was rediscovered in 2005 (Gehler 2006). The existence of this type material is widely unknown and a lectotype of *Coelodonta antiquitatis* has never been selected.

080

Molecular diversity assessment of ectomycorrhizal basidiomycetes from Alaska

József Geml, Gary A. Laursen, Ian C. Herriott, D. Lee Taylor

Institute of Arctic Biology, 311 Irving I Building, 902 N. Koyukuk Drive, P.O. Box 757000, University of Alaska Fairbanks, Fairbanks, AK 99775, U.S.A.

Due to its importance to the global climate system and position at the forefront of climate change, we have targeted boreal and arctic regions of Alaska for extensive surveys of fungal molecular biodiversity. We have generated ITS and partial LSU sequences in a high throughput fashion from both curated sporocarp collections (700 specimens) and soil PCR clone libraries (60,000+ clones). The soil sampling for clone-library construction was carried out at various plots of the Bonanza Creek LTER site in interior Alaska. The herbarium collections were gathered from across Alaska over 35 years of collecting effort, spanning all three major ecoregions and six subregions in Alaska. Here, we evaluate operational taxonomic unit discrimination methods along with phylogenetic diversity patterns in three basidiomycete genera that are particularly diverse in high-latitude ecosystems and have great ecological importance as ectomycorrhizal symbionts of plants: *Cortinarius, Lactarius*, and *Russula.*

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Pollen morphology in *Medicago* (Fabaceae)

Farangis Ghanavati[1], Mahnaz Ghobbei[1], Javad Mozafari[1], Shahrokh Kazempour[2]

[1] Seed and Plant Improvement Institute, Karaj, Iran, [2] Tarbiat Modaress University, Tehran, Iran

Iran is a centre of diversity of *Medicago*, having more than 23 species. Because of close similarity in sexual organs and pod-characteristics, taxonomical classification of these species based on morphological characteristics is difficult. Scanning Electron Microscopy (SEM) was used to study the major characteristics of pollen among Iranian *Medicago* species. Pollen grains were mostly tricolpate, but quadricolpate or hexacolpate pollen was also seen in one species. The equatorial view was oval-rectangular or spherical and the polar view obtuse-triangular, truncate-triangular or square. The majority of species showed reticulate and verrucate exine surface. *M. rigiduloides* with quadric or hexic colpate pollen was barely distinguishable from M. rigidula with tricolpate pollen exine surface. On the other hand, *M. tornata* with its spherical pollen and verrucate exin surface was obviously different from *M. polymorpha* with rectangular pollen and reticulate exine surface. This is the first report of *M. rigiduloides* and *M. tornata* from Iran.

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Direct and rapid protocol for somatic embryogenesis and plant regeneration from immature explants of chick pea (*Cicer arietinum*) – a recalcitrant grain legume

Kiran Kumar Ghanti

Gulbarga University, Gulbarga-585 106, Bangalore, India

A protocol for plant regeneration via somatic embryogenesis was developed in two chickpea verities. Somatic embryos were induced from immature cotyledons on Murashige and Skoog's (MS) medium fortified with different concentrations of 2,4-dichlorophenoxyacetic acid (2,4-D), 2,4,5-trichlorophenoxyacetic acid (2,4,5-T), naphthalene acetic acid (NAA) and picloram singly or in combination with 0.5-2.0 mg l^{-1} N^6-benzylaminopurine (BAP) or 0.5-2.0 mg l^{-1} kinetin (KN). Type of auxin, its concentration and genotype influenced the frequency of somatic embryogenesis. NAA was better for somatic embryo induction compared to other auxins. The well formed, cotyledonary shaped embryos germinated into plantlets with 36.6% frequency on MS medium supplemented with 2.0 mg l^{-1} benzylaminopurine + 0.5 mg l^{-1} abscisic acid (ABA). The frequency of embryogenesis and plantlet regeneration was higher in ICCV-10 then other cultivar tested. Regenerated plants were transferred to soil and grown to maturity produced viable seed with 40% survival. The ability of this regeneration system to produce embryos with a high frequency and their conversion to whole plants offers potential for gene transfer and development of transgenics in this important grain legume and also in the production of synseeds.

074

Stem species pattern of the orbitotemporal region in the cranium of the Tenrecidae (Afrotheria, Mammalia)

Peter Giere

Museum für Naturkunde, Invalidenstraße 43, 10115 Berlin, Germany, peter.giere@museum.hu-berlin.de

Tenrecidae, as part of the newly established taxon Afrotheria, have recently received increased attention from systematists using both morphological and molecular approaches. This group, which formerly was included in the Insectivora, contains Recent species mostly from Madagascar with a few exceptions from western Africa. Based on an existing phylogeny, the stem species pattern of characters from the orbitotemporal region is reconstructed using both skeletal and histological material of different ontogenetic stages. Both museum material and literature data on living members of the Tenrecidae is included in this reconstruction. Using members of the Chrysochloridae (golden moles) as an outgroup, morphological characters found in the orbitotemporal region of the skull of tenrecids are assessed and polarized in this reconstruction as a contribution to eventually increase the morphological support for the Afrotheria.

056

The first comprehensive molecular phylogeny reveals ancient vicariance, parallel evolution of viviparity and extensive convergence in shell morphology of thiarid freshwater gastropods

Matthias Glaubrecht, Thomas von Rintelen

Museum für Naturkunde, Humboldt-Universität zu Berlin, Invalidenstrasse 43, 10115 Berlin, Germany, matthias.glaubrecht@museum.hu-berlin.de

Freshwater gastropods of the large and morphologically diverse pantropical Thiaridae have figured prominently in evolutionary biology when discussing phenomena such as e.g. speciation and adaptive radiation, the colonization of new adaptive zones and the role of key innovations. However, to date, both the family and its constituent taxa have been delineated using morphological features, with some debate as to the actual extent of the entire family. More importantly, the various evolutionary hypotheses have not been tested within a rigorous phylogenetic framework. We now use a molecular phylogeny for about one hundred representative thiarids, based on a c. 900 bp fragment of the mitochondrial large ribosomal subunit gene (16S), to unravel their systematics. The resulting phylogeny reveals that some well known and important lineages hitherto subsumed within the thiarids actually form the palaeotropic Paludomidae. The Thiaridae proper comprise two major clades both representing apparently ancient lineages, viz. (i) the palaeotropic Thiaridae sensu stricto and (ii) its sistergroup comprising two subclades that correspond on the one hand to the West African Pachymelaniinae and on the other hand the Neotropic Hemisininae. It can be hypothesized that the separation between these latter two subclades has been caused by the vivariant event isolating Africa and South America during the late Mesozoic, indicating a Gondwanan origin. Within the Thiaridae sensu stricto a lack of resolution of the basal branching events is considered to indicate a rapid ancient radiation particularly in Southeast Asia and Australia into the diverse array of recent lineages. On the generic level, several well-known and speciose taxa, such as e.g. *Thiara*, *Tarebia* and *Stenomelania* or Melanoides , are shown to be para- or polyphyletic in the molecular phylogeny, suggesting that shell characters such as the highly-turreted shells of *Stenomelania* or the stepped-shape shells of *Thiara* are the result of convergent evolution of conchological features rather than an expression of phylogenetic relationships. We will also discuss the parallel origin of viviparous reproductive strategies. As a consequence we anticipate that a large-scale revision of thiarid taxonomy is the prerequisite for any meaningful study on the evolution and historical biogeography of these freshwater gastropods.

058

Basal or derived? - The phylogeny of the Acteonoidea (Gastropoda, Opisthobranchia)

*Katrin Göbbeler, Annette Klussmann-Kolb

Institute for Ecology, Evolution and Diversity, Phylogeny and Systematics, J.W. Goethe-University, Siesmayerstrasse 70, 60054 Frankfurt am Main, goebbeler@bio.uni-frankfurt.de

The phylogenetic position of the Acteonoidea (Gastropoda, Opisthobranchia) has been a matter of debate for decades. Phylogenetic analyses of morphological data support a position at the basis of the Opisthobranchia. By contrast, analyses of different molecular datasets have revealed a more derived position within the Opisthobranchia. The Acteonoidea are commonly divided into three families: the Acteonidae, the Bullinidae and the Hydatinidae. The phylogenetic interrelationships of these three families are unresolved until now. Some authors even doubt the monophyly of the Acteonoidea because of the lack of synapomorphies. The purpose of the current study is to clarify the monophyly of the Acteonoidea, the phylogenetic relationships of its families and the position of the Acteonoidea within the Opisthobranchia. The present molecular systematic study includes eight different acteonoid taxa representing seven different genera. Among the investigated taxa are members of all three families. Thus, this is the first comparative investigation of the interrelationships of acteonoid taxa. The dataset for this study is completed by members of the main opisthobranch subgroups, the main pulmonate subgroups, some basal heterobranchs and caenogastropods. Four different markers were used: the complete 18S rRNA, partial 28S rRNA, partial 16S rRNA and partial mitochondrial CO1 sequences. Phylogenetic reconstruction was performed using Baysian inference approaches and maximum likelihood. The results of this study strongly support the monophyly of the Acteonoidea. They seem to have a more derived position within the Opisthobranchia. However, the molecular data do not confirm the current grouping into families.

046

Maximum age for a Carabid beetle radiation in New Zealand (Coleoptera: Broscini: *Mecodema*)

*Julia Goldberg, Steve Trewick

Allan Wilson Centre for Molecular Ecology and Evolution, Institute of Molecular Biosciences, Massey University, Private Bag 11-222, Palmerston North, New Zealand, J.Goldberg@massey.ac.nz

New Zealand is believed to be a hot spot for endemism comparable to island biota such as Hawaii and the Galapagos. It has often been a focus of speciation and colonization studies because of its Gondwanan origin and geographical isolation during the past 80 my. However there is still much debate about origins and age of the New Zealand biota, which has traditionally been viewed as a Gondwana element. By implication biodiversity in New Zealand is perceived as old, a relic of its ancient origin. On the other hand, it is increasingly apparent from molecular studies that diversification, and in many cases origination of taxa, postdate the break-up of Gondwana. In particular, studies of many New Zealand plant groups indicate colonization and species radiation in relatively recent times. Fewer examples of extensive species radiation in animals have been documented, and here we report on a species-rich genus (*Mecodema*) of Carabid beetles. We present a molecular phylogeny based on mitochondrial and nuclear gene regions and an approach to time the radiation of this genus in New Zealand. Due to the lack of adequate fossil evidence, constrained stratigraphic information was used to calibrate relaxed molecular clock estimates for diversification of *Mecodema*. Divergence times were inferred from mitochondrial gene regions using the Bayesian relaxed molecular clock approach (BRMC) and the commonly applied fixed divergence rate for invertebrates of 2.3%/my. The inferred timings indicate radiation of these beetles no earlier than the mid-Miocene (12 mya) with most speciation events being younger, dating to the Plio-Pleistocene (<5 my) and making *Mecodema* an impressive example of recent insect species radiation in New Zealand.

072

Phylogenetic relationships of the Cape Verde Sparrow (*Passer iagoensis*) based on mitochondrial and nuclear DNA

*Javier Gonzalez[1], Melanie Siow[1], Eduardo Garcia-del-Rey[2], Guillermo Delgado[3], Michael Wink[1]

[1] Institut für Pharmazie und Molekulare Biotechnologie, Universität Heidelberg, Im Neuenheimer Feld 364, 69120 Germany, [2] Departamento de Ecología, Facultad de Biología, Universidad de La Laguna, 38260 La Laguna, Tenerife, Canary Islands, Spain, [3] Museo de Ciencias Naturales, Organismo Autónomo de Museos y Centros, Calle Ramón y Cajal, Edificio Salesianos, Semisótano 2, 38003 Santa Cruz de Tenerife, Canary Islands, Spain

The phylogenetic relationships of the Cape Verde Sparrow (*Passer iagoensis*) have been investigated using nucleotide sequences of mitochondrial and nuclear genes. To elucidate the evolutionary relationships of Cape Verde Sparrow we have included a total of eight other species of the genus *Passer*: the Tree Sparrow (*P. montanus*), the Spanish Sparrow (*P. hispaniolensis*), the Southern Grey-headed Sparrow (*P. diffusus*), the Grey-headed Sparrows (*P. griseus*), the Rufous Sparrow (*P. motitensis*), the Pegu Sparrow (*P. flaveolus*) the Cape Sparrow (*P. melanurus*), the House Sparrow (*P. domesticus*) and the Cape Weaver as an outgroup (*Ploceus capensis*). We have obtained the sequences of the mitochondrial cytochrome b gene and three nuclear introns: ornithine decarboxylase, myoglobin and glyceraldehyde-3-phosphodehydrogenase. The data set consists of approximately 2,500 base pairs. Maximum likelihood, maximum parsimony and Bayesian inference algorithms were used to reconstruct phylogenetic trees and calculate genetic distances. Findings are discussed in terms of a recent colonization of Cape Verde Islands by the Cape Verde Sparrow and the relative abundance of pseudogenes, probably nuclear copies of the cytochrome b, in the genus Passer.

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Analysis of polymorphism and phylogeny of genus *Aegilops* based on AFLP- and RGA-profiling date

S. V. Goryunova[1], C. G. van der Linden[2], M. J. Smulders[2], N. N. Chikida[3], E. Z. Kochieva[4]

[1] Vavilov Institute of General Genetics, Russian Academy of Sciences, Moscow, 119991 Russia, [2] Plant Research International UR, P.O.Box 16, 6700 AA Wageningen, The Netherlands, [3] All-Russian Institute of Plant Industry, St. Petersburg, 190000 Russia, [4] Bioinzheneriya Center, Moscow, 117372, Russia

Aegilops L. is a genus of annual grasses closely related to cultivated wheat. The *Aegilops-Triticum* group is an example of taxa with reticulate evolution. The genus is composed of 25 species with diploid, allotetra- and allohexaploid genomes. In spite of considerable interest in *Aegilops*, relationships between *Aegilops* species remain unclear. To clarify the phylogeny of *Aegilops* AFLPs and RGA-profiling were used. Whereas AFLPs mainly reveal the variability in arbitrary selective-neutral genome sequences, RGA-profiling was designed to reveal polymorphisms in the genome. In total, 63 specimens of all 25 *Aegilops* species and 5 specimens of *Triticum* were examined. *Aegilops* accessions were chosen according to the results of preliminary RAPD-analysis of intraspecific polymorphism. In total, 2144 polymorphic DNA-fragments for AFLP and 581 for RGA-profiling were obtained. For each pair of accessions Nei-Li genetic distances were computed. To compare data from two different methods, a 2-way Mantel test was performed. Intraspecific distances from RGA-data were higher than from AFLP. It seems that RGAs evolve more rapidly then the main part of the genome. Traditional cluster analysis (UPGMA) and network reconstruction (NeighborNet) were performed for phylogeny reconstruction and revelation of structure within the *Aegilops-Triticum* group. Several groups of species were resolved. Each of the groups included either species with similar diploid genomes or one parental diploid and some related polyploid species. Borders between species were less clear on the RGA-dendrogram than on the AFLP-dendrogram, due to intraspecific variability and the presence of notably differing accessions in some species.

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Taxonomic re-arrangements in the Coridaceae (Boraginales)

Marc Gottschling[1,2], Hartmut H. Hilger[3], James S. Miller[4,2]

[1] Charité – Universitätsmedizin Berlin, Klinik für Dermatologie, Venerologie und Allergologie, Hauttumorcentrum Charité, Charitéplatz 1, 10117 Berlin, Germany, Marc.Gottschling@charite.de, [2] Missouri Botanical Garden, 4344 Shaw Boulevard, St. Louis, MO 63110, USA, [3] Freie Universität Berlin, Systematische Botanik und Pflanzengeographie, Altensteinstraße 6, 14195 Berlin, Germany, Harmut.Hilger@fu-berlin.de, [4] New York Botanical Garden, 200th St. & Kazimiroff Blvd., 10458-5126, Bronx, NY, USA, JMiller@nybg.org

Modern authors have not agreed on a satisfactory system of generic delimitation among woody Boraginales. Recent treatments have recognized a broadly defined *Cordia* with 3 through 7 subgenera or sections. *Auxemma, Patagonula*, and *Saccellium* have been all described as distinct from *Cordia* because of highly specialized fruit morphologies, and subsequent authors have universally continued to maintain them. Molecular ITS sequence data now suggest an alignment of genera that is consistent with morphological, anatomical, and palynological data. *Coldenia*, formerly considered a member of Ehretiaceae, is sister to *Cordia* s.l. *Cordia* s.l. segregates into four monophyletic assemblages, more or less corresponding to established taxonomic units as previously inferred from morphology, ecology, and biogeography. (1) The *Varronia* clade is a well-differentiated taxon and has a sistergroup relationship to the other three clades (*Cordia* s. str.). (2) The *Collococcus* clade comprises *Cordia* sect. *Superbiflorae* and the New World species of *Cordia* sect. *Myxa* (excluding *Cordia dentata* and *Cordia lutea*). (3) The *Myxa* clade includes all of the Old World species of *Cordia* sect. *Myxa* and the New World species *C. dentata* and *C. lutea*. (4) The Sebestena clade includes *Cordia* sects *Cordia* and *Gerascanthus*, three species of *Cordia* sect. *Rhabdocalyx*, and *Auxemma*, *Patagonula*, and *Saccellium*. *Auxemma, Patagonula*, and *Saccellium* are no longer tenable as separate taxa and should be reduced under *Cordia*. Furthermore, *Varronia* is the sistergroup to the rest of *Cordia* s.l., and its resurrection as a distinct genus has been recently proposed. Thus defined, Cordiaceae comprise *Coldenia*, *Cordia*, and *Varronia* at the generic level, all of which are monophyletic and consistent with vegetative, floral, and pollen morphology.

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Taxonomic revision of *Bourreria* (Ehretiaceae, Boraginales)

Marc Gottschling[1,2], James S. Miller[3,2]

[1] Charité – Universitätsmedizin Berlin, Klinik für Dermatologie, Venerologie und Allergologie, Hauttumorcentrum Charité, Charitéplatz 1, 101 17 Berlin, Germany, Marc.Gottschling@charite.de, [2] Missouri Botanical Garden, 4344 Shaw Boulevard, St. Louis, MO 63110, USA [3] New York Botanical Garden, 200th St. & Kazimiroff Blvd., 10458-5126, Bronx, NY, USA, JMiller@nybg.org

Bourreria (Ehretiaceae, Boraginales) is an important element of the Neotropics and comprises trees and shrubs that grow mostly in dry scrubby habitats and deciduous forests. More than 100 species and varieties from the New World have been described in *Bourreria*, but the total number of species is considered significantly lower. *Bourreria* has been recognized as one of the taxonomically most complex taxa of the woody Boraginales and was considered in serious need of taxonomic revision. Species delimitation is difficult due to three main reasons: 1) populations are morphologically variable, 2) many species are only imperfectly known, and diagnostically important characters of the fruit remain unknown, 3) taxonomic studies of *Bourreria* have mostly been regional during the past century and frequently have not evaluated morphological variation of species throughout their full geographic ranges. Based on the study of more than 6000 herbarium specimens, we now treat *Bourreria* as comprising 30 species that are distributed from Baja California east to Florida and south throughout Central America and the Caribbean Islands to northern South America, with a center of diversity in México (15 species). Delimitation of species in *Bourreria* varies from that of previous authors, and morphological data are reviewed in order to support our taxonomic circumscriptions. Most species of *Bourreria* have discrete distributions and are characterised by exclusive, well-recognisable traits, despite high morphological variability. *Bourreria* probably segregates into five monophyletic species groups: 1) *B. baccata* and relatives may represent an ancestral group of species of the Caribbean archipelago, with many plesiomorphic character states; 2) the *B. exsucca* species group (= *Crematomia*) is characterised by unique schizocarpic fruits; 3) *B. huanita* and its relatives have a densely velutinous interior calyx; 4) the style of the *B. microphylla* species group is extraordinarily short; 5) *B. spathulata* and relatives may represent an ancestral group of species on the Central American mainland, with many plesiomorphic character states. Within *Bourreria*, the development of large flowers has taken place several times independently (within the species groups of *B. exsucca* and *B. huanita*).

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The interior construction of the stamen lever in *Salvia* (Lamiaceae)

Matthias Gröteke, Sascha Thimm, Regine Claßen-Bockhoff

Institut für Spezielle Botanik, Johannes Gutenberg-Universität, Mainz, Germany

More than 100 years ago, Correns (1891) presented the first and until today the only theory about the movement of the staminal levers in *Salvia*. Based on anatomical studies he hypothesized that the movement is based on torsion of the thin ligament between the filament and the connective. The insect moving the stamen would elastically deform the joint that immediately swings back into its initial position when the pressure slows down. Our anatomical studies, however, indicate that the ligament is a stiff structure throughout not being twisted in the course of the movement. It is composed of a central vascular bundle surrounded by a collenchyma of a species-specific diameter and the epidermis. On both ends the collenchyma merges into the soft parenchyma of the filament and connective, respectively, each being characterised by large cells and intercellular spaces. At the same sites, the epidermis usually forms pronounced swellings caused by both cell division and cell enlargement. Histological sections of stamens that were fixed in the released stage illustrate that it is the parenchyma that becomes distorted during the movement. We conclude that the push against the lower lever arm causes an elastic deformation of the connective parenchyma that is passively transferred to the filament parenchyma by the stiff ligament. The shorter the ligament and the larger the parts of parenchyma involved the easier the movement will be carried out. During the movement the joint is elastically extended and the connective slides across the epidermal swellings thereby increasing the distance between filament and connective. Obviously the swellings not only enhance the precision of the lever movement by guiding the connective arms but also increase the reset force of the released lever.

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Origin and development of mesoderm in *Membranipora membranacea* (Bryozoa)

Alexander Gruhl

Freie Universität Berlin, AG Evolution und Systematik der Tiere, Königin-Luise-Str.1-3, 14195 Berlin, agruhl@zoosyst-berlin.de

The origin of the third germ layer in Bryozoa is still only insufficiently known. Earlier descriptive studies postulate the mesoderm to originate from a quartet of presumptive endodermal cells at the vegetal pole of the blastula. These cells are said to divide off cells into the blastocoel, which subsequently begin to proliferate. In addition to the lack of detailed documentation for this process, most observations were made in species with non-feeding larvae that are either gutless or bear a non-functioning intestinal tract. As the planktotrophic cyphonautes larva is widely regarded to resemble the ancestral larval form in Bryozoa, the mode of mesoderm formation in such larvae is suggested to be of greater phylogenetic significance, especially in comparisons with other metazoan phyla. I have conducted TEM and cLSM studies to trace origin and fate of mesodermal cells in developmental stages of the cheilostome bryozoan *Membranipora membranacea*. Shortly after gastrulation, one ectodermal cell from the prospective larval anterior pole ingresses into the primary body cavity. This cell gives rise to two muscular cells that gain elongate shape and connect the basis of the developing apical organ to the anterior blastoporal rim, the presumptive site of the pyriform organ. Further muscles can be derived from the first set of cells. Undifferentiated mesodermal blastemal cells, that occur in later stages are unlikely to be derived from muscle cells, but are located directly underneath the outer epithelium and therefore likely to arise by repeated ingression or delamination of ectodermal material. Although initial mesoderm formation takes place in proximity to the ectoderm-endoderm boundary, proliferations from endoderm have not been observed. These results are compared to patterns of mesoderm formation in other metazoan groups.

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Molecular phylogeny of bluebells, *Hyacinthoides*

Michael Grundmann[1], Harald Schneider[1], Fred. J. Rumsey[1], Stephen W. Ansell[1], Jane Squirrell[2], Pete Hollingworth[2], Stephen J. Russell[1], Johannes C. Vogel[1]

[1] Department of Botany, The Natural History Museum, Cromwell Road, London SW7 5BD, UK, [2] Royal Botanic Garden, 20A Inverleith Row, Edinburgh EH3 5LR, UK

The genus *Hyacinthoides* (Hyacinthaceae), closely related to Scilla, consists of nine currently accepted species, distributed across Western Europe and North Africa. Here we provide the first molecular phylogeny that includes all species. Sixty-seven accessions representing seven outgroup taxa and the entire natural distribution range of each *Hyacinthoides* taxon were analysed using c. 4200 bp of chloroplast DNA sequence, derived from five non-coding regions: atpB-rbcL, psbH-trnH, trnCD, trnG, trnLF. Two well supported clades were recovered by phylogenetic analyses. Clade I comprised three species (*H. aristidis, H. lingulata*, and *H. italica*) from North Africa and the Maritime Alps of Italy and France. Clade II comprised six species from Western Europe and North Africa, arranged as two sub-clades, firstly (IIa) grouping *H. mauritanica* and *H. reverchonii*, and secondly (IIb) *H. algeriensis, H. hispanica, H. paivae*, and *H. non-scripta*. Southern Moroccon specimens of *H. mauritanica* potentially represent a new taxon, as they are sister to *H. reverchonii*, which together are sistergroup to Northern Moroccan-Portuguese specimens of *H. mauritanica*. Within clade IIb, both *H. algeriensis* and *H. paivae* are nested within *H. hispanica*. Taxa within this clade are distinguished by their derived bell-shaped flowers, with the exception of *H. paivae*, which has reverted to an open-stellate arrangement. Root-tip squashes confirmed the North African *H. algeriensis* to be a tetraploid (n=32), derived from a widespread lineage of the diploid Iberian *H. hispanica*. The lack of sequence diversity is compatible with a hypothesis of a single origin of polyploidy. In contrast to the genetically highly structured *H. hispanica*, *H. non-scripta* was almost uniform across its range from Northern Spain to Great Britain, a feature supporting a scenario of a Pleistocene bottleneck.

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Comparative analysis of the chloroplast DNA phylogeography of a myrmecophytic and a non-myrmecophytic species of *Macaranga* (Euphorbiaceae)

Daniela Guicking[1], Brigitte Fiala[2], Frank R. Blattner[3], Kurt Weising[1]

[1] Systematics and Morphology of Plants, Institute of Biology, University of Kassel, 34132 Kassel, Germany [2] Animal Ecology and Tropical Biology (Zoology III), Biocentre, University of Würzburg, 97074 Würzburg, Germany [3] Leibniz-Institute of Plant Genetics and Crop Research (IPK), 06466 Gatersleben, Germany

The genus *Macaranga* (Euphorbiaceae) comprises some of the most important pioneer tree species in lowland tropical rain forests of Southeast Asia. About 30 species of *Macaranga* are obligate ant-plants (myrmecophytes), and several species are facultatively associated with ants. Despite their ecological importance, to date nothing is known about the factors structuring genetic diversity in these dioecious pioneer species. Most importantly, the potential influences that the ant partners exert on differentiation processes of their hosts remain obscure. Myrmecophytic *Macaranga* species are unable to survive without their symbiotic ants in the wild, suggesting that the two partners cannot migrate separately from each other. We hypothesize that this obligatory symbiosis may have had a negative impact on gene flow and recolonization processes from refugial populations during the Pliocene or Pleistocene and hence, may have accelerated differentiation and speciation in myrmecophytic species.

To test this hypothesis, we compared the chloroplast DNA (cpDNA) phylogeography of two closely related *Macaranga* species in Borneo, *M. pearsonii, a myrmecophyte,* and *M. gigantea*, a non-myrmecophyte. A clear phylogeographical structure was found for the cpDNA haplotypes of both species ($N_{ST} >> G_{ST}$), with moderate to high coefficients of differentiation: *M. gigantea* $G_{ST} = 0.698$, $N_{ST} = 0.857$; *M. pearsonii* $G_{ST} = 0.563$, $N_{ST} = 0.848$. The differentiation between Sabah and East Kalimantan in northern/eastern Borneo was particularly pronounced, and was also stronger in the myrmecophyte *M. pearsonii* as compared to the non-myrmecophyte *M. gigantea.* These observations lend support to our hypothesis of a putative influence of the associated ants on differentiation processes. However, alternative factors, e.g. different evolutionary histories, may as well explain the observed differences. Further analyses are therefore necessary to finally decide whether the life history strategy ‘obligate myrmecophytism’ may have affected population structure and genetic diversity in *Macaranga.*

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Phylogenetic relationship analysis of *Genista* (Fabaceae) species from Turkey as revealed by Inter-Simple Sequence Repeat Amplification

Erdoğan E. Hakki[1], Bekir Doğan[2], Ahmet Duran[3], Muhittin Dinç[3], Esra Martin[3]

[1] Selcuk University, Faculty of Agriculture, Department of Field Crops, Konya, Turkey,
[2] Selçuk University, Education Faculty, Department of Science Education, Konya, Turkey,
[3] Selçuk University, Education Faculty, Department of Biology Education, Konya, Turkey

Genista L. (Fabaceae) is wide spread in Europe, South Africa, and West Asia and represented by almost 90 species. Thirteen species occur in Turkey. In this study phylogenetic relationship among the *Genista* taxa were investigated using the Inter-Simple Sequence Repeat (ISSR). ISSR gives more reliable results than Randomly Amplified Polymorphic DNA (RAPD) markers. The phylogenetic relationship were revealed with dendrograms prepared by NTSYSpc 2.1 software.

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Second chance for old-known "*Capsella apetala*" - characterizing a homeotic mutant of shepherd´s purse

*Steffen Hameister[1], Pia Nutt[2], Guenter Theißen[2], Barbara Neuffer[1]

[1] Department of Special Botany, University of Osnabrueck, Barbarastr. 11, 49076 Osnabrueck Germany, [2] Department of Genetics, Friedrich Schiller University, Philosophenweg 12, 07743 Jena, Germany

In several genera within the Brassicaceae family quite a few evolutionary tendencies can be observed, which are possibly involved in speciation, e.g. variations in flower morphology. A floral variety of the shepherd's purse *Capsella bursa-pastoris* (L.) Medik. defined by "staminoide petals"(SPE) is the focus of our studies. This homeotic variety was first described in the early 19th century and is characterized by a second whorl of stamens instead of petals, which leads to a decandric flower structure. Such a naturally occurring homeotic mutant, known from several habitats in Central Europe and Russia, provides the ability to study evolutionary trends. On the one hand we focus on the chromosomal localization of the putative locus which is responsible for the transformation of petals. By crossing a decandric with a wild type parent followed by selfing of F_1, we obtained an F_2 segregating population (University of Jena) in which we found evidence for a singular locus determining the petal morphology. This mapping population was applied to conduct a linkage analysis using AFLP data. Currently, our floral trait is arranged in one linkage group with six molecular markers. Otherwise we try to uncover possible variations between both *Capsella* types. Therefore we study population genetics and ecological parameters such as flowering time for a huge mixed population in vineyards of "Rheinhessen". Yet we found evidence for a lower genetic variability of SPE individuals and a divergence in onset of flowering. Especially because the distinct floral variation appears in wild populations, a promising model system seems to have been identified, which provides the chance to investigate evolutionary processes on molecular and population genetic level.

030

The phylogeny of Branchiopoda – summarizing molecular, morphological and fossil data

Carolin Haug, Joachim T. Haug, Andreas Maas, Dieter Waloszek

Biosystematic Documentation, University of Ulm, Ulm, Germany, Carolin.haug@uni-ulm.de, Center of 'Orsten' Research and Exploration C.O.R.E. (http://www.core-orsten-research.de)

Traditional views of the phylogenetic position of Branchiopoda within Crustacea and its in-group phylogeny have been questioned by recent publications. Of special interest is the positioning of the Branchiopoda as a sister group to Insecta (Glenner et al. 2006, Science 314). These data result from molecular analyses and should be tested against morphological characters. Since the basis for any reliable phylogeny is the reconstruction of ground patterns, the sister group of Branchiopoda can be judged, but a stable in-group phylogeny is also needed. Yet, the in-group phylogeny of Branchiopoda is also under discussion, and long-established monophyla have been doubted to be valid. For example, phylogeny hypotheses based on molecular data see Notostraca as an in-group taxon of Diplostraca rather than being an in-group taxon of Calmanostraca (= Notostraca + †Kazacharthra), the sister group to Diplostraca in morphologically-based analyses. Paraphyly of 'Conchostraca' has been detected using morphological and ontogenetic features. The former spinicaudatan *Cyclestheria hislopi* shows the same brood-care behaviour and direct development as the Cladocera, now included in the Cladoceromorpha as the sister taxon to the remaining spinicaudatans. Furthermore, all phylogenetic trees must be able to handle fossil taxa. Usually it is not possible to directly include fossil species in molecular analyses, and even for morphological studies it depends on the qualitity of the fossils. Even then, most do not show enough details for comprehensive comparisons – one exception are 'Orsten'-type fossils. Yet, the results of a computer-based phylogenetic analysis can be tested against available fossils of the studied group, and it is clear that a phylogeny contradicting the fossil record is not parsimonious. The well-established sister taxon to the crown-group of the Branchiopoda is the Cambrian †*Rehbachiella kinnekullensis*. We summarize current phylogenetic hypotheses including evidence from two more well-preserved fossils of Branchiopoda from the much younger Devonian Rhynie Chert, the famous †*Lepidocaris rhyniensis* and †*Castracollis wilsonae*.

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4D reconstruction of †*Henningsmoenicaris scutula* and heterochrony in early crustacean evolution

Joachim T. Haug, Andreas Maas, Dieter Waloszek

Biosystematic Documentation, University of Ulm, Ulm, Germany, joachim.haug@uni-ulm.de, Center of 'Orsten' Research and Exploration C.O.R.E. (http://www.core-orsten-research.de)

Originally the three-dimensionally preserved †*Henningsmoenicaris scutula* from the Middle Cambrian 'Orsten' of Sweden was described on the basis of three specimens by Walossek & Müller (1990, Lethaia 23). These authors placed †*H. scutula*, together with three additional species, †*Goticaris longispinosa*, †Cambropachycope clarksoni and †*Martinssonia elongata*, in the stem-lineage of Crustacea. This placement founded on a special mixture of features of these taxa: 1) features plesiomorphically retained from the euarthropod ground pattern, 2) others shared with crown crustaceans, Eucrustacea, 3) other characteristics of Eucrustacea are lacking in these taxa. Here we describe the ontogenetic sequence of †*H. scutula* in a detailed SEM study of 40 specimens. Precise morphological comparisons between the different specimens and application of morphometrics permitted the recognition of ten successive instar stages and a single significantly older stage. This ontogenetic sequence provides a detailed insight of the morphogenesis of all major external structures, e.g., the morphology of several of the appendages including even gradual changes in their setation pattern. Another interesting structure traceable through ontogeny are the lateral eyes: These start as elevations on right and left side of the inner shield margin anterior to the hypostome, become more developed subsequently to receive possibly movable stalked eyes in late instars. All ontogenetic stages were reconstructed as virtual 3D models used for a 4D reconstruction (3D over time) of †*H. scutula*. Comparable data are also available for other species of Crustacea from the same fossil deposit, e.g., of the one-eyed micro-predators †*Goticaris longispinosa* and †*Cambropachycope clarksoni*, the phosphatocopine †*Hesslandona unisulcata*, and the branchiopod †*Rehbachiella kinnekullensis*. Based on these data and those of additional species a preliminary small-scale phylogenetic analysis of the Crustacea was carried out including ontogenetic data. The four species putatively regarded as early Crustacea indeed turned out to be derivatives of the early crustacean stem lineage. Based on ground-pattern reconstructions for each node and tracing of the character evolution on the resulting phylogram heterochronic events reveal to have occurred in early crustacean evolution.

005

Species delimitation and testing using binary multilocus data

Bernhard Hausdorf[1], Christian Hennig[2]

[1] Zoological Museum, University of Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany, hausdorf@zoologie.uni-hamburg.de, [2] University College London, Department of Statistical Science, 1-19 Torrington Place, London WC1E 6BT, United Kingdom, chrish@stats.ucl.ac.uk

We propose an approach for alpha taxonomy consisting of a species concept and methods for species delimitation and testing based on this concept. The cohesion concept is favoured as theoretical species concept. Species are operationally defined as genotypic clusters, groups of individuals with similar genotypes that are separated from other such groups by gaps in the allele composition. A method for delimiting species based on binary multilocus data (like AFLP data) using Gaussian clustering is introduced. A statistical test for clustering of specimens indicating distinct species using Monte Carlo simulations is proposed. The hypothesis that the observed degree of clustering of specimens can be explained by the frequency distribution of the alleles and the spatial autocorrelation of the occurrences of the alleles alone is tested. In comparison to approaches to delimit species based on phylogenetic species concepts, this approach has the advantage that non-exclusive groups can be classified and that Gaussian clustering provides a decision about the number and the delimitation of candidate species.

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Phylogeny, biogeography and the evolution of dioecy in the southern hemisphere genus *Leptinella* (Compositae, Anthemideae)

*Sven Himmelreich[1], Ilse Breitwieser[2], Christoph Oberprieler[1]

[1] Institute of Botany, University of Regensburg, Regensburg, Germany, [2] Allan Herbarium, Landcare Research, Lincoln, New Zealand

The genus *Leptinella* Cass. includes 44 taxa and is distributed mainly in New Zealand, but also in Australia, New Guinea, South America, Tasmania, and on the subantarctic islands. The genus is characterised by astonishing transitions in breeding systems: *Leptinella* species form populations with monoecious, subdioecious or dioecious plants. Additionally *Leptinella* species form also an impressive polyploid complex with ploidy levels ranging from tetraploid chromosome numbers to $2n = 24x$. In order to gain insight into the evolutionary history and the biogeography of *Leptinella* along with the evolution of polyploidy and dioecy in this genus, we conducted phylogenetic analyses based on sequence information from nrDNA ITS and two spacer regions of the chloroplast genome (psbA - trnH, trnC - petN). Our results indicate that a) *Leptinella* is member of a strongly supported monophyletic group comprising the southern hemisphere genus *Cotula* and the S American genus *Soliva* together with seven S African genera, b) the classification of the genus into three subgenera as proposed by Lloyd (1972) is only partly supported, c) there were several long-distance dispersal events from New Zealand to Australia, South America, and the subantarctic islands, d) the radiation of the polyploid complex of *Leptinella* species in New Zealand was very fast. Analyses of character evolution of *Leptinella* demonstrate that the ancestor of the genus was tetraploid and monoecious. Dioecy or subdioecy evolved at least three times in the genus, sometimes not connected with a change in chromosome number or in conjunction with polyploidy. In the monophyletic subgenus *Leptinella*, a close connection between polyploidy and dioceous sex expression is observed.

029

Phylogeny of Remipedia (Crustacea) - current status

*Mario Hoenemann, Stefan Koenemann

University of Veterinary Medicine Hannover, Buenteweg 17, 30559 Hannover, Germany

Recent phylogenetic analyses of remipede crustaceans based on morphological characters yielded ambiguous and partly conflicting results. The morphologic data did not support the current taxonomic concept, with three families in the order Nectiopoda. However, clade stability was relatively low, and for more reliable and stable phylogenetic reconstructions, the use of molecular data seems indispensable. In an ongoing research project, we are sequencing five mitochondrial and four nuclear markers to resolve phylogenetic relationships within the Nectiopoda. Here we present preliminary results based on sequences of mtCO 1 and 16S rDNA for the majority of currently known species of Remipedia.

004

Molecular analysis in systematics: a method-dependent approach

*Thomas Hülsken, Stefan Schreiber, Carina Marek, Michael Hollmann

Lehrstuhl für Biochemie I – Rezeptorbiochemie, Fakultät für Chemie und Biochemie, Ruhr-Universität Bochum, Universitätsstrasse 150, 44780 Bochum, Germany

The application of molecular systematics to phylogenetic and taxonomical analysis has changed the fields of systematic and phylogenetic studies. To date, however, only a few scientists (e.g., Williams & Knowlton 2001, Zhang et al. 2002, Will et al. 2005) have ever discussed the genetical background and biochemical methodology behind the molecular analyses. In many recent studies, phylogenetic analyses based on sequences amplified from live-collected or ethanol-preserved tissues were successfully performed. However, in this context the accuracy and consistency of the methods are of fundamental importance. Heterogenous amplifications have been demonstrated in many species groups, and pseudogenes and gene duplications are known for many vertebrate and invertebrate taxa. RNA-based analyses as performed by Williams & Knowlton (2001) can help to identify paralogous sequences in cases of variable amplification results. In this study we want to show that the success of molecular systematics is highly dependent on the appropriate biochemical methods, reagents, and logistics applied, including tissue preservation and storage conditions, quality of DNA extraction, efficiency of PCR, fidelity of sequencing and reliability of DNA database entries. Albeit technically difficult, RNA-based analysis is possible of ethanol-fixed tissue and can be used to amplify transcribed genes as positive controls in cases of gene variability as we have schown for marine gastropod families such as Conidae and Naticidae. Thus, RNA-based analyses can be used to reduce the perils of erroneous sequences and improve the reliability of phylogentic analyses based on these sequences. As the correct identification of the analyzed species is the cornerstone for any sustainable phylogenetic work, the first and foremost task is the reliable recognition of species and the knowledge of the literature published. Thus, there can be little doubt that experienced taxonomists are needed to perform a reliable species identification, not despite but rather because of the great potential of molecular systematics.

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Diversification patterns of leaf traits and habitat in Iberian columbines

*Rafael Jaime, J.M. Bastida, P.J. Rey, J.M. Alcántara

Área de Ecología. Universidad de Jaén. E-23071 Jaén, Spain, rjaime@ujaen.es

The genus *Aquilegia* has become an example of adaptive radiation from studies developed on North America, where the radiation seems related to selection exerted by diverse types of pollinators. The number of taxa in Europe and North America is similar but there are fewer types of pollinators in Europe. European columbines are differentiated mainly in vegetative characters and radiation of European columbines might therefore have been driven by adaptation to abiotic environment. The Iberian Peninsula is a centre of diversification of columbines and a suitable area to study morphological differentiation in relation to environmental heterogeneity. We recorded 10 leaf traits and 6 environmental traits of 9 populations of *A. vulgaris vulgaris*, 6 of *A. vulgaris nevadensis*, 8 of *A. vulgaris dichroa*, 3 of *A. pyrenaica pyrenaica*, 1 of *A. pyrenaica discolor* and 6 of *A. pyrenaica cazorlensis*. Traits of leaf size and structure show strong positive correlations across populations. On the other hand, the populations with glandular leaf pubescence show higher SLA and less dense cover of non-glandular pubescence. Habitat selection at species level is determined by abiotic factors varying at local geographical scale (soil moisture, canopy cover), at the level of subspecies at wider geographical scales (mean precipitation, altitude). Correlations between leaf traits and habitat characteristics reflect two general patterns. The split between the ancestral *A. vulgaris* and *A. pyrenaica* seems to have occurred through specialization of the latter species in dry, open, rocky substrates typical of higher elevations, by acquisition of smaller leaves with shorter petioles. Convergent acquisition of glandular pubescence is observed in taxa endemic to southern Spain (*A. vulgaris nevadensis* and *A. pyrenaica cazorlensis*).

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Surviving the Pleistocene without genetic and spatial restriction: phylogeographic analysis and paleodistributional niche modeling of diploid Patagonian *Hordeum* species (Poaceae)

Sabine S. Jakob[1], Enrique Martinez-Meyer[2]

[1] Leibniz Institute of Plant Genetics and Crop Research (IPK), Corrensstr. 3, 06466 Gatersleben, Germany, [2] Instituto de Biologia, Universidad Nacional Autonoma de Mexico, 04510 Mexico City, Mexico

In southern Patagonia three diploid *Hordeum* species occur, which form a monophyletic group within the genus. Although they are mostly sympatric, their habitats are ecologically differentiated on a local scale. These species evolved during the last two million years from a common progenitor, thus providing a system for the study of speciation processes in a young radiation. Phylogeographic analyses based on chloroplast haplotypes as well as modelling of present and past climatic niches of the species were conducted. The distribution of the genetic variation indicates at least one vicariance event, separating one of the later three species from the last common ancestor of the remaining two. However, neither the geographic distribution of haplotypes nor phylogeographic analysis allowed the clear definition of potential ice age refuges. In fact, the observed haplotype patterns indicate that quite large populations survived the ice ages without any spatial restriction. These findings were supported by models of the recent and Pleistocene species' distribution, which suggested the occurrence of *Hordeum in situ* even during the last glacial maxima about 18,000 years ago. Thus, the combination of phylogeographic analyses and paleoclimatic niche modelling enabled us to generate a conclusive hypothesis about the evolutionary history of the three species. Although they occur today in sympatry and are adapted to different ecological niches on a local scale, the analysis shows that this differentiation was not the reason for speciation, but evolved in allopatry after the species became reproductively isolated by geological barriers. The nature of these barriers is, however, currently unclear, as the Patagonian steppe east of the Andes was probably never completely fragmented by glaciers stretching from the Andes to the Atlantic Ocean.

003

Biodiversity data resources for West Africa – accessibility and possible solutions to property rights issues

Thomas Janssen[1], Marco Schmidt[2], Karen Hahn-Hadjali[2], Georg Zizka[1,2]

[1] Research Institute Senckenberg, Dpt. of Botany and Molecular Evolution, Senckenberganlage 25, 60325 Frankfurt, Germany, [2] University of Frankfurt, Institut for Ecology, Evolution and Diversity, Siesmayerstr. 70, 60323 Frankfurt, Germany

The countries of West Africa cover diverse landscapes ranging from evergreen rainforests to the sahel. Regardless of the vegetation zone concerned, the local population depends on natural resources for a part of their subsistence. Furthermore, policy makers recognized biodiversity as a non-negligible economic factor for the welfare of their countries. It is hence a common understanding that action needs to be taken quickly to preserve and sustainably manage the local diversity ressources in the view of high anthropogenic and climatic pressures on habitats, fauna and flora. Research on conservation and sustainable management of natural resources is currently under way and depends on the availability of biodiversity data with good spatio-temporal coverage. Hence, a sufficient biodiversity data foundation can only be provided through international cooperation. Biodiversity data is here defined as single occurrence data (specimens) and group occurrence data (floristic and faunistic relevés). A large amount of such data has been and is currently being acquired in West Africa in the frame of large scale research projects such as BIOTA or SUN, but also on smaller scales by many researchers. Global access to an overview of existing data and ongoing projects is a prerequisite to concerted, time- and resource-efficient research action and helps to avoid redundant data collection, promotes the closure of data gaps and fosters research synergies. Taking into account current dynamics in the research system and especially the modus of funding attribution, it has to be considered, that putative cooperation partners will pursue common as well as specific aims with acquired data, which may impose constraints on data exploitation. We here present largely web-based approaches to the resolution of data accessibility and data property issues susceptible to promote targeted cooperative research on the conservation and sustainable management of natural biodiversity resources in West Africa.

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When zoochory becomes disadvantageous - genecology and population genetics of *Galium aparine* (Rubiaceae)

*Markus Jerominek, Frank H. Hellwig

Institut für Spezielle Botanik, Friedrich Schiller Universität Jena, Germany

Due to morphological and phenological characters, *Galium aparine* L. is separated into field and hedge ecotypes. To test how far the ecotypes are genetically differentiated we cultivated individuals from three different locations (three field and three hedge populations) under equal garden conditions and analysed their genetic diversity via AFLP (Amplified Fragment Length Polymorphism). To characterize the ecotypes morphologically we examined the length and number of fruit spines. While the hedge ecotype shows long and numerous fruit spines that are well adapted to zoochory, the field ecotype has either shorter or less fruit spines. We concluded that the adaptive significance of the observed reduction depends on a speirochor dispersal strategy. This means that fruits of the field ecotype were harvested together with crop diaspores and dispersed with them. Probably the seed treatment of crops favours fruits with reduced spines because they are similar to crop diaspores and not sorted out like fruits with long and numerous spines. Thus zoochory become disadvantageous in field habitats. Cultivation over two generations shows that the ecotype specific fruit-characters remain unchanged and therefore must be genetically fixed. The analysis of five AFLP primers reveals a genetic differentiation between the two ecotypes (AMOVA, 13.3%). Furthermore, neighbour joining analysis shows that the field individuals from three different locations cluster together and do not originate from the respective hedge habitat. We conclude that at least the field ecotype evolved only once.

022

Some water bears (Tardigrada) from Bulgaria with description of two new species of the genus *Macrobiotus*

Łukasz Kaczmarek[1], Bartłomiej Gołdyn[2], Łukasz Michalczyk[3]

[1]Department of Animal Taxonomy and Ecology, A. Mickiewicz University, Umultowska 89, 61-614 Poznań, Poland, kaczmar@amu.edu.pl, [2]Department of General Zoology, A. Mickiewicz University, Umultowska 89, 61-614 Poznań, Poland,: glodny@amu.edu.pl, [3]Centre for Ecology, Evolution and Conservation, School of Biological Sciences, University of East Anglia, Norwich NR4 7TJ, UK, agnostic@poczta.fm

Tardigrada of Bulgaria are very poorly known and complex tardigradological studies have never been conducted in this country. This study is based on a few samples only, however even in such scarce material we were able to identify some very interesting species. Up to now 35 species have been described for Bulgaria (compare Romania: 50 species; Greece: 57 species; former Yugoslavia: 74 species). The 35 species recorded in Bulgaria constitute about 4 % of all known Tardigrada species. In August 2007 17 moss samples were collected in the Western part of Bulgaria, most of them in Vitosha Mountains (1400-2300 m) and two from Sofia (600 m). In this material 6 species of Tardigrada were identified. Two of the species are new to science (*Macrobiotus* sp nov. 1, *Macrobiotus* sp. nov. 2). Additionally, one species, *Isohypsibius prosostomus*, is a new record to the Bulgarian tardigrade fauna. *Macrobiotus hufelandi*, *Hypsibius convergens* and *Ramazzottius oberhaeuseri* were previously reported from Bulgaria. *Macrobiotus* sp nov. 1 is most similar to *M. pallari* but differs by the absence of dentate lunulae on claws and in some aspects of the egg morphology. *Macrobiotus* sp. nov. 2 is similar to *M. coronatus* but is different in some morphological and morphometric characters of adults and eggs.

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Species concept problem for asexual green euglenoids: conclusions from studies on the genus *Phacus*

*Anna Karnkowska, Rafał Milanowski, Bożena Zakryś

Department of Plant Systematics and Geography, University of Warsaw, Al. Ujazdowskie 4, PL-00-478 Warszawa, Poland, ankarn@biol.uw.edu.pl

The central question concerning the nature of species has been whether asexual organisms diversify into species. Green euglenoids are well known as asexual organisms. Moreover, there are also a lot of criptic species in this group of organisms (difficult to distinguish based on morphology only). One of such cryptic species is known from the literature as "*Phacus parvulus*". In this work we have studied morphological diversity and analysed chloroplast and cytoplasmic SSU rDNA of several strains representing the "*Phacus parvulus*" together with other taxa from the genus *Phacus*. The topology of the phylogenetic tree, obtained from the Bayesian analyses of combined sequences coding chloroplast and cytoplasmic rRNA genes, suggest the existence of seven species in the "*Phacus parvulus*" - *P. inflexus, P. oscillans, P. parvulus, P. polytrophos, P. pusillus, P. similis* and *P. skujae*. Such result is in agreement with the morphological data, but on the other hand the sequence diversity within the seven taxa is very small (2 - 4%), much smaller than among the rest of the species of the genus *Phacus* (sequence diversity is 7- 20%). Such situation that morphological characteristics are more distinct than the molecular ones is pretty unique for photosynthetic euglenoids. We concluded that only combined genetic and morphological analyses seem to be an appropriate method to study the critical species of Euglenales, because in some clades morphology is more variable than nucleotide sequence diversity, while in most clades it is conversely.

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vifabio – aggregating library and internet resources for biologists

Gerwin Kasperek, Judith Dähne, Jashar Rexhepi, Berndt Dugall

Universitätsbibliothek Johann Christian Senckenberg, Bockenheimer Landstraße 134-138, 60325 Frankfurt am Main, Germany, vifabio@ub.uni-frankfurt.de

The Virtual Library of Biology – vifabio - has been established as a central library portal (www.vifabio.de). This ongoing project is conducted by the University Library Johann Christian Senckenberg, Frankfurt/Main, with several partner institutions in Germany and Austria. The project's objective is to create a single point of access to various resources for biologists, such as printed materials in libraries, databases and internet sites. The core elements of vifabio are:
(1) A meta-catalogue (virtual catalogue of biology) where multiple libraries with important holdings of biological literature are integrated for parallel search. In the starting phase, libraries in Berlin, Frankfurt, Gatersleben (Germany) and Vienna (Austria) are participating. In the near future, more biological libraries form Germany and abroad will join. In addition, the tables of contents of almost 1,900 biological journals with data on 1.7 mio. articles have been integrated.
(2) In cooperation with Kurt Stübers BioLib, digitised versions of historic biology books are now available as Portable Document Files, among them many titles relevant to taxonomy and systematics.
(3) The Internet Guide is a collection of quality-checked links to biological internet resources. Access is provided via search tools, as well as via browsing through multiple alternative systems of resource arrangement (e.g. subjects/themes, geographic coverage, resource type).
(4) An inventory of important online databases for biologists provides access via searching and browsing. This collection comprises bibliographical databases as well as factual and pictorial databases for all sub-disciplines of biology. DFG-funded licences permit nationwide usage of some bibliographic databases, for example, Biological Abstracts 1926-2004, and Zoological Record 1864-2006.
Access on electronic journals is enabled through the Electronic Journals Library (EZB). Further enhancements of vifabio will include improved linking features to electronic full-texts as well as integration of more bibliographic databases into the meta-catalogue. A repository for electronic documents, to be established as part of vifabio, shall provide a platform for open access publication.

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Evolution of morphological characters within *Astragalus* s. str in the context of nrDNA ITS phylogeny

N. M. Kazemi[1], S. Kazempour Osaloo[1], A. A. Maassoumi[2]

[1] Department of Plant Biology, Faculty of Basic Sciences, Tarbiat Modares University, Tehran, Iran, [2] Department of Botany, Research Institute of Forests and Rangelands, Tehran, Iran

In this study, the evolutionary trend of 22 vegetative and reproductive morphological characters was assessed in the phylogenetic context deduced from nrDNA ITS data for 115 species including 109 members of *Astragalus* senso stricto clade and 6 representatives of related genera as outgroups (Kazempour Osaloo et al. 2005). Character state information of these selected characters were obtained from available literature and examined specimens and were scored based on numerical unordered scoring. nrDNA ITS phylogeny was reconstructed using Neighbor Joining method as implemented in PAUP*. The morphological dataset was then investigated in the context of molecular data by mapping onto the nrDNA ITS phylogeny with MacClade 4. Based on the results of this study the highest CI (Consistency Index) and RI (Retention Index) is 0.50 and 0.96 respectively for the gum ducts (absence/presence) character. So this character shows the lowest level of homoplasy. Also the lowest CI and RI is 0.03 and 0.35 respectively for the inflorescence (lax/dense) character. So this character shows the highest level of homoplasy. All studied characters evolves several times among different groups of *Astragalus* s. str. clade and show high levels of homoplasy so that none of them are synapomorphy for the genus *Astragalus* and thus are of less taxonomic value, although some of them support monophyly of some recognized clades.

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Phylogeny of selected species of *Astragalus* (Fabaceae) based on cpDNA trnL-F and nrDNA ITS sequences data

N. M. Kazemi[1], S. Kazempour Osaloo[1], A. A. Maassoumi[2], E. Rastegar Pouyani[3]

[1] Department of Plant Biology, Faculty of Basic Sciences, Tarbiat Modares University, Tehran, Iran, [2] Department of Botany, Research Institute of Forests and Rangelands, Tehran, Iran, [3] Department of Biology, Faculty of Basic Sciences, Teacher Training University, Sabzevar, Iran

This study represents a chloroplast trnL-F and nrDNA ITS based-phylogenetic analyses of certain Old World *Astragalus* and representatives of Astragalean clade and phylogenetic status of *A. memoriosus* (sect. *Caraganella*). Phylogenetic relationships among 27 Old World *Astragalus* species plus representatives of aneuploid Neo-Astragalus clade as place holders and other representatives of Astragalean clade including *Colutea*, *Oxytropis, Phyllolobium, Podlechiella vogelii, Oreophysa microphylla, Chesneya astragalina* and two species of *Caragana* as outgroups are inferred using Maximum Parsimony (MP) approach as implemented in PAUP*4. A total of 1089 and 645 nucleotide sites were respectively analyzed for cpDNA trnL-F and nrDNA ITS of which 123 and 169 ones were phylogenetically informative, respectively. Based on the analysis of cpDNA trnL-F sequences, *Astragalus* species are not gathered in a clade, so called *Astragalus* s. str. as idefined in previous studies. These results like our previous studies based on nrDNA ITS and cpDNA ndhF data show that annual species are scattered among perennial *Astragalus*. So monophyly of this group is not confirmed again. Also this study is concordant with ndhF data, in close relationship of *A. hemsleyi* and *A. ophiocarpus*, but this relationship is in conflict with nrDNA ITS data. The sister relationship of *Biserrula pelecinus* to subclade of *A. annularis-A. epiglottis* as inferred from cpDNA trnL-F sequences is congruent with nrDNA ITS one, but phylogenetic position of the clade comprising of these taxa is not equal in deduced phylogenies. Another incongruency between these two phylogenies is the position of *Phyllolobium* sp. Also phylogenetic position of subclade of *A. grammocalyx, A. coelicolor* and *A. capito* inferred from this analysis is congruent with nrDNA ITS data and in conflict with ndhF one, although all three phylogenies are agree in sister relationships of these taxa. this study shows that *A. memoriosus* (sect. *Caraganella*) is closely allied with *A. stocksii*, another member of this section. Based on both datasets, *Podlechiella vogelii* forms a subclade at the base of the Cluteoid clade and *Oreophysa microphylla*, a member of coluteoid clade is nested among other *Colutea* species and allied with *Colutea persica*.

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Is the genus *Lithops* (Aizoaceae) monophyletic?

*Alexandra Kellner[1], Christiane M. Ritz[2], Peter Schlittenhardt[3], Frank H. Hellwig[2]

[1] Institut für Allgemeine Botanik und Pflanzenphysiologie, AG Spezielle Botanik, Justus-Liebig-Universität Gießen, Germany, [2] Institut für Spezielle Botanik, Friedrich-Schiller-Universität Jena, Germany, [3] Ispra, Italy

The genus *Lithops* (Aizoaceae, Ruschioideae) is distributed in the Cape flora of southern Africa and comprises about 40 species. Not only the taxonomy within the genus is difficult, but also its delimitation from other genera of the subfamily Ruschioideae is sometimes challenging due to the extreme reduction of vegetative characters. We analysed two different chloroplast markers (atpB-rbcL IGS, trnS-trnG IGS), one nuclear marker (nrITS) and Amplified Fragment Length Polymorphism (AFLP) to investigate the phylogeny of Lithops and its relationships to other taxa of the Ruschioideae. None of these phylogenetic analyses supported the monophyly of *Lithops*. There are several hypotheses explaining these results. First, the very recent origin of the Ruschioideae is responsible for the very low sequence variation which does not suffice to resolve the deep branches in the trees. Second, the genus *Lithops* is an artificial taxonomic unit based on very few and ambiguous morphological characters. Some genera, e. g. *Dinteranthus* and *Schwantesia* are morphologically very similar to *Lithops*. *Dinteranthus* is distinguished from *Lithops* by the number of locules per capsule and the surface of the seeds. Schwantesia has triquetrous leaves, whereas the leaves of *Lithops* are isomeric and wedge-shaped. The third hypothesis is that phylogenetic trees are not suited to present the relationships between *Lithops* and its allies, because the evolution of these taxa might be influenced by reticulation as it could shown by the existence of interspecific and intergeneric hybrids.

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Oxytropis species in Northeast Asia: genetic diversity and cryopreservation

Alla B. Kholina, Olga V. Nakonechnaya, Nina M. Voronkova

Institute of Biology and Soil Science, Far Eastern Branch Russian Academy of Sciences159 Prospect Stoletiya, Vladivostok, 690022, Russia

Oxytropis is a large and diverse genus comprising about 300 species (Yurtsev, 1999), among them many rare, endemic and medicinal plants that are in danger of extinction due to natural disasters and human pressure. To conserve the genetic resources of these species, it is necessary to assess its genetic diversity, revealing the centers of diversity for sample collecting and suitable temperature regimes for seed storage. We explore allozyme variation in eight *Oxytropis* species from Northeast Asia: *O. kamtchatica, O. revoluta* (sect. *Arctobia*), *O. ochotensis*, *O. erecta*, *O. retusa, O. hidakamontana, O. calcareorum* (sect. *Orobia*), *O. chankaensis* (sect. *Baicalia*); and we tested the effect of deep freezing in liquid nitrogen (–196°C) on seed viability. The highest level of polymorphism was observed in octoploid *O. ochotensis* (P = 61.9%), the lowest in the rare endemic species from Kurils, *O. retusa* and *O. hidakamontana* (P = 14.3% for both species). The results indicated that the freezing did not lead to seed death. Responses to cryopreservation appeared as significant increase of germination without scarification, especially in *O. chankaensis* (seed germination was about 90%).

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Boechera or not – that's the question. Phylogenetic position and phylogeography of Eastern North American *Boechera* (Brassicaceae)

*Christiane Kiefer, Christoph Dobes, Marcus Koch

University of Heidelberg, Heidelberg Institute of Plant Science, Department I, Biodiversity and Plant Systematics, Im Neuenheimer Feld 345, 69120 Heidelberg, Germany

The genus *Boechera* (Brassicaceae) comprises 110 species distributed primarily in the western United States, with a centre of greatest diversity in California. Only a few western species have distribution ranges extending into eastern North America, and seven are exclusively restricted to eastern and central Canada and eastern United States. Analysis of cpDNA sequence variation (trnLF region) shows that these seven species constitute two separate lineages apart from the three major evolutionary lineages of *Boechera* recovered in previous cpDNA studies. Analysis of the nuclear internal transcribed spacer (ITS1 and ITS2) places the eastern species in two separate clades within one lineage distinct from all other *Boechera* species that form a major monophyletic group. Because the resolution of both marker systems is low where the different lineages split, we suggest to retain the eastern North American *Boechera* species in the genus, rather than splitting them into two or three different genera. Phylogeographic analyses revealed a geographic structure for *Boechera canadensis* and *Boechera laevigata* haplotypes and a potential hybrid zone for *B. laevigata* and *B. missouriensis*.

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Thoracic morphology of Mantophasmatodea (Insecta)

Rebecca Klug[1], Jürgen Goebbels[2]

[1] Institut für Zoologie und Anthropologie, Abteilung Morphologie, Berliner Straße 28, 37073 Göttingen, Germany, rklug@gwdg.de, [2] Bundesanstalt für Materialforschung Berlin (BAM), Unter den Eichen 87, 12205 Berlin, Germany

The thoracic morphology including the musculature of Mantophasmatodea is described and illustrated for the first time. Based on x-ray tomography data, the cuticule and musculature of one representative of Mantophasmatodea (*Austrophasma*) was reconstructed based on x-ray tomography data. This non-invasive method is very useful to clarify the anatomy of rare specimens. The musculature of Mantophasmatodea shows an overall similarity with that of Grylloblattodea. Potential synapomorphies of Mantophasmatodea and Grylloblattodea are the presence of a spino-coxal muscle (M. metaspina-coxalis, origin: on the metaspina, insertion: on the posterior rim of the third coxa) in the Metathorax, and the absence of two dorso-ventral muscles (M. metacoxa-subalaris of meso- and metathorax) and two sterno-coxal muscles (M. mesofurca-coxalis posterior, M. metafurca-trochanteralis). These findings support a sister group relationship of Grylloblattodea and Mantophasmatodea.

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Phylogeny and historical biogeography of the leafy liverwort *Marchesinia* (Jungermanniopsida: Lejeuneaceae)

Fanny Klugmann[1], Jörn Hentschel[1], Rosemary Wilson[1], Harald Schneider[2], Jochen Heinrichs[1]

[1] Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, [2] Department of Botany, The Natural History Museum, London SW7 5BD, UK

The liverwort genus *Marchesinia* occurs throughout the Neotropics and Africa, but also in Atlantic Europe. The results of phylogenetic analyses based on nuclear ribosomal ITS and chloroplast DNA trnL-F sequences recovered existing classifications as non-natural. A new generic classification is, therefore, proposed here. This classification takes into account the results of the phylogenetic analyses as well as careful examination of morphological evidence. Marchesinia brachiata is split into three species (*M. languida, M. bongardiana, M. brachiata* s.str.) that are separated by characters of the underleaves, and leaf dentation. The European / North African *Marchesinia mackaii* is placed sister to the remainder of the genus. A reconstruction of the historical biogeography of the genus based on DNA sequence variation and the fossil record provides evidence for an origin of *Marchesinia* in the Late Creataceous and subsequent diversification in the Oligocene and Miocene. The African-South American range of populations assigned to *Marchesinia brachiata* is likely the result of migration by spore dispersal. The European / North African *Marchesinia mackaii* clade dates back to the Early Tertiary. Possibly *Marchesinia mackaii* represents a boreotropical element.

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Phylogeny of silverfishes (Zygentoma) and the origin of the winged insects: insights derived from internal anatomy

Markus Koch, Nicola Dolgener

Freie Universität Berlin, Institute of Biology, AG Animal Systematics and Evolution,
Königin-Luise-Str. 1-3, 14195 Berlin, Germany

The diversity of life habits in silverfishes ranges from 'free-living' soil dwellers to hypogean forms and cave-dwellers, as well as psammophily, myrmecophily, and termitophily. The evolution of these life habits has not yet been worked out as the interrelationships of the high-ranking subgroups still remain unknown. Since characters of the external morphology are apparently insufficient to resolve their affinities, the internal anatomy of 16 species covering each of the major zygentoman subgroups has been studied comparatively by histological sections. Among the internal organs, high variability is recognized for the structure of the gut and the composition of the gonads. A comparatively short foregut seems to be maintained in *Tricholepidion*, whereas a marked crop extending into the abdomen characterizes all other zygentomans. Proventricular denticles proved to be present in all zygentomans (including *Tricholepidion*) except for the Atelurinae. The composition of the proventricle in Maindronia is overall identical to the state in Lepismatidae, but is situated more posteriorly in the 7th abdominal segment. The gonads significantly differ in the number of ovarioles as well as testicular follicles. Absence of spermatolophids and the cercal articulation in *Trinemophora* supports the current view that Protrinemuridae are not nicoletiids, but are most closely related to Maindroniidae and Lepismatidae. The absence of labial nephridia in *Trinemophora* and its uniquely shaped tentorium seem to support the monophyly of Protrinemuridae though the former character is shared with pterygote insects. The ventral nerve cord proved to be non-informative in being consistently composed of three thoracic and eight abdominal pairs of ganglia. Results obtained are combined with characters of external morphology and analyzed cladistically to test new evidence for the view that Zygentoma is paraphyletic with respect to Pterygota.

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On distribution and variability of hepatics in Svalbard

Nadezhda Konstantinova, Anna Vilnet, Anatoliy Savchenko

Polar-Alpine Botanical Garden-Institute of the Kola Sci Center of RAS Kirovsk, Murmansk Province, Russia 18425, nadya50@list.ru

The results of study of hepatics of Svalbard were summarized and revised by A. Frisvoll & A.Elvebakk (1996). These authors accepted a totally 85 hepatic species for archipelago. We studied hepatics of Svalbard since 2004 and collected them in eastern coast of Grønfjorden including the lower part of Grøndalen, valley of Linnevatnet, western coast of Bockfjorden, middle part of Reindalen and Nordauslandet, Prins Oscar Land. As result a new for archipelago as well as rare and poorly known species were found and knowledge on distribution of many taxa were greatly expanded. Four taxa (*Anastrophyllum sphenoloboides* R.M.Schust., *Lophozia silvicoloides N. Kitagawa, Marsupella boeckii* (Austin) Lindb. *Marsupella sprucei* (Limpr.) H.Bern.) were collected in Spitsbergen for the first time. The presence in Spitsbergen of three species excluded early from the list of hepatics of archipelago by Frisvoll & Elvebakk (1996) was confirmed. Of them *Lophozia excisa* (Dicks.) Dumort. was collected in most areas visited while *Dichiton integerrimum* (Lindb.) H.Buch and *Odontoschisma elongatum* (Mart.) Dumort. were gathered only once. New localities were discovered for 7 very rare in Svalbard species (*Diplophyllum albicans* (L.) Dumort., *Gymnomitrion apiculatum* (Schiffn.) Muell. Frib., *Scapania spitsbergensis* (Lindb.) Muell Frib., *Lophozia polaris* (R.M.Schust.) R.M.Schust., *Schistochilopsis grandiretis* (Lindb.) Konst., *Nardia geoscyphus* (De Not.) Lindb.) as well as for a number of rare species. Majority of these species are arctomontane species, while several ones are worldwide rare or poorly known and critical species. Distribution of these species are maped and discussed. Morphology of several studied specimens of *Anastrophyllum sphenoloboides*, *Scapania spitsbergensis*, *Gymnomitrion apiculatum, Lophozia silvicoloides, Marsupella boeckii*, etc. collected in Svalbard differ very little from that of specimens collected in Europe or Asia. This corresponds with very low genetic variability of species. The sequences of ITS1-2 nrDNA and trnL-F cpDNA of most studied species sampled in Spitsbergen, Siberia and European part of Russia differs not more the 1%. But in some species (particularly *Lophozia excisa*) both morphological and genetical variability are very high and will be discussed in details. This research has been supported partly by Russian Foundation for Basic Researches grant (06-04-48225).

049

A story of success: toward the phylogeny of the cleptoparasitic Nyssonini (Hymenoptera: Apoidea, Crabronidae)

*Stefanie Krause, Michael Ohl

Museum für Naturkunde, Humboldt Universität, Invalidenstr. 43, 10115 Berlin, Germany, stefanie.krause@museum.hu-berlin.de

Most of the approximately 28,000 species of Apoidea build their own nests and provision them with larval food. A remarkable exception are the members of the Nyssonini (Crabronidae, Bembicinae): all of the more than 200 extant species are assumed to be obligate clepto- (or brood) parasites of other crabronid wasps. The adult female enters the nest of its host and uses the hosts provision for its own eggs. Apart from *Stizoides* (Bembicinae), the Nyssonini are the only known brood parasites within the paraphyletic assemblage of apoid wasps and are therefore of special interest. However, only little is known about the biology and taxonomy of this taxon. Although taxonomic catalogues of the Nyssonini are available, a broad overview or a comprehensive key to species level are lacking and a modern cladistic analysis of the Nyssonini does not exist. The current work aims at producing a cladistic analysis at the genus level. The preliminary analysis presented is based on a large number of morphological characters and includes 30 species representing the 18 genera of the Nyssonini as well as three species of the Alyssontini and Bembicini (both Bembicinae).

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Fossil jumping genes – witnesses of evolutionary history in bird genomes

Jan Ole Kriegs, Andreas Matzke, Erin Arms, Denise Kelsey, Gennady Churakov, Jürgen Schmitz

Institute of Experimental Pathology, University of Münster, Von-Esmarch-Str. 56, 48149 Münster, Germany, kriegs@uni-muenster.de

Reconstruction of Avian evolutionary trees by morphological and molecular methods has undergone diverse revisions leaving numerous aspects hotly debated. Retroposed elements integrate randomly into genomes with negligible probabilities of the same element integrating independently into orthologous positions in different species. Thus, presence/absence analyses of these elements are an auspicious strategy for molecular systematics. Here we present such „fossil jumping genes“ of the CR1 family of retroposed elements as powerful markers of evolutionary history in different parts of the avian phylogenetic tree.

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The morphological, anatomical and ecological properties of *Allium* (Liliaceae) taxa on the Cihanbeyli-Konya salt lake

Mustafa Küçüködük, Ayşe Pektaş, Murad Aydın Şanda

Selcuk University, Science and Art Faculty, Biology Department, Campus-Konya, Turkey

The morphology, anatomy and ecology of three taxa (*A. cappadocicum, A. flavum subsp flavum var. flavum, A. vuralii*) of the genus *Allium* have been investigated. In the anatomical investigation, sections of the root, scape, bulb and leaf of the species were examined and similarities and differences between the species were determined. The root epiderma cells of *A. cappadocicum* are larger than those of the other two species. There are shuttle-like cavities with thick-walled cells in the transverse section of the bulbs of these three species as a result of drying. In all taxa the cuticles of the scape are thick, *A. cappadocicum* having the thickest cuticle scape. Epidermis cells bear longitudinal striation over most cells between cuticle and epidermis in *A. vuralii*. Leaves of *A. flavum* and *A. vuralii* are fistulose, terete and mesophyll is unifasial; leaves of *A. cappadocicum* are flat and the mesophyll isolateral. In all taxa stomata are numerous, slightly too deeply sunken, xerophytic and anomocytic. The leaves of *A. flavum* and *A. vuralii* are different from those of *A. cappadocicum* having hairs and ribs. The stomata cells of *A. cappadocicum* are larger than the stomatas of other two species. Another charecteristic feature of *A. cappadocicum* is the row of micropapillae in the cuticle of leaves. The spongy mesophyll cells increase in size inwards and break down to a large central cavity in all species; the largest cavity is seen in *A. vuralii*. The most important morphological difference is the number of valves of the spathe. A. cappadocicum has a 1-valved spathe with a long beak; *A. vuralii* and *A. flavum* spathes are 2-valved. All taxa grow on saline and strongly alkaline loamy soils containing excessive calcium carbonate. Their soils are poor in organic matter (P_2O_5, K_20, Ca, Mg, Mn), but rich in iron content.

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Phylogeography of *Schmidtea mediterranea*

*Eva Lázaro, J. Baguñà, M. Riutort

Dpt. de Genètica, Fac. Biologia, Universitat de Barcelona, Spain

Schmidtea mediterranea presents a distribution limited to the Western Mediterranean (Catalonia, Balearic Islands, Corsica, Sardinia, Sicily and Tunisia). There exist two races according to their mode of reproduction: sexual and fissiparous, the latter present only in Catalonia and Minorca. The fissiparous race differs from the sexual by the presence of a chromosomic heteromorphism due to a translocation, and can be both diploid and triploid. Basing on the distribution of the biotypes known until that time and on the microplate's theory of the formation of the Mediterranean, Baguñà et al. proposed a biogeographical hypothesis to explain the known distribution of the species. This hypothesis allowed these authors to predict that the species could likely be found also in other parts of the Catalan Coast, the Balearic Islands and the Kabylie, predictions that have all been confirmed with successive descriptions of the species in Majorca, Minorca, Empordà and Tunisia. The phylogenetic analysis of these biotypes based on protein data suggested that the chromosomal heteromorphosys would be a recurring phenomenon, and so the acquisition of asexuality. We have sampled all the known populations of this species in order to study their genetic variability with nuclear and mitochondrial markers and also to infer the phylogenetic relationships among the populations. The preliminary results show a phylogenetic tree that seems to confirm the biogeographical hypothesis. However, the genetic variability analyses have found all the markers used not to present any variability at the intrapopulation level, neither for the fissiparous nor for the sexual populations, this surprising result will be discussed.

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An Andean diaspora: taxonomy, biogeography, and phylogeny of the fern genus *Melpomene* (Polypodiaceae)

Marcus Lehnert[1], Michael Kessler[1], Alexander N. Schmidt-Lebuhn[2], Susan A. Klimas[3], Shannon Fehlberg[3], Thomas A. Ranker[3]

[1] Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, [2] Institut für Biologie, Abt. Pflanzenökologie, Martin-Luther-Universität Halle-Wittenberg, Am Kirchtor 1, 06108 Halle (Saale), Germany, [3] University Museum and Department of Environmental, Population, and Organismic Biology, University of Colorado, 265 UCB, Boulder, CO 80309-0265, USA, mlehner1@uni-goettingen.de

Melpomene is genus of small tropical ferns and comprises 28 species with ten varieties. They are characterized by pinnatifid fronds and clathrate, often iridescent scales with apical glands. Most have a strong aromatic scent that persists in dried specimens. Many species grow strictly or mainly epiphytically in moist montane forests; some species are characteristic páramo elements and grow as terrestrials or saxicolous. The genus is common in the moist, tropical-montane areas of South America, but most diverse in the Andes. One species, *M. flabelliformis* (Poir.) A.R. Sm. & R. C. Moran, also occurs in Africa, Madagascar and the Mascarenes. The results of our phylogenetic analysis confirm the monophyly of the genus. The basal species, which are geographically restricted to southern Mexico and the high regions of the Andes, are morphologically distinct from the rest of the genus (e.g., fronds especially thin textured or with gibbose free segments vs. fronds coriaceous with adnate segments). The core group of *Melpomene* is divided into two main clades, one of mainly epiphytic species with hairs to 2 mm long and erect rhizomes (*M. pilosissima*-group), and one containing many terrestrial species with hairs to 1 mm long and prostrate rhizomes (*M. moniliformis*-group). Short branch lengths in the cladograms of the core group indicate a relatively young diversification in *Melpomene.* A connection with the final uplift of the Andes (ca. 1.5 Mya until today) is suspected because the most diverse clades grow mainly above 2000 m a.s.l. The distribution patterns suggest several dispersals from the Andes to the Caribbean, Mesoamerica, the Guyana Highlands, SE Brazil, and the Old World.

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Do mycorrhizae in ferns contain a phylogenetic signal? - a review

Marcus Lehnert, Hans-Peter Kreier, Michael Kessler

Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, mlehner1@uni-goettingen.de

We gathered information about presence, type, and abundance of mycorrhizal fungi in the sporophytes of ferns and lycophytes, and compared it with the phylogenetic position of the host plants. We have records for 1298 samples representing 1009 species and 36 of the 40 recognized fern and lycophyte families, which show an average presence of fungal infections of 62%. Only mycorrhizae involving arbuscular mycorrhizal fungi (AMF; 75% of infected samples) and ascomycetes (25% of infected samples) are known from these taxa. AMF are dominant in terrestrial ferns and change in prevalence according to soil fertility. The percentage of non-mycorrhizal and facultatively mycorrhizal ferns increase with advanced phylogenetic position. This general trend is disturbed by young radiations in old phylogenetic lineages (e.g., Selaginellaceae, Hymenophyllaceae) and in mainly epiphytic groups (Polypodiaceae), which are either non-mycorrhizal or have changed to a more derived type of mycorrhiza (i.e., with ascomycetes). The information for some groups (e.g., lycophytes, Oleandraceae, Dennstaedtiaecae, Tectariacaeae) is still insufficient and calls for more intensive studies. Reports for gametophytes indicate a much clearer trend of successive independence of ferns and lycophytes from mycorrhizae with advancing evolution. Our works in progress investigate the fungal infection rate of terrestrial ferns in relation to changing soil fertility, and compare the phylogeny of selected fern groups and its mycorrhizal fungi.

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Taxonomic assessment of morphological and molecular data from selected clones of the family Surirellaceae (Bacillariophyta)

*Sabine Lenz, Regine Jahn, Birgit Gemeinholzer*Botanical Garden and Botanical Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Str. 6-8, 14195 Berlin, Germany*

Diatoms are unicelled eucaryotes which inhabit any wet or moist ecosystem. The most important characteristics of diatoms are their silicate frustules which are produced within the plasmalemma and delimit the cell to the outside. The frustule has an epitheca and a hypotheca which interlock like two parts of a box interconnected through girdle bands. Diatoms undergo cell division in which each daughter cell gets one theca and the corresponding valve is formed inside and between the two mother theca. After several consecutive divisions, the size of the frustules of one part of the population is obviously decreasing. When a certain size is reached, enlargement is regained by sexual reproduction. Diatoms are classified on the basis of their symmetry: centrics and pennates. The pennates are classified according to the possession of a raphe into araphids and raphids; within the raphids according to the type and position of the raphe. The taxa with a canal-like raphe surrounding the valve face are classified within the family Surirellaceae. For the lower ranks, the different architecture of their frustules are important features for differentiating genera and species. In this study, we want to test if these pronounced morphological features are supported by selected molecular data. A taxonomic evaluation of selected clones belonging to the genera *Surirella, Cymatopleura, Campylodiscus* was carried out. The morphological evaluation of their features was performed by qualitative and quantitative investigation of their silica frustules using light microscopy (LM) and scanning electron microscopy (SEM). The morphometrics of the valves such as outline, size (length and width), costae and striae per 10 μm was calculated. For the molecular evaluation, the total genomic DNA was isolated using the Dynabeads method, and the large subunit of RuBisCO (rbcl) region was amplified and sequenced. The obtained sequences were compared with a molecular reference database (GenBank; www.AlgaTerra.net). This data was used for phylogenic analysis calculated by maximum-parsimony (MP) and maximum-likelyhood (ML).

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Multiple origin of autogamy in Marantaceae

*Alexandra C. Ley, Regine Claßen-Bockhoff

Institut für Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Germany, aley@uni-mainz.de

The Marantaceae are the most derived family in the order Zingiberales. They evolved sophisticated flowers characterised by an irreversible explosive pollination mechanism and extreme proterandry. During bud development pollen is deposited on the back of the style head to be secondarily presented by the style. After that, tension is built up between the style and the enveloping hooded staminode. The deflection of the trigger appendage at the hooded staminode releases the style from its tension which rapidly curls in. During this movement the stigmatic cavity scrapes off the foreign pollen from the insect and immediately hereafter deposits own pollen from the pollen plate onto the insect. Due to the strong hold of the style by the hooded staminode and the strict spatial separation of stigmatic cavity and pollen plate the self-fertile Marantaceae usually depend on a pollinator to get fertilised. However, autogamy arose at least four times independently within the family. In the respective species pollen transfer is mediated via subtle changes in the morphology of the style head (*Halopegia azurea*) or of the hooded staminode (*Maranta noctiflora, Marantochloa leucantha, Pleiostachya pruinosa*). In the first species, own pollen slides into the stigmatic cavity during the style movement because the pollen plate beats against the fleshy staminode that pushes the pollen over the low proximal rim of the stigmatic cavity. In the remaining three species the specific arrangement of the hood around the style head promotes the squeezing of pollen grains over the distal rim of the stigmatic cavity after pollen deposition. Pollen is finally taken up by the stigmatic cavity during the rapid style movement resulting in 100% selfing in all species. The four presented species illustrate that small morphological changes may have considerable effects on the breeding system. We assume that the driving evolutionary forces for the switch towards autogamy are self-assurance in the absence of pollinators and compensation for reduced vegetative propagation.

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Intraspecific variation in Viola suavis in Europe - parallel evolution of white-flowered morphotypes

Judita Lihová, Pavol Mereďa, Iva Hodálová

Institute of Botany, Slovak Academy of Sciences, Dúbravská cesta 14, 845 23 Bratislava, Slovak Republic, judita.lihova@savba.sk

Viola suavis (*Viola* sect. *Viola*) represents a taxonomically critical species with a series of morphologically and geographically defined races treated at different taxonomic levels. It is widely distributed in the Mediterranean from Morocco eastwards to the Middle East but due to cultivation its distribution area expanded also to Central and northern Europe. In the present study we aimed to explore its morphological and genetic (by means of AFLP fingerprinting) variation in Central and southeastern (C & SE) Europe, but including also populations from Spain. We focused on resolving the status and origin of white-flowered populations (vs common blue-flowered ones), which have not been previously reported from C & SE Europe. The white-flowered morphotype was, however, previously recorded from Spain, and treated as *V. suavis* subsp. *catalonica*. Our results indicated clear differentiation between Spanish and C & SE European populations, and white-flowered populations appeared biphyletic. Spanish white-flowered populations shared a single AFLP phenotype that was close to those resolved in Spanish blue-flowered populations. White-flowered populations from C & SE Europe, on the other hand, formed a separate subcluster among the blue-flowered accessions from that area. Parallel evolution and derived status of white-flowered morphotypes is thus invoked. Further sampling and detailed investigation of populations across the entire distribution range of *Viola suavis* is needed to resolve its infraspecific patterns and propose a sound taxonomic concept.

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Evolutionary relationships and speciation in the genus *Pozoa* (Apiaceae) in southern South America

*Patricio López S. [1], Tod Stuessy [1], Karin Tremetsberger [1,2], Gudrun Kohl [1]

[1] *Department of Systematic and Evolutionary Botany, Faculty Center of Botany, University of Vienna, Rennweg 14, 1030 Vienna, Austria, plopez@udec.cl,* [2] *Facultad de Biología Vegetal y Ecología, Universidad de Sevilla, Avenida Reina Mercedes, 41080, Sevilla, Spain*

The genus *Pozoa* includes two species, *P. coriacea* Lag. and *P. volcanica* Matthias & Constance, restricted geographically to the Andes mountains (30°54' to 44°30' S) between Chile and Argentina. The genus is divergent morphologically from other known genera of subfamily Hydrocotyloideae. The goal of this study is to use DNA sequences and AFLP markers to understand the modes of speciation at the populational level of the two species within the genus. For AFLP investigations, five primer combinations were used to analyze 22 populations from throughout the geographical range of both taxa. Analysis of matK and ITS regions in the related genera *Asteriscium*, *Gymnophyton*, *Domeykoa* and *Mulinum* suggest that the former two are closest to *Pozoa*. AFLP data reinforce the idea that the genus is monophyletic and that two major populational systems exist, corresponding to each of the two species. Greater amounts of genetic variation in *P. coriacea*, plus its broader geographic range, suggest that it is ancestral to *P. volcanica* rather than the reverse. Genetic variation in *P. volcanica* is not partitioned into different subpopulations, instead appearing as a single metapopulation. Pioneer populations on Volcan Lonquimay, which exploded in an eruption in 1988, tie genetically to nearby populations.

052

Parasitoids of some fruit flies (Diptera: Tephritidae) in Iran

Hosseinali Lotfalizadeh[1], Babak Gharali[2], Jafar Khalghani[3]

[1] *Department of Insect Taxonomy, Iranian Research Institute of Plant Protection, Tehran, P. O. B. 19395-1454, Iran, hlotfalizadeh2001@yahoo.com,* [2] *Department of Plant Protection Research, Agricultural Research Centre of Ghazvin,Iran* [3] *Agricultural Researches and Education Organization Tehran, Iran*

The parasitoid complex of fruit flies (Diptera, Tephritidae) on different host plants was studied in Iran. Previously reported species of parasitoids from Iran are also included. As a result, nine species from three families of Chalcidoidea (Hymenoptera) and two species of Braconidae are listed as parasitoids of fruit flies. It includes four new records (2 Eulophidae and 2 Eurytomidae) for Iran as Colotrechnus viridis (Masi), *Pronotalia carlinarum* (Szelényi & Erdös), *Eurytoma compressa* (Fabricius) and *Eurytoma strigifrons* Thomson.

048

Hymenopterous parasitoids (Hym.: Chalcidoidea) of xylophagous beetles in Iran

Hosseinali Lotfalizadeh[1], Jafar Khalghani[2]

[1] *Department of Insect Taxonomy, Iranian Research Institute of Plant Protection, Tehran, P. O. B. 19395-1454, Iran, hlotfalizadeh2001@yahoo.com,* [2] *Agricultural Researches and Education Organization Tehran, Iran*

A survey was conducted in Iran on xylophagous beetles, to collect and determine the natural enemies of these beetles. Fifteen species of hymenopterous parasitoids (Hym.: Chalcidoidea) were recorded, from four families: Chalcididae, Eulophidae, Eupelmidae, Eurytomidae and Pteromalidae. Five species are new records for the fauna of Iran: *Callocleonymus pulcher* Masi (Pteromalidae), *Eurytoma blastophagi* Hedqvist (Eurytomidae), *Eusandalum inerme* (Ratzeburg) (Eurytomidae) and two Chalcididae, *Trigonura ruficaudis* (Cameron) and *Trigonura sphenoptera* Nikol'skaya. Biological information and distribution of each are provided. *Heydenia pretiosa* Förster and *Trigonura sphenoptera* Nikol'skaya are recorded for the first time parasitizing on *Xylopertha reflexicauda* Lesne (Col.: Bostrychidae) and buprestid beetles, respectively.

020

A three-dimensionally preserved nemathelminth from the Cambrian

Andreas Maas, Klaus J. Müller, Dieter Waloszek, Joachim T. Haug

Biosystematic Documentation, University of Ulm, Ulm, Germany, andreas.maas@uni-ulm.de, Center of 'Orsten' Research and Exploration C.O.R.E. (http://www.core-orsten-research.de)

A new, 145 µm long, three-dimensionally preserved fossil from Middle Cambrian rock collected in Queensland, Australia is presented. The possibly immature form, named *Shergoldana australiensis* Maas, Waloszek, Haug & Müller, 2007, shares features with several Recent Nemathelminthes, i.e. with the minute gastrotrichs and among cycloneuralians with the priapulids, kinorhynchs, and larval nematomorphs. Similarities include the body tagmosis and structural details but occur in a mixed assemblage. The tubular annulated anterior part of the body of *S. australiensis*, for example, resembles that of extant nematomorph larvae, with the difference that the accordion-like annulated region is somewhat irregular in the fossil. Nematomorph larvae can contract but not intrude this region, which we also assume for the fossil. A comparable region exists, in our view, also in all scalidophoran taxa, i.e. in kinorhynchs, priapulids and loriciferans, the so-called neck region. The body region anterior to the neck of scalidophorans, the introvert, can be ex- and intruded. Other similarities of *S. australiensis* with cycloneuralians concern a ring of structures located around the frontal opening, the presumed mouth area, possibly representing a pharyngeal armature consisting of inwardly pointing tooth-like outgrowths. Backwardly pointing spines on plates on the region behind the annulations resemble structures found on different parts of the body of priapulids. At least some shared features may represent plesiomorphies with regard to the ground pattern of Nemathelminthes or Cycloneuralia, such as the bifurcated tail end. *S. australiensis* is presented here as possibly the first record of a free-living immature cycloneuralian from the Cambrian, even if it remains uncertain whether it has closer affinities to the one or other in-group. The new data provided by S. australiensis are expected to enlighten the systematic status of the various macroscopic, 2D- and 3D-preserved Cambrian fossils previously described as roundworms or even priapulids, including the slim but cm long palaeoscolecids and the embryonic stages of *Markuelia* sp., both co-occurring with *S. australiensis*. The new find also adds to the discussion whether the scalid-bearing body region called introvert in Scalidophora stems from the cycloneuralian ground pattern ("Introverta"). It seems that the introvert is indeed a scalidophoran novelty.

085

Study of *Navicula* Bory diatoms in Tajan river, Mazandaran province, Iran

*Nahid Masoudian[1], Fattolah Fallahian[2], Taher Nejadsattari[2], Ramezanali Khavari nejad[2], Mohammmad Naderpour[1]

[1]Islamic azad university damghan branche Damghan, Iran, [2]Islamic azad university, Science and Research Branch, Tehran, Iran

The Tajan river originates from Alborz mountains of Iran and is the most important source of water for agriculture and economic purposes in Sari, the centre of Mazandarn province. The study of the microorganisms in this river is very important for water quality determination. Diatoms are major constituents of the flora of freshwater habitats. This study was carried out from March to September 2007. Samples were taken in monthly interval periods and immediately fixed in situ with 4% Formaldehyde. For identification, permanent mounts were prepared using the Patrick & Reimer procedure. Species identification was done by means of light microscope and the counting method was used for recognition of diatom communities. Among 14 species identified of *Navicula*, *N. cryptocephala*, *N. halophila, N .placentula* and *N.lanceolata* were the dominant taxa. The study also revealed that the density of diatom species was higher in stone beds than in sediments, also in cold months.

097

Web based digital taxonomic tools, center pieces in the multidisciplinary approach of elucidating evolution and systematics of the giant genus *Peperomia* (Piperaceae)

Guido Mathieu[1], Paul Goetghebeur[1], Stefan Wanke[2], Marie-Stéphanie Samain[1]

[1]Ghent University, Department of Biology, Research Group Spermatophytes, B-9000 Gent, Belgium, [2]Technische Universität Dresden, Institut für Botanik, Plant Phylogenetics and Phylogenomics Group, D-01062 Dresden, Germany

With currently 1615 accepted taxa, about 1400 synonyms and over 1500 'herbarium names' (unpublished names mentioned on herbarium specimens), *Peperomia* is generally considered as a 'difficult' genus.

The establishment of several digital taxonomic tools has enhanced a renewed interest in this genus and boosted research efforts during the last few years. Taxonomic tools include the TRGP (Taxonomic Repertory of the genus Peperomia), the PBO (Peperomia Bibliography Online; currently more than 900 references) and the DPP (Digital Peperomia Photobase; currently about 100.000 digitalised herbarium specimens from 60 herbaria in Europe, South and North America). The TRGP and PBO are online at www.peperomia.net, whereas (parts of) the DPP can be distributed on a transportable medium or uploaded to a FTP server.

Research projects in the genus *Peperomia* supported by these web based tools include floristic studies worldwide, ex situ collection management, phylogenetic research (both morphology and molecular based), the compendium of herbarium names, several *Peperomia* expeditions to Madagascar and Latin American countries, and the NeMys Biological Information System (online at www.nemys.ugent.be). The latter system is an extension of the TRGP core data providing access to recent and historic literature on *Peperomia* as pdf-files, digitalised herbarium specimens, distribution maps, morphological data and interactive identification keys. Digital pictures of living *Peperomia* species are already available on NeMys.

To conclude, the digital taxonomic tools are an essential precondition to carry out research in systematics and evolution of a giant genus, but the effort to compile the information, establish an up to date database and make it accessible online is not frequently made.

095

Evidence for gene flow and introgression among the Mediterranean firs

*Eike Mayland-Quellhorst[1], Birgit Ziegenhagen[2], Sascha Liepelt[2]

[1] Senkenbergstraße 19, Institut für Allgemeine Botanik, Justus-Liebig-Universität Giessen, Germany, [2] Karl-von-Frisch Straße 8, Conservation Biology, Philipps Universität Marburg, Germany

The morphologically distinct *Abies* species in the Mediterranean exhibited generally low variation in plastidal genomes in former studies, compared to the American and Asian section of this genus. Inside the European *Abies* species the conservationally and economically important species *Abies alba* Mill. takes an important position. One reason for this is the large and central range of the silver fir in Europe. For another reason the silver fir seems to be a pool for cpDNA haplotypes and mtDNA haplotypes of the Mediterranean fir species. This emphasizes the importance of this species for nature conservation on the background of climate change. In this study the trnC-trnD locus of the chloroplast genome, with a length of 2,500 bp was used as a marker. Investigated were 21 populations of *A. alba* and one population of each of the seven other Mediterranean species, which exhibited 22 haplotypes. The genetic differences among the haplotypes were small, which also applies to other loci in the Mediterranean species. The small degree of variation did not help to clarify the phylogenetic relationships between the cpDNA haplotypes. Population genetic analysis revealed a moderate degree of differentiation for the entire data set (Gst of 0.23), which could be confirmed by Analysis of Molecular Variance. Bayesian analysis of the data set allowed us to infer a spatial genetic structure with four geographically consistent groups. The distribution of haplotypes and the observed spatial genetic structure led to the hypothesis of *Abies alba* as a melting pot for genetic variation and recent gene flow among parapatric species.

094

A new checklist of the North Iranian Equisetum

Ali Mazooji[1], Fahimeh Salimpour[2]

[1] *Biology Deartment, Islamic Azad University, Roodehen Branch, Iran,* [2] *Biology Department, Islamic Azad University, North Branch of Tehran, Iran*

In a new study on the North Iranian *Equisetum*, conducted in the hyrcanian phytogeographic region during the years 2004 to 2007, a total of 8 species has been reported. Five species, *E. arvense*, *E. fluviatile*, *E. palustre*, *E. telmateia* and *E. ramosissmum*, were already known from Iran, while three (*E. pratense*, *E. variegatum*, *E. hyemale*) are recorded as new to the country.
E. pratense has three angled branches and *E. variegatum* has simple stems or is branched only from base. *E. hyemale* has caducous teeth of the leaf sheaths.

032

Molecular markers from ESTs can give new insights for arthropod phylogeny

*Karen Meusemann, Björn v. Reumont, Bernhard Misof, W. Wägele

Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany

The phylogeny of arthropods, especially the phylogenetic position of key taxa like Remipedia, Copepoda out of the Crustacea as well as the enthognath hexapod taxa (Collembola, Diplura, Protura) is still not resolved, analyses of mitochondral and nuclear protein coding data currently arrive at different conclusions. EST-databases which become more and more common deliver a large amount of sequence data. It is now possible to look for new molecular markers suitable for resolving deep phylogenetic relationships within arthropods. Focused on crustaceans and apterygot hexapods we produced EST-libraries for key taxa of Crustacea (Branchiopoda, Cirripedia, Copepoda) and for key taxa of apterygot insects (Collembola, Archaeognatha, Diplura). We analysed over 40 arthropod taxa for more than 60 genes and reconstructed a phylogeny of arthopods based on the included EST-data. A preliminary analysis of EST-data shows already a well supported resolution of the arthropd phylogeny. Furthermore, we are working on a "primer-toolbox" of protein coding genes based on the EST-data to establish primers for reliable amplification from genomic DNA which can then be easily applied to a large number of arthropod taxa. These two subprojects (one focused on crustaceans, one on "basal" hexapods) are embedded in the projects "Molecular phylogenetic analyses of crustaceans (Entomostraca + Malacostraca)" and "The "Atelocerata" - a vanishing hypothesis?". Both are part of the priority program „Deep Metazoan Phylogeny", SPP 1174, financed by the German Science Foundation (DFG).

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Repeated evolution of succulent basal organs in Apocynaceae

Ulrich Meve, Sigrid Liede-Schumann

Lehrstuhl für Pflanzensystematik, Universität Bayreuth, 95440 Bayreuth, Germany

Biosystematical research in the monophyletic family Apocynaceae (373 genera with ca. 5,000 species) caused a tremendous scientific output in the last years emphasising molecular analyses, but including also studies on morphology, karyology, reproduction biology, and biogeography. These results, almost evenly covering the complete family, allow a much improved insight into the phylogenetic structures mirrored by a fine-tuned taxonomy at all levels. Statements on the evolution of different characters within the family now become possible as well. In the present study, the evolution of succulence of basal organs in Apocynaceae s.l., whether root, stem or leaf succulence, is analysed. Succulence is predominantly confined to the Old World, and here to the most highly developed and diverse subfamily Asclepiadoideae where it is typically associated with the tribe Ceropegieae that includes the species-rich stem-succulents stapeliads and *Ceropegia*. Nevertheless, succulent plants occur in 61 genera of Asclepiadoideae, and these are not monophyletic. Apart from Asclepiadoideae, succulent taxa are restricted to two genera of Apocynoideae, and nine of Periplocoideae, which are also not monophyletic. Succulence is only missing in two of the five subfamilies (Rauvolfioideae, Secamonoideae). In the three other subfamilies all types of succulence evolved manifold and independently from each other: Root succulence evolved independently at least twelve times, stem succulence at least eleven times, and leaf succulence, generally less frequent and typically confined to Marsdenieae and Ceropegieae (Asclepiadoideae), evolved at least eight times.

013

Sipunculan hemerythrin protein family has strong annelid affinity

*Achim Meyer, Bernhard Lieb

Institut für Zoologie, Johannes Gutenberg-Universität Mainz, Germany

Hemerythrin an oxygen carrier in erythrocytes suspended in the coelomic fluid is only known for the sipunculids, brachiopods and priapulids. Additionally, other members of the hemerythrin family e.g. myohemerythrins have been found in several annelid species, the oligochaetes and polychaetes. By sequencing 2000 ESTs from Sipunculus nudus we found 17 hemerythrin sequences including two new hemerythrins: (i) hemerythrin C which is closely related to S. nudus hemerythrin A and (ii) a second isoform which is similar to the more basal monomeric hemerythrins, myohemerythrin, neurohemerythrin and MPII (Metalloprotein II). Phylogenetic analyses using 'Maximum Likelihood' and 'Baysian inferences' reveal a close relationship between monomeric annelid and sipunculan hemerythrins and suggest a derived status for the sipunculid oxygen carriers hemerythrin A, B and C. Additionally, this dataset stresses the extraordinary and basal position of S. nudus in Sipuncula and indicates a monophyletic clade of sipunculan hemerythrins with octameric quarternary structure.

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A three-year study of weed management on plant community in field margins in an openfield landscape

Nadia Michel, Louis de Redon, Aurélie Garnier, Sovuthy Him-Thean, Marina de Miguel, Aude Sourisseau, Jean-Michel Dreuillaux, Robert Haïcour, Agnès Ricroch[1]

[1] *Université Paris-Sud, Lab. Ecologie, Systématique et Evolution, UMR 8079 CNRS, Bât. 360. F-91405 Orsay cedex, France, agnes.ricroch@u-psud.fr*

Our study assessed the weed abundance and diversity in 27 field margins (FM) to examine the effects of three years of herbicide use and/or mowing on the similarity and composition of the floristic richness and diversity of plant community. The influence of year and weed control on floristic patterns were analysed to measure the dynamics of weeds in a 46 km^2 open field landscape in France (2005-2006-2007). We quantified management intensity and examined the local characteristics of FM, and used principle component analyses to ordinate the environmental variables. Data showed that all the parameters describing plant richness were affected by the farming system (weed control) but differently according to the year. Moreover the total richness in all FM increased from 2005 to 2007. Indeed 102 species were found in 2005, 122 in 2006, and 134 in 2007. Interestingly we noted that this increase in species richness coincided with the decrease of the number of treated FM. Since 2007 no weed treatment was applied in FM adjacent to roads following the new application of usual good farming practices validated by the French Departmental Commission for Agricultural Policy. This new measure enhanced at once the quality of FM for plant preservation. Diversity of local weed species was influenced by both FM characteristic (type of adjacent road) and farming system (weed control). No evolutionary reproductive strategy of a botanical group was predominant in relation to the decrease of weed control as the proportion of annuals was similar to perennials each year. However ubiquitous species were able to be maintained in FM with very low plant richness under strong conditions resulting from intensive and repeated weed treatments. The increase in the number of insect-pollinated species in all FM that were surveyed over time is a good indicator for the persistence of both the pollinator-requiring species in plant communities and the community of pollinators. The persistence of pollinator-requiring species provided sustainable local nectar resources for insects and thereby can prevent insect-mediated gene flow over long distances in the landscape. The increase in the richness of not insect-pollinated species, i.e. autogamous and wind-pollinated species, showed that these types of species, generally known to be more sensitive to disturbances than insect-pollinated species, were however able to persist in disturbed habitats such as intensively managed FM.

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Genetic variation in populations of *Microdracoides squamosus* (Cyperaceae) on inselbergs in Cameroon

*Irma Mika[1], Reiner Finkeldey[1], Stefan Porembski[2]

[1] Department of Forest Genetics and Forest Tree Breeding, Büsgen-Institute, University of Göttingen, Germany, [2] Allgemeine & Spezielle Botanik und Botanischer Garten, Institut für Biowissenschaften, University of Rostock, Germany

Inselbergs are isolated dome-shaped Precambrian rock outcrops which are completely differentiated from their surroundings concerning their edaphic and microclimatic conditions: The soil cover is thin or absent and evaporation rates are high. Inselbergs occur all over the tropics and also in actual temperate regions with a former tropical climate. They represent terrestrial habitat islands resembling islands in the ocean. Therefore they have been suggested as model systems for ecological and evolutionary studies. Investigating the molecular ecology and genetics of inselberg radiations can be the key towards the understanding of continental adaptive radiations. Inselberg vegetation differs significantly from that of their surroundings. A set of typical habitats, e.g. monocotyledonous mats, evolved with a high number of endemic species. On African inselbergs Cyperaceae are dominant in monocotyledonous mats. They developed a treelet-like habit and several adaptations to water scarcity like roots possessing a velamen radicum and poikilohydry. One of the endemic species of inselbergs in Cameroon is *Microdracoides squamosus* Hua. It is disjunct in its distribution and occurs in Guinea/Sierra Leone as well as in Nigeria and Cameroon. Some other inselberg species share this distribution pattern which is possibly caused by Pleistocene climatic perturbations. The aim of this work is to assess the genetic variation within and between five fragmented inselberg populations of *Microdracoides squamosus* in Cameroon using AFLPs. We will test the hypotheses that genetic variation is low within populations due to small, isolated habitats, and that there is a correlation between genetic and geographical distance due to limited and rare dispersal events.

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Cynoglossum paraphyletic

*Oliver Mohr, Christian Schwarzer, Hartmut H. Hilger

Institut für Biologie, FU Berlin, Systematische Botanik und Pflanzengeographie, Altensteinstr. 6, 14195 Berlin, Germany

Boraginaceae s.str. have a cosmopolitan distribution with centres of diversity in the northern temperate zone and the Mediterranean climates and comprises some 300 genera and over 2,000 species. Various authors viewed the infrafamilial classification of the family very differently and up to 20 tribes have been proposed. The traditional and most widely used classification (Gürke 1893) recognizes four large tribes: Boragineae, Eritrichieae, Lithospermeae and Cynoglosseae. A recent study with molecular markers (Långström and Chase 2002, Plant Syst. Evol. 234: 137-153) proposed an additional, well-defined tribe Echiochileae, but indicated that the Eritrichieae and Cynoglosseae in their traditional circumscription are not natural groups and propose the fusion of these two tribes in a single, more widely defined Cynoglosseae. The present study attempts to resolve the relationships between the members of these Cynoglosseae on the basis of three different molecular markers (trnL-F, ITS, rpS16) and a wide taxon sampling. The genus *Cynoglossum* appears to be highly paraphyletic and/or polyphyletic and its members are retrieved in several different clades. Consequently, extensive rearrangements and nomenclatural changes must be performed. To support our assumptions, in addition to the molecular data, flower-, inflorescence-, fruit morphological and palynological facts had been consulted. Further results are: the species of *Cynoglossum* fall into two monophyletic groups, a mainly Eurasian-N.-African clade, in which lineages of *Cynoglossum* occur next to species of e.g. *Lindelofia*, *Pardoglossum*, *Rindera* and *Solenanthus*. The taxa of the second clade have their centre of diversity in America. This second monoplyletic group will informally be called “Cryptantheae” since the American genus *Cryptantha* represents the largest group within it. Other genera included are *Plagiobothrys*, *Amsinckia*, *Pectocarya*). However, “Cryptantheae” is not used as proposed by Brand (1925), who adopted it erroneously instead of the tribal name Eritrichieae, but as a circumscription for the monophyletic group described here.

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Systematic implications of nutlet morphology in the tribe Mentheae (Nepetoideae: Lamiaceae)

*Hye-Kyoung Moon[1], Erik Smets[1,2], Suzy Huysmans[1]

[1] Laboratory of Plant Systematics, Institute of Botany and Microbiology, K.U.Leuven, Kasteelpark Arenberg 31, P. O. Box 2437, 3001 Leuven, Belgium, [2] National Herbarium of The Netherlands, Leiden University Branch, P. O. Box 9514, 2300 RA Leiden, The Netherlands.

The tribe Mentheae sensu Harley et al. (2004) is an economically important tribe in Lamiaceae with many ornamentals and culinary herbs. Although the tribe is a well supported monophyletic group, subtribal delimitation and the intergeneric relationships are still poorly understood. The nutlet morphology of the tribe, representing 57 out of 65 genera, is documented (SEM) here in order to assess the systematic value of nutlet characters and to evaluate the existing molecular phylogenies for this group. Significant variation was found in nutlet shape, morphology of the abscission scar, distribution of trichomes, and surface sculpture. Surface ornamentation varies considerably and is potentially a systematically important nutlet character in Lamiaceae. Seven different surface types are recognized in Mentheae based on differences in cell outline, anticlinal walls, cell boundary relief and curvature of the outer periclinal wall. A combined cladistic analysis was performed based on molecular data and 15 selected nutlet characters and included 41 taxa for which molecular data were available (411 variable characters of nuclear ribosomal ITS and chloroplast trnL-F sequences). For comparison, the nutlet characters and molecular data were also analysed separately. The resulting topologies indicate that nutlet characters are systematically useful at various taxonomic levels and in particular at generic level. The character evolutions of major nutlet traits are discussed within tribe Mentheae.

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Palynological study of *Trifolium* sect. Lotoidea in Iran

*Golaleh Mostafavi, Fahimeh Salimpour, Youcef Shahali

Department of Biology, Faculty of Science, Islamic Azad University, North Tehran Branch, P.O.Box 19585-935, Tehran, Iran

Lotoidea is the largest section of *Trifolium* and contains 5 perennial and 2 annual species in Iran. Among them, *T. repens* and *T. nigrescens* as well as *T. ambiguum* and *T. montanum* are morphologically very similar. The aim of this survey was the differentiation of these species through a palynological approach. SEM has been used to compare and characterize pollen grains. Characters studied included polar axis (P), equatorial diameter (E), P/E proportion, pollen surface ornamentations, furrow amounts, furrow lengths and furrow ornaments. Results indicate that pollen grains of this section are tricolpate and surface ornamentation reticulate to regulate. The longest and shortest polar axis are found in *T. repens* and *T. glomeratum* respectively. P, P/E proportion, plant growth period and stipule appear to be considered as reliable factors of differentiation for these species. *Trifolium* repens has been previously differentiated by inflorescence characters. Our observations show that this perennial species can also be separated by its particulate pollen polar axis measuring 33/4 μm. (P/E = 1/97μm from above species with P/E = 1/54, 26/21 μm axis length). On the other hand, *Trifolium montanum* and *T. ambiguum* which have been morphologically differentiated by their inflorescence shape and their calyx teeth length proportion to floral calyx tube length, can be identified by using P and P/E measurements. Finally, our studies show that *T. radicosum* which is endemic to Iran, does not belong to this section.

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Mitochondrial genome data of *Sipunculus nudus* gives evidence for an inclusion of Sipuncula into Annelida

*Adina Mwinyi[1], Achim Meyer[2], Christoph Bleidorn[3], Bernhard Lieb[2], Thomas Bartolomaeus[1], Lars Podsiadlowski[1]

[1] Institut für Zoologie, Freie Universität Berlin, Berlin, Germany, [2] Institut für Zoologie, Johannes Gutenberg Universität Mainz, Mainz, Germany, [3] Institut für Biochemie und Biologie, Universität Potsdam, Potsdam-Golm, Germany

The position of the marine Sipuncula within the metazoan tree is currently under debate. While morphological results sometimes place them next to molluscs, more and more molecular studies favour a classification near annelids. In this regard, analyses of mitochondrial genomes have been proven to provide valuable markers for phylogenetic questions. We studied the mitochondrial genome of the sipunculid *Sipunculus nudus*, using both, amino acid sequence information and gene arrangements, as characters for systematic analyses. According to the most parsimonious explanation, the specific gene order of *Sipunculus nudus* can be derived from the hypothetical ground pattern of the Lophotrochozoa, placing sipunculids close to annelids. Due to insufficient genomic data of additional species, the comparison of gene arrangements could not reveal the intrataxonomic correlations of different lophotrochozoan groups so far. However, the outcome of our phylogenetic analyses (Maximum likelihood, Bayesian inference) of amino acid sequence data indicates that sipunculids are closely related to annelids. Moreover the results suggest the inclusion of the Sipuncula into the traditional taxon Annelida, giving reason that sipunculids can be regarded as unsegmented annelids.

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An ecological study of plant associations of Hajaligholi desert in Damghan, Iran

Mohammmad Naderpour, Nahid Masoudian

Islamic azad university damghan branch, Damghan, Iran, mohammadnaderpoor@yahoo.com

The Hajaligholi desert in semnan province situated between 35° 45′ to 36° north latitude and 54° 25′ to 55° east longitude. In this survey flora and plant associations of Hajaligholi desert have been studied.Totally 41 species were determined. These species belong to 17 families and 37genera.The plant associations have been studied using the method of Braun- Blanquet. 93 releves have been taken from area.9 releves have been deleted due to similarity with others, and phytosociological data analysis on 84. Remained releves have been done according to the C.A.H (Classification Asendante Hierachique) and A.F.C (Analyse Factoriel des Correspondance) methods. 13 associations have been defined. The physical and chemical speciality of the soil including texture, EC, N, P, K$^+$ (absorbable) Na$^+$,Ca^{++}and Mg^{++} (soluble) are the important factors for controling the distribution of this communities. Plants are mainly hemicryptophyte (31.7%) and therophyte (26.8%). Gheophytes are less frequent (9.8%). Irano-Touranian elements are 70% and the rest are pluriregional.

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Taxonomic revision and molecular studies of *Garcinia* sect. *Garcinia* (Guttiferae)

M. Nazre

Faculty of Forestry, Universiti Putra Malaysi, 43400 UPM Serdang Selangor, Malaysia

A taxonomic revision of *Garcinia* sect. *Garcinia* (Guttiferae) reduced the number of species from 44 to 16 with 5 varieties. A total of nine species are excluded, 19 species are reduced to synonyms and five species have sufficiently known to be classified. Species of sect. *Garcinia* are typically understorey trees of rain forest distributed from eastern India to Malesia. Within sect. *Garcinia*, three species, *Garcinia acuticosta*, *G. exiguus* and *G. sangudsangud* are newly described while *G. diospyrifolia* var. *arborea*, *G. diospyrifolia* var. *minor* and *G. malaccensis* var. *pseudomangostana* are new varieties. Species limits are defined on the basis of combination of characters from the male flower, i.e. shape of stamens, presence of pistillode or types of fruit and characters from the leaf (shape and size, venation pattern and glandular lines). Using molecular data from sequence of ITS region, most of the sections delimited by Jones (1980) proved to be monophyletic but sect. *Garcinia* is paraphyletic because of *G. maingayi*, *G. trianii* and *G. costata* are in clade that is strongly supported as sister to sect. *Brindonia*. These species should be excluded from sect. *Garcinia*, as is also indicated by morphology. The most significant characters supporting monophyly of sect. *Garcinia* are those of the shape of the stamen bundles.

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Genome sharing patterns in south-east Australian eucalypts

*Paul G. Nevill[1], Gerd Bossinger[2], Peter K. Ades[2]

[1] The University of Melbourne, The School of Forest and Ecosystem Science, and Cooperative Research Centre for Forestry, Water Street, Creswick, Victoria 3363, Australia, [2] The School of Forest and Ecosystem Science, The University of Melbourne, and Cooperative Research Centre for Forestry, Parkville, Victoria 3010, Australia

Interspecific hybridization and introgression appears to have played an important role in the evolution of *Eucalyptus* species. Previous studies, mostly on species in subgenus *Symphyomyrtus*, have found high levels of intraspecific chloroplast DNA (cpDNA) polymorphism and extensive sharing of chloroplast haplotypes between species within regions. Similar to *Quercus*, geographical location is more important than species when it comes to determining chloroplast type in subgenus *Symphyomyrtus*. Less was known about the extent of cpDNA sharing between species in subgenus *Eucalyptus*, as well as the extent of sharing of the nuclear genome between *Eucalyptus* species. In this study we examined sharing of the nuclear and cytoplasmic genome between 200 individuals from 10 species at 25 locations using nuclear and chloroplast microsatellite markers. Preliminary results indicate that cpDNA haplotypes are extensively shared between subgenus *Eucalyptus* species. Twenty five different haplotypes were found in 10 different species at 25 locations where the species occurred together. All species at a location were more likely to share exact haplotypes in areas thought to have been treeless during the Last Glacial Maximum (LGM) than the same species in hypothesised glacial refugia. Preliminary results on the sharing of the nuclear genome indicate extensive sharing of alleles between some species, and little sharing between other species. Further work will help to elucidate the patterns of sharing of both nuclear and cytoplasmic genetic markers.

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Molecular phylogeny of tribe Dipterocarpeae (Dipterocarpaceae, subfamily Dipterocarpoideae) based on sequence data of chloroplast and nuclear ribosomal DNA

*Nga Phi Nguyen, Oliver Gailing, Reiner Finkeldey

Department of Forest Genetics and Forest Tree Breeding, Georg August University of Göttingen, Germany

Dipterocarpaceae is the most important tree family in the flora of Southeast Asia. Southeast Asian dipterocarps belong to subfamily Dipterocarpoideae and are divided into two tribes (Shoreae and Dipterocarpeae). Many studies have been carried out to resolve the taxonomic relationships of subfamily Dipterocarpoideae based on chloroplast and nuclear DNA. Almost all of them focused on the resolution intra- and interspecific relationships within tribe Shoreae and genus *Shorea* while information on the fine scale phylogenetic structure of tribe Dipterocarpeae is rare. The aims of our research are to (1) solve phylogenetic relationships among the genera and species of tribe Dipterocarpeae using coding and non-coding sequences of the chloroplast and nuclear genomes, (2) test the utility of these sequences for phylogenetic construction of interspecific relationships. A total of 51 taxa of tribe Dipterocarpeae was investigated to construct a molecular phylogeny with two non-coding regions (trnL-trnF) and one coding region (petD) of the chloroplast genome and with ITS-2 (internal transcribed spacer) of the nuclear ribosmonal DNA. The results showed that tribe Dipterocarpeae is divided into two clades with significant bootstrap support. One clade consists of genus *Dipterocarpus* and all remaining genera are in the other clade. Genus *Upuna* is the sister group to genera *Vatica*, *Anisoptera*. Generally, the results are consistent with previous phylogenetic analyses of tribe Dipterocarpeae (Tsumura et al 1996; Kayima et al 1998; Dayanandan et al 1999, Gamage et al 2006 and Indrioko et al 2006) but show a higher resolution.

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Urtica Mediterranea – Evolutionary history of stinging nettles (*Urtica*, Urticaceae) in Europe

*Nicolai M. Nürk[1,2], Maximilian Weigend[2]

[1] Leibnitz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), 06466 Gatersleben, Germany, [2] Institut für Biologie, Systematische Botanik und Pflanzengeographie, FU Berlin, 14195 Berlin, Germany

Twenty-one taxa (13 species, 4 subspecies, and 4 varieties) of *Urtica* L. occur in Europe, eight of them endemic on islands of the Mediterranean or Macaronesian region. No data on their phylogenetic relationships, biogeography and character evolution have so far been published and the origin of the endemic species is not understood. Molecular data were generated to elucidate the evolutionary history of *Urtica* in Europe, using the internal transcribed spacer region (ITS) and the chloroplast marker *psb*A-trnH in a representative sample of species of the entire genus. The phylogenetic trees obtained retrieve the annual Mediterranean species of the genus in a basal position, while the perennial taxa form a derived monophyletic group. *Urtica dioica* with its several European subspecies is monophyletic, if *U. kioviensis* is included. The island endemics group in three different lineages: (i) the two annual Macaronesian species *U. stachyoides* and *U. portosanctana* closely allied to *U. urens*, (ii) the perennial species from Macaronesia, Sicily, and northern Lebanon, (iii) and the perennials from Corsica/Sardinia, Majorca, and Cyprus. The first clade of perennial species (*U. morifolia*, *U. rupestris*, *U. fragilis*) is closely allied to Middle East endemics, while the second clade (*U. atrovirens*, *U. bianorii*, *U. cypria*) includes also the East African species. Studies of fruit morphology and reproduction strategies revealed three different types of propagation, which are related to phylogenetic groups. Annual species release mature achenes out of the opening perianth, whereas achenes remain enclosed in the perianth in perennials and are dispersed as a unit. Vegetative propagation by runners is only known from *U. dioica* and members of its clade. In *U. atrovirens* the fruits float and are seawater tolerant, possibly explaining its presence in the northern Tyrrhenian archipelago.

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Diagnostic marker to identify the geographic origin of *Shorea leprosula* (Dipterocarpaceae)

*Hani Sitti Nuroniah, Oliver Gailing, Reiner Finkeldey

Department of Forest Genetics and Forest Tree Breeding, Büsgen-Institute, Georg-August-Universität University of Göttingen, Büsgenweg 2, 37077 Göttingen, Germany

Shorea leprosula Miq is common tree and widespread emergent species in lowland Dipterocap forests in Indonesia. Forest destruction, degradation and exploitation for their valuable timber are the main threats for Dipterocarp forests. In the context of forest certification it is important to test the geographic origin of wood and wood products. Maternally inherited cpDNA marker of *S. leprosula* showed virtually no variation among geographic region of the species. However, AFLP (Amplified Fragment Length Polymorphism) fragments were identified that were fixed in one region (Borneo) but nearly absent from another region (Sumatra). Those diagnostic AFLP fragments have been extracted from polyacrylamide gels and their DNA sequences were determined. The AFLP markers were converted into a simple SCAR marker. We identified deletion and a SNP (Single Nucleotide Polymorphism) in the AFLP (restriction) site. The developed SCAR marker clearly differentiated *S. leprosula* from Borneo and Sumatra and it is high valuable for wood certification in this species.

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Evolution of sex chromosomes in *Bryonia* (Cucurbitaceae)

Ryan K. Oyama, Stefanie M. Volz, Susanne S. Renner

Department of Biology, Ludwig Maximilian University, 80638, Munich, Germany.

Very few dioecious angiosperms are known to have XY sex determination. Studies in *Silene latifolia* and *S. dioica*, the two best understood XY systems in plants, have found that the diversity of Y-linked genes is substantially lower than that of their X-linked homologs and have also revealed geographic population structure among Y-linked loci. We are testing this finding in *Bryonia dioica* (Cucurbitaceae), the first angiosperm in which XY sex determination was proven. Our approach uses sequence-characterized amplified regions (SCARs) developed from male-linked AFLP markers, from accessions taken from populations throughout northern Europe and the Mediterranean. We also generated sequences from the related dioecious species *B. cretica*, *B. marmorata*, *B. syriaca*, and the monoecious species *B. alba* for use as outgroups. A phylogeny constructed from the first sequenced SCAR marker shows a clear clade of Y chromosomes and a clade of X chromosomes from *B. dioica*, with the Y sequences having substantially less diversity. However, it also reveals a paraphyletic grade of "intermediate" *B. dioica* sequences that are neither clearly X nor clearly Y. These findings suggest that the XY system in *Bryonia* is labile and that not all populations lose diversity on the Y chromosome. Our results add to the emergence of the family Cucurbitaceae as a promising system in which to study the evolution of sex chromosomes in plants. Not only does *Bryonia* contain monoecious and dioecious species, but its sister group, *Ecballium elaterium*, has well-characterized monoecious and dioecious populations and also XY sex determination. In addition, more distantly related species in the family have dimorphic sex chromosomes. Finally, phylogenies are available for *Bryonia* and for the family Cucurbitaceae as a whole.

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Cytomorphological analysis of two triploid hybrids from *Solanum melongena* 'Golden' x *S. nigrum* subsp. *nigrum* (Solanaceae)

Olatunji Oyelana[1], Kayode Ogunwenmo[1], Cyril Nwagburuka[2], Okunola Alabi[1]

Babcock University, [1]Department of Basic and Applied Sciences, [2] Department of Agriculture, PMB 21244, Ikeja, Lagos 100 001, Nigeria

Basic genotype manipulation through the introduction of novel genes for value-added yields informed the number of past intergeneric and interspecific hybridization efforts. The interspecific cross effected between *Solanum melongena* 'Golden' (2n = 2x = 24) and *S. nigrum* subsp. *nigrum* (2n = 4x = 48) was aimed at creating a new genome for improving species' agronomic qualities and cytogenetic status, and possibly expand the genetic base for the genus. The only F_1 fruit contained eight seeds and recorded 100% germination. The two surviving triploid hybrids (2n = 3x = 72) were morphologically similar to the diploid parent. Leaves were simple, hairy, and deeply lobed and L/B was 14.75 x 10.57 cm and glabrous, margin entire and L/B 11.42 x 10.83 cm respectively in the diploid and tetraploid parents while they were fairly lobed, sparsely hairy and L/B 13.52 x 8.57 cm in the triploid hybrids. Inflorescences were raceme in the hybrids as in the diploid parent. Flowers were few and many dropped before they were opened. Pollen viability was 71 % and 97.4 % in diploid and tetraploid parents and 38.2 % in the triploid hybrids. Fruits were globose and yellow (384 seeds), round and purple (67 seeds) in the diploid and tetraploid parents but were round, red and seedless in the triploid hybrids. Meiosis was regular and the few univalents and impaired bivalents encountered in the triploid hybrids were linked to dissimilar genomes. Mitotic chromosomes were asymmetrical and sizes varied. Epistasis and other mechanisms including negative gene interactions were implicated in the hybrids' low quality and breakdown. A number of repeated backcrosses to the tetraploid parent are suggested in order to explore the possibility of allelic realignment and possible rearrangement of genes for desirable phenotypes at F_2 and subsequent generations.

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Nuclear and non-nuclear interactions in F_1 hybrids of three *Solanum* species in the subgenus *Leptostemonum* section *Melongena* (Solanaceae)

Olatunji Oyelana, Kayode Ogunwenmo

Babcock University, Department of Basic & Applied Sciences, School of Science & Technology, P.M.B 21244, Ikeja, Lagos, Nigeria

The occurrence of hybrids among *Solanum* species and the attendant phylogenetic misconceptions underscore the need for a re-examination of the breeding systems. A number of reciprocal crosses involving *S. gilo*, *S. anguivi* and *S. macrocarpon* in the subg. *Leptostemonum* (Dunal) Bitter sect. *Melongena* Dunal were effected to assess inherent nuclear and non-nuclear influence on hybrid fitness and determine the extent of genomic changes and species compatibility. The hybrids expressed intermediacy and overlaps in morphometric characters of leaves, petioles, petals and plant height. Maternal influence was dominant in growth habit, leaf shape and texture, flower colour and fruit size while paternal control was limited to fruit color in *Solanum gilo* x *S. macrocarpon.* Pollen viability was depressed from 97.3 - 86.5 % in parents to 53.8 - 20.1 % in hybrids. Stomata were anomocytic in the hybrids except a few contiguous. *S. gilo* x *S. macrocarpon* produced single flowered inflorescence while the reciprocal *S. macrocarpon* x *S. gilo* developed perennating ability indicating heterogeneity of the parental genome. Fruits were generally intermediate in size and seed number or smaller and fewer in the hybrids. They were wrinkled in *S. gilo* x *S. macrocarpon* with a number of aborted seeds. Meiosis was irregular with few laggards and isolated uni- and bivalent chromosomes associated with the presence of foreign genes in the parent species. On the other hand multivalenlency and chromosome clumps revealed the extent of homogenization of parental genomes and species' affinity. Maternal genome exerted profound influence on hybrid phenotype and fitness and should inform and direct future hybridization efforts.

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Taxonomic studies of *Vicia* species in Iran

Niki Pakbin[1], Ahmad Ghahreman[2], Mahmood Mousavi[3]

[1] Department of Botany, College of Science, Tehran Universit,. Tehran, Iran, [3] Department of Botany, Iran herbarium, Agriculture ministry, Tehran, Iran

The genus *Vicia* L. (Papilionaceae) with 150 species is one of the most important legumes and is used as food, forage, fertilizer and sometimes ornamental. About 46 species of *Vicia* are reported for Iran. Based on 700 herbarium specimens, 40 species were recognized in this investigation. Results of the taxonomic research revealed four sections, which were described and analysed using numerical taxonomy. The dendrogram confirmed the relationship among the species. Distribution maps of each species are presented. Six species of *Vicia* are endemic: *V. iranica*, *V. kotchyana*, *V. venulosa*, *V. sojakii*, *V. aucheri*, and *V. rechingeri.*

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Origin and evolution of agamospermic *Potentilla* species (Rosaceae) in Central Europe

*Juraj Paule, Christoph Dobeš

University of Heidelberg, Heidelberg Institute of Plant Science, Department of Plant Systematics and Biodiversity, Im Neuenheimer Feld 345, 69120 Heidelberg, Germany

The aggregates of *Potentilla verna* and *Potentilla argentea* are both agamospermic species complexes of overlapping geographic distribution, which integrate into each other by extensive hybridisation. Hybrid populations are found in a multitude of isolated places throughout Europe and are currently treated as species within the *Potentilla collina* agg. (Collinae sensu Th. Wolf). Chloroplast and nuclear DNA sequence polymorphisms within the putative paternal aggregates but also within other related taxa were analysed in order to identify those parental evolutionary lineages which gave rise to *P. collina* forms. In a first phase of the project, we have focused on the origin of *Potentilla alpicola* De la Soie, a member of the Collinae, in southern Tyrol and adjacent areas. In this study on hybrid speciation we assessed the question whether *P. alpicola* populations are of single or multiple origin and whether they have been established by a uniform evolutionary process or if a more complex scenario of evolution applies. For that purpose AFLP, morphological and cytological data were combined. Finally, we address the question which criteria should be fulfilled in order to give *P. collina* hybrid forms the rank of a species.

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The family Hydrophyllaceae in Guerrero, Mexico

Silvia Pérez-Mota, Nelly Diego-Pérez

Laboratorio de Plantas Vasculares, Departamento de Biología Comparada, Facultad de Ciencias, Universidad Nacional Autónoma de México (UNAM) 04510 Mexico City, México

The state of Guerrero, on the west coast of the country, is one of the most biodiverse Mexican states. Unfortunately, available data on either flora or fauna occurring in this state is rather scarce. The "Flora de Guerrero" project, being carried out at the Vascular Plants Laboratory at the Faculty of Sciences in the National Autonomous University of Mexico (UNAM), seeks to contribute to the knowledge of such diversity by listing, describing, mapping the distribution, as well as making keys to both existing and new floral taxa occurring there. In Mexico only 4 genera of Hydrophyllaceae occur, just like in the state of Guerrero where we found 6 species: *Hydrolea spinosa*, *Nama dichotomum*, *Nama origanifolium*, *Nama undulatum*, *Phacelia platycarpa*, *Wigandia urens*; and two varieties of *Hydrolea*: *Hydrolea spinosa* var. *spinosa* and *Hydrolea spinosa* var. *cervantesii*. Some Hydrophyllaceae have medicinal and/or economic uses in our country, especially the genera *Wigandia* and *Phacelia*. However, the importance of the Hydrophyllaceae lies in the fact that they are successful pioneers colonizing disturbed vegetation areas.

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The mitochondrial DNA of *Xenoturbella bocki*: genomic architecture and phylogenetic analysis

*Marleen Perseke[1], Thomas Hankeln[2], Bettina Weich[2], Guido Fritzsch[3], Peter F. Stadler[3], Olle Israelsson[4], Detlef Bernhard[1], Martin Schlegel[1]

[1] Institut für Zoologie, Molekulare Evolution und Systematik der Tiere, Universität Leipzig,Talstr. 33, 04103 Leipzig, Germany, perseke@rz.uni-leipzig.de, [2] Institut für Molekulargenetik, Johannes Gutenberg Universität Mainz, J. J. Becherweg 32, 55099 Mainz, Germany, [3] Interdisziplinäres Zentrum für Bioinformatik, Universität Leipzig, Härtelstr. 16-18, 04107 Leipzig, Germany, [4] Museum of Evolution, Uppsala University, Norbyvagen 16, 75236 Uppsala, Sweden

The phylogenetic position of *Xenoturbella bocki* has been a matter of controversy since its description in 1949. We sequenced a second complete mitochondrial genome of this species and performed phylogenetic analyses based on the amino acid sequences of all 13 mitochondrial protein-coding genes and on its gene order. Our results confirm the deuterostome relationship of *Xenoturbella*. However, in contrast to a recently published study (Bourlat et al. in Nature 444: 85–88, 2006), our data analysis uggests a more basal branching of *Xenoturbella* within the deuterostomes, rather than a sister-group relationship to the *Ambulacraria* (Hemichordata and Echinodermata).

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A supermatrix approach resolves phylogenetic relationships in danthonioid grasses

Michael D. Pirie[1], Aelys M. Humphreys[1], Chloe Galley[1], Nigel P. Barker[2], G. Anthony Verboom[3], Kelvin Lloyd[4], Suzy J. Draffin[4], David Orlovich[4], C. Marcelo Baeza[5], Maria Negritto[5], Eduardo Ruiz[5], Hugo Cota Sanchez[6], Elizabeth Reimer[6], H. Peter Linder[1]

[1] University of Zürich, Switzerland, [2] Rhodes University, South Africa, [3] University of Cape Town, South Africa, [4] University of Otago, New Zealand, [5] University of Concepcion, Chile, [6] University of Saskatchewan, Canada.

Variation in branch lengths, inter-locus conflict, and the necessity of dense taxon sampling present challenges for phylogeny reconstruction in large groups. Recent studies have proposed sampling and analysis strategies which could solve difficult to resolve relationships with the minimum sequencing effort. We test the usefulness of such an approach, using a supermatrix to reconstruct a phylogeny of the grass subfamily Danthonioideae. Danthonioideae comprises ca. 288 species found in temperate regions worldwide, but mostly in the southern hemisphere. Generic delimitation in Danthonioideae is unstable, and most danthonioid genera as currently defined have been shown to be non-monophyletic. To date, insufficient taxon and character sampling and apparent inter-gene conflict have prevented delimitation of monophyletic genera. We generate cpDNA and nrDNA gene trees, and a total combined tree with 79% representation of species, by analysing variable non-coding DNA sequences with high taxon sampling density with more conservative protein coding DNA sequences with low taxon sampling density. This supermatrix approach efficiently improves resolution and support whilst maximising representation of taxa and their sometimes composite evolutionary histories. In this phylogeny we now have a tool which can be used to address a range of evolutionary questions and which will allow us to make recommendations for predictive, useful, and thus hopefully robust generic delimitations in Danthonioideae.

166

Ecological modelling and GIS analysis to evaluate the conservation status and protection level of *Heliotropium* sect. *Cochranea* species (Heliotropiaceae) in Chile and Peru

Patricio Pliscoff[1], Hartmut H. Hilger[2], Federico Luebert[2]

[1] World Wildlife Fund - Chile, Carlos Anwandter 624, Casa 4, Valdivia, Chile, [2] Freie Universität Berlin, Institut für Biologie, Systematische Botanik und Pflanzengeographie, Altensteinstraße 6, 14195 Berlin, Germany.

The 19 species of *Heliotropium* sect. *Cochranea* are endemic to the arid zones of the coastal deserts of northern Chile and southern Peru. Some of the species have very narrow distribution ranges, but are not protected as species. Their conservation status has not been evaluated so far. An evaluation of the conservation status following the area of occupancy (B2) criteria from the "IUCN Red List Categories and Criteria" was carried out. The area of occupancy was determined for each species from geo-referenced field records by means of ecological modelling. This analysis classifies two species, *Heliotropium eremogenum* and *H. longistylum*, as endangered and four, *H. filifolium*, *H. glutinosum*, *H. jaffuelii* and *H. philippianum*, as vulnerable. Given the fact that the models largely overestimate the area of occupancy of some species, these results might be considered as a conservative scenario, i.e., some species might eventually be more threatened than suggested by these results. An overlay of the predicted area of occupancy for each species, and the maps of the already Chilean and Peruvian protected areas was performed using GIS. This analysis yields that four of the 19 species are not protected by any area, one of them is the endangered *H. eremogenum* and the other three fell in the category of Vulnerable (*H. glutinosum*, *H. jaffuelii* and *H. philippianum*). The predicted area of occupancy of *H. longistylum*, the other endangered species, is to 17% protected, whereas a protection of 22% is given for the area of occupancy of *H. filifolium*, the other vulnerable species. Three additional species are protected in less than 1% of their predicted area of occupancy and five more in less than 5%. This means that less than a half of the species may be really protected. Conservation actions must be adopted in the area if the protection of the specific diversity is a priority.

059

Diversity, disparity, and evolution in the "*Thiara scabra*"-species complex (Gastropoda: Cerithioidea: Thiaridae) in Indonesia

*Kathrin Podlacha, Thomas von Rintelen, Matthias Glaubrecht

Museum für Naturkunde, Humboldt-Universität, Invalidenstrasse 43, 10115 Berlin, Germany, kathrin.podlacha@museum.hu-berlin.de

Among the mostly marine Cerithioidean gastropods, particularly the freshwater Thiaridae have generated special interest due to their large taxonomical diversity, unparalleled morphological disparity, and phenotypical plasticity in concert with their ecological adaptability. Also they possess peculiar reproduction modes, including viviparity and parthenogenesis. In the past, the conchological variability of thiarids have resulted in the description of a number of named taxa, attributed to various morphospecies and changing genus concepts. One example is the species complex of the so-called "*Thiara*" *scabra*, to which several other morphospecies have been attributed, such as "*Thiara*" *acanthica* and "*Thiara*" *mirifica*, which differ in their viviparous strategy. We here describe preliminary results for those taxa in addition to another enigmatic taxon, viz. "*Thiara*" *rudis*. In our study we particularly focus on collections from the island of Sulawesi, within the biogeographically rich Wallacea region. We use our own collections, as well as material from all major museums, in order to reconstruct the geographical ranges for the constituent taxa of this species complex, to evaluate critical morphological data, and to determine the reproduction mode. Our comparative analyses of morphological and molecular genetic data suggest the necessity to revise the systematization of the traditionally delineated genus *Thiara* (which is defined by the type species *amarula*) and morphospecies subsumed within. We propose the transference of several nominal species to the genus *Plotia* (with *scabra* as type species) instead. We expect to obtain an even more robust phylogenetic reconstruction in the future, based on an expanded data-set which will eventually allow for testing more general systematic and biogeographic hypotheses using these limnic gastropods.

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Colonization of potash mining dumps by halophytes: a case study with *Spergularia media* (Caryophyllaceae)

*Kathleen Prinz[1,2], Isabell Hensen[2]

[1] Plant Systematics and Morphology, University of Kassel, Germany, [2] Institute of Geobotany, Martin-Luther-University Halle-Wittenberg, Halle, Germany

In the last decades, the sizes and biodiversity of many natural inland salt marshes have experienced a tremendous decrease due to human activities. Consequently, anthropogenically influenced salt sites such as the vicinity of potash mining dumps have become valuable secondary habitats for many halophytic species that are currently endangered in the natural landscape. Our study aims to examine the genetic structure and genetic diversity of *Spergularia media* (Caryophyllaceae) as a typical representative for C European halophytes that colonize both natural and anthropogenic salt-influenced habitats. Populations were sampled from several inland salt sites in C and SE Europe, as well as from coastal areas of the North Sea and the Baltic Sea. AFLP markers and nuclear microsatellites were used to assess the geographical distribution of genetic variation and to reveal the geographic origin of *S. media* populations growing in the neighbourhood of potash mining dumps. Our preliminary results indicate that (1) coastal and inland populations are differentiated from each other, with a higher genetic diversity occurring within the former, (2) C European inland populations of this halophytic species are probably not derived from the coasts of the North Sea and the Baltic Sea, and (3) inland populations of *S. media* have experienced considerable fragmentation and founder effects. In future studies, Mediterranean and Pannonian populations will be included in an extended sampling in order to identify putative donor populations for C European inland salt habitats.

015

Undescribed diversity in the genus *Polygordius* (Annelida: Polychaeta): Pygidial glands as a useful taxonomic character

Patricia A. Ramey[1], Dieter Fiege[2]

[1] Institute of Marine and Coastal Sciences, Rutgers the State University of New Jersey, 71 Dudley Rd., New Brunswick, NJ, 08901, United States, [2] Forschungsinstitut Senckenberg, Sektion Marine Evertebraten II, Senckenberganlage 25, 60325, Frankfurt am Main, Germany

There has been renewed progress in documenting and understanding marine biodiversity on a global scale. Members of the Polygordiidae are commonly found in all oceans in intertidal and shallow subtidal sandy sediments. They are relatively small, have indistinct external segmentation, and lack certain typical polychaete characters such as parapodia and chaetae. Characters previously used to distinguish species of the single genus *Polygordius* include body size, number of segments, color, shape of pygidium, ciliation on the body surface, and pattern of the circulatory system. While comparing species of *Polygordius* for the description of *Polygordius jouinae* Ramey, Fiege & Leander, 2006 from the inner continental shelf off New Jersey, USA, the shape of the pygidium and associated structures such as pygidial glands and anal lobes proved useful taxonomic characters. A general biogeographic overview of the diversity of pygidial morphology is presented, focusing on the number, shape and orientation of the glands using SEM images. To date 16 species and 2 subspecies are known for *Polygordius*. It appears, however, that several more species remain to be described. Thus, the view that the Polygordiidae represent a relatively small, homogeneous group (uniformity in morphological features) appears unfounded and diversity is greater than previously thought. Re-evaluation of morphological characters using morphological and molecular techniques will aid greatly in distinguishing among species so they can be accurately identified in ecological surveys, environmental assessments, and evolutionary analyses.

070

Skull comparison between *Neurergus microspilotus* and *Salamandra infraimmaculata semenovi* (Amphibia: Salamandridae)

Nasrullah Rastegar-Pouyani, Fahimeh Akia, Hiwa Faizi

Department of Biology, Faculty of Science, Razi University, 67149 Kermanshah, Iran, nasrullah.r@gmail.com

In the present paper cranial characters of *Neurergus microspilotus* collected from Kavat River, Paveh, Kermanshah province and *Salamandra infraimmaculata semenovi* from Sarvabad, Kurdistan province, western Iran, have been described and comparatively analyzed based on 10 dry skull preparations. Individual variations within each of these two species discussed and compared together. Prominent discrepancies between skulls of the two species observed as follows: individual bones thickness, maxillary dentition, frontal form, premaxilla form, parietal form and palate and associate structures. With regard to the more primitive status of *Salamandra* relative to *Neurergus* (from an evolutionary perspective), in the *S. i. semenovi* most parts of skull not being completely ossified, having a membranous state and even in the ossified parts the elements have no solidity. The frontal in *N. microspilotus* bearing an ossified process toward the eye corner which creates a ring by cartilaginous part as frontosquamosal; this ring created among three parts including frontal, parietal, and squamosal. Whereas the frontosquamosal bone is absent in *S. i. semenovi*. In *N. microspilotus* almost all parts of skull elements bearing solid structures but this is not the case with *S. i. semenovi*.

071

Geographic variation in the Scincid lizards of the genus *Trachylepis* (Sauria: Scincidae) in Iran

Nasrullah Rastegar-Pouyani, Hiwa Faizi

Department of Biology, Faculty of Science, Razi University, 67149 Kermanshah, Iran, nasrullah.r@gmail.com

The genus Trachylepis Fitzinger, 1843 encompasses two-three species in Iran: *Trachylepis vittata* (Olivier, 1804) distributed in western Iran, west of the Zagros Mountains; *T. septemtaeniata* (Reuss, 1834) in southern regions of the Zagros Mountains and *T. aurata transcaucasica* Chernov, 1926 from northern to central parts of the Zagros Mountains. For study of geographic variation in the latter two taxa, 58 specimens of these two taxa (*T. aurata transcaucasica* and *T. septemtaeniata*) were collected from five distinct localities in the Zagros Mountains and adjacent regions. Post-ANOVA pair- wise analysis (Tukey test) and two multivariate analyses including Principal Component Analysis (PCA) and Discriminant Function Analysis (DFA) based on 22 metric and five meristic characters across all the studied groups verified significant intra- and-interspecific differences in some important characters. Especially, results of the multivariate analyses suggest that most of the studied populations have acquired certain degree of morphological divergence. For instance, 88.9% of west Azerbaijan, 95% of Kurdistan, 90% of Kermanshah, 80% of Lorestan, and 77.8% of Khuzestan populations were assigned to their correct *a priori* group by classification resulted in discriminant analysis. The specific status of *T. septemtaeniata* is questioned and it is concluded that this species being just a subspecies of *T. aurata*.

027

Genetic variability and morphometric studies of *Ligia oceanica* (Crustacea: Isopoda: Oniscidea)

Michael J. Raupach, Jobst Pfaender

Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany

Isopod crustaceans are exemplary of the evolutionary transition of animals from aquatic to terrestrial habits, and exist in all gradations from strictly marine to strictly terrestrial forms. Of currently known 10,500 species of isopods, some 4,200 are in the terrestrial suborder (Oniscidea), and these have diversified into habitats of shore, savannah, marsh, forest and even desert. The genus *Ligia* exemplifies the semi-terrestrial phase of the sea-to-land continuum and prototypal land isopod, showing numerous features of its morphology, physiology, and behaviour which are transitional between ancestral marine and fully terrestrial forms. Representatives of the species *Ligia oceanica*, commonly known as rock lice or sea slater, inhabit a narrow rocky supralitoral area of the Atlantic coast of Europe. Despite the fact that *Ligia oceanica* is abundant and widespread at the European Atlantic coast, no studies of their population structure or phylogeography exist. In our project we analysed mitochondrial DNA sequence variations (CO1 and 16S rDNA) in population samples over a wide geographic range (Norvay, Germany, Wales, Ireland, France, Spain and the Netherlands), revealing a remarkably complex genetic variability, probably a consequence of isolation and bottlenecks caused by glaciations. In addition to the molecular data, landmark-based morphometric studies of headstructures were included to compare patterns revealed by mitochondrial markers.

045

Molecular taxonomy in Middle European Carabidae (Insecta: Coleoptera)

Michael J. Raupach[1], Karsten Hannig[2], Thomas Wagner[3], Bernhard Misof[1], Johann-Wolfgang Wägele[1]

[1] Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany, [2] Dresdener Str. 6, 45731 Waltrop, Germany [3] Institut für Integrierte Naturwissenschaften, Abteilung Biologie, Universität Koblenz-Landau, Universitätsstrasse 1, 56070 Koblenz, Germany

The Carabidae, or ground beetles, are one of the largest and best known families of Coleoptera, with more than 35,000 described species worldwide. Because Carabidae show different levels of habitat selectivity, ranging from generalists to specialists, ground beetle assemblages can be used as valuable bioindicators to characterize disturbance in various habitats such as forests or meadows. However, the identification of many species is difficult, and many carabid species are often very variable. Therefore, a DNA-based taxonomy analysing a vast number of specimens will be useful to ensure accurate species identifications and biodiversity research. Beside this, the genetic cohesiveness and taxonomic integrity of species with widespread or disjunct geographical distributions can be evaluated using DNA sequence data. In addition to the mitochondrial CO1 gene fragment, we analyze highly variable regions of the nuclear D1-D2 LSU gene to avoid known molecular problems only using mitochondrial data (e.g. introgression or ancient polymorphisms).

065

Origins and biomechanical evolution of teeth in echinoids and ophiocistioids (Echinodermata)

Mike Reich[1], Andrew B. Smith[2]

[1] *Geowissenschaftliches Zentrum der Universität Göttingen, Museum, Sammlungen & Geopark, Göttingen, Germany,* [2] *The Natural History Museum, Department of Palaeontology, London, UK*

Echinoid teeth are without doubt the most complex and highly evolved skeletal component to have evolved in echinoderms. They are biomechanically constructed to be resilient and tough while maintaining a shelf-sharpening point. Recently, new collections of well-preserved teeth of both echinoids and ophiocistioids have been made from the Late Ordovician and Silurian of Sweden. Based on SEM analysis of these isolated tooth elements, we provide a detailed structural analysis of the earliest echinoderm teeth. Eight distinct constructional designs are recognized encompassing various degrees of sophistication, from a simple vertical battery of tooth spines, to advanced teeth with multiple tooth plate series and a reinforced core of fibres. These provide key data on the early stages of tooth evolution. Despite the obvious homology between the lanterns of ophiocistioids and echinoids, their teeth are very different in microstructural organization and they have evolved different forms of self-sharpening mechanism. Whereas echinoid teeth evolved from a biseries of mouth spines, ophiocistioid goniodonts evolved from a uniseries of mouth spines.

075

The rediscovery of type material of *Mammuthus primigenius* (Mammalia: Proboscidea)

Mike Reich[1], Alexander Gehler[1], Dick Mol[2], Hans van der Plicht[3], Adrian M. Lister[4]

[1] Geowissenschaftliches Zentrum der Universität Göttingen, Museum, Sammlungen & Geopark, Göttingen, Germany, [2] The Natural History Museum Rotterdam, The Netherlands, [3] Centre for Isotope Research, University of Groningen, The Netherlands, also at Faculty of Archaeology, Leiden University, The Netherlands, [4] The Natural History Museum, Department of Palaeontology, London, UK

The woolly mammoth *Mammuthus primigenius* (Blumenbach, 1799) is one of the bestknown large mammals of the Late Pleistocene and was a very common species during this epoch. Thousands of localities have been discovered in Europe since the first finds in the 16th century, but unfortunately the exact stratigraphy is unknown for most of them. The European records consist mainly of single bones and molar teeth, but well preserved parts of skeletons and skulls are not uncommon. Two specific scientific names for the woolly mammoth were proposed in 1799. Johann Friedrich Blumenbach (1752–1840), at Göttingen University, proposed the name *Elephas primigenius,* while Georges Cuvier (1769–1832) proposed *Elephas mammonteus*. Blumenbach's 6th edition of his „*Handbuch der Naturgeschichte*" appeared a few months earlier than Cuvier's paper and *E. primigenius* was the name adopted by subsequent authors, including G. Cuvier himself (Cuvier 1806). The following 200 years of mammoth taxonomy turned out difficult, and after the Second World War, Blumenbach's original specimens were declared to be lost or destroyed and a neotype for *Mammuthus primigenius* from the Taimyr Peninsula, Arctic Siberia – the so-called Taimyr Mammoth, excavated in 1948 – was designated in 1990. We report here the rediscovery of the paralectotype of *Mammuthus primigenius* (Blumenbach, 1799) – now once again available for further scientific study (GZG.V.010.018). The absolute age of the paralectotype, based on AMS 14C dating (Groningen University), is 34,340 ± 230/± 210 BP (lab reference number GrA-32611).

039

Speciation in process between small isolated populations of the bush cricket *Barbitistes serricauda* caused by anthropogenic fragmentation

Christian Richter[1], Jochen Gottwald[1], Christoph Knorr[2], Andreas Stumpner[1]

[1] Johann-Friedrich-Blumenbach-Institut für Zoologie und Anthropologie, Berliner Straße 28, 37073 Göttingen, Germany ,[2] Tierärztliches Institut Göttingen, Burckhardtweg 2, 37077 Göttingen, Germany

The central European area populated by the ratite bush cricket *Barbitistes serricauda* (Fabricius 1798) has first been fragmented in Prehistoric times by the settling of the copper beech, which was presumably promoted by man. The specimen with low mobility cannot use the copper beech as a means of nourishment. Therefore populations of this type of bushcricket can only be found in places where the copper beech does not grow. These populations are characterized by an outstanding poverty in regard of the number of individuals – sometimes less than 15 specimen – that remains constant for any length of time. The AFLP-analysis of population genetics show no obvious connection between genetical and geographic distance. Filial generations of single populations that were bred under standartized conditions, indicate processes of differentiation in locally isolated populations by significantly diverse lengths of leg and also differences in the progress of embryonic development influenced by endogenic factors of maternal origin. Population hybrids bred in the labratory under identical testing conditions, whose parents derived from different subpopulations, indicated a postzygotic isolation developing between several populations. Deliberately bred lines of inbreeds showed no signs of reduced fitness in comparison to control breeds. The fragmentation of the habitat of *Barbitistes serricauda* did indeed lead to a drastic restriction of genetical exchange between single populations, but the isolation of local populations also led to processes of diversification within the population in general and generated a large genetical variation within the species, which in turn might result in speciation. Therefore, any fragmentation of habitat may contribute to biodiversity in the long run, even if some populations extinguish locally. Hence a positive evaluation of anthropogenic fragmentation of habitat is possible in some cases, since it may have the same results as processes of a natural, i.e. geologic kind.

011

Phylogeny of Dicranophoridae (Rotifera: Monogononta)

*Ole Riemann, Wilko H. Ahlrichs

Carl von Ossietzky Universität Oldenburg, Germany, Institut für Biologie und Umweltwissenschaften (IBU), 26111 Oldenburg, Germany, o1Riemann@gmx.net

A claistic analysis of Dicranophoridae (Rotifera: Monogononta) based on morphological characters with species as terminal taxa is presented. The analysis covers 76 ingroup and 4 outgroup taxa (*Notommata glyphura*, *Itura myersi*, *Lindia tecusa*, *Dorria dalecarlica*). The data matrix in total comprises 59 binary and multistate characters. Character coding is based on personal observations and on a broad survey of the literature. Characters included cover general body organisation (rotatory organ, trunk, foot), internal morphology and the fine structure of the jaw apparatus revealed by SEM. Examples of SEM preparations are provided. All charaters are given equal weight, character states are treated as unordered. A maximum parsimony analysis firmly supports monophyly of Dicranophoridae. A monophyletic clade comprising the genera *Dicranophorus* and *Dicranophoroides* is the sister group to all other dicranophorid rotifers. Representatives of the polyphyletic genus *Encentrum* are the most strongly derived species within Dicranophoridae. Overall parsimony suggests that key events in the evolution of this species rich rotifer family are the development of accessory jaw elements and modifications of the gastric tract.

098

The Lauraceous collections by Friedrich Sellow

Pedro Luís Rodrigues de Moraes

Universidade Estadual de Campinas, IB – Depto. Botânica, PO Box 6109, 13083-970, Campinas, SP, Brazil

Among the travelers of the beginning of the 19th century, the Prussian naturalist Friedrich Sellow (1789 – 1831) gathered major collections of plants in Brazil in the region between Bahia and the former Cisplatine Province (Uruguay). Although he is the most cited collector of new species in Martius' *Flora Brasiliensis*, he deceased at little more than 42 years of age without publishing any scientific work or journey books. Sellow's legacy has its major restriction in problems with labels. Generally, the majority of his extant gatherings at Berlin (B) has no complete information on the labels and in many plant families label data is restricted to "Sellow, Brasilia". Fortunately, many Lauraceae specimens have original field labels and collection numbers. From the numbered collections, it is possible to determine their places of origin since Urban provided an elaborate list of Sellow's six itineraries in Brazil (during 1814 – 1831), each having been coded by Sellow with different combination of letters and numbers. In the present study, all Lauraceae specimens mentioned in the works by Nees von Esenbeck, Carl Meissner, Carl Mez and recent revisors have been searched in the herbaria B, BM, BR, CGE, E, F, G, GZU, HAL, HBG, K, KIEL, L, LE, M, MO, NY, P, US, VT, and WRSL. To date, 448 specimens have already been located, 193 of them being numbered collections. Herbarium B is the principal resort of Sellow's collections, housing 207 specimens, 142 of them being types. It appears that Sellow collected material of 69 currently accepted species of Lauraceae. The taxonomic status of all species names has been updated and 13 lectotypifications have been proposed.

099

Current taxonomic status of Daniel Rolander's species published by Rottbøll in 1776

Pedro Luís Rodrigues de Moraes[1], James Dobreff[2], Lars Gunnar Reinhammar[3], Olof Ryding[4]

[1] *Department of Botany, IB, Unicamp, P.O. Box 6109, 13083-970 Campinas, S.P., Brazil.* [2] *Centre for language and literature, Lund University, P.O. Box 201, 221 00 Lund, Sweden,* [3] *The Bergius Foundation at the Royal Swedish Academy of Science, P.O. Box 50017, 104 05 Stockholm, Sweden,* [4] *Botanical Museum, Natural History Museum of Denmark, University of Copenhagen, Gothersgade 130, 1123 Copenhagen K, Denmark*

Christen Friis Rottbøll, in his dissertation "*Descriptionis rariorum plantarum*" published in 1776, described 12 species based on specimens and the original descriptions given by Daniel Rolander in "*Diarium Surinamicum*", a 699-page unpublished manuscript currently in the library of the herbarium in Copenhagen, from his stay in Suriname from 20 June 1755 to 20 January 1756. Rottbøll's dissertation had an almost verbatim version published in the journal *Acta Literaria Universitatis Hafniensis* 1: 267-304 (1778), which has been repeatedly indicated by several authors as the place of its valid publication, hence overlooking the former. Likewise, a second edition was published in 1798 and has also been mistakenly considered as the place of publication of those species by other authors that were likely unaware of the original source. This situation has caused several Rottbøll's species to be misleadingly placed under synonymy, instead of being taken as basionyms to species names. Rolander's species published by Rottbøll have been assumed to have specimens housed at the Copenhagen Herbarium (C), although only few Rolander specimens have been attributed and located there. In fact, Rolander lived in Copenhagen for 4-5 years from 1760/1-1764/5. During this period, he sold part of his herbarium and the complete *Diarium* respectively to Rottbøll and to Christian Gottlieb Kratzenstein. However, up to the present, the major parcel of gatherings by Rolander is known to be kept at the Bergius Foundation in Stockholm (SBT), from specimens P.J. Bergius received as gift from Rolander. With 231 years having passed since Rottbøll's publication, these species still deserve special attention, since seven of them are basionyms for current accepted species names, and another has never had its status changed, being the generitype of *Nectandra* (*Nectandra sanguinea* Rol.). Although several of them are important elements of the Flora of Suriname, they still require lectotypification. Here, we update the taxonomic identity of those species, discoursing, whenever pertinent, on their nomenclatural status. Nine of the 12 taxa and also one synonym from a species described by Linné *filius* are lectotypified. Type localities and dates are provided, whenever possible.

077

Some unclear questions in systematics of Early Miocene bats (Vespertilinini, Chiroptera, Mammalia) of Eastern and Central Europe

Valentina Rossina

Paleontological Institute of Russian Academy of Science, Prophsouznaya str. 123 Moscow, 117997 Russia, ros@paleo.ru

Frequently, the incompleteness and small sample numbers of fossils render the systematic definition of extinct taxa difficult. Especially this concerns fossil bats. Recently we have discovered a new representative of the Vespertilionini tribe from the late Miocene deposits of Gritsev locality (MN 9) in the Ukraine. This vespertilionid bat is distinguished from *Myotis* in 1) the strong reduction of P/3, 2) I/3 is the smallest one and is shifted outwards, 3) the talonid of M/3 is reduced. Our specimen is most similar to the Early Miocene *Hanakia* Horacek, 2001 (MN 3-5), and *Paleptesicus* Zapfe, 1970 (MN 6). Unlike *Hanakia* the dentition of our specimen is shorter and the shape of the mandible is different. Gritsev specimen differs from *Paleptesicus* in 1) P2 is more reduced, 2) the crown of P4 has additional antero-lingual tip of cingulum, 3) the rostrum part of the skull is wider and shorter. On the basis of several morphological criteria the Ukraine specimen can be related to *P. priscus*. In this case it is necessary to suppose that the more ancient *P. priscus* had two small premolars in the lower jaw (not found until now). In accordance with Ziegler (2003), however, the lower tooth row of *Paleptesicus* had only one small premolar. We assume that the tooth row of *Paleptesicus* had two small premolars. Furthermore, we suggest that oldest species of *Hanakia* must have at least one small premolar in the upper jaw. Thus, the specimen from Gritsev combines plesiomorphic and more advanced features which is why for now it cannot be referred to any of the known members of the tribe. The exact definition of the Gritsev specimen will allow not only to determine its position in Vespertilionini, but also to reconsider the systematical positions of some of the earlier described taxa (for example *P. noctuloides*).

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The ploidy level in Iranian species of *Trifolium*

Fahimeh Salimpour, F. Sharifnia

Department of Biology, Faculty of Science, Islamic Azad University, North Tehran Branch, P.O.Box 19585-936, Iran

Chromosome numbers were counted for the first time in 140 accessions of 37 annual and perennial *Trifolium* species in Iran. *T. radicasum* with 2n = 16 is newly reported. Also, new cytotypes of *T. tumens*, *T. fragiferum*, *T. ambiguum*, *T. nigrescens*, *T. stellatum* and *T. montanum* are confirmed. The observations showed an increase of ploidy level in this genus. Karotypic formula showed that most of the chromosomes are meta- , submeta- and acrocentric. The smallest chromosomes are found in sections *Versicaria* and *Mistyllus*, and the largest in sects. *Trifolium* and *Tricocephalum*. Based on these results, *Trifolium* is heterogeneous; the morphological characters support the findings.

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Pollen morphology of ***Stachys*** (Lamiaceae) in Iran

Yasaman Salmaki[1], Shahin Zarre[1*], Ziba Jamzad[2]

[1] *Department of Plant Biology, School of Biology, University College of Science, University of Tehran, PO Box: 14155-6455, Tehran, Iran, zarre@khayam.ut.ac.ir,* [2] *Research Institute of Forests and Rangelands, PO Box: 13185-116, Tehran, Iran,*

Stachys is one of the largest genera of Lamaiaceae containing approximately 275 to 300 species. It is centred in the warm-temperate regions of the Mediterranean and SW Asia, with a secondary centre in North and South America, and in southern Africa. Iran with about 34 species is one of the diversity centres of this genus. Pollen grains of 30 taxa of the genus *Stachys* (29 spp., 1 subsp.), representing 9 of the currently recognized sections, and 1 species of the closely related genus *Sideritis* (*S. montana*) were examined by Light and Scanning Electron Microscopy. Pollen grains of *Stachys* were single, isopolar, radial symmetrical and tricolpate. The basic shape of the pollen grains in the most taxa studied is prolate-spheroidal, but subprolate and oblate-spheroidal pollen grains can also be found in few species. The pollen grains are usually tricolpate, but tetracolpate were found in a few species, i.e. *S. iberica*, *S. atherocalyx* and also in *Si. montana*. The lumina are separated by smooth or sinuate muri which make them polygonal, more or less rounded and elongate. The mean of polar axis varies from 23.69 µm, in S. laxa to 33.00 µm, in *S. persepolitana*, but the equatorial axis ranges from 20.03 µm, in *S. sylvatica*, to 34.8 µm, in *S. atherocalyx*. The wall thickness ranges from 1.21 µm in *S. sylvatica* to 2.80 µm in *S. ixodes* with equal thickness on apocolpia and mesocolpia in each pollen. The basic sculpturing types observed among studies species are microreticulate (the frequent type), reticulate, perforate, and foveolate. The results of this study show that several characters can be characterized by the type micro sculpturing. For example in *S.* sect. *Aucheriana* all species show elongate lumens arranged in a reticulate pattern. Although pollen morphological characters provide some evidences useful in delimitation of species in some sections (e.g. sect. *Eriostemum*), in other cases like sect. *Fragilicaulis* (one of the taxonomically difficult groups of *Stachys*), pollen morphological characters provide no support in circumscribing and delimitating the species.

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Indel evolution and secondary structures of group I & II introns in asterids

K. Salomo[1], T. Borsch[2], A. M. Barniske[1], C. Neinhuis[1], D. Quandt[1]

[1] Institut für Botanik, Technische Universität Dresden, Germany, [2] Carl von Ossietzky Universität Oldenburg & Nees Institute, University of Bonn, Germany

The *trnL* group I, the *petD* group II intron and the *trnL-F* and *petB-D* spacers, all located within the large single copy region (LSC) of the chloroplast genome, were analysed from 74 taxa, representing all orders and major families of asterids, and 9 outgroup taxa. Mutational hotspots show high similarity in location, number and extension to hotspots already known from former studies. Within the predicted secondary structures of both introns they are most of the time restricted to terminal stem-loop regions. After exclusion of hotspots the arisen dataset comprised 4925 aligned sequence positions and a binary indel matrix of 1335 characters. Phylogenetic analyses following likelihood, parsimony and Bayesian inference approaches reveals in a highly resolved and well supported phylogeny of asterids comparable to multi-gene analysis. All the backbone nodes receive high confidence and are also resolved in analyses of *pet-D* data alone. Rapidly evolving non-coding chloroplast regions are already known to contain a large number of length mutations like insertions and deletions (indels). Recent studies have shown that most insertions within non-coding chloroplast DNA are direct repeats supposed to be the result of slipped strand mispairing during DNA replication, repair and recombination. Interestingly, both, the *petD* and *trnL* region show a high congruence in length distribution of simple sequence repeats (SSR's) with an unexpected bias towards SSR's with a length of 4-6 nucleotides. As the likelihood of repeat events should decrease with size this bias might indicate a general mechanism of molecular evolution that deviates from the current slipped strand mispairing (SMM) concept.

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Independent loss and duplication of Hox genes during evolution of the mollusc cluster

*Leyli Samadi, Gerhard Steiner

Molecular Phylogenetics, Department of Evolutionary Biology, Faculty of Life Sciences, University of Vienna, Austria, leili.samadi@univie.ac.at, gerhard.steiner@univie.ac.at

Hox genes are a particular subgroup of homeobox genes, a family of transcription factors characterized by a 60-amino-acid-long DNA binding motif called the homeodomain. These genes are found in special gene clusters and function in the patterning of anterior-posterior body axis of bilaterian animals. The number of Hox genes identified in molluscs varies considerably among major taxa. We identified orthologs of Hox genes in six species of Bivalvia, Gastropoda and Scaphopoda. Among these are at least one anterior, five central, and one posterior Hox genes. Paralog 3 gene (zerknult) was not recovered in any of the species, probably as the result of multiple substitutions of primer binding sites. Gene loss occurred independently in different paralog groups. Independent gene duplications were observed in members of central class genes. The homeodomain sequence and the parapeptides in the flanking regions of homeobox are highly conserved. Lox5, Antp, Lox2, and Lox4 of the central class orthologs have an intron which ranges in size between 1.2-1.5kb and the position of the intron is conserved in the genes of this class. The two genes of posterior class share a 5´exon and probably undergo alternative splicing. Since in the ecdysozoans only one single posterior gene exists, further investigation about the alternative splicing event may provide some insights about the duplication of this gene in the ancestor of lophotrochozoans.

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The heavy, trace and nutrient elements contents in some wild edible *Agaricus* (Agaricales) taxa from Turkey

Murad Aydın Şanda, Hasan Hüseyin Doğan

Selcuk University, Science and Art Faculty, Biology Department, Campus Konya, Turkey

The concentrations of Ag, Al, As, B, Ba, Bi, Ca, Cd, Co, Cr, Cu, Fe, Ga, In, K, Li, Mg, Mn, Na, Ni, P, Se, Sr, Tl, V, and Zn were determined in wild edible *Agaricus* L. taxa (*A. arvensis* Schaeff; *A. comtulus* Fr., *A. cupreobrunneus* (Schöff.) Pilát, *A. urinascens* (Schöff.) Singer var. *urinascens*, *A. silvaticus* Schöff. and *A. essettei* Bon.) from Turkey by ICP-AES eqipment. The highest Ag, As, Cd, Cu, Ga, P, and Zn contents were detected in *A. essettei* as 2.69 mg.kg^{-1} for Ag, 80.39 mg.kg^{-1} for As, 60.52 mg.kg^{-1} for Cd, 68.30 mg.kg^{-1} for Cu, 1.87 mg.kg^{-1} for Ga, 18040 mg.kg^{-1} for P, and 95.34 mg.kg^{-1} for Zn. The highest Al, Fe, Mg, Mn, Pb, and Ni concentrations were determined in *A. silvaticus* as 2182, 1736, 2433, 45.62, 2.51, and 7.56 mg.kg^{-1} respectively. The highest Bi, Ca, Cr, Na, Sr, and V contents were determined in A. cupreobrunneus as 9.59 mg.kg^{-1} for Bi, as 14250 mg.kg^{-1} for Ca, as 25.74 mg.kg^{-1} for Cr, as 5436 mg.kg^{-1} for Na, as 49.45 mg.kg^{-1} for Sr, and as 31.70 mg.kg^{-1} for V. The Tl, V, B, Ba, Co, and In concentrations were not detected in our mushroom samples.

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The morphological and anatomical characteristics of three endemic and threatened taxa (*Hyacinthella campanulata*, *H. lazulina* and *H. heldreichii*; Liliaceae) in Turkey

Murad Aydın Şanda, Ebru Atayeter

Selcuk University, Science and Art Faculty, Biology Department, Campus Konya, Turkey

Sections of root, scape, bulb and leaf of three endemic and threatened taxa, *Hyacinthella campanulata*, *H. lazulina* and *H. heldreichii*, from Turkey were examined and anatomical similarities and differences between the species were determined. In all taxa the leaves are smooth and amphistomatic, the cuticle is thin, the stomata are of the amaryllis and anomocytic type and the mesophil is isolateral. The stomata cells of *H. lazulina* are larger than in other taxa although stoma cell number per unit area are greater than in other taxa as well. The root epiderma cells of *H. heldreichii* are smaller than in the other two species. The protoxylem vessel number of *H. lazuliana*, *H. campanulata* and *H. heldreichii* are 5, 6 and 7 respective. The cristal number of leaves and root cortex parenchyma in *H. campanulata* is larger than in the other two species. Finally, the pedicel of *H. lazulina* is (sub)sessil.

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Species delimitation and speciation in a Cretan land snail radiation

*Jan Sauer, Bernhard Hausdorf

Zoological Museum, University of Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany

We investigated the performance of different methods based on mitochondrial sequences (*cox1*, 16S rDNA) and multilocus (AFLP) data as well as morphological characters of the shell and the genitalia for delimiting species of the Cretan land snail genus *Xerocrassa*. We identified twelve *Xerocrassa* species occurring on Crete, six of which have not been described so far. Based on phylogenies and distribution data, we tested hypotheses concerning the geographic mode of speciation and the factors that promote radiation. The most recent sister clades show no range overlap indicating a predominantly allopatric mode of speciation. However, the hypothesis that the radiations were the result of a fragmentation of Crete into several palaeoislands during the late Miocene and Pliocene could be rejected. Contrary to the predictions of this hypothesis, Monte Carlo simulations showed that the distribution areas of the Cretan endemics are not significantly clustered. This result indicates that the land snail radiations on Crete were not caused by a common sequence of vicariance events. Although most sister clades show strong range size asymmetry as predicted by the peripatric speciation model, a test for peripatric speciation based on a Monte Carlo simulation of range size asymmetry was not significant. This indicates that different speciation modes might have been involved in the Cretan land snail radiations. Nevertheless, stochastic events like chance colonization of isolated habitats were probably most important. Body size differences are significantly larger between sympatric than between allopatric species indicating that body size plays a role in competitive interactions between species. A randomization of independent contrasts of body size over the tree shows that size changes are significantly concentrated towards the root of the tree of the Cretan *Xerocrassa* species. Thus, size differences did not facilitate speciation, but did promote persistence and/or subsequent radiation of lineages. This result and the lack in appreciable differences in ecology indicate that the *Xerocrassa* radiation on Crete is mainly non-adaptive as has been claimed for the radiations of *Albinaria* and *Mastus*.

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Invasion without sex in *Veronica filiformis*

*Romain J. Scalone, Dirk C. Albach

Institut für Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Germany, albach@uni-mainz.de, scalone@uni-mainz.de

Mankind is changing its environment in a hitherto unprecedented way. One aspect of change is the introduction of organisms to a new environment, thus creating hundreds of evolutionary experiments. While most of these "experiments" fail, it is those that succeed that are important to understand evolution. One exceptional case is the introduction of *Veronica filiformis* from the Caucasus to Europe. *Veronica filiformis* does not reproduce sexually but exclusively by vegetative means within the introduced area. This is caused by the self-incompatibility of the species combined with spatially very limited dispersal by vegetative means. By analyzing patterns of gene flow and dispersal routes in the native and introduced areas, we aim at understanding the importance of vegetative and sexual reproduction in the whole distribution area. For this it is necessary to know the origin of the introduced plants, the dispersal of potential clones on different scales (transcontinental to local) and the potential of adjacent clones to produce seeds with each other. Molecular markers (AFLP fingerprints) and crossing studies are being conducted to give the appropriate information to answer the above-mentioned questions regarding the dispersal ability of *Veronica filiformis* in its native and introduced area with two different strategies. Initial crossing studies (done between March to Mai 2007) with plants from 26 (on 33) populations collected on a transsect between Tübingen and Münich (190 km) demonstrate that multiple clones (with a maximum of 8 different S-alleles) are present, sometimes separated by at most 23 km. Some preliminary AFLP-results showed differences in the intra-population diversity.

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Phylogeny of Caryophyllales based on petD group II intron sequences and effects of indel coding on phylogeny inference

*Bastian Schäferhoff[1], Kai Müller[1], Dietmar Quandt[2], Thomas Borsch[3]

[1] Nees-Institut für Biodiversität der Pflanzen, Rheinische Friedrich-Wilhelms Universität Bonn, Meckenheimer Allee 170, 53115 Bonn, Germany, [2] Technische Universität Dresden, Institut für Botanik, Zellescher Weg 20b, 01062 Dresden, [3] Institut für Biologie und Umweltwissenschaften, Carl von Ossietzky Universität Oldenburg, Ammerländer Heerstraße 114-118, 26129 Oldenburg

With about 12,000 species, Caryophyllales represent one of the major orders of angiosperms and contain some economically important plants like spinach, beet, amaranth, and horticultural plants like Cactaceae or pinks. Previous phylogenetic studies using coding markers could not clarify all intraordinal relationships, but provided evidence that some families might not reflect natural groups. In this study, the non-coding chloroplast petB–petD region, consisting of a transcribed spacer and a group II intron, was analysed for 45 taxa of Caryophyllales. The aligned matrix contains 1705 characters, 40% of which were variable. Length variation was coded in a seperate indel matrix of 184 characters. Phylogenetic relationships were reconstructed using parsimony and Bayesian inference. The largest clade found in Caryophyllales was Caryophyllales I including Phytolaccaceae, Petiveriaceae, Nyctaginaceae, Gisekiaceae, Molluginaceae, Aizoaceae, Cactaceae, Portulacaceae, Basellaceae, Didiereaceae, Halophytaceae, Amaranthaceae, Chenopodiaceae, Caryophyllaceae, Achaocarpaceae, Stegnospermataceae and Simmondsiaceae, and was recovered with high statistical support. Within Caryophyllales I, six major lineages were observed. The first includes Amaranthaceae, Chenopodiaceae, Caryophyllaceae and Achatocarpaceae, the second comprises Cactaceae, Portulacaceae, Basellaceae, Didiereaceae, Halophytaceae and Molluginaceae, with Molluginaceae being sister to the remaining families. The third clade includes Phytolaccaceae, Petiveriaceae, Nyctaginaceae, Gisekiaceae, Aizoaceae and surprisingly *Hypertelis* (Molluginaceae) as sister to Gisekiaceae. Therefore, *Hypertelis* is not closely related to the remaining Molluginaceae that are represented by *Mollugo* in this study. Stegnospermataceae, *Microtea* and Simmondsiaceae constitute three minor lineages in Caryophyllales I. the formerly unplaced Simmondsiaceae and *Microtea* (Phytolaccaceae - Microteoideae) are successive sisters to the remaining Caryophyllales I. *Microtea*, which had never before been included in a phylogenetic study , is not closely related to other Phytolaccaceae. There is only weak evidence for the monophyly of Caryophyllales II, including Polygonaceae, Plumbaginaceae, Tamaricaceae, Frankeniaceae and a number of carnivorous families. Evolution of microstructural changes of the petD group II intron was studied within Caryophyllales. Regarding the length mutations of the petD intron, a bias towards insertions was observed. Insertions that are once acquired seem to have a low probability to get lost again. Most insertions (about 83%) were simple sequence repeats (SSRs), the remaining insertions were either unknown sequence motifs or microsatellite-like.

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Flowering sequence and breeding system in protogynous Bruniaceae

*Lavinia Schardt, Regine Claßen-Bockhoff

Institut für Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Germany

The Bruniaceae (75 species, 12 genera) are a (sub-)endemic family of the South African fynbos biome. Species are often found in small and isolated populations, part of them being threatened with extinction. Except for the beetle pollinated, almost self-incompatible *Audouinia capitata* (De Lange et al. 1993) there is nearly nothing known about the floral biology and the breeding system of the species. To get a deeper insight into the reproductive biology of the Bruniaceae and to reconstruct the evolutionary significance of reproductive characters in the family field investigations are being conducted in the South Western Cape. The most exciting findings so far are the documentation of protogyny in *Berzelia* ssp. and *Staavia* ssp. and of a different dependence on pollinators. In the self-compatible *Berzelia lanuginosa* the pincushion-blossoms are composed of about 130 densely aggregated flowers blooming for about four weeks. During anthesis male and female stages in the inflorescence do overlap. Bagging experiments clearly indicate that the flowers set fruit in the absence of pollinators. In *Staavia radiata*, however, the straw-blossoms include more than 150 flowers blooming for over three months and presenting only few flowers per day. Again, an overlap of female and male stages was observed, but no fruits are produced in the absence of pollinators. Obviously, at least two different mating systems evolved in the family, one relying on a long anthesis and thereby increasing the chance of outcrossing (*Staavia*) and a second one relying on a short anthesis with the ability to self-pollinate without pollinators (*Berzelia*). In any case, protogyny guarantees outcrossing in at least the first flowers of the inflorescences.

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Architecture and flowering sequence in the Apiaceae-Saniculoideae

Christian Scharhag, Regine Claßen-Bockhoff

Institut für Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Germany

Within the Apiaceae, the subfamily Saniculoideae is characterised by densely aggregated flower clusters originating from compound inflorescences with mixed flowering patterns (Froebe 1979). Except the dioecious *Arctopus* ssp. and the monoclinous *Eryngium* ssp. all Saniculoideae are andromonoecious, i.e. have hermaphrodite and (functionally) male flowers. In the current project we monitored the flowering sequence of four species to test the influence of the plants' architecture to their breeding systems.

- *Astrantia major* is multicyclic proterandrous and extremely dichogamous while *Petagnaea gussonei* is also protandrous, but flowers in a duodichogamous manner with a strong tendency to geitonogamy.
- *Sanicula marilandica* and *Hacquetia epipactis* are both protogynous with a weak phase separation in the flowers of *H. epipactis* probably resulting in delayed selfing; due to a high phase overlap the individuals pass a female stage first, then an extended hermaphrodite and finally a male phase.
- *Astrantia major* and *Sanicula marilandica* correspond to the protandrous and protogynous andromonoecious species in the Apioideae with respect to the increase and decrease of male flowers with increasing branch order.

No close correlation exists between inflorescence architecture, flowering sequence and patterns of dichogamy pointing to an independent regulation of the flowering sequence from the underlying architecture. Proterandry appears to be the ancestral stage from which protogyny evolved one time within the Saniculoideae. Though the latter slightly increases the genetic diversity among the offspring it obviously is not a serious alternative in the group including predominantly proterandrous species.

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Phylogeographical inferences of *Hypericum perforatum* and *H. maculatum* (Hypericaceae)

*Charlotte Scheriau, Marcus Koch

Heidelberg Institute of Plant Sciences, Biodiversity and Plant Systematics, University of Heidelberg, Im Neuenheimer Feld 345, 69120 Heidelberg, Germany

St. John's wort (*Hypericum perforatum* L.) is a medical plant and therefore well studied for its anti-depressive, anti-cancer and anti-inflammatory metabolites. *H. perforatum* has a basic chromosome number of 8. Its populations are mainly composed of tetraploids (2n=4x=32) (Robson NKB 2002). However, little is known about its evolutionary history. *H. perforatum* is assumed to be of hybrid origin, because of some morphological similarities between it and *H maculatum* Crantz. *H. maculatum* is considered as one putative parent from an ancient hybridization event, and it is obvious that there is ongoing gene flow between both species (a putative frequent hybrid is H. x *desetangsii* Lamotte). For phylogeographical analysis we used cpDNA (trnL intron and trnL-F intergenic spacer) and nrDNA (ITS 1 and ITS 2) to show possible refuge areas and former migration routes. We also compared our phylogeographical results with a representative screening of ploidy levels. The aims of this study are to provide information on 1) centres of genetic diversity, 2) possible migration routes, 3) hybridization and suture zones, and 4) temporal estimates of the various speciation events.

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Arabidopsis thaliana's wild relatives: an updated overview on systematics, taxonomy and evolution

*Roswitha Schmickl, Marcus A. Koch

Heidelberg Institute of Plant Science, Biodiversity and Plant Systematics, University of Heidelberg, Im Neuenheimer Feld 345, 69120 Heidelberg, Germany

Since the introduction of *Arabidopsis thaliana*, the Thale Cress, to a broader scientific community in 1965, nearly 40 years passed until the phylogenetic position of this species was resolved and its closest relatives were characterized. More and more molecular data is available for *Arabidopsis thaliana* and it has become the most important model system among dicotyledonous plants. However, *Arabidopsis thaliana* provides only a limited set of traits and characters. We are now in the position that scientists move into the more diverse relatives of *Arabidopsis*, transferring knowledge from the model plant to these species. Hereby past taxonomy and phylogenetic concepts may lead to misunderstanding and confusion. Consequently there is great need to provide a comprehensive overview on current knowledge of systematics, evolution and diversity of *Arabidopsis* considering also the closest wild relatives. On this conference we aim to discuss critically the most recent taxonomic and systematic conclusions in the light of a worldwide screening of genetic diversity within the whole genus *Arabidopsis*.

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Evolutionary position of the enigmatic monotypic genus *Hypagophytum* (Crassulaceae) from Ethiopia: evidence from molecular and morphological data

Sabrina Schmidt[1], Barbara Rudolph[1], Ulrich Knapp[2], Joachim Thiede[3]

[1] Universität Hamburg, Biozentrum Klein Flottbek, Ohnhorststrasse 18, 22609 Hamburg, Germany, sabalexaschmidt@yahoo.de, b.rudolph@botanik.uni-hamburg.de , [2] Blumenstraße 4, 66509 Rieschweiler-Mühlbach, Germany, [3] Schenefelder Holt 3, 22589 Hamburg, Germany, joachim.thiede@gmx.de

Ever since its first description as Sempervivum abyssinicum Hochst. ex A. Rich. in 1847, this small tuberous herb from the Ethiopian Semien Mountains caused considerable classification problems: its generic placement and relationships were discussed controversially due to a unique combination of specialised morphological features. The plant was variously associated with the Macaronesian Aichryson (formerly placed in Sempervivum), Sedum (as Sedum abyssinicum (Hochst. ex A. Rich.) Hamet), Crassula (as Crassula malladrae (Chiovenda) Chiovenda nom. illeg.) or placed in a genus of its own (= Hypagophytum abyssinicum (Hochst. ex A. Rich.) A. Berger) with an uncertain position. The seed surface structure of *Hypagophytum* was described as costate, which prompted its placement in subtribe Telephinae. However, the seed surface structure corresponds to the sinuate-papillate type only found in *Crassula* (Knapp 1997), thus favouring a placement close to that genus within Crassuloideae (Thiede & Eggli 2005). Here, we investigate the evolutionary position, generic placement and phytogeographic relations of Hypagophytum based on analysis of nuclear ITS 1 & 2 as well as chloroplast trnL-F spacer sequence data in order to reinterpretate its specialised morphological features.

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A first indication of polyploidy in *Polylepis* (Rosaceae)

Alexander N. Schmidt-Lebuhn[1], Jörg Fuchs[2], Dietrich Hertel[3], Johanna Toivonen[4,5], Michael Kessler[5]

[1] Abt. Pflanzenökologie, Institut für Biologie, Universität Halle-Wittenberg, Germany, [2] Abt. Cytogenetik und Genomanalyse, IPK Gatersleben, [3] Department of Plant Ecology and Ecosystem Research, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany [4] Section of Biodiversity and Environmental Science, University of Turku, Finland, [5] Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany

The genus *Polylepis* (Rosaceae) consists of ca. 26 species of trees and some shrubs inhabiting the high Andes from Venezuela to central Argentina and northern Chile. *Polylepis* forests constitute the potential natural vegetation of much of the high Andes and support highly specialized animal communities. While the genus is easily recognizable, species delimitation is difficult and traditionally controversial, with high numbers of intermediate specimens and morphological plasticity. The exact reasons for this are still poorly understood. One of the possible explanations is a combination of hybridisation and polyploid speciation, but repeated previous attempts at chromosome counts have failed and available estimates are limited to very few taxa. In a first assessment of genome sizes conducted in *Polylepis*, we used flow cytometry to examine eleven species of *Polylepis* covering the whole range of morphological diversity found in the genus. While flow cytometry does not allow to directly infer chromosome numbers, our results reveal three distinct groups in a proportion of ca. 1 : 2 : 4. This indicates the occurrence of tetraploidy and octopoloidy and thus lends credibility to the hypothesis of polyploid speciation in the genus.

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Stabilization of novel morphological character states within 3 generations of hybrids in *Caiophora* (Loasaceae subfam. Loasoideae)

*Joana Schulz, Michaela Achatz, Markus Ackermann, Maximilian Weigend

Institut für Biologie der Freien Universität Berlin - Systematische Botanik und Pflanzengeographie, Altensteinstraße 6, 14195 Berlin, Germany

Caiophora (Loasaceae subf. Loasoideae) is a largely High-Andean genus with ca. 30-60 species. Its morphology contains a remarkable diversity concerning in habit, floral and leaf morphology as well as pollination syndromes. In spite of the morphological, molecular divergence appears to be very low between species, possibly indicating recent diversification. Also, several natural, fertile, interspecific hybrids have been documented in the wild and this further argues for a close relationship between taxa. To investigate possible reproductive barriers between taxa in the genus, experimental hybridization was carried out in the greenhouse and subsequent generations raised (F2, F3). Species used ranged from different populations of the same species to taxa from divergent species groups. Morphological parameters such as length and breadth of petals and bracts as well as the colour of the flowers were measured and compared between and within the generations (P, F1, F2, F3). The interspecific crosses between the *C. chuquitensis*- and the *C. carduifolia* groups resulted in an F1 with floral and leaf morphology parameters intermediate between the parental species *C. deserticola* and *C. carduifolia.* In the F1 a strong heterosis effect was observed, which was still perceptible, although weaker, in the subsequent generations. The F2-progeny showed strong morphological segregation, but the divergent morphotypes were stabilized and could be retrieved (after selfing of the F2) in the F3. The combination of novel characters, arising from hybridization, appears to be a very rapid process. Thus interspecific hybridization is a real possibility for the arisal of new lineages in the genus. This is all the more likely in nature because there appears to be no barrier to interspecific hybridization.

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Occurrence and distribution of serotonin-like immunoreactivity in larval *Haminoea hydatis* (Opisthobranchia, Cephalaspidea)

*Corinna Schulze, Annette Klussmann-Kolb

Institute for Ecology, Evolution and Diversity – Phylogeny and Systematics, J.W. Goethe-University, Siesmayerstr. 70, 60054 Frankfurt am Main, Germany

Haminoea hydatis is a member of the Cephalaspidea (Opisthobranchia). It occurs on the European Atlantic coast and the west coast of Africa. Cephalaspideans characteristically have a cephalic shield and a Hancock´s organ as cephalic sensory organs (CSOs). These are considered to have chemo- and mechanosensory functions. This study is part of a project reconstructing the evolution of the CSOs in the Opisthobranchia. It focusses on the pre- and postmetamorphic development of the *Haminoea hydatis* nervous system. We describe developmental stages based on morphological characteristics. These stages are investigated for serotonin-like immunoreactivity by means of antibody-staining in conjunction with confocal laser scanning microscopy (CLSM). *Haminoea hydatis* has a poecilogonous development. In early ontogeny 6 stages up to hatching can be distinguished. The average period until hatching takes 15 days. The first serotonin-like immunoreactivity is detected in stage 1 (days 1-3) in form of non-differentiated structures. First structures of the central nervous system can be observed in stage 2 (< day 3). The cerebral and pedal ganglia are visible in stage 4 (< day 5). From stage 5 (between days 7 and 8) projections appear, emerging from the cerebral ganglia towards the periphery. These results confirm other investigations on several gastropod species that serotonin has a regulatory effect on cleavage and plays a role in peripheral processing of sensory input.

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Induction of fertile male offsprings in *Plectus* (Nematoda)

*René Seiml-Buchinger

AG Evolutionsbiologie, Institut für Biologie / Zoologie, Freie Universität Berlin, Königin-Luise-Str. 1-3, 14195 Berlin, Germany

Generally, males of *Plectus* Bastian, 1865 are extremely rare. The identification of males found in soil samples is extremely difficult, only by comparing with the corresponding females. In cultures males are usually not found; the assumption is that the reproduction should be strictly parthenogenetic. By changing the environmental conditions it was possible to induce residual male offspring. The factor, which plays the decisive role, is the increased temperature. Like in *Caenorhabditis elegans* it has to be over 30°C, but for at least 14 days, not only six hours. The males show a high variability in their genital structures. The number of precloacal tubes varies from one to three. Even the morphological shape of the tubes shows strong distinctions. To test weather *P. acuminatus* males are fertile, virginal females were cultured with males at 20°C. In the progeny males were present at rates from 4%-53%. In control experiments without males, no males occurred in the progeny. The males found in the cultures used in the mating experiments also show a high diversity in the number (zero to four) and the shape of the precloacal tubes. Another aspect of the mating experiments was to quantify the number of transferred sperms. It could be shown, that only very few sperms are transferred (max. 7). In unmated females sperms or sperm like structures never were discovered. Finally it can be seen, that the reproduction processes of *P. acuminatus* are complex issues, where parthenogenetic plays a mayor role.

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Morphological and anatomical differentiation of *Cupressus arizonica* varieties planted in Tehran (Iran)

Youcef Shahali, Ahmad Majd, Golaleh Mostafavi

Department of Biology, Faculty of science, Islamic Azad University, North Tehran Branch, P.O.Box. 19585-935, Tehran, Iran

During the last two decades, the perfect adaptation of Arizona cypress trees (*Cupressus arizonica*) to climatic conditions has led to large-scale plantation of several varieties in reforestation, wind barriers and urban landscaping programs in Iran. A literature search yielded no investigations to identify and characterize the varieties planted in Iran. We have conducted a comparative study into the differentiation of the major varieties of *C. arizonica* in Tehran. Morphological characteristics of bark, branches, ramification, leaves and scale arrangements were compared. Vegetative and germinative anatomical structures were analyzed by using standard cellular and histological methods. Pollen samples were collected from mature male cones and compared with SEM. Our investigations indicate that var. *glabra* and var. *arizonica* constitute the great majority of the Arizona cypress trees planted in Tehran. The two varieties differ in their ramification patterns, bark, presence or absence of white spots on leaves and scale arrangements. Furthermore we detected major similarity between two varieties in anatomy but appreciable differences in pollen morphology.

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Embryology of *Tanacetum polycephalum*: a new and rare type of embryology

Abbas Shahsavari, Fariba Mohsenzade , Somayeh Hajsadeghi, Abdolkarim Chehregani

Department of Biology, Bu-Ali Sina University, Hamedan, Iran.

Embryological studies indicated species of *Tanacetum* to have *Antennaria* type diplospory with precocious embryology. The embryo sac is of the polygonum type, 8 cells (an ovule, two synergids, two polar nuclei and three antipodal cells) and the polar nuclei fuse before anthesis. Embryological characteristics of *Tanacetum polycephalum* were evaluated in this study. The flower and buds in different developmental stages were removed, fixed in FAA70, stored in 70% ethanol, embedded in paraffin and sectioned at 7-10 μm with a microtome. Staining was carried out with PAS according to protocol suggested by Yeung (1984) and contrasted with Meyers Hematoxylin. Chromosome behavior was studied using squashing of anthers. The results show that the embryology of *Tanacetum polycephalum* should be regarded an exceptional type. The embryo sac is a many-celled deviation of the *Polygonum* type, having 6-12 large antipodal cells with condensed cytoplasm. Study of microsporogenesis revealed abnormalities in chromosome pairing with result in the formation of univalents, bivalents, trivalents, and higher polyvalents, with the consequent production of lagging chromosomes, unbalanced nuclei and sterile pollen.

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Deep Molecular Phylogeny of the Pterygota

*Sabrina Simon[1], Jennifer Angermann[1], Heike Hadrys[1,2]

[1] ITZ, Ecology & Evolution, Stiftung Tierärztliche Hochschule Hannover, Bünteweg 17-d, 30559 Hannover, Germany, [2] Department of Ecology and Evolutionary Biology, Yale University, New Haven, CT, 06511, USA

Insects are among the most successful organisms of our planet and likely compose some 60% of the diversity of life. Unraveling their phylogenetic relationships, however remains a challenge. Despite the substantial amount of studies, the phylogenetic relationships among insects remain ambiguous. The pterygote data sets available hitherto show a strong bias towards the derived orders of insects. Especially studies of gene organization and complexity, EST approaches and mitochondrial genome analyses are mostly focusing on model systems such as *Drosophila*, *Apis*, *Tribolium*, *Anopheles* etc. (see Savard et al. 2006). Most phylogenies approaching basal pterygote insects are based on individual molecular sequence markers (e.g. 18S rRNA, partial 28S rRNA and Histone 3 sequences) and reveal conflicting results (Hovmöller et al., 2002; Kjer, 2004; Terry and Whiting, 2005). The potential of rRNA genes for phylogeny reconstruction has been hindered by alignment problems. Recently new rRNA substitution models and semi-automated secondary structure analyses have been introduced as a promising new approach to reduce those problems and gain additional information on molecule morphology (Misof et al., 2006). The current knowledge suggests that the origin of winged insects and their major bauplan innovations cannot be resolved by the standard sequence markers only. The use of ESTs for isolating new markers is a straightforward quantitative approach to increase the number of characters and improve the explanatory power of sequence analyses. Several arthropod EST projects have been published, but with a strong bias towards the holometabolous insects and a gap of information at the base of the Pterygota. Therefore we will focus our EST projects on Odonata, Ephemeroptera and Plecoptera. In addition our approach will be not only to increase the number of sequence markers but also select rRNA molecule morphology and mitochondrial genome structures as discriminative markers between different levels of genetic organization. This work is supported by the DFG special priority program "Deep Metazoan Phylogeny "SP1174 grant given to H.H. (DFG HA 1947/5-1 and 5-2).

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Phylogeny and phylogeography of *Allium* section *Rhizirideum*

*Tatiana Sinitsyna[1], Nikolai Friesen[2]

[1] -All-Russian N.I.Vavilov research institute of plant industry, B .Morskaya str. 42, Saint-Petersburg, 190000, Russia. [2] - Botanical Garden of the Osnabrück University, Albrecht-strasse, 29, Osnabrück, 49076, Germany

Section *Rhizirideum* is the typical section of *Allium* subgenus *Rhizirideum* and characterized by having bulbs enclosed in membranous tunics and attached to horizontal rhizomes. The section is widely distributed from Europe to Far East and includes 21 species. The centre of species diversity is in the steppes of Siberia and Mongolia. According to the phylogeny and intrageneric classification of the genus (Friesen et. al., 2006), the section *Rhizirideum* is monophyletic. The phylogeny of this section is complicated due to polymorphism and hybridization (polyploidy). To study this group, methods of sequencing of ITS fragments of nuclear DNA, trnL-Leo and trnL- trnF spacer fragments of chloroplast DNA and RAPD analysis were used; 23 representatives were analysed. Analysis with cpDNA markers showed minimal differences between species in the section. Use of ITS fragments resolved 2 distinct groups of species: a European group (*A. lusitanicum*, *A. angulosum*, *A. albidum*, *A. flavescens*, *A. pseudoalbidum*, *A. czelghauricum*, *A. incensiodorum*) and an Asian group (rest of the species of the section).

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Phylogeny of selected *Cryptocoryne* species in Malaysia based on 5' trnK sequence variation of chloroplast DNA

[1]Ahmad Sofiman Othman, [2]Niels Jacobsen

[1]School of Biological Sciences, Universiti Sains Malaysia, 11800 Penang, Malaysia. [2] Dept. of Ecology,Faculty of Life Sciences, University of Copenhagen, Rolighedsvej 21, 1958 Frederiksberg, Copenhagen, Danmark.

Cryptocoryne is an aquatic plant genus within the family Araceae. The genus is native to south east Asia which includes both the Malay Peninsular and the island of Borneo. Several species are widely exploited as foliage plants in tropical fish aquaria. A phylogeny was constructed using sequence variation of the 5' trnK intron including a partial of the matK region of chloroplast (cp) DNA to elucidate species relationships among representative of *Cryptocoryne* species present in both the Malay Peninsular and Borneo. Within the *Cryptocoryne* species surveyed, the 5' trnK intron ranged from 679 to 691 base pairs (bp) while the partial matK region sequenced ranged from 157 to 164 bp. The cpDNA phylogeny provides a strong relationship between *C. ellipica* and *C. schulzei*. The molecular data also grouped *C. xpurpurea* (a putative hybrid species) and *C. griffithii* (a putative parent of C. xpurpurea) together within a subclade but are distantly apart from *C. cordata* (the oher putative parent). This suggests that *C. xpurpurea* might be of hybrid origin having had *C. griffithii* as the maternal parent. Overall the cpDNA phylogeny however, did not provide sufficient resolution of species relationships among *Cryptocoryne* species used in this study.

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Phylogeography of *Gnaphalium salicifolium* (Asteraceae) in high mountains of Guatemala

*Sylvia Söhner[1], Frank Blattner[2], Klaus Bernhard von Hagen[1]

[1]Institute for Biology, Martin-Luther-University Halle-Wittenberg, Halle (Saale), Germany, [2]Institute of Plant Genetics and Crop Plant Research (IPK), Gatersleben, Germany

Many plant species in temperate mountain ranges have survived in refugia during cold stages of the Pleistocene and have later recolonized previously ice-covered regions. For other regions, e. g., tropical high alpine mountains phylogeographical information is rather scarce. Patterns in such mountains may differ because ice shields were not present and therefore migrations are expected on a smaller scale. As an indicative species, we have studied 15 different populations of *Gnaphalium salicifolium* from the Cadeña Volcanica and other mountains of Guatemala using sequences of the nuclear internal transcribed spacer (ITS), different cp regions, and AFLPs. The cp regions did not show informative characters. Following the ITS ribotypes the genetic diversity is much more equally distributed between populations than typically found in temperate mountains. Ribotype dispersal seemed to have happened in several directions repeatedly and all this might be connected to a comparably undisturbed population history. In contrast the phylogeography of *Halenia decumbens* (Gentianaceae) established in a previous study shows a directed migration starting from geologically old highlands via highlands of intermediate age into the young chain of volcanoes. It is concluded that these very different distribution patterns may be caused by different seed dispersal capabilities.

035

Eocene amber fauna from India – a paleogeographic study

*Mónica Morayma Solórzano Kraemer, Jes Rust

Institut für Paläontologie, Universität Bonn. Nussallee 8, 53115, Bonn, Germany msolorzanokraemer@gmail.com, jrust@uni-bonn.de

Eocene Indian amber with organismic inclusions was recently found more or less accidently together with spectacular fossil vertebrates. The amber derives from the Vastan lignite mine, which is located approximately 30 km northeast of Surat (Gujarat, West Indian). The deposits have been dated as lower Eocene (about 52 Ma), founded on foraminiferal biostratigraphy and also on the presence of fossil otoliths assemblages. The age of the amber implicates that the insects were embedded before or close to the time of the collision of the Indian plate with Asia. The amber is of great importance, because the fossils afford the possibility to study the evolution of the terrestrial ecosystems of India on a geological time scale. If India was an isolated continent during most of the Cretaceous and the Paleocene, its high extant biodiversity with a distinctive endemism should also be reflected by the arthropods and other organisms.The Vastan amber fauna is mainly composed of Arachnida and Diptera, however, also other insects have been found: Hymenoptera, Psocoptera, Auchenorrhyncha, Microlepidoptera and some unidentified specimens. Two of the insects, a Psychodidae and a Mycetophilidae, have been studied more precisely in terms of their systematic postion and biogeographic relationship. First results of the investigation of the two taxa imply the presence of a characteristic fauna in India before the collision with Asia.

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A hybrid zone of two gomphocerine grasshopper species on the Tomaros mountain in Northern Greece

*Jan Sradnick, *Anja Klöpfel, Norbert Elsner

Georg-August-Universität, Göttingen, Johann-Friedrich-Blumenbach-Institut für Zoologie und Anthropologie, Berliner Str. 28, 37073 Göttingen, Germany

The two grasshopper species *Stenobothrus rubicundus* and *Stenobothrus clavatus* are found on the northern und southern slopes, respectively, of the Tomaros mountain in north-west Greece. The habitat of both species crosses at the saddle area. Both species can be clearly distinguished based on morphology of the antennae, position of the stridulatory pegs, numerous characters of the fore and hind wings, and most notably on the different courtship behaviour of the males, which normally acts a powerful pregametic isolating mechanism in grasshoppers. Nevertheless, intermediate forms can be found frequently in a small overlapping area of *St. clavatus* and *St. rubicundus* on the saddle region. These hybrids display an abundance of intermediate morphological and behavioural characters. In comparison with populations of either *St. rubicundus* or *St. clavatus* on other mountains the populations on the Tomaros mountain seem to influence each other genetically. This suggests introgression of genes towards both *Stenobothrus* populations, which needs further corroboration by molecular means.

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Comparative mitochondrial genomics of Tunicata

Thomas Stach[1], Anke Braband[2], Lars Podsiadlowski[1]

[1]Institut für Zoologie, Freie Universität Berlin, Berlin, Germany , [2]Institut für Biologie, Humbodt-Universität Berlin, Germany

With respect to mitochondrial gene order Tunicates are among the most diverse animal taxa. With the exception of a single doliolid species (*Doliolum nationalis*), only members of Phlebobranchiata and Stolidobranchiata ("Ascidiacea") have GenBank records for complete mitochondrial genomes. We sequenced the mitochondrial genome of *Clavelina lepadiformis*, a member of Aplousobranchiata (Tunicata: "Ascidiacea"). Comparison of the mitochondrial gene order with the CREX software (Berndt et al. 2007, Bioinformatics 23:2957) shows that gene order changes in tunicates cannot easily be reconstructed, even if the highly mobile tRNA genes are neglected. The reasons for this extreme case of gene order variation remain obscure. Two distinct apomorphic similarities, present among tunicate mitochondrial genomes are apparent: (i) all genes are encoded on the same strand, a character state that is otherwise only found in some lophotrochozoan taxa, and (ii) all but *Clavelina lepadiformis* share an adjacency of the cox2 and cob genes. Comparative analyses of nucleotide composition, substitution rates and strand biases in deuterostome taxa demonstrate the high degree of variation and thus reveal the strongly derived character of tunicate mitochondrial genome sequences. For these reasons, a phylogenetic analysis of Tunicata based on mitochondrial genomes and sequence data in general remains challenging.

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Organization of the mesoderm in ascidian larvae

Thomas Stach, Conny Peschel, Anne Paasch

Freie Universität Berlin, Fakultät für Biologie, Zoologie, AG Sytematik und Evolution der Tiere, Königin-Luise-Str. 1-3,14195 Berlin, Germany

The larval stage of ascidian tunicates has played a pivotal role in understanding chordate evolution. While the organization of the mesoderm has been given high importance in comparative anatomical studies of Bilateria, this morphological character remains largely unexplored in ascidian larvae. In the only available transmission electron microscopic (TEM) study available (Katz 1983) the presence of two mesodermal pockets is claimed, raising the possibility that paired coelomes are present in the larval ascidian. Here we present a comparative anatomical study of larval semaphoronts from four major tunicate clades: Aplousobranchiata, Phlebobranchiata, Stolidobranchiata, and Appendicularia. We used computer assisted 3D-reconstruction based on complete series of 1µm-sections analyzed by light microscopy complemented by TEM-investigation of selected regions. Mesodermal tissue is widely distributed in the trunks of the larvae. In Aplousobranchiata numerous mesodermal cells can be found from the anterior to the posterior trunk forming a sheet between ectodermal epidermis and endodermal gut rudiment. In Phlebobranchiata, massive mesodermal components occur in the posterior trunk, whereas more anteriorly situated mesoderm consists of loose streaks of cells or isolated cells. This is also the case in part of Stolidobranchiata. In other Stolidobranchiata and larval Appendicularia the anterior trunk is entirely free of mesodermal cells. The TEM-investigation revealed that all mesodermal structures in larval tunicates were mesenchymal with the exception of a ventral portion of the mesoderm in the larva of the aplousobranch *Clavelina lepadiformis*, which probably corresponds to the developing pericard. Thus we could not find evidence for paired coelomic cavities in Tunicata. Outgroup comparison suggests that an ealy development of the pericard, as observed in Aplousobranchiata and Appendicularia is plesiomorphic within Tunicata, with the heterochronic shift towards a later development apomorphic for the remainder of Tunicata. Within Tunicata the stepwise evolutionary reduction of the anterior mesoderm is documented.

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Phylogenetic status of the genera *Calligonum*, *Pteropyrum* and *Atraphaxis* based on chloroplast and nuclear DNA sequences

*Solmaz Tavakkoli[1], S. Kazempour Osaloo[1], A.A. Maassoumi[2]

[1]Department of Plant Biology, Faculty of Basic Sciences, Tarbiat Modares University, Tehran, Iran, [2]Department of Botany, Research Institute of Forests and Rangelands, Tehran, Iran

This study deals with the phylogenetic status of three woody polygonaceous genera *Calligonum*, *Pteropyrum* and *Atraphaxis* (Polygonoideae-Polygoneae / Atraphaxideae), using both nrDNA ITS and trnL-F sequencing for the first time (for the remaining taxa analyzed here, the sequences were obtained from GenBank). All phylogenetic analyses were performed using the Maximum Parsimony approach as implemented in PAUP*4.0b10. Twenty-two ingroup taxa including *Calligonum* p.p. (with winged fruit), *Calligonum* p.p. (with bristled fruit), *Calliphysa* (with membranous saccate fruit), *Pteropyrum* (3 *species), Atraphaxis (2 species), Fagopyrum (3 species), Fallopia (3 species), Polygonum* (1 species), *Persicaria* (4 species) and *Rumex* (3 species) plus *Triplaris gardneriana* as an outgroup, were included in a phylogenetic analysis based on nrDNA ITS data. cpDNA trnL-F sequences were obtained for a subset of these taxa. Phylogenetic analysis was also performed on the aligned data matrice of combined nrDNA ITS and trnL-F sequences for nine of these species. All inferred phylogenies show that *Calligonum* and *Pteropyrum* are closely related taxa forming a single clade, while *Atranphaxis* is related to *Polygonum*. Both nrDNA ITS and trnL-F phylogenies revealed that *Calligonum*, *Pteropyrum* and *Atraphaxis* are monophyletic. The three sampled species of *Calligonum* have no nucleotide differences in trnL-F sequences and are of only 2 nucleotide substitutions in nrDNA, and thus, the species relationships were not resolved. Our data demonstrate that placement of *Calligonum* and *Pteropyrum* in the tribe Polygoneae/Atraphaxideae is erroneous. It is suggested to place these two genera in their own tribe Calligoneae, as already proposed by Roberty & Vautier (1964).

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Principles of plant evolution in the Arctic: a comparison of *Artemisia* and *Ranunculus*

*Natalia V. Tkach[1], Elvira Hörandl[2], Matthias H. Hoffmann[1], Martin Röser[1], K. Bernhard von Hagen[1]

[1] Institute of Biology, Department of Geobotany and Botanic Garden, Martin-Luther-University Halle-Wittenberg, Neuwerk 21, 06099 Halle, Germany, [2] Department of Systematic and Evolutionary Botany, Institute of Botany, University of Vienna, Rennweg 14, 1030 Vienna, Austria

Artemisia L. with 33 of c. 450 species and *Ranunculus* L. with 45 of c. 600 species recorded from arctic habitats are among the most diverse genera of the Arctic, and the aim of our study was to identify whether typical ecological, geographical, morphological, karyological, or temporal patterns can be observed which are most likely connected with colonization of arctic habitats. Therefore, we have produced molecular phylogenies of 133 and 279 taxa for *Artemisia* and *Ranunculus*, respectively, including almost all arctic lineages recorded. We then tried to compare independent arctic lineages with their respective sistergroups. We found that both genera have colonized arctic habitats multiple times, but arctic lineages of *Artemisia* were on average much older than lineages of *Ranunculus*. Another difference was that arctic Ranunculi seem to fit to the general rule of higher ploidy levels in arctic habitats but not *Artemisia*. Instead, arctic *Artemisia* lineages evolved significantly larger flower heads and lesser plant height subsequent to the colonization of the arctic. Similar morphological adaptations were not apparent in arctic *Ranunculus*. The number of arctic lineages present in major arctic regions was different, for example, there is only single arctic *Artemisia* species in Europe but several species of *Ranunculus*. We conclude that the divergent patterns found between both genera are connected with the different age of the groups and different reactions to the glaciation history.

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The thorax of the Anoplura (Insecta, Acercaria) reconstructed from MCT

Gert Tröster, Benjamin Wipfler

Johann-Friedrich-Blumenbach Institut für Zoologie und Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie mit zoologischem Museum, Berliner Strasse 28, 37073 Göttingen, gtroest@gwdg.

The Anoplura, or sucking lice, are a wingless taxon of insects grouped together with Psocoptera (book lice), Amblycera and Ischnocera (biting lice), and Rhynchophthirina (elephant lice) within Psocodea. The morphology of the thorax and the thoraric muscles is adapted to the special way of life of the Anoplura, as ectoparasites of mammals. To improve the mobility in the hosts fur and furthermore to resist grooming attacks the legs are enlarged and evolved into brace legs. Each leg bears a robust claw on its tip allowing the animal to cling to the hosts hairs. The leg musculature is well developed. Additionally the thoraric muscles moving the base of the legs are dramatically enlarged. The origin of the coxal muscles has moved from the pleural towards the dorsal thoraric region. In some taxa a strong apodeme protrudes vertically from the middle of the dorsal region of the thorax into its lumen. The muscles supplying the coxae originate from these apodemes. All muscles, which are inherent in winged insects, used for flying are reduced. The three thoraric segments are completely fused. Dorsally no differentiation into pro-, meso- and metathorax is possible any more. On the ventral side the segmentation can be retraced by the three pairs of legs. In *Hybophthirus notophallus* the ventral apodemes of the thorax, the pro-, meso- and metafurca still exist while these structures are completely reduced in all other Anoplura. This reduction causes the loss of several muscles originating from these structures. The presented facts of this study support the thesis of *Hybophthirus* being the most basal taxon of the Anoplura.

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A comparative morphological study of the '*Quercus ilex* group' in western Eurasia

*Georg F. Tschan, Thomas Denk

Department of Palaeobotany, Swedish Museum of Natural History, Box 50007, 10405 Stockholm, Sweden, Georg.Tschan@nrm.se

The *Quercus ilex* group in western Eurasia comprises three species, *Q. ilex, Q. coccifera,* and *Q. aucheri*. Material for the present study was collected from the entire distribution ranges of the three taxa. A comparative morphological study was undertaken using leaf morphology (leaf architecture and micromorphology) and characters from cupules and acorns. The following questions have been addressed: (i) Do the three species form distinct morphological units? (ii) Is there morphological overlap between them? (iii) Is *Q. aucheri* a good species? (iv) Are hybrids between *Q. ilex* and *Q. suber* (cerris oaks) common? (v) How are members of the *Quercus ilex* group related to a widespread European Neogene (fossil) species *Q. mediterranea*? Based on this, an attempt was made to reconstruct the evolutionary history of the *ilex* group in western Eurasia. One of the main findings of this study is that hybrids are much less common in western Eurasian oaks than commonly assumed. Hybridization can be traced at the molecular level, but most of the hybrid signal can be attributed to ancient hybridization (G. W. Grimm et al., unpublished data) and is seen not only between closely related species but also between members of more distantly related groups (e.g. cerris oaks and *ilex* group). The fact that species boundaries among oaks are permeable (gene flow) does not affect species integrity of extant oak species.

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Distribution and threat status of the endemic taxa *Centaurea* sect. *Acrolophus* (Asteraceae) in Turkey

Osman Tugay, Kuddisi Ertuğrul, Tuna Uysal

Selçuk Universty, Faculty of Science and Letters, Department of Biology, Konya, Turkey, otugay@selcuk.edu.tr

Centaurea is one of the largest genera in the flora of Turkey. Section *Acrolophus* is represented by 31 taxa, 24 of which are endemic to Turkey; 10 of the endemic taxa have local and 14 of them regional or larger distributions. The endemic species are (threat status in brackets): *Centaurea aggregata* Fisch. & Mey. ex DC. subsp. *albida* (C.Koch) Bornm (EN), *C. anthemifolia* Hub.-Mor. (CR), *C. austro-anatolica* Hub.-Mor. (EN), *C. calolepis* Boiss. (LC), *C. cariensiformis* Hub.-Mor. (CR), *C. cariensis* Boiss. subsp. *cariensis* (VU), *C. cariensis* Boiss. subsp. *longipapposa* Wagenitz (LC), *C. cariensis* Boiss. subsp. *maculiceps* (O.Schwarz) Wagenitz (LC), *C. cariensis* Boiss. subsp. *microlepis* (Boiss.) Wagenitz (NT), *C. cariensis* Boiss. subsp. *niveotomentosa* (Hub.-Mor.) Wagenitz (EN), *C. consanguinea* DC. (LC), *C. dichroa* Boiss. & Heldr. (LC), *C. kilaea* Boiss., (EN), *C. nydeggeri* Hub.-Mor. (CR), *C. olympica* C. Koch (CR), *C. pinetorum* Hub.-Mor. (VU), *C. polyclada* DC. (VU), *C. sipylea* Wagenitz (CR), *C. sivasica* Wagenitz (LC), *C. tuzgoluensis* Aytaç & H.Duman (CR), *C. werneri* Wagenitz (CR), *C. wiedemanniana* Fisch. & Mey. (CR), *C. yozgatensis* Wagenitz (CR) and *C. zeybekii* Wagenitz (CR). The information on the distribution and threat categories of these taxa, especially of the narrow endemics were incomplete and are updates based on the present study.

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The rediscovery of *Centaurea demirizii* (Asteraceae) in Turkey

Osman Tugay, Tuna Uysal

Selçuk Universty, Faculty of Science and Letters, Department of Biology, Konya, Turkey
otugay@selcuk.edu.tr

During the project 'The Revision of genus *Centaurea* L. Sections *Acrolophus* (Cass.) DC. ve *Ammocyanus* Boiss. (Asteraceae) in Turkey', founded by the Scientific Research Projects Coordination Office (BAP-06401023), *Centaurea demirizii* Wagenitz, a local endemic taxon, was collected in Ağrı area. The first specimens of this species were collected during an expedition by Demiriz to the area around Doğubeyazıt, East Anatolia in July 1956. These specimens were described as new species by Wagenitz in 1961. In the Flora of Turkey (1975) the author indicated that the capitula of *Centaurea demirizii* are very similar to those of *C. glastifolia*, but the habit is quite different and the characters of the pappus are aberrant for *Chartolepis* (Cass.) DC. section. Some deficiences in the description of *Centaurea demirizii* were remedied, and a new description of the species has been prepared.

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Molecular phylogeny of the genus *Ononis* (Fabaceae)

*Florian Turini[1], Christian Bräuchler[1,2], Günther Heubl[1]

[1] LMU München, Department Biologie I, Systematische Botanik, Menzinger Str. 67, 80638 München, Germany, [2] Botanische Staatssammlung München, Menzinger Str. 67, 80638 München, Germany

Ononis L. (Fabaceae, Papilionoideae), consisting of about 85 species, is a very common genus in the circummediterranean region, with a center of diversity in the Iberian Peninsula and adjacent northern Africa. It is part of the papilionoid temperate herbaceous clade, with *Medicago* and *Trigonella* as closest relatives. To re-evaluate the infrageneric concept of *Ononis*, 77 species were analyzed using nuclear ITS and plastid trnL-F sequences. Trees resulting from maximum parsimony analyses and Bayesian inference revealed *Ononis* monophyletic. Topologies indicate five major lineages within the genus, which are morphologically supported by a specific combination of peduncle length and flower color each. This contradicts the traditional infrageneric classification presented by Širjaev (1932), who recognized the two sections *Ononis* and *Natrix*. However, the majority of the proposed 22 subsections are well reflected by the molecular data. A few exceptions can be explained by former misinterpretation of certain non-reliable characters like seed number or -surface structure. In particular, subsections *Reclinatae* and *Villosissimae* are indicated to be polyphyletic. Subsections *Antiquae* and *Rhodanthae* are placed in a basal position and consequently are confirmed to comprise ancestral taxa, as suggested by former studies. Major clades within the genus are also discussed in a biogeographic context, showing a correlation between the life strategies dominant in the different groups and the climatic factors in their specific habitats. Some of the subsections are likely to be secondary perennial, like the Central European-distributed subsection *Ononis* and the subsections *Mauritanicae* and *Canariensis*, which could serve as examples for secondary high altitude- or insular woodiness, respectively.

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Ultrastructure of potential photoreceptors in echinoplutei of *Strongylocentrotus purpuratus* (Echinodermata, Echinoida)

*Esther Ullrich, Harald Hausen

Institut für Biologie / Zoologie, Systematik und Evolution der Tiere, Freie Universität Berlin, Königin-Luise Str. 1-3, 14195 Berlin, Germany

The evolution of photoreceptive cells within the animal kingdom has been a challenging field of research for more than a hundred years. Lately molecular methods enable us to determine photoreceptors by a set of molecules involved in the photoreception- and transduction cascade. Opsins are one group of those molecules and it has been a big surprise to find six different opsins in the recently sequenced genome of the sea urchin *Strongylocentrotus purpuratus*. Although there is proof for behavioural and neurological phototactic responses in adult sea urchins and echinoplutei, structural investigations alone never resolved specialized photoreceptive cells. Based on reported expression of an opsin, which is typical for rhabdomeric photoreceptors, in the armtips of a larva of *S. purpuratus* we examined the structure of all tissues in the larval arms using cLSM and TEM. Phalloidin and antibodies against α- acetylated tubulin were used for labelling F-actin rich microvillar structures and nerve fibres associated with them to identify potential rhabdomeric photoreceptor cells. Microvilli bearing sensory cells were not detectable in the armtips. Subsequent ultrastructural analysis revealed exactly one type of nerve cell located in the region of interest. These epidermal cells have long sensory apical extensions supported by microtubules and two axons running beneath the ciliary band. The arrangement of the microtubuli differs however from that in ciliary structures. A comparable cell type has been described from other echinoderm and enteropneust larvae. A potential photoreceptive function of this cell type bears consequences for photoreceptor evolution in deuterostomes.

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Patterns of genetic diversity of *Fagus sylvatica* in Rodopi Mountains, N.E. Greece

*Amaryllis Vidalis[1], Aristotelis Papageorgiou[2], Seraphim Hatziskakis[2], Ioannis Tsiripidis[3], Oliver Gailing[1], Reiner Finkeldey[1]

[1] Abteilung für Forstgenetik und Forstpflanzenzüchtung, Büsgen-Institut, Georg-August-Universität Göttingen, Büsgenweg 2, 37077 Göttingen, Germany, [2] Department of Forestry, Environment and Natural Resources, Democritus University of Thrace, P.O. Box 129, Pantazidou 193, 68200 Orestiada, Greece, [3] Biology Department, Aristotle University of Thessaloniki, 54006 Thessaloniki, Greece

The taxonomic classification of the European beech has lately been subject of scientific discussion. In the present study, genetic variation at AFLPs, chloroplast microsatellites and variation in leaf morphology have been analysed in four populations of *F. sylvatica* in Rodopi Mountains, N.E. Greece. The analysis of morphological traits reveals differences between the western and the eastern part of Rodopi Mountains. Moreover, high levels of haplotype diversity were observed within populations, while in central and western Europe no variation at cpDNA markers was detected. Clinal variation patterns occurred in both morphological and molecular markers, with the variation increasing from the west to the east. Differentiation among populations was found, as expected, stronger at maternaly inherited cpDNA. The results obtained in this study can be explained either by considering the Rodopi an introgression zone between subspecies *sylvatica* and subspecies *orientalis* or by the existence of a main glacial refugium of european beech during the last glaciation.

088

Phylogeny of suborder Jungermanniineae (Hepaticae) based on ITS1-2 nrDNA and trnL-F cpDNA sequences data

Anna Vilnet[1], Nadezda Konstantinova[1], Alexey Troitsky[2]

[1] Polar Alpine Botanical Garden, Kirovsk-6, Murmansk, Province 184236, Russia, anya_v@list.ru, [2] A. N. Belozersky Institute of Physicochemical Biology, M. V. Lomonosov Moscow State University, Moscow 119991, Russia, tav@genebee.msu.ru

The suborder Jungermanniineae is one of the most complex groups of leafy liverworts. We have tried to reconstruct the phylogeny of the group including a wide sampling of Lophoziaceae, Scapaniaceae, Gymnomitriaceae and Jungermanniaceae based on combined ITS1-2 and trnL-F data from 139 species (233 samples). Phylogenetic trees were inferred by Bayesian, maximum likelihood and parsimony methods. The topologies of the resulting trees are congruent and similar to previous molecular ones but disagree with modern conceptions of Jungermanniineae based on morphology. Jungermanniaceae and Lophoziaceae appear to be polyphyletic families, Gymnomitriaceae and Scapaniaceae are monophyletic. The taxa of Jungermanniaceae are located in the basal part of the trees far removed from Lophoziaceae. The location of *Mylia* species in a distinct clade supports its treatment in the separate family Myliaceae. *Leiocolea* is combined in one clade with *Mesoptychia*, giving reason to expand the Mesoptychiaceae. Phylogenetic relationships of *Jamesoniella* remain unclear: *J. autimnalis* (DC.) is placed within Jungermanniaceae and *J. undulifolia* is related to Lophoziaceae. Within Lophoziaceae the narrow generic concepts of *Lophozia*, *Anastrophyllum* and *Tritomaria* are supported. *Isopaches, Schistochilopsis, Obtusifolium, Barbilophozia, Sphenolobus, Crossocalyx* and *Saccobasis* should be treated as separate genera. *Lophozia* s.str. and *Orthocaulis* are polyphyletic genera. The separation of Diplophyllaceae from Scapaniaceae is not confirmed by tree topologies. *Gymnomitrion* and *Marsupella* are polyphyletic genera. The position of *Eremonotus* accepted by most bryologists is not supported. The results obtained suggest the necessity of the revision of Gymnomitriaceae.

067

Uncovering the trail of a mass murderer – the phylogeography of *Acanthaster planci*

*Catherine Vogler[1], John Benzie[2], Paul Barber[3], Gert Wörheide[1]

[1] Courant Research Centre Geobiology, Georg-August-Universität Göttingen, Goldschmidtstr. 3, 37077 Göttingen, Germany, [2] Moana Technologies, Hawaii, USA, [3] Biology Department, Boston University, USA

Due to their high dispersal potential and the apparent lack of barriers in the marine realm, widespread marine organisms have long been expected to display little genetic structuring. Yet recent studies on marine invertebrates challenge this belief. Distributed throughout the Indo-Pacific, and as such an ideal model for understanding patterns influencing its genetic structure, the conspicuous crown-of-thorns starfish *Acanthaster planci* has drawn much public and scientific attention over the last 40 years. Despite being a natural predator of corals, it is notoriously infamous for its dramatically destructive "outbreak" phenomena that have devastated coral reefs throughout its distribution range. However, until today, little is understood about its larval dispersal patterns, the connectivity among populations, and the spread of outbreaks among reefs - all essential elements to appreciate the scale of *A. planci*'s threat to coral reefs and devise appropriate management plans. Previous studies on *A. planci* have allowed uncovering substantial gene flow among populations over large distances; nonetheless a major genetic differentiation between the Indian and Pacific Oceans was also detected. However, the lack of resolution of the markers used in these studies limited the interpretability of the data at a finer scale. By investigating *A. planci*'s phylogeography using sequences of the mtDNA control region, and increasing the sampling to its whole distribution range, this study allowed distinguishing several differentiated clades - probably influenced by past geotectonic events and sea level changes, as well as current oceanographic patterns - and understanding more about the dispersal patterns of this ecologically important corallivore.

008

Phylogeny of Calcareous Sponges: resolving relationships of morphological highly problematic taxa

*Oliver Voigt, Eilika Wülfing, Gert Wörheide

Courant Research Centre Geobiology, Georg-August-Universität Göttingen, Goldschmidtstr. 3, 37077 Göttingen, Germany

Resolving the phylogeny of phylum Porifera still remains a challenge. Relationships among and within the recognized three extant classes of Porifera (Demospongiae, Calcarea and Hexactinellida) are not satisfactory solved. One reason for this is the limited amount of morphological traits with taxonomic value (mainly consisting of skeletal elements and their architecture) and the presence of many homoplasies in the remaining ones. While in class Hexactinellida, phylogenies inferred from molecular sequence data are in good concordance with morphological evidence, this is not the case in the other sponge classes. Especially in calcareous sponges (Class Calcarea), molecular phylogenies suggests that most of the recognized orders, families and genera are not monophyletic, which brings forward completely unexpected novel hypotheses of relationships and questions the currently accepted typological system of Calcarea. It also raises additional questions on the experimental design required to test these hypotheses. We present refined new phylogenies, mainly based on molecular data and sophisticated analyses that allow testing of current calcarean taxonomic hypotheses and suggesting novel scenarios of character evolution, e.g. reconstructing the evolutionary history of aquiferous systems in Calcarea. Further, 'DNA barcoding' approaches to overcome crucial problems of identification and taxon sampling in the light of an animal group which posseses so many homoplasic characters are discussed.

021

Sperm ultrastructure as a significant contribution to morphological data sets for nemertean systematics

*Jörn von Döhren, Thomas Bartolomaeus

Freie Universität Berlin, Institut für Biologie, Evolution und Systematik der Tiere, Königin-Luise-Str. 1-3, 14195 Berlin, Germany

Nemertea is a spiralian clade of unsegmented, predatory worms that consists of about 1000 species. Up to present, ingroup phylogeny with morphological data sets has been restricted to certain subtaxa including Paleonemertea, Eureptantia and Pelagica but no attempt has been made regarding the whole of the taxon. This is mainly due to a lack of characters that are suitable to be compared on a higher level especially in the presumably basal subtaxa. This study aims at broadening the morphological data set by introducing ultrastructural data obtained by means of transmission and scanning electron microscopy on spermatozoa of 10 species representing members from most of the nemertean subtaxa. The resulting matrix is complemented by literature data on spermatozoa of 20 species already published. We can show that data on sperm morphology in Nemertea represents a significant contribution to unraveling the ingroup phylogeny of this taxon. The obtained results also show extensive congruence with molecular phylogenies of Nemertea.

031

New approach to test the Mandibulata concept and to infer the phylogeny of Crustaceans

Björn v. Reumont[1], Wolfgang Wägele[1], Dieter Waloskek[2]

[1] Zoologisches Forschungsmuseum Alexander Koenig, Bonn, Germany, reumont.zfmk@uni-bonn.de. [2] Universität Ulm, Sektion für Biosystematische Dokumentation, Ulm, Germany

In our project we reconstruct the phylogeny of crustaceans within arthropods with a focus on lower crustaceans or Entomostraca. The project is integrated in the DFG priority program „Deep Metazoan Phylogeny". We use two different molecular approaches to reconstruct phylogeny. First, we sequenced the complete ribosomal 18 and 28S rRNA genes and additionally the 12S, 16S and Histone 3 genes. For the ribosomal RNA genes we constructed an improved alignment based on secondary structures. This analysis was performed using the new software RNASalsa. Phylogeny was computed applying PHASE 2.0 using a Bayesian approach. We implemented a time-heterogeneous model to scope with non stationary base frequencies. In the second approach we sequence ESTs and analyse data in cooperation with the bioinformatic group of A. von Häseler (University Vienna). The goals are to reconstruct the internal phylogeny of lower crustaceans including important groups like Remipedia, Pentastomida, and Mystacocarida. But we also intend to address arthropod phylogeny and the Mandibulata concept using these new methods and marker genes. We also use an expanded and carefully selected taxon sample to include arthropod groups with putative less derived characters.

040

Digging for the offspring, or how to bury an ootheca underground (Insecta: Dictyoptera: Mantodea)

*Frank Wieland

Georg-August-Universität Göttinegn, Johann-Friedrich-Blumenbach-Institut für Zoologie & Anthropologie, Abteilung für Morphologie, Systematik & Evolutionsbiologie, Berliner Str. 28, 37073 Göttingen, Germany, fwielan@gwdg.de

Mantodea (praying mantids) is a monophyletic group which is supported by numerous autapomorphic characters, often being closely related with the raptorial lifestyle. The phylogenetic relationships between the mantodean taxa, however, are poorly understood. In the current classification the 2,300 extant species are categorized in 15 "families" comprising 48 "subfamilies". However, only very few apomorphic characters supporting the monophyly of these taxa have been mentioned and described. Thus the monophyly of many of the mantodean subgroups is doubtful. Evidence for the artificial nature of most of the major traditional groupings based on molecular data was presented by Svenson & Whiting (2004, Systematic Entomology 29: 359-379). Mantodea deposit their eggs in oothecae (egg packages), where they are embedded in a foamy secretion from the accessory glands of the genital apparatus, a synapomorphic feature of Mantodea and their closest relatives, the cockroaches and termites (Blattodea). In most Mantodea, the females choose a suitable substrate above the ground for attaching the ootheca, usually a twig, a leaf, the bark of a tree, or a stone. The ootheca is then built onto the substrate, and the fluid secretion hardens, thus gaining its typical foamy structure. In captivity, some species have been observed burying their oothecae in the ground when the climatic environment in captivity does not suit the demands for a proper embryonic development. However, several species living in very arid habitats generally bury them this way. Four different morphological solutions to the problem of digging for the deposition of oothecae below the surface have been identified and are here presented in their morphological details. They are informally named the "Eremiaphilidae-type" (spines originating from sternite 6), the "*Rivetina*-type" (spines originating from the proximal part of sternite 7), the "*Chroicoptera*-type" (hooks originating from the distal part of sternite 7), and the "*Ligaria*-type" (hooks originating from the gonapophyses of the 8th abdominal segment). The identification of the corresponding apomorphic structures allows to support the monophyly of Eremiaphilidae and (at least a part) of Chroicopterinae.

016

Central nervous system and photoreceptor-like sense organs in *Polygordius appendiculatus* (Annelida), an interstitial polychaete with uncertain phylogenetic affinities

*Verena Wilkens, Günter Purschke

Zoologie, Fachbereich Biologie/Chemie, Universität Osnabrück, 49069 Osnabrück, Germany

The phylogenetic position of *Polygordius* is still unclear; relationships to either Opheliidae or Protodrilida, especially to *Saccocirrus*, are the most favored hypotheses. The present study in *Polygordius appendiculatus* was designed to look for morphological characters supporting either of these two hypotheses. For this purpose the homology of the anterior appendages should be clarified as well as the structure of the central nervous system and nuchal organ; we also examined whether photoreceptor-like sense organs exist in adults. From their innervation pattern it is unlikely that the anterior appendages represent antennae rather than palps. However, these palps lack structures typical of palps in Canalipalpata such as musculature and coelomic cavities, which would be expected in the case of a saccocirrid relationship. In adult individuals 13 photoreceptor-like sense organs were found in front of the brain, the only structures resembling photoreceptors in adult *P. appendiculatus*. Most likely, such structures first develop in the larvae and persist in the adults. These sense organs are multicellular and comprise a supportive cell and several sensory cells enclosing an extracellular cavity. There are three different types of sensory cells, one rhabdomeric and two ciliary. These sensory cells are combined differently to form three types of sense organs, the most frequent employing all three types of sensory cells; the second possesses a rhabdomeric and one ciliary cell type, and the last one the two types of ciliary sensory cells. Whereas similar sensory cells are frequently found in various polychaetes including *Saccocirrus* and Opheliidae, their combination in one sensory organ is unique for *Polygordius* and is considered to represent an autapomorphy. The nuchal organs exhibit features typical of polychaetes but there are no specific features in common with *Saccocirrus*. Instead, the covering structures show obvious similarities to Opheliidae, as can also be found in the central nervous system. Altogether, the current observations do not contradict a relationship to opheliids but give no evidence of a relationship to *Saccocirrus* such as has been found in certain molecular analyses, and thus currently leave the phylogenetic position of *Polygordius* unresolved.

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Molecular systematics and morphological diversification of *Euphorbia* sect. *Monadenium*

*Maria Will, Frank H. Hellwig

Institut für Spezielle Botanik, Friedrich-Schiller-Universität Jena, Germany

According to molecular studies (Brunys et al. 2006) the formerly accepted genera *Monadenium* Pax, *Synadenium* Boiss. and *Endadenium* L.C.Leach form a monophyletic group (section *Monadenium* (Pax) Bruyns) of *Euphorbia* L. subgen. *Euphorbia*. In the present investigation, we try to light up the relationships within the formerly circumscribed genus *Monadenium* using nrITS- and $\mathrm{trnL_{UAA}}$-$\mathrm{trnF_{GAA}}$-IGS sequence data of 28 taxon samplings. Our data support earlier findings (Park & Elisens 2000, Steinmann and Porter 2002, Bruyns et al. 2006) that the *Monadenium*-group is closely related to *Euphorbia* and that the section is a well supported (BP = 100%; PP = 1.00; BS = 27) monophyletic group nested in *Euphorbia*. The phylogenetic tree (MP) shows *Euphorbia neopedunculata* Bruyns as sister to all further investigated taxa. This species is characterised by the absence of a caruncula and the occurrence of non-fused involucral bracts. Thus our results support the hypothesis, that the herbaceous life form and free involucral bracts represent ancestral character states (Bally 1961). Within the remaining species we found six well supported clades almost homogenous in the basic chromosome number, life form and seed morphology. However, succulence and life forms appear to have evolved several times in parallel. In one of the six clades, *Euphorbia neogossweileri* Bruyns and *E. cupularis* Boiss. (syn. *Endadenium gossweileri* L.C.Leach and *Synadenium cupulare* (Boiss) Wheeler ex A.White, R.A.Dyer & Sloane, respectively) cluster together with three woody species of the *Monadenium*-group. In this clade we found gradual changes in floral morphology, e.g. a notched involucral gland as in the *Monadenium*-group instead of a rim-like one as it is described for *Synadenium*. There seem to be no significant morphological and molecular phylogenetic differences between the formerly accepted genera *Endadenium* and *Monadenium*. The clade clearly shows the tendency of reduction, fusion of glands and involucral bracts as well as the trend towards increased zygomorphy.

090

Steady diversification of derived liverworts under Tertiary climatic fluctuations

Rosemary Wilson, Jochen Heinrichs, Jörn Hentschel, S. Robbert Gradstein, Harald Schneider

Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, rwilson@uni-goettingen.de

Tropical forests contain the majority of extant plant diversity and their role as a cradle and/or museum of biodiversity is an important issue in our attempts to assess the long-term consequences of global climate change for terrestrial biomes. Highly diverse groups of liverworts are an often ignored but extremely common element in rainforests, and thus their evolution may shed light on the ecological robustness of rainforest biomes to climate fluctuations. We record a remarkable constant accumulation of diversity through time for the most species-rich family of liverworts, Lejeuneaceae, inferred by divergence time estimates. The observed pattern supports the recently developed concept of a dual role of the tropics as both a museum and a cradle of biodiversity.

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Cytogeography and chromosome evolution of *Helictotrichon* subgenus *Pratavenastrum* (Poaceae) in the Mediterranean and adjacent high mountains

Grit Winterfeld, Martin Röser

Institute of Biology, University of Halle-Wittenberg, Neuwerk 21, 06099 Halle, Germany

A chromosomal survey revealed that taxa of *Helictotrichon* subg. *Pratavenastrum* (Aveneae, Poaceae) include two groups of karyotypes with respect to the number of satellite chromosomes (SAT) per haploid set. Within the mesomorphic diploids the two groups show different distributions: the mainly eastern, Balkanic-Pontic group with two SAT and the west European and Mediterranean group with only one SAT. This is the region with highest species diversity. The central Mediterranean allotetraploid and xeromorphic *H. cincinnatum* contains both kinds of chromosome sets. Since two SAT was considered as ancestral, it is inferred that chromosome sets with only one SAT originated and expanded in the western Mediterranean. But as indicated by the conspicuous distribution pattern of the east Mediterranean highly polyploid and strongly xeromorphic *H. agropyroides* containing also the derived state of only one SAT, this is by no means sure. The Aegean dekaploid *H. agropyroides* may be the remnant of diploids with this derived karyotype structure that have become extinct in the East or they have yet to be found. Presumably, these diploids were mesomorphic and not xeromorphic as *H. agropyroides* which survived. Alternatively, chromosome sets with only one satellite chromosome originated independently in the East and the West.

041

The head morphology of *Hymenopus coronatus* (Insecta, Mantodea) reconstructed from micro computer tomography

*Benjamin Wipfler, Thomas Hörnschemeyer

Johann-Friedrich-Blumenbach Institut für Zoologie und Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie mit zoologischem Museum, Berliner Strasse 28, 37073 Göttingen, Germany, bwipfle@gwdg.de

Mantodea is a group of approximately 2300 mostly tropical species, all sharing a carnivorous way of life. The mantodean head is strongly sclerotized and is characterized by its triangular shape, the presence of a parietal suture in combination with the reduction of the frontal and occipital suture, enlarged compound eyes, and a strongly reinforced tentorium with equally sized corpotentorium and anterior tentorial bridge. The mouthparts are well developed and of the chewing type. The mandibular molae are altered into blade shaped structures that articulate with each other like a pair of scissors thus increasing the cutting effect of the mandible. These modifications constitute adaptations towards the carnivorous and predatory way of life. *Hymenopus coronatus* Olivier, 1792 is traditionally placed along with the taxon Hymenopodidae on relatively basal branches of the mantodean phylogenetic system. However, the first genetic analysis by Svenson and Whiting (2004, Sys. Ent. 29(3): 359-370) indicated the Hymenopodiae to be paraphyletic and placed a part of this group within the highly derived Empusidae.The remaining Hymenopodidae including *Hymenopus* along with some other taxa are hypothesised as the sistergroup of Empusidae. The head capsule of *Hymenopus coronatus* is characterized by the rather slim appearance and the huge conical compound eyes. Other typical features are a cone-shaped process of the vertex called fastigium, which contains musculature as well as tracheae, and a scutellum with dorsal apodemes. A possible autapomorphy is the corpotentorium which is reduced to a slim bar while the anterior tentorial bridge is very strong. This has not been observed in any other mantid, yet. The mandibles are elongated and show a strongly developed molar ridge with two well defined apodemes that give the ridge a flash-shaped appearance. Except for the reduction of the corpotentorium all these modifications are shared by the Empusidae, thus giving additional morphological evidence for such a relationship.

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The Huertales clade identified to contain *Dipentodon, Perrottetia, Huertea, Tapiscia* and *Gerrardina*, and to be sister to Brassicales plus Malvales

Andreas Worberg[1], Mac H. Alford[2], Dietmar Quandt[3], Thomas Borsch[4]

[1] Rheinische Friedrich-Wilhelms-Universität Bonn, Nees-Institut für Biodiversität der Pflanzen, Meckenheimer Allee 170, 53115 Bonn, Germany, [2] Department of Biological Sciences, University of Southern Mississippi, 118 College Drive #5018, Hattiesburg Mississippi 39406, USA [3] Dresden University of Technology, Institute of Botany, Plant Phylogenetics & Phylogenomics Group, 01062 Dresden, Germany, [4] Institut für Biologie und Umweltwissenschaften, Universität Oldenburg, 26111 Oldenburg, Germany

Soon after *Tapiscia* was inferred as an isolated eudicot lineage (Soltis et al. 2000, Bot. J. Linn. Soc. 133: 381-461), the angiosperm order Huerteales has been proposed to accommodate *Tapiscia* and *Huertea* (Doweld, 2001, Bull. Misc. Inform. Kew 1911: 310-313; Peng et al., 2003, Bot. Bull. Acad. Sin. (Taipei) 44: 217–222). The taxa of Huerteales, however, are poorly known and have been considered as members of various groups, often shuffled among families such as Celastraceae and Flacourtiaceae. The order Huerteales was formally described by Doweld (2001) to include the genus *Dipentodon* (Dipentodontaceae) and the two small genera *Tapiscia* and *Huertea* (Tapisciaceae). Recently, Zhang and Simmons (2006, Syst. Bot. 31: 122–137) inferred *Perrottetia* as being associated with *Tapiscia* and *Dipentodon* based on molecular data. Alford (2006, Taxon 55: 959-964) showed that the former Flacourtiaceae genus *Gerrardina* does in fact represent an isolated rosid lineage and recognized the distinct family Gerrardinaceae. We applied sequence data of the rapidly evolving matK gene and the group II trnK intron to cover a broad representative sampling of the rosids and the eudicots. For the first time *Tapiscia, Perrottetia, Dipentodon* and *Gerrardina* were all included in a molecular phylogenetic dataset. All genera were found in a Huerteales clade with maximum statistical support. Also, we were able to position the Huerteales clade to branch after Sapindales, and to be sister to a Brassicales-Malvales clade. The highly supported topology inferred in this study now permits first hypotheses about the evolution of the order Huerteales and provides further insights into patterns of morphological evolution within the Eurosids II (malvids). Our results support a classification of the Huerteales as one of the rosid orders within angiosperms.

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Endemic plants of Başarakavak and environs, Turkey

*Evren Yildiztugay, Yavuz Bağci

Selçuk University, Faculty of Arts and Sciences, Department of Biyology, Campus, 42075, Selçuklu, Konya, Turkey, eytugay@selcuk.edu.tr

Turkey has about 3778 endemic species of flowering plants. Its rich flora is due to its geographic position, a great geomorphological diversity, different climate types and its location on the border of three phytogeographic regions. This study was based on a master thesis dealing with the flora of the surroundings of Başarakavak Town. 1222 plant specimens were collected between 2004-2006, of which 691 species (90 families, 370 genera) have been determined. The number of endemic taxa is 100 (14.5 %); their threat categories were evaluated according to IUCN 2001. *Clypeola ciliata* Boiss. and *Silene lycaonica* Chowdh. are endangered (EN), and *Dianthus ancyrensis* Hausskn. & Bornm., *Astragalus suberosus* Banks & Sol. subsp. *ancyleus* (Boiss.) Maththews, *Centaurea bourgaei* Boiss., *Onosma sieheanum* Hayek, *Veronica macrostachya* Vahl. subsp. *sorgerae* M.A. Fisch., *Sideritis brevibracteata* P.H. Davis, *Thesium bertramii* Aznav. and *Iris stenophylla* Hausskn. & Siehe ex Baker subsp. *stenophylla* are vulnerable (VU). *Clypeola ciliata* Boiss., *Centaurea bourgaei* Boiss., *Cephalaria paphlagonica* Bobrov, *Colchicum baytopiorum* C.D. Brickell are new records. The phytogeographic spectrum of the plants in this area is as follows; Irano-Turanien 23.1 %, Mediterranean 9.8 %, Euro-Siberian 6.6 %.

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Taxonomic review of the *Agropyron cristatum* complex (Poaceae: Triticeae) in Iran

Mehdi Yousofi

Department of Biology, Payam Noor University, Esfahan, Iran, muosofi@yahoo.com

The genus *Agropyron* Gaertn. (Poaceae: Triticeae), from which 23 species have previously reported from Iran, is today restricted to *Agropyron cristatum* (L.) Gaertn. complex sensu lato. In this study the taxonomy of this complex in Iran was reviewed using morphological and cytological analysis. For this purpose, Principal Component Analysis (PCA) and Cluster Analysis were performed on morphological data from 35 characters of the thirteen populations of *A. cristatum* collected from different habitats in the country. Observations were also made on root tip cells of the same materials as included in the present investigation. In support of the obtained results many published literature, herbarium specimens and field observations were also reviewed. The cytological results showed three ploidy levels ($2n=2x=14$; $2n=4x=28$ and $2n=6x=42$) among the populations. A diploid population of *A. cristatum* was also reported from Hamadan province in the west of Iran. The diploid taxa are important for their rarity. The presence of *A. cristatum* subsp. *puberulum* Nevski was confirmed in the flora of Iran and a new taxon as *A. cristatum* subsp. *hamadanicum* Yousofi (subsp. novo) was also reported. Therefore, this complex in Iran consist of 4 subspecies and 3 varieties as: 1) *A. cristatum* subsp. *pectinatum* (M.Bieb.) Tzvelev with three varieties; var. *pectinatum*, var. *imbricatum* (Roemer et Schultes) G.Beck and var. *minor* Yousofi (var. novo), 2) *A. cristatum* subsp. *incanum* (Nab.) Melderis, 3) *A. cristatum* subsp. *puberulum* (Boiss. ex Steud.) Tzvelev and 4) *A. cristatum* subsp. *hamadanicum* Yousofi (subsp. novo). Finally, a taxonomic key for separating the subspecies and varieties and a distribution map of the *A. cristatum* complex in Iran were provided.

014

Molecular and structural characterization of cells involved in chaetogenesis in larval *Platynereis dumerilii* (Annelida)

*Anne-C. Zakrzewski[1], Florian Raible[2], Harald Hausen[1]

[1] Institut für Zoologie, Evolution und Systematik der Tiere, FU Berlin, Königin-Luise-Str. 1-3, 14195 Berlin, Germany, [2] EMBL Heidelberg, Meyerhofstr. 1, 69117 Heidelberg, Germany

Chaetae are one of the most characteristic features of annelids with a very specifc structure and mode of formation. The chaetae consist of ß-chitin and each chaeta arises from an own epidermal follicle. The shape of the chaetae results from chitin polymerisation on the surface of highly dynamic microvilli of the basal cell, the chaetoblast. The lateral follicle cells secret additional chaetal material. Annelid-like chaetae are also common in taxa such as Echiura, Myzostomida and Siboglinidae (which by now are subordinated taxa of Annelida). However, also within Mollusca, Bryozoa and Brachiopoda similar structures are present, whose homology is controversially discussed. Comparisons are hitherto restricted to structural and biochemical data. For the first time we report specific gene expression data for the cells, which are involved in chaetal formation in larvae of the annelid *Platynereis dumerilii.* Cellular localization was possible by combination of in situ-hybridization techniques, immunohistochemistry and transmission electron microscopy. Some of the genes are expressed either by the chaetoblast or by follicle cells. Other genes are simultaneously expressed by the chaetoblast and by follicle cells. Expression does not occur in any other cell type in developing individuals. The data thus provide a highly specific set of molecular markers for chaeta forming cells and add a new level for comparative analyses.

006

Comparison of methods and protocols for routine DNA extraction in the DNA-Bank Network

Holger Zetzsche[1], Hans-Peter Klenk[2], Michael Raupach[3], Thomas Knebelsberger[4], Birgit Gemeinholzer[1]

[1] Botanischer Garten und Botanisches Museum Berlin-Dahlem (FU-Berlin), Königin-Luise-Strasse 6-8, 14195 Berlin, Germany, h.zetzsche@bgbm.org, b.gemeinholzer@bgbm.org, [2] Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, Mascheroder Weg 1b, 38124 Braunschweig, Germany, Hans-Peter.Klenk@dsmz.de, [3] Zoologisches Forschungsinstitut und Museum Alexander König, Adenauerallee 160, 53113 Bonn, Germanmy, w.waegele.zfmk@uni-bonn.de, [4] Zoologische Staatssammlung München (SNSB), Münchhausenstr. 21, 81247 München, Germany, haszi@zsm.mwn.de

The DNA Bank Network comprises DNA banks from the Botanic Garden and Botanical Museum Berlin-Dahlem (BGBM), the Bavarian State Collection of Zoology Munich (ZSM), Forschungsmuseum Alexander Koenig Bonn (ZFMK), and the German Collection of Microorganisms and Cell Cultures Braunschweig (DSMZ) covering a range of biological diversity. While protocols for DNA extraction from various biological sources develop steadily, comparisons among methods for routine extractions remain rare. Ten extraction protocols based on five extraction methods were compared to obtain DNA from material of three different ages from each of 12 representative taxa. These included bacteria, fungi, invertebrates, vertebrates, plants, and algae. Commercially available kits (INVITEK, MACHEREY-NAGEL, QIAGEN, ROCHE, SIGMAALDRICH, and VWR-OMEGA) using silica-membranes were evaluated, so that five suitable protocols were tested for each taxon. Additional methods based on magnetic beads (AGOWA© mag, AGOWA), anione exchange (*Genomic Tip*©, QIAGEN), salting-out precipitation (*Puregene Genomic* DNA Purification©, Gentra/QIAGEN), contaminates and inhibitor binding by sorbent matrix (Nexttec™, Nexttec), and modified CTAB protocols were also compared. Total DNA yield was measured by a spectrometer based on absorbance at 260nm. DNA quality was estimated by using the OD260/280 absorbance ratio and agarose-gel electrophoresis.

Results indicate decreasing DNA yields and quality as samples age. In general, DNA could be separated from cell material more efficiently (resulting in higher DNA yields) by applying salting-out precipitation, anione exchange, and CTAB, whereas DNA yields were lower but more consistent with silica-membrane kits and magnetic beads. DNA quality differed most among extraction protocols. Salting-out precipitation reduces shearing of DNA molecules during extraction. If processing time and cost are considered, silica-based kits should be preferred for routine extractions of most taxa.

Workshop I

Phylogeny and Biogeography of Poales

The backbone problem: hunting for informative characters in DNA sequences of Tillandsioideae (Bromeliaceae) for reconstructing a well-resolved phylogeny

Michael H. J. Barfuss, Walter Till, Rosabelle Samuel

Department of Systematic and Evolutionary Botany, University of Vienna, Rennweg 14, 1030 Wien, Austria

Plastid genomes have shown to be very uniform in recently diverged plant groups (like in Bromeliaceae) mainly caused by rapid radiation (and subsequent quick speciation / isolation). In addition to the less variable chloroplast regions which we analysed in our previous studies, we sequenced another set of cpDNA markers, which are supposed to be phylogenetically much more informative. Nevertheless, avoiding results of still insufficiently resolved phylogenies derived from this additional chloroplast data we also established primers for nuclear DNA regions, especially with the target of getting well resolved backbones in our trees. Attempts of several research groups to amplify the nrDNA region ITS (Internal Transcribed Spacer) in Bromeliaceae failed so far, because of very strong bounded secondary structures caused by repetitive GC-rich motives in the ITS 1 region. While we were able to successfully amplify and sequence over this difficult region for a set of species of Bromeliaceae by modifying PCR programs and sequencing chemistries, results of sequence analysis again showed very poor amounts of phylogenetically informative characters among taxa, having a similar substitution rate as it can be found in the investigated chloroplast regions (which is in contrast to many other plant groups). All resulting trees (even from combined analyses) did not yet allow an unambiguous interpretation of phylogenetic relationships of the whole subfamily Tillandsioideae; especially not at the backbone of very species-rich genera like *Tillandsia* and close relatives (*Racinaea, Viridantha*), and *Vriesea* and associates (*Alcantarea*, *Werauhia*). Therefore, sequences (including exons as well as introns) of the assumed single-copy nDNA genes PRK (Phosphoribulokinase), PHYC (Phytochrom C) and MS (Malate Synthase) have been analysed, and results compared with phylogenies derived from ITS and more than 10 different plastid regions; this nuclear markers seems to be much more promising in giving higher phylogenetic signals per sequenced base pair than any of the other previously investigated DNA regions does.

Clades, lemmas and awns in Rytidosperma s.l. (Danthonioideae: Poaceae)

Aelys M. Humphreys, H. Peter Linder

Institute for Systematic Botany, University of Zürich, 8008 Zürich, Switzerland

Systematic biology is in an age of reciprocal illumination, where new insights from phylogenies based on molecular data allow reassessment of taxonomic groups and their evolutionary history. Rytidosperma s. l. (Danthonioideae: Poaceae) comprises ca. 100 species that are distributed in temperate areas on all Southern Hemisphere continents. Much controversy has plagued circumscription of and relationships between the genera in this group ever since the genus Danthonia D.C. was described for grasses with 'twisted column bases' over two centuries ago. Seven genera are currently recognized in *Rytidosperma s.l.*: *Tribolium*, *Karroochloa* and *Schismus* in Africa and Austrodanthonia, *Notodanthonia*, *Joycea* and *Rytidosperma* in Australasia, with *Rytidosperma* extending to South America.

We present the first molecular phylogeny of *Rytidosperma s.l.*, with representatives from all continents. We show that the Australasian and South American species form a monophyletic group embedded within the African species, that none of the genera as currently delimited is monophyletic and that Australian lowland species are distinct from their American equivalents Danthonia. We discuss the inferred hypothesis of phylogeny, based on both cpDNA and nrDNA markers, in the light of other lines of evidence: morphology, ecology and geography. A striking array of lemma morphologies are found in *Rytidosperma s.l.*: lemmas are awned or not, glabrous or hairy, with hairs scattered or arranged neatly in rows. Lemma morphology is likely to affect dispersal and establishment of caryopses. Further, the group includes both mesic and sclerophyllous species, annuals and perennials and occurs in a range of habitats from open, sunny grasslands, to wet margins of temperate rainforests, to marshy peatlands above the treeline.

Many of the members of this group are important fodder grasses in Australia and others are ecologically dominant in New Zealand. A robust hypothesis of phylogeny, based on a clear understanding of its underlying biology, will enable establishment of a sound generic delimitation. This will be of considerable practical consequence for many users, both scientific and non-scientific.

Independent wheat B and G genome origins in outcrossing *Aegilops* progenitor haplotypes

Benjamin Kilian[1,3], H. Özkan[2], O. Deusch[1], S. Effgen[3], A. Brandolini[4], J. Kohl[5], W. Martin[1], F. Salamini[3,6]

[1]Institute of Botany III, Heinrich-Heine-Universität, Düsseldorf, Germany; [2] Faculty of Agriculture, University of Cukurova, Turkey; [3]Max Planck Institute for Plant Breeding Research, Köln, Germany; [4]Instituto Sperimentale per la Cerealicoltura, S. Angelo Lodigiano, Italy; [5]Institute of Bioinformatics, Heinrich-Heine-Universität, Düsseldorf, Germany; [6]Fondazione Parco Tecnologico Padano, Localita Cascina Codazza, Italy

Wheat evolution has received great interest, because of its great economic significance. Cytogenetically, the wheat species fall into three groups based upon their ploidy level: I) diploid 2n = 14 = einkorn wheat; II) tetraploid 4n = 28 = emmer wheats; III) hexaploid 6n = 42 = bread wheats.

Bread wheat, *Triticum aestivum*, has no direct wild hexaploid progenitor and possesses three sets of homoeologous chromosomes, designated as AABBDD, whose origins have differing degrees of certainty. The D chromosomes stem from wild diploid *Aegilops tauschii* through alloploidization with the wild AABB tetraploid *T. dicoccoides.*

The A and B chromosomes of that tetraploid derive from an earlier hybridization between the wild AA diploid *T. urartu* and a wild diploid B genome donor frequently reported from within *Aegilops* section *Sitopsis.*

The challenge was to determine if *Aegilops speltoides* was the donor of the B and G genomes in tetraploid AABB and AAGG wheats. We studied molecular diversity in a large collection using genome specific AFLP loci and haplotypes. The identification and use of B genome specific markers allowed us to pinpoint the origin of the wheat B genome to S chromosomes of *Ae. speltoides.* It is shown that the outbreeding nature of *Ae. speltoides* influences its molecular diversity and bears upon inferences of B and G genome origins. Haplotypes at nuclear and chloroplast loci reveal that the B and G genomes of polyploid wheats are unique samples of *Ae. speltoides* haplotype diversity. These have been sequestered by the AABB *T. dicoccoides* and AAGG *T. araraticum* lineages during their independent origins.

Allopolyploid origin and hybridization in an allohexaploid grass *Elytrigia intermedia* (Poaceae, Triticeae)

Václav Mahelka, Judith Fehrer, František Krahulec

Institute of Botany, Academy of Sciences of the Czech Republic, 252 43 Průhonice, Czech Republic

The tribe Triticeae (family Poaceae) is an excellent example for reticulate evolution. Events and processes like ancient hybridization, introgression, recurrent hybridization and multiple origin of particular taxa have likely occurred in this tribe and resulted in its reticulate structure. Proven recurrent hybridizations revealed surprising genomic histories of the respective taxa and might have promoted their adaptation to a diverse array of ecological conditions. We focused on the genomic history of an allopolyploid wild grass from the tribe Triticeae, *E. intermedia* (syn. Thinopyrum intermedium) from its native area in Central Europe. To analyse its genome composition, we chose one chloroplast DNA marker to infer the maternal origin of the species, and two kinds of nuclear DNA sequences: the internal transcribed spacer (ITS) region of nuclear ribosomal DNA, and the granule-bound starch synthase gene (GBSSI). This approach enabled us to combine two nuclear loci which are supposed to undergo different intragenomic processes. In contrast to single-copy genes (GBSSI), multigene families (ITS) in allopolyploid taxa tend to experience concerted evolution, leading to the elimination of variation present among distinct parental ITS copies. Our results largely confirmed this assumption and revealed quite different fates of the two loci, which, despite of considerable homogenisation of ITS variation, both represent valuable markers for phylogenetic and hybrid speciation reconstruction. The data show that *E. intermedia* experienced hybridization at the tribal level in the course of its evolution, which resulted in a more variable genome than was so far assumed.

Biogeography of the genus *Fosterella* (Bromeliaceae)

Jule Peters[1], Christoph Nowicki[2], Martina Rex[1], Katharina Schulte[3], Kurt Weising[1], Georg Zizka[3], Pierre L. Ibisch[2]

[1]Institute of Biology, University of Kassel, Germany,[2]Faculty of Forest and Environment, University of Applied Sciences Eberswalde, Germany,[3]Research Institute Senckenberg & J. W. Goethe-Universität, Frankfurt/M., Germany

The neotropical genus *Fosterella* (Bromeliaceae) currently includes 30 species with a centre of distribution and diversity in the Andes of Bolivia, particularly in the montane rain forests of the Yungas ecoregion. Most of the species are characterized by rather small ranges and can be found from lowland Amazon forest and isolated mountain ranges of the Brazilian shield to cool cloud forest and high arid valleys in the Andes. Morphological delimitation of several species is difficult due to a scarcity of characters. In our collaborative project involving three institutions, we combine molecular, morphological and biogeographical data in order to get insights in (1) the taxonomy and phylogeny of the genus *Fosterella*, (2) its origin and expansion into its current range, and (3) the formation of endemic species within the Bolivian Andes.

Here we present a first detailed biogeographical analysis, which will be discussed in the light of recent taxonomic and phylogenetic findings. Potential distribution ranges of Bolivian *Fosterella* species are extrapolated and actual diversity patterns are visualized with the help of a computational model that is based on a climatic envelope approach. Conclusions on the evolution and spread of the genus derived from biogeographical patterns are discussed.

Phylogeny and biogeography of Danthonioideae (Poaceae)

Michael D. Pirie

University of Zurich, Switzerland

Danthonioideae is one of the smaller grass subfamilies, comprising ca. 288 species found in temperate regions worldwide, but mostly in the southern hemisphere. It was erected by the Grass Phylogeny Working Group (2001), following molecular work of Barker (1995) and the identification of a diagnostic feature, haustorial synergids, by Verboom (1994). Recent phylogenies based on chloroplast and nuclear encoded DNA sequence markers representing 70 % of the species provide us with a powerful tool with which to test evolutionary hypotheses. Most danthonioid genera are para- or polyphyletic. The 'basal' danthonioid clades include taxa endemic to the African continent, such as Afromontane and Cape clades of *Merxmuellera*, and the widespread and species rich *Pentaschistis* clade. The current worldwide distribution originated through a series of dispersals within the last 10 million years, primarily out of Africa and then more frequently across the Pacific. Dispersals were followed in some cases by radiations within continents, resulting in the species diversity of groups such as the New Zealand snow grasses (*Chionochloa*) and *Danthonia s.s.* in the Americas. Some immigrants back-crossed with native relatives, spawning hybrid lineages, such as South American Cortaderia (the pampas grasses), and monotypic *Notochloe* in Australia. The complexities in patterns of morphological diversity across the subfamily which in the past fuelled discord in generic delimitation, have proven to reflect an equally complex and reticulate species history.

Molecular phylogeny of *Fosterella* (Pitcairnioideae, Bromeliaceae) based on four chloroplast DNA regions

Martina Rex[1], Katharina Schulte[2], Georg Zizka[2], Jule Peters[1], Pierre L. Ibisch[3], Kurt Weising[1]

1Plant Molecular Systematics, Dept. of Sciences, University of Kassel, Germany, 2Research Institute Senckenberg and J.W. Goethe-University, Frankfurt/M., Germany, 3Faculty of Forest and Environment, University of Applied Sciences, Eberswalde, Germany

The neotropical genus *Fosterella* (Bromeliaceae) comprises about 30 species, distributed in Central and South America. The geographical range of the genus extends from Mexico in the north to Argentina in the south and Brazil as well as Paraguay in the southeast. The highest species diversity is found in semiarid to humid habitats of the Andean slopes and valleys of Bolivia. Most *Fosterella* plants are mesophytic terrestrial herbs with small and inconspicuous flowers. The morphological differentiation of species used to be difficult due to a paucity of diacritic characters. Thanks to the intensification of collection efforts and advancing molecular phylogenetic studies, the taxonomic revision of the genus has made good progress. *Fosterella* is included in the subfamily Pitcairnioideae s. str., but its exact sister group relationships are unsettled, and little is known about the infrageneric phylogeny.

To resolve relationships between *Fosterella* species and their putative allies, we conducted a phylogenetic analysis based on chloroplast DNA (cpDNA) sequence variation. Here we present the results obtained from sequencing the atpB-rbcL and psbB-psbH spacer, the rps16 intron and the matK gene of 62 bromeliad species from 19 genera, including 24 of the 30 recognized *Fosterella* species. The combined analyses of all four loci yielded a well-resolved phylogeny, which strongly supports the monophyly of *Fosterella*. Species boundaries and phylogenetic relationships suggested by the cpDNA consensus trees are mainly congruent with those revealed by our previous AFLP study (Rex et al., 2007, Genome 50: 90-105), but show higher resolution and better support for individual clades.

The tree topology will be discussed in conjunction with available morphological and anatomical data.

Diversity patterns of grasses (Poaceae) in Burkina Faso

Marco Schmidt[1, 2], Thomas Janssen[1, 2], Konstantin König[1], Georg Zizka[1],[2]

[1]Institut für Ökologie, Evolution und Diversität, J.W.Goethe-Universität Frankfurt am Main, [2]Abt. Botanik und molekulare Evolutionsforschung, Forschungsinstitut Senckenberg, Frankfurt am Main

Among the monocots, grasses are of outstanding economic and ecological importance on a worldwide scale. In Burkina Faso in West Africa, they constitute the largest family of vascular plants with 254 species, but their diversity is not evenly distributed across the country. In the savannas they are the most important family in terms of abundance and species richness, in other habitats - such as gallery forests - there are only a few species. On the country scale there is a change in growth form from small therophytic grasses in the sahelian North of the country to tall perennial grasses in the sudanian South. Furthermore, habitat preferences are dependent on the photosynthetic (sub)type. We collected data on the photosynthetic type, height and growth form of Poaceae from Burkina Faso and will link these to modelled distributions derived from collection and observation records, using the program MaxEnt with environmental grid data, including remote sensing data. General countrywide distribution patterns and habitat preferences of these groups will be identified and compared. We will draw conclusions for a sustainable management of natural grass resources in Burkina Faso.

Phylogeny, classification and morphological evolution in the grass subfamily Pooideae

Julia Schneider, Elke Döring, Martin Röser

Institut für Biologie, Martin-Luther-Universität Halle-Wittenberg, Neuwerk 21, 06099 Halle, Germany

The subfamily Pooideae comprises roughly 150 genera and 3300 species, which is about 33% of all grass species, rendering it the largest subfamily of grasses. It contains some of the world's most important crops such as wheat, barley, rye, and oat as well as many important pasture grasses (e.g., bluegrass, false oat, fescue). The Pooideae are worldwide distributed but evolved most extensively in temperate regions of the northern hemisphere. To circumscribe the subfamily, identify and delineate its major lineages, and the sequence of their evolutionary divergence a broad sampling of taxa was used for the first time across all acknowledged tribes and subtribes for sequence analyses of chloroplast and nuclear DNA. The results suggest a number of re-alignments for traditional tribes within the Pooideae, including the abandonment of several tribes previously recognised, such as the Triticeae and Bromeae. The branching order of major lineages in the subfamily is very well resolved. Among the early-diverging lineages are several clades with "bambusoid" or strongly aberrant morphological characters and the Stipeae (feathergrass alliance), which is firmly nested within this subfamily. Judging from the topology of the molecular trees in this study, there is no good evidence that spikelets with a single floret, although widely accepted, had been original in this subfamily. Many species-poor lineages or genera identified as diverging early in the evolution of the subfamily Pooideae are biogeographically confined to high mountain regions at the border between tropical and subtropical climates on all continents except Africa. These groups with partly unique combination of morphological characters are seemingly remnants of the early radiation of Pooideae from tropical into non-tropical climates.

Systematics and biogeography of Chilean *Puya* species (Bromeliaceae)

Katharina Schulte[1,2], Nicole Haußner[1,2], Elke Kiehlmann[2], Marco Schmidt[1,2], Konstantin König[2], Patricio Novoa[3], Georg Zizka[1,2]

[1]Research Institute Senckenberg, Frankfurt am Main, Germany [2]J.W. Goethe-University, Frankfurt am Main, Germany, [3]Jardin Botánico Nacional, Viña del Mar, Chile

The neotropical genus *Puya* (Bromeliaceae) comprises app. 200 species of perennial rosette herbs and rosette trees with principally Andean distribution. The Chilean representatives of *Puya* (8 species) are endemic to the country which constitutes a distinct centre of endemism for the genus. According to recent molecular studies the Chilean *Puya* species form a monophyletic group of basal position within the genus. Up to now the inter- and infraspecific relationships of the Chilean *Puya* species remained largely unclear.

In the course of a taxonomic revision of the Chilean *Puya* species morphological and biogeographical data were collected from herbarium specimen and in extensive field work. The biogeographic data was used to analyze the potential distribution of the species by different modelling approaches.

The delimitation of several species/subspecies has proven to be difficult mainly due to considerable morphological variability. In order to elucidate inter- and intraspecific relationships of all Chilean *Puya* taxa AFLP analyses have been conducted. The analyses include more than 70 accessions more or less covering the distributional range of the taxa. Results from the molecular analysis are presented and compared to the morphological and biogeographical data.

Workshop II
Biodiversity Informatics

The EDIT desktop taxonomic editor

Pepé Ciardelli

Botanischer Garten und Botanisches Museum Berlin-Dahlem (BGBM), Zentraleinrichtung der Freien Universität Berlin, Königin-Luise-Str. 6-8, 14195 Berlin, Germany

The core of the European Distributed Institute of Taxonomy (EDIT) Platform for Cybertaxonomy is the Common Data Model (CDM) for modeling taxonomic information. However, experience has shown that a well-designed model alone will not win acceptance within the taxonomic community. It is crucial that taxonomists are provided with editing tools that are intuitive to learn and easy to use, and which fit as closely as possible with the way they are accustomed to working. Therefore, we have begun development of a desktop Taxonomic Editor for the editing of CDM data, with which a taxonomist can do anything from fine-tuning an imported checklist to compiling a complete dataset from scratch.

To optimize the application's workflow, we relied on use cases developed within the EDIT project, i.e. creating a monography, or editing a database which uses concept relations extensively. The application's user interface is based largely on our experience in programming the Web Editor for the Berlin Model, and in constantly improving it according to the needs of the taxonomists who use it every day. While we have not completely done away with forms-based editing, we will offer an alternative word processor-like input window, which offers autocompletion, syntax hints, and on-the-fly parsing; our hope is that this approach will be instantly recognizable and attractive to taxonomists used to working in Microsoft Word.

We chose to make the editor a desktop application for other reasons as well. A desktop application offers the ability to download either a complete copy or a slice of the data in a centralized data store; it would then use the synchronizing components of the CDM programming library to save any changes done locally to the central data store, and to resolve any resulting conflicts. Furthermore, with a desktop application, the user can work entirely offline; with future releases, we hope to take advantage of this fact, for example, with modules designed for fieldwork and/or hand-held devices. This will also allow applications specializing in different areas of the CDM to work on the same dataset. For more information: http://dev.e-taxonomy.eu/trac/wiki/TaxonomicEditor

Developing the EDIT platform for cybertaxonomy

Markus Döring

Botanischer Garten und Botanisches Museum Berlin-Dahlem (BGBM), Zentraleinrichtung der Freien Universität Berlin, Königin-Luise-Str. 6-8, 14195 Berlin, Germany

The platform brings the taxonomic work process to the Internet. A growing set of applications, standards and recommendations allows scientists to handle taxonomic data electronically, fostering collaboration and reuse of data.

The Common Data Model (CDM) is at the heart of the EDIT Platform - based on the hard-won lessons from more than 10 years of modeling taxonomic data, it describes the information taxonomists process within the platform.

EDIT has been working to ensure that the Common Data Model suits the needs of taxonomists working across the entire spectrum of biological data. Eventually, this could even result in taxonomic data from all participating institutions being accessed as one dataset. But even if these lofty heights are not reached, collaboration across geographic and disciplinary boundaries will be made easier.

So far the actual software development has focused on a shared data repository, the CDM store, an editor for this store and a customizable webportal delivering taxonomic information and at a later stage location-centric biodiversity inventory data. The Portal provides means for basic online contributions, but to take full control over a CDM store a taxonomic desktop editor is being developed. A specialized application for managing structured descriptions of species and specimens to generate keys is planned, either by extending an existing application or the taxonomic editor itself. Last but not least, tools for creating maps from CDM data are a core functionality of the platform, too.

The data store provides immediate GBIF integration delivering occurrence data. A unique and stable way of referencing data in the CDM exists as well as simple ways of searching and subscribing to the latest changes in the search results.

The CDM data portals are built using the open source content management system Drupal, which allows the creation of flexible websites adapted in look and functionality to the needs of each community. They will be used to publish data from the EDIT WP6 exemplar groups responsible for the Palm, Cichorieae, and Diptera datasets. Initially, these portals will be read-only, displaying data that has already been imported into the CDM; in future versions, simple forms will be created to allow remote contributors to quickly add new images, common names or personal annotations. For more information: http://wp5.e-taxonomy.eu/blog/cdmcommunity.

The DNA bank network in Germany

Gabriele Dröge, Holger Zetzsche, Anton Güntsch, Birgit Gemeinholzer

Botanic Garden and Botanical Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Str. 6-8, 14195, Berlin, Germany

The DNA Bank Network was established in spring 2007 and is funded by the German Science Foundation (DFG).

The network intends to cover the whole range of biological diversity (microorganisms, algae, plants, fungi and animals) and will be maintained by four partner institutions with complementary collections and expertise: the Bavarian State Collection of Zoology in Munich (ZSM); the Botanic Garden and Botanical Museum Berlin-Dahlem (BGBM); the German Collection of Microorganisms and Cell Cultures in Braunschweig (DSMZ); and the Zoologisches Forschungsmuseum Alexander König in Bonn (ZFMK).

The main target of the network is to enhance taxonomic, systematic, genetic and evolutionary studies, by providing complete online documentation of each DNA sample in order to offer the scientific community more transparency.

It is possible - and a desired outcome - to offer DNA ordering at cost price, as well as to donate DNA with information about the respective voucher.

A DNA Bank database module has been developed to enable participating institutions to capture DNA-related information not yet covered by their specimen collection databases. Alternately, information held in existing specimen information systems can be linked using the BioCASe protocol and ABCD-encoded collection and observation records. Common access to distributed DNA Bank Network data is facilitated by a central web portal developed and hosted at the BGBM. The portal can be used to explore DNA material in stock at the partner institutions, as well as associated information including the provenance of the original material, place of the voucher deposit, and information on DNA quality and extraction methods. Additionally, digital images and links to published molecular data are provided where existing. The specimen and DNA voucher information will also be made accessible via the international network of the Global Biodiversity Information Facility (GBIF).

Biodiversity research leaks data. Create the biodiversity data archives!

Anton Güntsch, Walter G. Berendsohn

Botanic Garden and Botanical Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Str. 6-8, 14195, Berlin, Germany

Efficient access to research results, as well as to the primary data gathered and generated by past and ongoing research, is of tremendous importance for science, both for the efficiency of work flows and for the support (or refutation) of hypotheses. Consequently, numerous electronic archives for scientific data have been built up. They provide access to information ranging from structured descriptions of scientific studies to raw data in various formats, which can then be further processed and incorporated into present-day studies. A good example of such repositories are the various data archives providing the means for depositing and accessing primary data generated in the course of social science studies.

Present global challenges require increased efficiency in the generation of biodiversity research. Unfortunately, while biodiversity research has proven to be very effective in storing and preserving physical material in scientific collections, it does not have a tradition of preserving and making accessible the data collections generated by studies and projects. Usually, data stay with the authors of a scientific publication, so that data access depends on personal contacts and the data holder often neglects the ongoing necessity to transform data files to contemporary formats. Sooner or later this results in data sets being lost.

However, with the advent of comprehensive and agreed data formats and standards for primary biodiversity data (e.g. ABCD, TCS, SDD, see www.tdwg.org), the community has taken a first step to facilitate data archives for biodiversity research. We propose using existing data standards to build a first working archive for biodiversity data. This service would be much more than merely a facility for storing and backing up documents and databases, even going beyond the aims of the Alliance for Permanent Access. It would implement at the very least the following functions:

- Depository service: software tools and manual operations for transforming source data and documents into standardized data formats and for inserting data into the archive.
- Metadata capture: software for storing data set descriptions of content and technical parameters supporting future migration services.
- Migration service: software for transforming archived documents and data collections into contemporary data formats, ensuring compliance with modern software environments.
- Software repository: storage of software associated with data sets ranging from specific scientific tools (e.g. a particular version of a collection management software) to entire server environments frozen as virtual machines in files.
- Access component: software for searching and browsing the archive, taking into account IPR and copyright issues and ensuring proper attribution.

As the proposed archive will store prior versions in the migration process, ensuring that a roll-back is always possible, we expect massive amounts of data to be stored, processed, and transmitted. The architecture needs to take this into account and will probably consist of a set of distributed archive servers sharing their data processing and storage capabilities, and adding redundancy to the system.

The biodiversity data archive would be a powerful tool for researchers, students, and the public. It will also be one of the core components of LifeWatch, the European infrastructure facility for biodiversity research, for which a preparatory project has just started. The return to the massive infrastructure investment consists in increased efficiency for most work processes associated with biodiversity assessment and research, and thus our increased capacity to tackle some of the most pressing questions of our time.

Publishing specimen & observation records using BioCASe technology

Jörg Holetschek

Botanischer Garten und Botanisches Museum Berlin-Dahlem (BGBM), Zentraleinrichtung der Freien Universität Berlin, Königin-Luise-Str. 6-8, 14195 Berlin, Germany

Natural history collections, observational databases as well as living collections in institutions throughout the world form a unique archive of biodiversity, each object documenting the occurrence of one species on a given location at a certain point in time. They are the subject of research and, together with the annotations attached to them, preserve the expertise of the present and the past.

The BioCASe project (Biological Collection Access Service) and the networking activities of its successor SYNTHESYS (Synthesis of Systematic Resources) aim at linking together those sources of knowledge and making it available to anyone through free Internet search portals. BioCASe technology can be used for all types of collections, from botanical to zoological, from marine to terrestrial, from specimen as well as living collections. Currently, BioCASe technology is used for connecting about 16 million records from 389 collections to several thematic-specific portals as well as to the Global Biodiversity Information Facility network (GBIF).

BioCASe technology consists of several standards and software implementations. The central part is the Access to Biological Collection Data schema (ABCD), which is used for packing collection information into XML documents and sending them across networks. The TDWG Access Protocol for Information Retrieval (TAPIR) enables web portals and other related services to send queries and the matching results across networks and thus manage the data flow between network components. The PyWrapper is a software implementing those standards, providing collection databases with the capability to accept and answer TAPIR requests, publishing the collection data represented in ABCD documents.

Future tasks involve the stepwise transition to the TAPIR protocol for all installations still running the BioCASe protocol, an improved handling of user feedback (annotations) as well as providing tools for improving data quality (duplicate detection, data integrity checks). For more information, visit http://www.biocase.org and http://search.biocase.org.

Checklist-driven access to European collection and observational data

Patricia Kelbert, Anton Güntsch, Niels Hoffmann, W. G. Berendsohn

Botanic Garden and Botanical Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Platz 6-8, 14195 Berlin Dahlem, Germany

Over the last ten years, a powerful international infrastructure has been developed and implemented to access distributed biological collections and observational data. Today, international networks such as GBIF (Global Biodiversity Information Facility) and BioCASE (Biological Collection Access Service for Europe) provide access to more than 130 million data records, from simple occurrence data to highly structured specimen information.

Almost all records available via these systems include the latin name of the organism and consequently, the primary term used in queries is that name. Especially for the systematist, search results could be significantly improved with a thesaurus system which allows for user controlled expansion of query terms to synonyms, to related taxa in the taxonomic hierarchy, and to related taxonomic concepts such as those designated by misapplied names.

We have translated this idea into a working access system to European specimens and observations (i.e. organisms collected or observed in Europe), based on the existing Biological Collection Access Service for Europe (BioCASE, www.biocase.org). The new query system (search.biocase.org/toto/) is currently capable of taking Latin names and expanding them with related query terms; the sources for this query expansion are the European checklists Fauna Europaea for zoological and Euro+Med PlantBase for botanical names and taxa. Users receive significantly richer responses uncovering specimen and occurrence data, which would otherwise be hidden to them. In a next phase, we plan to broaden the system's taxonomic coverage by including checklist data for European marine species. The software can accommodate any reasonably structured taxonomic thesaurus – as an example we have also used it with the German Standard List data for vascular plants and mosses (see search.biocase.org/toto_de), which will be integrated with the German GBIF Botany portal. In addition, we will include non-taxonomic terms and relations in the expansion process, such as place names associated with collection events, thus further enriching the query process.

Data portals for biological systematics

Wolf-Henning Kusber, Elke Zippel, Anton Güntsch, Walter G. Berendsohn

Botanic Garden and Botanical Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Str. 6-8, 14195 Berlin, Germany; email: biodiversityinformatics@bgbm.org

Distributed information on biological systematics in a broad sense (species, taxonomic, specimens, and observation data) is held by a wide range of scientists and curators in natural museums and universities. These actors in biological systematics are data users as well as data providers.

Advanced Internet data portals such as GBIF (www.gbif.org) and BioCASE (www.biocase.org) provide common access to distributed specimen and occurrence data and are an increasingly important information resource for systematics and taxonomy. To date, 150 million records have been made available using the GBIF infrastructure - 1 billion records should be available by the end of 2008.

GBIF provides fast access to a relatively restricted set of common data elements stored in a central index database and in several mirror databases. More complex data records – for example, those making full use of the highly structured ABCD data schema - are less accessible, because users must consult the respective individual XML record encoding the required information. In contrast to GBIF, the BioCASE Portal renders the raw information (XML record) into a human-readable format using a style-sheet transformation. Based on this technique, two specialized BioCASE portals have been set up as case studies for further data portal development: GBIF-Deutschland Botanik (covering the German Flora; see: http://search.biocase.org/gbif-de-botany/) and BioCASE (covering data on all taxa occurring in Europe). Both portals are multilingual and include additional data such as ecological data, notes, references, metadata etc.

Over the long run, taxonomists will require fast and comprehensive access to subsets of data according to their scientific needs (taxonomic groups, geographical regions, geological ages, host-parasite-systems, etc.). Main topics are digitized images of specimens held by Natural History Museums, as well as detailed protologue data of species including evaluated information. Assumed that a wide range of checked quality data is provided, more search functions are needed, such as collector's numbers and collection dates. With the increasing amount of information on the Internet, data cleaning mechanisms will be ever more important to guaranteeing high quality standards.

Workshop III

Piperales: an integrative multidisciplinary approach

Genomic and functional resources for *Aristolochia fimbriata*, an emerging basal angiosperm model species

Claude W. dePamphilis[1], Barbara J. Bliss[1], Stefan Wanke[1,2], Jill Duarte[1], P. Kerr Wall[1], Ali Barakat[1], Siela N. Maximova[1], Lena Landherr[1], Yi Hu[1], Jim L. Leebens-Mack[3], Hong Ma[1]

[1]Department of Biology, Institute of Molecular Evolutionary Genetics, and the Huck Institutes of the Life Sciences, 201 Life Sciences Building, Pennsylvania State University, University Park, PA 16802, USA, [2]Technische Universität Dresden, Institut für Botanik, Plant Phylogenetics and Phylogenomics Group, D-01062 Dresden, Germany, [3]Department of Plant Biology, University of Georgia, Athens, GA 30602, USA

Evolutionary innovation in early angiosperms include the evolution of the flower in many diverse forms, the fruit, double fertilization, vessel elements, specialized biochemical pathways, and a variety of angiosperm- and lineage-specific traits. Through the Floral Genome Project, we have gained insight into the sets of genes and gene duplication processes involved in the evolution of the earliest lineages of flowering plants. A missing component of these earlier studies has been the availability of a rapidly growing transformable species that would support functional analysis and potentially emerge as a useful genetic model system for basal angiosperms. We introduce *Aristolochia fimbriata* as a model species for basal angiosperm developmental evolution and functional genomics. To develop molecular genetic resources necessary to grow a community of researchers, we have performed large-scale EST sequencing of protein-coding and small RNAs, identifying a large diversity of genes and potential microRNA regulators. Parallel large-scale transcriptome sequencing is being done on several other basal angiosperms, making it possible to infer common and specific genes present in early flowering plant lineages. To illustrate the utility of these large EST datasets for phylogenetic purposes, we have isolated homologs of conserved single copy genes from *Aristolochia* and other basal angiosperm species. The phylogenies provide hints of the future utility of large-scale use of nuclear genes in angiosperm phylogenetics.

Local uses and chemistry of *Aristolochia* species – a global assessment based on bibliographic sources and chemical analysis

Michael Heinrich[1], Jennifer Chan[1], Monique S.J. Simmonds[1, 2]

[1]*Centre for Pharmacognosy and Phytotherapy, The School of Pharmacy, Univ. London, 29-39 Brunswick Square, London, WC1N 1AX, UK,* [2]*Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AB, UK*

Aristolochia (birthwort) has a long history of medicinal use in Europe, Asia (incl. China), Africa and Central America, although it is known to contain toxic aristolochic acids (AAs) with nephrotoxic and genotoxic effects (Muniz Martinez et al. 2002). During the mid 1990s several patients with renal failure and severe atrophy of the proximal renal tubules were admitted to Belgian hospitals after taking a Traditional Chinese Medicine (TCM) thought to contain AAs. Removal of the native kidneys and ureters in end-stage patients provided a high prevalence of urothelial carcinoma (46%; Muniz Martinez et al 2002).

A range of *Aristolochia* species are utilised in Central America (Kufer et al 2005). For example, the Cho'rti of Guatemala use *Aristolochia maxima* Jacq. against gastrointestinal pain and the Popoluca of Veracruz utilize six *Aristolochia* species (esp. *A. ovalifolia* Duch. and *A. asclepiadifolia* Brandegee) against stomach-ache and colic (Leonti et al 2001). Other species have been used globally, especially those species used in TCM (esp. *A. fangchi* Y.C. Wu), *A. indica* L., *A. debilis* Sieb & Zucch. (China), *A. trilobata* L. (Central America, Caribbean), *A. serpentaria* L. (North America), *A. clematitis* L. (Europe) and *A. bracteolata* Lam. (Africa). The presentation will provide an overview of the phytochemistry of the most widely used species, especially as it relates to the distribution of AAs and an assessment of the toxicological risk of these species.

Leaf calcium oxalate crystal macropatterns and their role in plant systematics and phylogeny: with special emphasis on *Peperomia* (Piperaceae)

Harry T. Horner[1], Stefan Wanke[2], Marie-Stéphanie Samain[3]

[1]Department of Genetics, Development and Cell Biology & Microscopy and NanoImaging Facility, Iowa State University, Ames, Iowa 50011-1020 USA, [2]Technische Universität Dresden, Institut für Botanik, Plant Phylogenetics and Phylogenomics Group, D-01062 Dresden, Germany, [3]Ghent University, Department of Biology, Research Group Spermatophytes, B-9000 Gent, Belgium

Microscopic calcium oxalate crystals formed by flowering plants have been known since Antoni van Leeuwenhoek observed them in the genus *Arum*. Since then, crystals have been collectively found in almost every organ and tissue in an estimated 75% of angiosperms. Leaves are typically the most available source in which to observe crystals because of leaf number, accessibility and longevity. Both living and herbarium specimens contain crystals. When leaves are chemically cleared and observed between crossed polarizers, the crystals are visible and easily identified as needle-like raphides, crystal sand, prisms, styloids and druses (spherical crystal aggregates). In a few recent studies crystals have served as an important character, such as in the Leguminosae and Rosaceae. However, no study has combined type and location of crystals with molecular systematic data, until recently. Such a study was initiated using leaves of 45 *Peperomia* species that vary in texture, shape, succulence, lamina size, coloration and venation. Each leaf contains druses in palisade parenchyma only, druses in palisade and raphides in spongy parenchymas, or druses in palisade and prisms in spongy parenchymas. These variations create distinct crystal macropatterns. These macropatterns were determined and compared to molecular data. The microscopic data identified two major crystal macropatterns and five variations of them. All but one species displayed typically either a single druse in almost all palisade cells forming one or more uniform crystal layers (81.8%, Uniform) or a single druse in palisade cells only above veins forming a reticulate pattern (18.2%; Reticulate). Most species (77.3%) did not display any crystals in spongy parenchyma (-/-); however, some clades showed spongy parenchyma raphide bundles (+/-) while others had prisms (-/+). Several clades displayed more than one macropattern. Based only on crystal macropatterns, data did not demonstrate a specific phylogenetic trend, and failed as synapomorphies for most of the clades. However, crystal macropattern evolution in *Peperomia* is generally characterized by an increasing complexity of the distribution of druses, raphides and prisms, with few reversals. These results indicate crystals may be useful characters at the species, genus, subfamily and family levels in some cases.

The role of B-class gene homologs in the evolution of petaloidy in Aristolochiaceae

M. Alejandra Jaramillo

University of Missouri-Columbia, Div. Biological Sciences, 109 Tucker Hall, Columbia, MO 65203, USA

Aristolochiaceae is a great model to study flower development for two main reasons, on the one hand it is one of the basal-most lineages of angiosperms, on the other hand its large diversity (>700 spp) is closely linked to its pollination ecology. We are testing the conservation of the B-function genetic network and its role in generating petaloid characteristics in the modified first whorl organs of Aristolochiaceae. There are four main lineages in Aristolochiaceae: *Saruma, Asarum, Thottea* and *Aristolochia*. *Saruma* has a differentiated perianth, with a first whorl of sepals and a second whorl of petals. Members of the other genera have a perianth that corresponds only to the first whorl, but has several petaloid characteristics. We have characterized the adaxial epidermis of the perianth of representative members of the family. As well, we have isolated B-class gene homologs from a number of Aristolochiaceae. We will discuss the molecular evolution of the B-class lineage in the Aristolochiaceae. Additionally we will compare the epidermal characteristics and expression patterns of B-class genes in the flowers of selected species.

Tropical species in nothern latitudes: why has the ancient relict plant *Aristolochia manshuriensis* survived?

O.V. Nakonechnaya, O.G. Koren, V.S. Sidorenko, Yu.N. Zhuravlev

Institute of Biology and Soil Sciences, Far East Department of Russian Academy of Sciences, pr. Stoletja 159, Vladivostok, 690022 Russia

Aristolochiaceae Juss. is an ancient family within Piperales L. The Aristolochiaceae family currently consists of 7 genera and about 600 species, 500 of them belong to the genus *Aristolochia*, which are spread mainly in the tropics and subtropics of both hemispheres. However, some *Aristolochia* species grow in more severe conditions in temperate areas. One of these, *Aristolochia manshuriensis* Kom., is an endemic of Manchurian floristic region. It is a woody liana distributed in Korea, China, and the south-eastern part of Russia. *Aristolochia manshuriensis* has a fragmented distribution because only certain habitats are suitable for this liana (broad-leaved forest, bottom of hills, watersheds). Probably, the origin of this species is related with a tropic climate within the territory of modern China.

However, climate changes have limited the species distribution and recent anthropogenic activity has led to further elimination of broad-leaved forests. Consequently the distribution area today is greatly reduced and the species rare. This plant is listed in the “Red Book of Russia” as an endangered species. Which features of *A. manshuriensis* made its survival since tertiary period? And why this species has become endangered today?

In this work we focus on seed reproduction of *A. manshuriensis* to answer these questions. Our data show high seed set (about 95%) and low fruit set (2%). The *A. manshuriensis* flower is adapted for cross-pollination, and a special pollinator is required for successful pollination. We believe this is one of causes for the low fruit set.

Thus, some features of reproductive biology provide stable revival of the species. Nevertheless, in present days some of these characteristics limit the prosperity of *A. manshuriensis* because of lack of suitable pollinators. Our results have applications for the conservation of rare relict plant.

Placing the origin of two species-rich genera in the late Cretaceous with later species divergence in the Tertiary: A phylogenetic, biogeographic and molecular dating analysis of *Piper* and *Peperomia* (Piperaceae)

James F. Smith, Angela C. Stevens, Chris Davidson

Department of Biology, Boise State University, 1910 University Drive, Boise, ID, 83725-1515, USA and Idaho Botanical Research Foundation, 637 Warm Springs, Boise, ID, 83712, USA

Nearly all of the species diversity in Piperaceae is encompassed within *Piper* and *Peperomia*. Both genera are distributed across the tropics with areas of diversification in the Neotropics and Southeast Asia. Piperaceae are less diverse in Africa with only two native species of *Piper*. Members of *Piper* and *Peperomia* are often narrow endemics although some species of both are found on three continents. This study examines the distribution of both genera with representative samples from the Neotropics, Asia, Pacific Islands, and Africa. Molecular dating is used to place an age for the crown clades of *Piper* and *Peperomia* as well as ages for diversification within the clades. Both genera have origins in the late Cretaceous, but diversification of both genera occurred much later in the Tertiary. Biogeography of both genera are correlated with paleoclimate and geological evidence to better explain the distribution and diversification of these large genera.

Independent evolution of different terrestrial life forms in the genus *Peperomia* (Piperaceae) and implications for biogeography of the tuberous species

Lars Symmank[1], Marie-Stéphanie Samain[2], Paul Goetghebeur[2], Guido Mathieu[2], Christoph Neinhuis[1], Stefan Wanke[1]

[1]Technische Universität Dresden, Institut für Botanik, Plant Phylogenetics and Phylogenomics Group, D-01062 Dresden, Germany, [2]Ghent University, Department of Biology, Research Group Spermatophytes, B-9000 Gent, Belgium

The tuberous geophytic species of *Peperomia* have been shown to be sister to the remaining mainly epiphytic species of *Peperomia.* However, these results were obtained from limited sampling and are only partially supported by our new findings based on comprehensive sampling. Phylogenetic tree reconstruction shows at least two independent lineages of tuberous species within the genus. Most of these species still belong to the subgenus *Tildenia*, sister to all other *Peperomia* clades, whereas some others occur scattered in the remaining clades. Leaves and inflorescences of *Tildenia* originate directly from the perennial tuber in contrast with species of the crown group where annual stems originate from the tuber.

The tuber is a derived character in other members of Piperales and most angiosperm lineages. However, as the tuber in *Peperomia* occurs in independent clades, radiation of the tuberous species seems to have been subject to convergent evolution. Species of the *Tildenia* clade are encountered in seasonally arid habitats in two biodiversity hot spots (Peru-Bolivia and Mexico-Guatemala) with few species reported from the countries in between. However, species from both areas are currently recovered as two monophyletic clades which are sister to each other. This supports the radiation of the groups after the forming of the Central American land bridge in the early Pleistocene. Tuberous species in the crown group are not yet well-characterized but it seems that they also occur in vegetation types without a seasonally unfavourable period such as tropical rainforest and are not necessarily geophytic.

In the terrestrial subgenus *Panicularia*, a clade closely related to *Tildenia*, adaptation to similar dry conditions has taken place through reduction of the surface/volume ratio and the elaboration of the multiple epidermises in the leaves. This results in a more efficient adaptation to xeric conditions compared to species with flat thin leaves.

Poster

Embryology of *Manekia naranjoana* (Piperaceae) and the origin of tetrasporic, sixteen-nucleate female gametophytes in Piperales

Tatiana Arias[1,2], Joseph H. Williams[2]

[1]University of Missouri, Division of Biological Sciences, 109 Tucker Hall, Columbia, MO 65211, USA, email: tavd4@mizzou.edu, [2]Department of Ecology and Evolutionary Biology, University of Tennessee, Knoxville, TN 37996, USA

The embryo-nourishing tissue of flowering plant seeds, endosperm, is typically triploid and is formed by a monosporic, *Polygonum* type female gametophyte. Four of the six other known genetic constructs of endosperm are found in the family Piperaceae, each a product of a different female gametophyte ontogeny. The embryology of *Manekia* is still undescribed and we report here that its female gametophyte is tetrasporic and sixteen-nucleate at maturity. There was variation in establishment of the body plan and this produced structural variation in the mature female gametophyte. Approximately 80 % of specimens had bipolar or weakly bipolar early organization and produced a binucleate central cell at maturity, whereas ca. 20 % of material had a distinctly tetrapolar early organization and produced a tetranucleate central cell. These ontogenies and mature structures correspond to the *Drusa* type and *Penaea* type patterns, respectively. *Penaea* type has not been reported in Piperaceae to date. Heterochrony, heterotopy, novelties and sequence deletions have all played roles in modulating variation within Piperales. Based on comparative analysis of development, and consistent with current phylogenies, the common ancestor of Piperaceae was tetrasporic with a bipolar body plan (a plesiomorphic trait inherited from a monosporic, bipolar Polygonum type ancestor) and produced a "functionally bisporic" form of triploid endosperm derived from two, not four, megaspore descendants and a sperm. Subsequent modification of this ancestral ontogeny can account for the origin of all three other known "true" tetrasporic endosperm genetic constructs, which are formed from derivatives of all four megaspores and a sperm. These derived endosperms in turn have higher ploidy, higher potential heterozygosity and a reduced opportunity for genetic conflicts.

Poster

Phylogeography and evolution of Near East Aristolochia - a diversity hotspot

Hafez Mahfoud, Christoph Neinhuis, Stefan Wanke

Technische Universität Dresden, Institut für Botanik, Plant Phylogenetics and Phylogenomics Group, D-01062 Dresden, Germany

The genus *Aristolochia* has a limited distribution in the temperate areas of the northern hemisphere. In North America only few species can be found (~5), whereas in Asia several more species had been reported. The only diversity hotspot is confined to the Mediterranean and Near East region, where up to 60 species have been described – all of which are endemics plus one introduced species. Especially the Near East Aristolochia have not been studied since almost 20-30 years and more detailed studies and collections date back to 1950 and earlier. For this reason a phylogenetic approach has been used to evaluate groupings and species boundaries. Most known species of this area are included by several populations. Represented Eastern Mediterranean and Near East species are both morphologically and molecularly recovered as monophyletic groups and are part of the subsection *Aristolochia*, sister to subsection *Podanthemum* both belonging to subgenus *Aristolochia*. Our study based on chloroplast sequences recovered several species as monophyletic (e.g. *A. cilicica, A. maurorum, A. paecilantha = A. scrabidula, A. bottea*). Some accessions, which had been clearly assigned to one species based on morphological characters, turned out to be independent lineages. These results might be due to cryptic speciation, but will need further investigation in the near future. Hybridisation, which had been assumed for some species (i.e. *A. maurorum*), could not be detected, as no nuclear marker has been studied, but is currently under investigation.

Poster

Web based digital taxonomic tools, center pieces in the multidisciplinary approach of elucidating evolution and systematics of the giant genus *Peperomia* (Piperaceae)

Guido Mathieu[1], Paul Goetghebeur[1], Stefan Wanke[2], Marie-Stéphanie Samain[1]

[1]Ghent University, Department of Biology, Research Group Spermatophytes, B-9000 Gent, Belgium, [2]Technische Universität Dresden, Institut für Botanik, Plant Phylogenetics and Phylogenomics Group, D-01062 Dresden, Germany

With currently 1615 accepted taxa, about 1400 synonyms and over 1500 'herbarium names' (unpublished names mentioned on herbarium specimens), *Peperomia* is generally considered as a 'difficult' genus.

The establishment of several digital taxonomic tools has enhanced a renewed interest in this genus and boosted research efforts during the last few years. Taxonomic tools include the TRGP (Taxonomic Repertory of the genus *Peperomia*), the PBO (*Peperomia* Bibliography Online; currently more than 900 references) and the DPP (Digital *Peperomia* Photobase; currently about 100.000 digitalised herbarium specimens from 60 herbaria in Europe, South and North America). The TRGP and PBO are online at www.peperomia.net, whereas (parts of) the DPP can be distributed on a transportable medium or uploaded to a FTP server.

Research projects in the genus *Peperomia* supported by these web based tools include floristic studies worldwide, ex situ collection management, phylogenetic research (both morphology and molecular based), the compendium of herbarium names, several *Peperomia* expeditions to Madagascar and Latin American countries, and the NeMys Biological Information System (online at www.nemys.ugent.be). The latter system is an extension of the TRGP core data providing access to recent and historic literature on *Peperomia* as pdf-files, digitalised herbarium specimens, distribution maps, morphological data and interactive identification keys. Digital pictures of living *Peperomia* species are already available on NeMys.

To conclude, the digital taxonomic tools are an essential precondition to carry out research in systematics and evolution of a giant genus, but the effort to compile the information, establish an up to date database and make it accessible online is not frequently made.

Poster

The trapping mechanism of *Aristolochia* pitfall flowers

Birgit Oelschlägel[1], Stanislav Gorb[2], Stefan Wanke[1], Christoph Neinhuis[1]

[1]Institut für Botanik, Technische Universität Dresden, Zellescher Weg 20b, D-01062 Dresden, Germany, [2]Evolutionary Biomaterials Group, Max-Planck-Institut für Metallforschung, Heisenbergstraße 3, D-70569 Stuttgart, Germany

The flowers of *Aristolochia* (Aristolochiaceae) are highly derived and specialised for capture, retention, and finally, releasing of pollinators. The flower surfaces of 41 representatives of all three subgenera (*Isotrema*, *Pararistolochia* and *Aristolochia*) were investigated by standard and Cryo-SEM. Furthermore, force measurements on the moveable weir hairs within the flower tube were performed. The trapping mechanism consists of the combination of two different principles, (A) sliding areas and (B) a highly derived type of trichomes (weir hairs). A) Sliding areas possess a specific epidermal cell morphology. The surface of each cell is characterised by a long, procumbent, conical papilla. Papillae are orientated proximally, and thus form a roof tile like structure ensuring the inward movement of the insect. Furthermore, in members of the subgenus *Aristolochia*, the cell surface is densely covered with wax platelets, and in the subgenera *Isotrema* and *Pararistolochia*, the epidermal surface has a thin film of a colourless liquid. Both, wax platelets and liquid films, are supposed to reduce insect adhesion. Sliding areas are situated on the lip and mouth region of representatives of subgenus *Aristolochia*, as well as in the tube of representatives of the subgenera *Isotrema* and *Pararistolochia*. (B) In addition to sliding areas, representatives of subgenera *Aristolochia* and *Pararistolochia* develop weir hairs in the flower tube. These multicellular trichomes possess a thin, moveable joint cell at the base. Force measurements on these hairs confirm their important role in the trapping mechanism of the flowers. Weir hairs allow insects to pass through the tube into the utricle with little effort by bending down the hairs. However, movement in the opposite direction causes the erection of the weir hairs. Escape from the flower is only possible by bending the weir hairs further up, which requires considerably larger forces. Furthermore, the surface of the trichomes is densely covered with long and brittle wax rodlets of the "*Aristolochia*"-type. They prevent adhesion for insect attachment structures. It is not possible for insects to escape due to antiadhesive properties of trichome surfaces until the trichomes shrivel.

Workshop IV

DNA sequence alignment for phylogenetic analysis – current approaches and future prospects

The impact of multiple sequence alignment on phylogenetic estimation

Claude W. dePamphilis[1], Li-San Wang[2], Jim Leebens-Mack[3], Kerr Wall[1], Kai Müller[4], Ali Barakat[1], Tandy Warnow[5]

[1]*Department of Biology and Huck Institutes of Life Sciences, 405B Life Sciences Building, The Penn State University, University Park, PA 16802,* [2]*Department of Pathology and Laboratory Medicine and Penn Center for Bioinformatics, University of Pennsylvania, Philadelphia, PA 19104,* [3]*Department of Plant Biology, University of Georgia, Athens, GA 30602,* [4]*Nees Institute for Biodiversity of Plants, University of Bonn, Meckenheimer Allee 170, 53115 Bonn, Germany,* [5]*Department of Computer Sciences, University of Texas, Austin, TX 78712*

Multiple sequence alignment is typically the first step estimating phylogenetic trees, with the assumption being that as alignments improve, so will phylogenetic reconstructions. Over the last decade or so, new multiple sequence alignment methods have been developed to improve comparative analyses of protein structure, but these new methods are often not used in phylogenetic analyses. In this talk, we report on a simulation study that we performed to evaluate the consequences of using these new multiple sequence alignment methods in terms of the resultant phylogenetic reconstruction. We find the surprising result that although the new alignment methods do indeed produce improved estimations of the true alignment, slight improvements in alignment accuracy have little consequence for phylogenetic accuracy. Several examples drawn from analyses of whole chloroplast genomes and plant gene families, provide some support for this finding, but also identify situations where alignment improvements can enhance alignment realism, phylogenetic resolution, and phylogenetic accuracy.

From the genome to the proteome: how phylogenetic relationships can be inferred from genomic data without the need for sequence alignment

Kay Hamacher

AG Bioinformatics and Theoretical Biology; Technische Universität Darmstadt;
Schnittspahnstr. 10, 64287 Darmstadt, Germany

Phylogenetic relations are largely determined by selection during the evolution of organisms. The functionality and complexity of the proteome of an organism is therefore a good measure for phylogenetic distances. In this talk we motivate a new measure which can be rationalized from statistical learning theory and show how phylogenetic trees can be derived. Comparison to other methodologies and standard taxonomy is further discussed. In addition we show the robustness of the methodology against perturbations such as errors in the input-data or insufficient sampling in the learning algorithms which provide for the extraction of proteomic data from genomes. We discuss further prospects of the method and speculate on the inclusion of another important part of genomic information such as regulatory elements.

A recursive alignment algorithm using a profile alignment with information about alignable and non-alignable regions

Frank Kauff[1], Cymon J. Cox[2], François Lutzoni[3]

[1]Universität Kaiserslautern, FB Biologie, Abt. Molekulare Phylogenetik, Postfach 3049, 67653 Kaiserslautern, Germany, [2]Natural History Museum, Dept. of Zoology, Cromwell Rd., SW7 5BD, London, UK, [3]Duke University, Dept. of Biology, Durham NC-27707, USA

The goal of the NSF-funded AFTOL project (Assembling the Fungal Tree Of Life, www.aftol.org) is to enhance the understanding of the evolution of the Kingdom fungi by sampling 1500+ species for eight genetic loci across all major fungal clades, plus a subset of taxa for a suite of morphological and ultrastructural characters. The WASABI system (Web Accessible Sequence Analysis for Biological Inference) was designed to facilitate the collection and dissemination of molecular data to (and from) the laboratories and to the public, and to provide storage and an automated analysis framework.An alignment algorithm was developed for WASABI which combines a profile alignment procedure with the principle of a new block-wise alignment method. Profile-alignments in NEXUS-format include character sets with information about non-alignable regions and indels, e.g. introns, hypervariable regions with multiple short indels. Additional sequences are aligned blockwise, starting with the largest alignable region, and omitting regions that cannot reliably aligned and which were previously denoted as such in the NEXUS file. Each aligned region subdivides both the profile alignment and the newly aligned sequence into an upstream and a downstream part relative to the aligned block. The algorithm is then applied recursively and separately to first the upstream parts of the profile and the new sequence, and then to the downstream parts of the profile and the new sequence. As the alignable regions in the core alignment may become smaller and smaller, so do the corresponding sequence parts, so that the difficulty of finding the correct alignment between profile block and sequence remains comparatively easy. Currently the local alignments are done using clustalw, however, most available alignment software could be easily incorporated into the software. Our results show that this alignment procedure can successfully deal with problematic regions, e.g. large introns, and that subsequent manual optimization can be kept to a minimum.

Aliscore - identifying random similarity within sequence alignments

Bernhard Misof, Katharina Misof, Patrick Kück

Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160; 53113 Bonn

It has been demonstrated that random similarity of sequences or sequence sections can impede phylogenetic analyses or the identification of gene homologies. Additionally, randomly similar sequences or ambiguously aligned sequence sections can negatively interfere with the estimation of substitution model parameters. Phylogenomic studies have shown that biases in model estimation and tree reconstructions do not disappear even with large data, but in fact can become pronounced. It is therefore important to identify possible random similarity within sequence alignments in advance of model estimation and tree reconstructions. Different approaches have been already suggested to identify and treat problematic alignment sections. We propose an alternative method which can identify random similarity within multiple sequence alignments based on Monte Carlo resampling within a sliding window. The method infers similarity profiles from pairwise sequence comparisons and subsequently calculates a consensus profile. In consequence, consensus profiles identify dominating patterns of non-random similarity or randomness within sections of multiple sequence alignments. We show that the approach clearly identifies randomness in simulated and real data. After the exclusion of putative random sections, node support drastically improves in tree reconstructions of both data. It thus appears as a powerful tool to identify possible biases of tree reconstructions or gene identification. The method is currently restricted to nucleotide data, but will be extended to protein data in the near future.

RNAsalsa -- alignment based on structure and sequence information

Roman Stocsits[1], Harald Letsch[1], Jana Hertel[2], Peter Stadler[2], Bernhard Misof[1]

[1]*Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160; 53113 Bonn,*
[2]*Bioinformatics Group, University of Leipzig, Härtelstrasse. 16-18; 04107 Leipzig*

RNAsalsa adapts known structure information to the considered sequences in several steps. Conserved structure features are verified via primary sequence conservation and the detection of consistent and compensatory substitutions, which requires internal alignment steps. Remaining highly variable sections, where conserved structures cannot be detected, are folded by minimizing free energy. The result is a complete individual secondary structure for each sequence. A final alignment is done by taking both structure and sequence information of each position into account. For further tree reconstruction analysis, a sequence alignment with a consensus structure is extracted, which can be used as an input for suitable programs like PHASE or MrBayes. The information of the consensus structure allows the application of RNA substitution models in the conserved paired regions of the considered RNA genes. It is important to notice, that RNAsalsa uses structure information for adjusting and refining the sequence alignment and vice versa.

When is homology important in alignment, and how do we use it?

David Morrison

SWEPAR, Swedish University of Agricultural Sciences, Uppsala, Sweden

Four objectives of molecular sequence alignment can be recognized: (i) structure prediction, which deduces the structure of a gene product from knowledge of its gene sequence, (ii) database searching, which maximizes the distinction between homologous and non-homologous sequences, (iii) sequence comparison, which juxtaposes residues representing conserved sequence features, and (iv) phylogenetic analysis, which produces plausible hypotheses of evolutionary relationships. Originally, all computerized alignment procedures were devised for sequence comparison, and only recently have specialist procedures been developed for the other three objectives. For structure prediction and database searching, many successful methods have been devised that ignore evolutionary homology as an optimality criterion. Phylogenetic analysis, on the other hand, demands that the historically equivalent residues must always be aligned. Indeed, meeting this requirement can be used as the definition of a successful phylogenetic alignment. Unfortunately, there has been little development of computerized procedures specifically for multiple alignment in the context of phylogenetic analysis. There are two strands that have arisen in practice. One uses methods that have been developed for the other three objectives, in an attempt to bring to bear all of the available evidence that might be useful for identifying homologous residues. Such methods include: multi-sequence consistency, iterative refinement, profile alignments, and structural considerations. There is, however, no theoretical model underlying this strand. The other strand combines the alignment and tree-building procedures, on the basis that homology can be distinguished from analogy only on a phylogenetic tree. Both parsimony and likelihood have been used as optimality criteria. Sadly, it seems that the models used by both methods are too simplistic to produce useful results, as they recognize substitutions and indels only. An alternative (third) approach to phylogenetic alignment would be to explicitly model the types of events that lead to sequence variation. These events include: duplications (notably tandem repeats and inverted repeats), substitutions, inversions, translocations and transpositions, deletions, and insertions. This approach should allow plausible hypotheses of residue homology to be developed, in a manner analogous to the use of transformation-series analysis, as originally developed for the phylogenetic analysis of phenotypic characteristics. This may be computationally difficult.

Homology assessment in the presence of microstructural changes

Dietmar Quandt[1], Kai Müller[2]

[1]Institute of Botany, TU Dresden, Zellescher Weg 22, 01062 Dresden, Germany, [2]Nees Institute for Biodiversity of Plants, University of Bonn, Meckenheimer Allee 170, 53115 Bonn, Germany

Applying rapidly evolving molecular markers for phylogenetic reconstructions is not as straightforward as using rather slowly evolving genes displaying low degrees of microstructural change. Extensive length mutations and inversions considerably complicate the homology assessment. Using alignment approaches based on repeat recognition (possibly guided by secondary structures) and an enhanced understanding of molecular evolutionary mechanisms might promote the utilization of more complexly evolving regions such as spacers and introns.

It appears that inversions are almost always associated with hairpins and display high degrees of homoplasy, unlike other kinds of microstructural changes (e.g., simple sequence repeats). A detailed investigation of differences in mutational patterns observed in the inverted as opposed to the non-inverted motif points towards multiple independent occurrences of such inversions among lineages.

Current automated alignment algorithms by design do not take into account inversions and, therefore, frequently create erroneous alignments. Similarly, motif recognition has not yet found its way into major alignment software packages, despite the commonness of simple sequence repeats (SSRs) mediated by slipped-strand-mispairing, a mechanism suggested 25 years ago. A modified slipped-strand-mispairing mechanism for SSRs provides a tool to differentiate between the original motif and its repeated variant and thus facilitates homology assessment.

Non-coding RNAs: alignment and structure prediction

Gerhard Steger

Institut für Physikalische Biologie; Heinrich-Heine-Universität Düsseldorf;40225 Düsseldorf, Germany

Alignment of RNA has a wide range of applications, for example in phylogeny inference, consensus structure prediction, and homology searches. Yet aligning structural or non-coding RNAs (ncRNAs) correctly is notoriously difficult as these RNA sequences may evolve by compensatory mutations, which maintain base pairing but destroy sequence homology. Ideally, alignment programs would take into account both RNA structure and sequence. The Sankoff algorithm for the simultaneous solution of RNA structure prediction and RNA sequence alignment was proposed 20 years ago but suffers from its exponential complexity. I will summarize features of recent alignment programs, which are able to account for both sequence and structure of ncRNA, and show the quality of predictions in dependence upon number of homologous sequences and similarity of sequences.

Workshop V

Pixel-Voxel-Morphology – introduction to working with µCT-data

Fish eye 3D

Martin Heß

BioZentrum, Ludwig-Maximilians-Universität München, Großhadernerstraße 2, 82152 Planegg, Germany

Thorough morphological studies on visual systems require acquisition, analysis and presentation of 3-dimensional image data with various methods, in different scales and several interlocked coordinate systems. Exemplarily such procedures are demonstrated with eyes and retina structures of teleosts.

The 3D-reconstruction of complete fish heads (position of eyes and supporting structures in the head, volumetry of anatomical compartments) based on mechanical section series is practicable - without conspicuous distortion - up to a specimen-diameter of about 5 mm. In future, image data of bigger objects shall be recorded with reasonable resolution using µMRT or µCT. On a smaller scale structures like retinal layers, cell patterns, neuroanatomy and synaptic connectivity can be accessed via mechanical (Epon) or optical sectioning (CLSM, 2-Photon Microscopy) down to the ultrastructural dimension (TEM-tomography). After acquisition digital 3D data are processed in application software like Photoshop, Amira Resolve RT and Acrobat 3D or programming languages like IDL for contrast optimization of raw image data, stack alignement, deconvolution, 3D pattern recognition, volumetry, volume- and surface-rendering and presentation.

Pixel-Voxel-Morphology - Introduction to working with µCT-data

Thomas Hörnschemeyer

University of Göttingen, Johann-Friedrich-Blumenbach-Institute for Zoology & Anthropology, Dept. of Morphology & Systematics, 37073 Göttingen, Germany,email: thoerns@gwdg.de

High resolution X-ray tomography (µCT) has meanwhile been used to study a variety of different aspects of the morphology of insects and other invertebrates as well as small vertebrates and different kinds of fossils.

The quality of the data produced with this range of techniques improved significantly during recent years and also a number of facilities now have the technical possibilities to do µCT scans.

The purpose of the workshop is to present a comprehensive overview of the current state of µCT techniques and their application to the investigation of morphology and function of small organisms. Together with the practical part of the workshop participants will get an impression of what is possible with these techniques.

The introduction to the workshop will give an overview of the physical background of computed X-ray tomography with a comparison of the different kinds of X-ray sources, like synchrotrons and X-ray tubes, and the differences in using these sources for µCT investigations.

The individual steps of data processing from the X-ray projection image to the virtual three-dimensional model will be explained and the necessary methods and steps for preparation and mounting of specimens will be illustrated. Finally, by means of some examples, the possible applications of µCT methods are demonstrated.

From segmentation to animation: combining the advantages of different 3D software packages

Thomas Kleinteich

Universität Hamburg, Biozentrum Grindel und Zoologisches Museum, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany, email: thomas.kleinteich@uni-hamburg.de

The possibilities that 3D datasets offer in the field of comparative anatomy are virtually infinite. Computer software packages for analysis of 3D datasets have been developed for different applications that comprise e.g. engineering, materials research, and computer aided design. For comparative anatomical studies, it often is necessary to combine different types of 3D software packages in order to yield optimal results. I will focus on the segmentation, rendering, and animation of 3D datasets with the software solutions TGS Amira®, VGStudio MAX®, and Autodesk Maya®. TGS Amira® and VGStudio MAX® are designed to process volume datasets, that are generated e.g. by µCT scanning. Both programs, however, differ notably in their general workflow and in the data segmentation process. Because TGS Amira® and VGStudio MAX® use volume datasets as input data, it is easy to combine both software packages; exchange formats are TIFF image stacks, DICOM data, and raw volume datasets. TGS Amira® can also be used to generate 3D models based on histological serial sections. Autodesk Maya® is designed for 3D modeling and animation; 3D models can be imported and exported as 3D surfaces. In the field of morphology, Autodesk Maya® is used to build 3D surfaces from histological data. The strengths of Autodesk Maya® are photo realistic rendering and character animation. However, the import of data from TGS Amira® and VGStudio MAX® to Autodesk Maya® is nontrivial due to the different data types (i.e. volume data vs. surface data). I will describe one option to generate surface data out of volume data using the VRML (i.e. virtual reality modeling language) export filters of TGS Amira® and VGStudio MAX®.

Participants

Achatz, Michaela Freie Universität Berlin, Altensteinstraße 6, 14195 Berlin, Germany, Tel: +49 (0)30-83853146, Michaela.Achatz@fu-berlin.de

Achigan Dako, Enoch Gbenato IPK Gatersleben, Corrensstraße 3, 06466 Gatersleben, Germany, Tel: +49 (0)39482-5117, dachigan@gmail.com

Ackermann, Markus Institut für Biologie der Freien Universität Berlin - Systematische Botanik und Pflanzengeographie, Altensteinstraße 6, 14195 Berlin, Germany, Tel: +49 (0)30-83856645, ackermal@zedat.fu-berlin.de

Ahlrichs, Wilko Carl von Ossietzky Universität Oldenburg, Fakultät V Mathematik und Naturwissenschaften, Institut für Biologie und Umweltwissenschaften, AG Molekulare Systematik, Carl-von-Ossietzky Str. 9-11, Postfach 2503, 26111 Oldenburg, Germany,
Tel: +49 (0)441-7983369, wilko.ahlrichs@uni-oldenburg.de

Akinnagbe, Akindele Department of Forest Genetics & Forest Tree Breeding, University of Goettingen, Buesgenweg 2, 37077 Goettingen, Germany, Tel: +49 (0)551-393540, akin.akinnagbe@gmail.com

Akinnagbe, Ruth Abosede Department of Microbiology, Federal University of Technology, Akure, Nigeria, c/o Akindele Akinnagbe, Department of Forestry & Wood Technology, Federal University of Technology, P.M.B. 704 Akure, Nigeria, ruth.akinnagbe@gmail.com

Akkoz, Cengiz Biology Department, Faculty of Art and Science, Selcuk University, 42031, Campus Konya, Turkey

Albach, Dirk Institut für Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Bentzelweg 9a, 55099 Mainz, Germany, Tel: +49 (0)6131 3923169, albach@uni-mainz.de

Álvarez-Presas, Marta Universitat de Barcelona, Dpt. de Genètica. Edifici annex., Av. Diagonal, 645, 08028 Barcelona, Spain, Tel: +34 (0)93-4031746, onaalvarez@ub.edu

Arida, Evy Zoologisches Forschungsmuseum Alexander König (ZFMK) Bonn, Adenauerallee 160, 53113 Bonn, Germany, Tel: +49 (0)228-9212285, arida@uni-bonn.de

Arunyawat, Uraiwan Department of Genetics, Kasetsart University, Paholyothin 50, Bangkhen, 10900, Thailand, Tel: +66 (0)25625444 ext. 4221, Uraiwan.A@ku.ac.th

Aspöck, Ulrike Naturhistorisches Museum Wien, 2. Zoologische Abteilung (Entomologie), Burgring 7, 1010 Wien, Austria, Tel: +43 (0)1-52177324, ulrike.aspoeck@nhm-wien.ac.at

Ayele, Taye Department of Forest Genetics and Forest Tree Breeding, Büsgen Institute, Georg-August University, Büsgenweg 2 37077 Göttingen, Germany, Tel: +49 (0)551-399522, tayele@gwdg.de

Azhar, Imran Ullah Punjab University Lahore, c/o Chand Bagh School Murid Ke Sheikhupura Road, Pakistan, Tel: +92 302-8965330, imran_ullah_cheema@hotmail.com

Baden, Christian Ulrich Biozentrum Grindel und Zoologisches Museum, Martin Luther King-Platz 3, 20146 Hamburg, Germany, Tel: +49 (0)40-428383867, Christian@cbaden.de

Bagci, Yavuz Selçuk University, Selçuk University, Faculty of Arts and Sciences, Department of Biyology, Campus, 42075, Selçuklu, Konya, Turkey, ybagci@selcuk.edu.tr

Bagusche, Frauke Universität Wien, Dep. Evolutionsbiologie, Molekulare Phylogenetik, Althanstrasse 14, Wien 1090, Austria, Tel: +43 (0)1-427754453, frauke.bagusche@gmx.de

Baier, Christina Leibniz-Institute of Plant Genetics and Crop Research (IPK) IPK, Department of Taxonomy and Evolutionary Biology 06466 Gatersleben, Germany, Tel: +49 (0)39482-5275, baier@ipk-gatersleben.de

Bakhshi Khaniki, Gholamreza Payame Noor University, P.O.Box 19395-4697, Tehran, Iran, Tel: +98 21-22292024, bakhshi@pnu.ac.ir

Bardy, Katharina Department of Biogeography and Botanical Garden, Faculty Centre Botany, University of Vienna, Rennweg 14, 1030 Wien, Austria, Tel: +43 (0)1 4277-54158, katharina.bardy@univie.ac.at

Barfuss, Michael H. J. Dept. of Systematic and Evolutionary Botany, University of Vienna, Rennweg 14, A-1030 Wien Austria, Tel: +43 (0)1-427754130, michael.h.j.barfuss@univie.ac.at

Barker, Nigel Department of Botany, Rhodes University, Department of Botany, Rhodes University, P.O. Box 94, Grahamstown, 6140, South Africa , Tel: +27 46-6038715, N.Barker@ru.ac.za

Bartolomaeus, Thomas Systematik und Evolution der Tiere, Freie Universität Berlin, FB Biologie, Chemie, Pharmazie, Königin-Luise-Str. 1-3, 14195 Berlin, Germany, Tel: +49 (0)30-83856288, tbartol@zoosyst-berlin.de

Bastida Alamillo, Jesús Mª Universidad de Jaén. Facultad de Ciencias Experimentales. Dpto. Biología Animal, Biología Vegetal y Ecologia, Paraje Las Lagunillas s/n Jaén (Jaén) C.P.: 23071, Spain, Tel: +34 (0) 953-213057, jbastida@ujaen.es

Bergmeier, Erwin Abteilung Vegetationsanalyse & Phytodiversität, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-395700, erwin.bergmeier@bio.uni-goettingen.de

Beutel, Rolf Friedrich-Schiller-Universität Jena, Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Erbertstr. 1, 07743 Jena, Germany, Tel: +49 (0)3641-949153, b5bero@rz.uni-jena.de

Blattner, Frank R. Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), Experimentelle Taxonomie, Corrensstraße 3, 06466 Gatersleben, Germany, Tel: +49 (0)39482-5202, blattner@ipk-gatersleben.de

Bleeker, Walter Department of Botany, University of Osnabrück, Barbarastr. 11, 49069 Osnabrück, Germany, Tel: +49 (0)541-9692248, bleeker@biologie.uni-osnabrueck.de

Bleidißel, Sabrina Zoologie und Biologiedidaktik, Bergische Universität Wuppertal, FB C-Zoologie, H10/01, Gaußstr. 20, 42097 Wuppertal, Germany, Tel: +49 (0)202-4392814, bleidiss@uni-wuppertal.de

Bleidorn, Christoph Insitut für Biochemie und Biologie, Evolutionsbiologie/Spez. Zoologie, Universität Potsdam, Karl-Liebknecht-Str. 24-25, Haus 26, 14476 Potsdam-Golm, Germany, Tel: +49 (0)331-9775604, Bleidorn@uni-potsdam.de

Blöch, Cordula Center of Botany, Department for Systematic and Evolutionary Botany, University Vienna, Rennweg 14, A-1030 Wien, Austria, Tel: +43 (0)1-427754027, cordula.bloech@univie.ac.at

Bos, Merijn M. State Museum of Natural History, Stuttgart Rosenstein 1, 70191 Stuttgart, Germany, Tel: +49 (0)711-8936238, boommarter@hotmail.com

Bradler, Sven Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Neurobiologie, Universität Göttingen, Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395430, sbradle@gwdg.de

Brandt, Angelika Zoological Museum, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany, Tel: +49 (0)40-428382278, abrandt@zoologie.uni-hamburg.de

Brandt, Ronny Plant Systematics & Morphology, Institute of Biology, University of Kassel, Milchlingstrasse 8, 34121 Kassel, Germany, Tel: +49 (0)561-81640642, ronny.brandt@gmx.de

Bräuchler, Christian LMU München, Department Biologie I, Systematische Botanik, Menzinger Str. 67, 80683 München, Germany, Tel: +49 (0)89-17861199, braeuchler@lrz.uni-muenchen.de

Braun, Michael Insitut für Pharmazie und Molekulare Biotechnologie (IPMB), Im Neuenheimer Feld 364, 69120 Heidelberg, Germany, Tel: +49 (0)6221-3262108, Michael.Braun@urz.uni-heidelberg.de

Brix, Saskia DZMB-Senckenberg, DZMB Hamburg, Biozentrum Grindel, Martin-Luther-King Platz, 20146 Hamburg, Germany, Tel: +49 (0)40-428385642, sbrix@senckenberg.de

Brochmann, Christian NCB - National Centre for Biosystematics, Natural History Museum University of Oslo, PO Box 1172 Blindern, NO-0318 Oslo, Norway, Tel: +47 (0)221-851611, christian.brochmann@nhm.uio.no

Brunken, Ulrike Palmengarten der Stadt Frankfurt am Main, Siesmayerstr. 61, 60431 Frankfurt am Main, Germany, Tel: +49 (0)69-21238328, Ulrike.Brunken@senckenberg.de

Bull-Hereñu, Kester Institut für Spezielle Botanik, Johannes Gutenberg-Universität, Mainz, 55099 Mainz, Germany, Tel: +49 (0)6131-3924286, bull@uni-mainz.de

Camenzind, Tessa FU-Berlin, Institut für Biologie, Systematische Botanik und Pflanzengeographie, Altensteinstr. 6, 14195 Berlin, Germany, Tel: +49 (0)30-51658800, Camtes@web.de

Carl-Ruprecht, Ulrike Department of Organismic Biology, University of Salzburg, Hellbrunnerstr. 34, 5020 Salzburg, Austria, Tel: +43 (0)662-80445529, ulrike.carl@sbg.ac.at

Castellani, Christopher Work Group Biosystematic Documentation, University of Ulm, Helmholtzstr. 20, 89081 Ulm, Germany, Tel: +49 (0)731-5031001, christopher.castellani@uni-ulm.de

Chase, Mark W. Royal Botanic Gardens, Kew, Jodrell Laboratory, Richmond, Surrey TW9 3DS PA, United Kingdom, Tel: +44 (0)20-83325311, m.chase@kew.org

Chatrou, Lars Nationaal Herbarium Nederland, Wageningen University branch, Generaal Foulkesweg 37, 6703 BL Wageningen, The Netherlands, Tel: +31 (0)317-483854, Lars.Chatrou@wur.nl

Ciardelli, Pepé Botanischer Garten und Botanisches Museum Berlin-Dahlem (BGBM), Zentraleinrichtung der Freien Universität Berlin, Königin-Luise-Str. 6-8, 14195 Berlin Germany, Tel: +49 (0)30-83850284, p.ciardelli@bgbm.org

Claßen-Bockhoff, Regine Institut für Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Bentzelweg 2, 55099 Mainz, Germany, Tel: +49 (0)6131-3924301, classenb@uni-mainz.de

Cusimano, Natalie LMU, Systematic Botany, Menzinger Str. 67, 80638 München, Germany, Tel: +49 (0)89-17861251, cusimano@bio.lmu.de

Degtjareva, Galina Botanical Garden, Lomonosov Moscow State University, 119991 Moscow, Leninskie Gory, Russia, Tel: +7 (0)495-9393193, degavi@genebee.msu.su

De Pamphilis, Claude Penn State University, 405B Life Sciences Bldg, University Park, PA 16802, USA, Tel: +1 814-8636412, cwd3@psu.edu

Deppermann, Jana University of Osnabrueck, Department of Biology/Chemestry, Division of Ecology, Barbarastr. 13, 49076 Osnabrueck, Germany, Tel: +49 (0)541-9692836, jana.deppermann@biologie.uni-osnabrueck.de

Diduszko, Dawid Department of Animal Taxonomy and Ecology, Adama Mickiewicz University Collegium Biologicum Umultowska 89, 61-614 Poznań, Poland, Tel: +48 61-829557, dawyyyid@yahoo.com

Dinapoli, Angela Institute for Ecology, Evolution & Diversity - Phylogeny and Systematics, J. W. Goethe-University, Siesmayerstr. 70, 60054 Frankfurt am Main, Germany, Tel: +49 (0)69-79824701, a.dinapoli@bio.uni-frankfurt.de

Dobler, Susanne Universität Hamburg, Biozentrum Grindel und Zoologisches Museum, Martin-Luther-King Pl. 3, 20146 Hamburg, Germany, Tel: +49 (0)40-428384288, susanne.dobler@uni-hamburg.de

Dogan, Hasan Huseyin Selcuk University Science and Art Faculty, Biology Department, Selçuk University, Faculty of Arts and Sciences, Department of Biyology, Campus, 42075, Selçuklu, Konya, Turkey, Tel: +90 3322231867, hhuseyindogan@yahoo.com

Dogan, Bekir Selçuk University, Selçuk University, Education Faculty, Biology Department, 42090 Meram, Konya, Turkey, Tel: +90 3323238220403, doganbekir@hotmail.com

Dohrmann, Martin Geoscience Centre Göttingen, Goldschmidtstr. 3, 37077 Göttingen, Germany, Tel: +49 (0)551-397908, mdohrma1@gwdg.de

Dressler, Carina Institut für Spezielle Zoologie und Evolutionsbiologie, FSU Jena, Erbertstraße 1, 07743 Jena, Germany, Tel: +49 (0)3641-949149, legeis.atopa@web.de

Dröge, Gabriele Botanic Garden and Botanical Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Str. 6-8, 14195, Berlin, Germany, Tel: +49 (0)30-83850150, g.droege@bgbm.org

Dural, Hüseyin Selçuk University, Faculty of Arts and Sciences, Department of Biyology, Campus, 42075, Selçuklu, Konya, Turkey, hdural@selcuk.edu.tr

Duran, Ahmet Selçuk University, Education Faculty, Biology Department, 42090 Meram, Konya, Turkey, Tel: +90 3323238220445, ahmetduran22@yahoo.com

Ehrendorfer, Friedrich Institute of Botany, University of Vienna, Rennweg 14, A-1030 Wien, Austria, Tel: +43 (0)1-427754154, friedrich.ehrendorfer@univie.ac.at

Eikel, Oliver Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie, Universität Göttingen Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395459, oeikel@gwdg.de

Eiserhardt, Wolf L. Universität Hamburg / Biozentrum Klein Flottbek, Ohnhorststraße 18, 22609 Hamburg, Germany, Tel: +49 (0)40-42816419, wolf.eiserhardt@botanik.uni-hamburg.de

El-Gendy, Amel Zoology Department, Faculty of Science, Alexandria University, 21511, Moharem Bek, Alexandria, Egypt, Tel: +2 (0)129393097, amelhosny@yahoo.com

El-Hedeny, Magdy Geology Department, Faculty of Science, Alexandria University, 21511, Moharem Bek, Alexandria, Egypt, Tel: +2 (0)127430978, m_elhedeny@yahoo.com

Eliades, Nicolas-George Department of Forest Genetics and Forest Tree Breeding, Universität Göttingen, Büsgenweg 2, 37077 Göttingen, Germany, Tel: 49 (0)551-399522, neliade@gwdg.de

Emadzade, Khatere Dep. of Systematics and Evolutionary Botany, University of Vienna, Rennweg 14, A-1030 Wien, Austria, Tel: +43 (0)1-427754163, emadzadekh@yahoo.com

Enke, Neela Botanisches Museum und Botanischer Garten, Freie Universität Berlin, Königin-Luise-Str. 6-8, 14195 Berlin, Germany, Tel: +49 (0)30-83850141, n.enke@bgbm.org

Epp, Laura Unit of Evolutionary Biology, University of Potsdam, Karl-Liebknecht-Str. 24-25, Haus 26, Germany, Tel: +49 (0)331-9775250, lauepp@uni-potsdam.de

Erpenbeck, Dirk Courant Research Center Geobiology, Georg-August-Universität Göttingen, Goldschmidtstr. 3, 37077 Göttingen, Germany, Tel: +49 (0)551-3991296, derpenb@gwdg.de

Ertugrul, Kuddisi Selcuk University Science and Art Faculty Selçuk University, Faculty of Arts and Sciences, Department of Biyology, Campus, 42075, Selçuklu, Konya, Turkey, Tel: +90 3322231862, ekuddisi@selcuk.edu.tr

Esfeld, Korinna Museum for Natural History, Rosenstein 1, 70191 Stuttgart, Germany, Tel: +49 (0)711-8936202, esfeld.smns@naturkundemuseum-bw.de

Fadaie, Fatemeh Faculty of Biology, Shahid Beheshty University, Tehran, Khakshenasy Houses, Beginning of Jorjan street, Shahid Beheshty Street, Gorgan, Iran, Po. Box: 4915694713, Iran, Tel: +98 (0)171-3338177, f_fadaie@sbu.ac.ir

Fahrein, Kathrin Institut für Zoologie, Freie Universität Berlin, Königin-Luise-Straße 1-3, 14195 Berlin, Germany, Tel: +49 (0)30-83856996, kathrin.fahrein@freenet.de

Fay, Michael F. Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AB, United Kingdom, Tel: +44 83325315, m.fay@kew.org

Fehrer, Judith Institute of Botany, Academy of Sciences of the Czech Republic, Zámek 1, 25243 Průhonice, Czech Republic, Tel: +420 271015415, fehrer@ibot.cas.cz

Feldberg, Kathrin Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany

Feldhaar, Heike Zoologie II, Biozentrum der Universität Würzburg, Am Hubland, 97074 Wuerzburg, Germany, Tel: +49 (0)931 8884305, feldhaar@biozentrum.uni-wuerzburg.de

Ferrufino Acosta, Lilian Florencia Botanischer Garten und Botanisches Museum Berlin, Dahlem, Königin-Luise Str. 6-8, 14195, Berlin, Germany, Tel: +49 (0)30-83850141, l.ferrufino@bgbm.org

Feuerstein, Verena Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie, Universität Göttingen Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395391, vfeuers@gwdg.de

Fey-Wagner, Christina University of Kassel, Heinrich-Plett-Str.40, 34123 Kassel, Germany, Tel: 49 (0)561-8044651, C.Fey-Wagner@gmx.de

Fiege, Dieter Forschungsinstitut und Naturmuseum Senckenberg, Senckenberganlage 25, 60325 Frankfurt/Main, Germany, Tel: 49 (0)69-75421265, Dieter.Fiege@senckenberg.de

Fischer, Christian Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie, Universität Göttingen, Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395454, cfische2@gwdg.de

Fleischmann, Andreas LMU München, Department Biologie I, Systematic Botany and Mycology, Menzinger Strasse 67, 80638 Munich, Germany, Tel: +49 (0)89-17861199, fleischmann@lrz.uni-muenchen.de

Förster, Stefanie Institut für spezielle Botanik, Johannes-Gutenberg-Universität Mainz, Bentzelweg 9a, 55128 Mainz, Germany, Tel: +49 (0)177-4143872, st_foerster_mz@yahoo.de

Franklin M. Jayaseelan, J. Benjamin Molecular Biophysics Unit, Indian Institute of Science, Bangalore 560 012,Karnataka, India, Tel: +91 (0)80-22932337, benjamin@mbu.iisc.ernet.in

Freitag, Helmut University of Kassel, Institute of Biology, Heinrich-Plett-Str. 40, 4132 Kassel, Germany, Tel: +49 (0)561-8044273, hfreitag@uni-kassel.de

Friedl, Thomas University of Goettingen, Dept. Experimental Phycology and SAG, Untere Karspuele 2, 37073 Goettingen, Germany, Tel: +49 (0)551-397868, tfriedl@uni-goettingen.de

Friedrich, Frank Entomology Group, Institut f. Sezielle Zoologie u. Evolutionsbiologie, FSU Jena, Erbertstr. 1, 07743 Jena, Germany, Tel: +49 (0)3641-949181, frank.friedrich@uni-jena.de

Friesen, Nikolai Botanical Garden of .University of Osnabrueck, Albrechtstrasse 29, 49076 Osnabrück, Germany, Tel: +49 (0)541-9692738, friesen@biologie.uni-osnabrueck.de

Fritz, Uwe Museum für Tierkunde, Staatliche Naturhistorische Sammlungen Dresden, Königsbrücker Landstr. 159, 01109 Dresden, Germany, Tel: +49 (0)351-8926325, Uwe.Fritz@snsd.smwk.sachsen.de

Fromm, Bastian Friedrich-Schiller-Universität, Zoologie Jena, AG Predel, Erbertstraße 1, 07743 Jena, Germany, Tel: +49 (0)3641-949190, B.Fromm@uni-jena.de

Fuentes, Susy Nees-Institut für Biodiversität der Pflanzen, Universität Bonn, Germany, and Herbario Nacional de Bolivia, La Paz Bolivia Meckenheimer Allee 170, 53115 Bonn, Germany, Tel: +49 (0)228-737025, sfuentes@uni-bonn.de

Fürst von Lieven, Alexander Institut für Biologie / Zoologie Königin-Luise-Str. 1-3, 14195 Berlin, Germany, Tel: +49 (0)30-83853838, lieven@zedat.fu-berlin.de

Gailing, Oliver Department of Forest Genetics, Büsgen-Institute., University of Göttingen, Büsgenweg 2, 37077 Göttingen, Germany, Tel: +49 (0)551-3914281, ogailin@gwdg.de

Gehler, Alexander Zentrum für Geowissenschaften, Universität Göttingen, Godschmidtstr. 3, 37077 Göttingen, Germany, Tel: +49 (0)551-397963, agehler@gwdg.de

Gehrig, Christine Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-392259, gehrigchristine@hotmail.com

Gehrke, Berit Institute for Systematic Botany, University of Zurich, Zollikerstrasse 107, CH 8008 Zurich, Switzerland, Tel: +41 (0)44-6348432, gehrke@systbot.uzh.ch

Geiser, Elisabeth St.Julien-Strasse 2 / 314, 5020 Salzburg, Austria, Tel: +43 (0)664-5434747, elisabeth.geiser@gmx.at

Geml, József Institute of Arctic Biology, University of Alaska Fairbanks, PO box 757000, 902 N Koyukuk Drive, Fairbanks, AK 99775-7000, USA, Tel: +1 9074741140, jgeml@iab.alaska.edu

Ghanavati, Farangis Seed and Plant Improvement Institute, Fahmideh Ave. Karaj, Iran, Tel: +98 9123774609, f_ghanavati83@yahoo.com

Ghanti, Kiran Kumar Dept. of crop physiology, University of agricultural science, GKVK, Bangalore, c/o Prof. Udaya kumar, Karnataka, India-5600065, India, Tel: 91 809448376357, ghantikiran@rediffmail.com

Ghobei, Mahnaz Seed & Plant Improvement Institute, Fahmide ST. Karaj, Iran,
Tel: +98 9122778683, Mahali_2002@yahoo.com

Giere, Peter Museum für Naturkunde, Berlin, Invalidenstraße 43, 10115 Berlin, Germany,
Tel: +49 (0)30-20938703, peter.giere@museum.hu-berlin.de

Glaubrecht, Matthias Museum für Naturkunde, Humboldt-Universität zu Berlin, Invalidenstr. 43, 10115 Berlin, Germany, Tel: +49 (0)30-20938504, matthias.glaubrecht@museum.hu-berlin.de

Göbbeler, Katrin Institute for Ecology, Evolution & Diversity - Phylogeny and Systematics, J. W. Goethe-University, Siesmayerstr. 70, 60054 Frankfurt am Main, Germany,
Tel: +49 (0)69-79824702, goebbeler@bio.uni-frankfurt.de

Goldberg, Julia Allan Wilson Centre for Molecular Ecology and Evolution, Institute of Molecular Biosciences, Massey University, Private Bag 11-222, Palmerston North, New Zealand,
Tel: +64 63569099 ext. 2574, J.Goldberg@massey.ac.nz

Gonzalez, Javier Institut für Pharmazie und Molekulare Biotechnologie, Abteilung Biologie, Im Neuenheimer Feld 364, 69120 Heidelberg, Germany, Tel: +49 (0)6221-327416, javier.gonzalez@urz.uni-heidelberg.de

Gonzalez Bravo, Ignacio Experimental Molecular Evolution, Institute for Evolution and Biodiversity. Westfaelische-Wilhelms Universitaet Muenster, Huefferstrasse 1, 48143 Muenster, Germany, Tel: +49 251-8321637, igbravo@uni-muenster.de

Gottschling, Marc Charité – Universitätsmedizin Berlin, Hauttumorcentrum, Charitéplatz 1, 10117 Berlin, Germany, Tel: +49 (0)30-450518339, Marc.Gottschling@charite.de

Gottwald, Jochen Hartmansweilerweg 18, 14163 Berlin, Germany, Tel: +49 (0)30-80496948, djgottwald@t-online.de

Gradstein, Claritza International Office, Faculty of Biology, University of Göttingen, Untere Karspüle 1a, 37073 Göttingen, Germany, Tel: +49 (0)551-395753, cgradst@gwdg.de

Gradstein, Robbert Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany,
Tel: +49 (0)551-392229, sgradst@uni-goettingen.de

Groeninckx, Inge Catholic University of Leuven (K.U.Leuven), Institute of Botany and Microbiology, Laboratory of Plant Systematics, Kasteelpark Arenberg 31, PO Box 2437, BE-3001 Leuven, Belgium, Tel: +32 16321535, inge.groeninckx@bio.kuleuven.be

Gruhl, Alexander FU Berlin, AG Evolution und Systematik der Tiere, Königin-Luise-Str. 1-3, 14195 Berlin, Germany, Tel: +49 (0)30-83854895, agruhl@zoosyst-berlin.de

Güntsch, Anton Botanic Garden and Botanical Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Str. 6-8, 14195, Berlin, Germany, Tel: +49 (0)30-83850166, a.guentsch@bgbm.org

Guicking, Daniela University of Kassel, Systematics and Morphology of Plants, Institute of Biology, Heinrich-Plett-Str. 40, 34132 Kassel, Germany, Tel: +49 (0)561-4084322, guicking@uni-kassel.de

Gurushidze, Maia Leibniz Institute of Plant Genetics and Crop Research (IPK), Department of Taxonomy and Evolutionary Biology, 06466 Gatersleben, Germany, Tel: +49 (0)39482-5268, maiko@ipk-gatersleben.de

Hamacher, Kay AG Bioinformatics and Theoretical Biology, Technische Universität Darmstadt, Schnittspahnstr. 10, 64287 Darmstadt, Germany, kay.hamacher@gmail.com

Hameister, Steffen Universität Osnabrück, Barbarastr. 11, 49076 Osnabrück, Germany, Tel: +49 (0)541-9692839, Hameister@biologie.uni-osnabrueck.de

Händeler, Katharina Institut für Evolutionsbiologie, Rheinische Friedrich-Wilhelms-Universität Bonn, An der Immenburg 1, 53121 Bonn, Germany, Tel: +49 (0)228-735751, uzsamk@uni-bonn.de

Haouala, Rabiaa Higher Institute of Biotechnology of Monastir, Av. Tahar Haddad, BP. 74 – 5000 – Monastir, Tunisia, Tel: +216 734654054, rabiahaouala@yahoo.fr

Haug, Carolin Work Group Biosystematic Documentation, University of Ulm, Helmholtzstr. 20, 89081 Ulm, Germany, Tel: 49 731-5031008, carolin.haug@uni-ulm.de

Haug, Joachim T. Work Group Biosystematic Documentation, University of Ulm Helmholtzstr. 20, 89081 Ulm, Germany, Tel: +49 731-5031008, joachim.haug@uni-ulm.de

Hausdorf, Bernhard Zoologisches Museum der Universität Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg Germany, Tel: 49 (0)404-28382284, hausdorf@zoologie.uni-hamburg.de

Hausen, Harald Institut für Zoologie, Systematik und Evolution der Tiere, FU Berlin, Königin-Luise Str. 1-3, 14195, Berlin, Germany, Tel: +49 (0)30-83854884, hhausen@zoosyst-berlin.de

Häusler, Darius Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie, Universität Göttingen Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395451, suirad@surfeu.de

Heinrich, Michael Centre for Pharmacognosy and Phytotherapy, University of London School of Pharmacy, 29-39 Brunswick Sq., London WC1N 1AX, UK, United Kingdom, Tel: +44 20-77535844, Michael.heinrich@pharmacy.ac.uk

Heinrichs, Jochen Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-392220, jheinri@uni-goettingen.de

Helmkampf, Martin Biocenter and Zoological Museum of the University of Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany, Tel: +49 (0)40-42818397, helmkampf@bni-hamburg.de

Henning, Tilo Systematische Botanik und Pflanzengeographie, Freie Universität Berlin, Altensteinstr. 6 14195 Berlin, Germany, Tel: +49 (0)30-51658800, HenningTilo@web.de

Hentschel, Jörn Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-395716, jhentsc@gwdg.de

Herrmann, Matthias Max Planck Institute for Developmental Biology, Spemannstr. 37-39, 72076 Tübingen, Germany, Tel: +49 (0)7071-601484, matthias.herrmann@tuebingen.mpg.de

Heß, Martin BioZentrum - AG Prof. Haszprunar, Ludwig-Maximilians-Universität München, Großhadernerstraße 2, 82152 Planegg, Germany, Tel: +49 (0)89-218074-130 / 185, hess@zi.biologie.uni-muenchen.de

Hesse, Bettina Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum Erbertstraße 1, 07743 Jena, Germany, Tel: +49 (0)3641-949154, bettina.hesse@uni-jena.de

Hilger, Hartmut H. Systematische Botanik und Pflanzengeographie, Freie Universität Berlin, Altensteinstr. 6 14195 Berlin, Germany, Tel: +49 (0)30-83856512, hartmut.hilger@fu-berlin.de

Himmelreich, Sven Universität Regensburg, Institut für Botanik, Universitätsstraße 31, 93053 Regensburg, Germany, Tel: +49 (0)941 9433128, sven.himmelreich@biologie.uni-regensburg.de

Hochkirch, Axel University of Osnabrück, Department of Biology/Chemistry, Ecology Group, Barbarastr. 11, 49069 Osnabrück, Germany, Tel: +49 (0)541-9692854, hochkirch@biologie.uni-osnabrueck.de

Hoenemann, Mario University of Veterinary Medicine Hannover, Buenteweg 17d, 30559 Hannover, Germany, Tel: +49 (0)511 9538887, mario.hoenemann@tiho-hannover.de

Hoffmann, Matthias H. Martin Luther University Halle-Wittenberg, Institute of Biology, Geobotany and Botanical Gardens, Am Kirchtor 3, 06108 Halle, Germany, Tel: +49 (0)345-5526229, matthias.hoffmann@botanik.uni-halle.de

Hoffmann, Jana Museum für Naturkunde der Humboldt-Universität zu Berlin, Invalidenstraße 43, 10115 Berlin, Germany, Tel: +49 (0)30-20938511, jana.hoffmann@museum.hu-berlin.de

Hohagen, Jennifer University of Veterinary Medicine Hannover, Richard-Wagner-Strasse 1, 30177 Hannover, Germany, Tel: +49 (0)511-2618989 jennyhoh@gmx.de

Holetschek, Jörg Botanischer Garten und Botanisches Museum Berlin-Dahlem (BGBM), Zentraleinrichtung der Freien Universität Berlin, Königin-Luise-Str. 6-8, 14195 Berlin, Germany, Tel: +49 (0)30-83850150, j.holetschek@bgbm.org

Holstein, Norbert Ludwig-Maximilians-Universität München, Institut für Systematische Botanik, Menzinger Str. 67, 80638 München, Germany, Tel: +49 (0)89-17861251, holstein@lrz.uni-muenchen.de

Hörandl, Elvira Department of Systematic and Evolutionary Botany, Faculty Center of Botany, University of Vienna, Rennweg 14, 1030 Vienna, Austria, Tel: +43 (0)1-427754044, elvira.hoerandl@univie.ac.at

Horner, Harry Iowa State University, 3A Bessey Hall, Department of Genetics, Development and Cell Biology & Microscopy and NanoImaging Facility, USA, Tel: +1 5152948635, hth@iastate.edu

Hörnschemeyer, Thomas Univ. Göttingen, Inst. f. Zoologie & Anthropologie, Abt. Morphologie & Systematik, Berliner Str. 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395566, thoerns@gwdg.de

Hubweber, Lasse Zoologisches Forschungsmuseum Alexander Koenig (ZFMK), Adenauerallee 160, 53113 Bonn, Germany, Tel: +49 (0)228-9122342, L.hubweber.zfmk@uni-bonn.de

Hülsken, Thomas Lehrstuhl für Biochemie I – Rezeptorbiochemie, Fakultät für Chemie und Biochemie, Gebäude NC Etage 6 Room 131, Universitätsstraße 150, 44780 Bochum , Germany, Tel: +49 (0)234-3227496, thomas.huelsken@rub.de

Humphreys, Aelys Institute for Systematic Botany, Zollikerstrasse 107, 8008 Zurich, Switzerland, Tel: +41 (0)44-6348351, Aelys.humphreys@systbot.uzh.ch

Hünefeld, Frank Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Entomology Group, Friedrich-Schiller-Universität Jena, Erbertstr. 1, 07743 Jena, Germany, Tel: +49 (0)3641-949149, Frank.Huenefeld@uni-jena.de

Hundsdörfer, Anna Museum für Tierkunde, Staatliche Naturhistorische Sammlungen Dresden, Königsbrücker Landstr. 159, 01109 Dresden, Germany, Tel: +49 (0)351-8926301, anna.hundsdoerfer@snsd.smwk.sachsen.de

Hunger, Marcel Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie, Universität Göttingen, Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395451, Marcel.Hunger@gmx.de

Husemann, Martin University of Osnabrück, Am Kalkhügel 16, 49080 Osnabrück, Germany, martinhusemann@yahoo.de

Jabbarpour, Saeedeh Islamic Azad University of Damghan, Km3 jade makhsose Karaj, shahrake farhangiyane gharb, block 108 unit 6, Tehran, Iran, Tel: +98 9122351260, S.Jabbarpour@gmail.com

Jäckel, Regina Biozentrum Grindel, Universität Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany, Tel: +49 (0)40-428383877, regina-jaeckel@onlinehome.de

Jacobs, Bart Laboratory of Plant Systematics, Universiteit Leuven, Kasteelpark Arenberg 31, 3001 Leuven, Belgium, Tel: +32 16321539, bart.jacobs@bio.kuleuven.be

Jahn, Regine Botanischer Garten und Botanisches Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Str. 6-8, 14195 Berlin, Germany, Tel: +49 (0)30-83859142, r.jahn@bgbm.org

Jaime Bueno, Rafael Universidad de Jaén. Facultad de Ciencias Experimentales. Dpto. Biología Animal, Biología Vegetal y Ecologia Paraje Las Lagunillas s/n Jaén (Jaén) C.P.: 23071, Spain, Tel: +34 953213057, rjaime@ujaen.es

Jakob, Sabine S. Leibniz Institute of Plant Genetics and Crop Science (IPK), Department of Taxonomy and Evolutionary Biology, Corrensstr. 3, 06466 Gatersleben, Germany, Tel: +49 (0)39482-5273, jakob@ipk-gatersleben.de

Janussen, Dorte Forschungsinstitut und Museum Senckenberg, Senckenberganlage 25, 60325 Frankfurt am Main, Germany, dorte.janussen@senckenberg.de

Janssen, Thomas Forschungsinstitut Senckenberg, Abt. Botanik u. molekulare Evolutionsforschung, Senckenberganlage 25, 60325 Frankfurt, Germany, Tel: +49 (0)69-970751614, thomas.janssen@senckenberg.de

Jaramillo, M. Alejandra University of Missouri-Columbia, Div. Biological Sicences, Div. Biological Sicences, 109 Tucker Hall, Columbia, MO 65203, USA, United States, Tel: +1 573-8828514, jaramilloa@missouri.edu

Jerominek, Markus Spezielle Botanik, Johannes Gutenberg Universität Mainz, Spezielle Botanik, Johannes Gutenberg Universität Mainz Bentzelweg 9a, 55099, Germany, Tel: +49 (0)6131-3924279, markus@jerominek.com

Joger, Klaus-Ulrich Staatliches Naturhistorisches Museum, Pockelsstr. 10, 38106 Braunschweig, Germany, Ulrich.joger@snhm.niedersachsen.de

Jonas, Rayko Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany

Jordon-Thaden, Ingrid University of Heidelberg, Heidelberg Institute of Plant Sciences, Dept 1: Biodiversity and Systematics, Im Neuenheimer Feld 345, 69120 Heidelberg, Germany, Tel: +49 (0)6221-544619, ijordonthaden@hip.uni-heidelberg.de

Kadereit, Joachim W. Institut für Spezielle Botanik und Botanischer Garten der Johannes-Gutenberg-Universität Mainz, 55099 Mainz, Germany, Tel: +49 (0)6131-3923755, Kadereit@uni-mainz.de

Kärnefelt, Ingvar The Biological museums, Östra Vallgatan 18, S-223 61 Lund, Sweden, Tel: +46 462229558, Ingvar.Karnefelt@botmus.lu.se

Karnkowska, Anna University of Warsaw, Department of Plant Systematics and Geography, Department of Plant Systematics and Geography, University of Warsaw, Al. Ujazdowskie 4, PL-00-478 Warszawa, Poland, Tel: +48 (0)22-5530552, ankarn@biol.uw.edu.pl

Kasperek, Gerwin University Library Frankfurt am Main, Bockenheimer Landstr. 134-138, 60325 Frankfurt am Main, Germany, Tel: +49 (0)69-79839365, g.kasperek@ub.uni-frankfurt.de

Kattari, Stefan G. LMU München, Department Biologie I, Systematische Botanik, Menzinger Straße 67, 80638 München, Germany, Tel: +49 (0)89-17861199, kattari@lrz.uni-muenchen.de

Kauff, Frank TU Kaiserslautern, FB Biologie, Abt. Molekulare Phylogenetik, Postfach 3049, 67653 Kaiserslautern, Germany, Tel: +49 (0)631-2052562, fkauff@biologie.uni-kl.de

Kazandjian S., Aniuska A. Simón Bolívar University, Departamento de Biología de Organismos, Sartenejas, Estado Miranda 89000, Venezuela, Te: +58 2129063076, akazandj@usb.ve

Kazemi, Nooreini Marzie Tarbiat Modares University, 14115-175, department of Plant Biology, Faculty of Basic sciences, Tarbiat Modares University, Jalale ale Ahmad highway, Tehran, Iran, Tel: +98 9124185042, marziekazemi@yahoo.com

Kelbert, Patricia Botanic Garden and Botanical Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Str. 6-8, 14195 Berlin, Germany, Tel: +49 (0)30-83850150, p.kelbert@bgbm.org

Kellner, Alexandra Institut für Allgemeine Botanik und Pflanzenphysiologie, AG Spezielle Botanik, Justus-Liebig-Universität Gießen, Senckenbergstr. 17, 35390 Gießen, Germany, Tel: +49 (0)641-9935136, Alexandra.Kellner@bot1.bio.uni-giessen.de

Kessler, Michael Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-395726, mkessle2@uni-goettingen.de

Kiefer, Christiane Universität Heidelberg, Heidelberg Institute of Plant Science, Department I, Biodiversity and Systematics, Im Neuenheimer Feld 345, 69120 Heidelberg, Germany, Tel: +49 (0)6221-544618, ckiefer@hip.uni-heidelberg.de

Kieneke, Alexander Institut für Biologie und Umweltwissenschaften, Carl von Ossietzky Universität Oldenburg, 26111 Oldenburg, Germany, Tel: +49 (0)441-798 3373, akieneke@senckenberg.de

Kilian, Benjamin Max Planck Institute for Plant Breeding Research, Department of Plant Breeding and Genetics, Carl-von-Linné-Weg 10, 50829 Köln, Germany, Tel: +49 (0)221-5062405, kilian@mpiz-koeln.mpg.de

Kilpert, Fabian Freie Universität Berlin, Institut für Biologie, Chemie, Pharmazie – Zoologie, Königin-Luise Straße 1 – 3, 14195 Berlin, Germany, Tel: +49 (0)30-83853915, fkil@zedat.fu-berlin.de

Klatt, Simone Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-395757, sklatt@uni-goettingen.de

Kleinteich, Thomas Universität Hamburg, Biozentrum Grindel und Zoologisches Museum, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany, Tel: +49 (0)40-428382283, thomas.kleinteich@uni-hamburg.de

Klöpfel, Anja Georg-August-Universität, Göttingen, Johann-Friedrich-Blumenbach-Institut für Zoologie und Anthropologie, Berliner Str. 28, 37073 Göttingen, Germany, Tel: +49 (0)551-392135, AKloepfel@web.de

Klug, Rebecca Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie, Universität Göttingen, Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395517, rklug@gwdg.de

Knebelsberger, Thomas Zoologische Staatssammlung München, Münchhausenstraße 21, 81247 München, Germany, Tel: +49 (0)89-8107124, knebelsberger@zsm.mwn.de

Koch, André Zoologisches Forschungsmueum Alexander Koenig, Bonn, Adenauerallee 160, 53113 Bonn, Germany, Tel: +49 (0)228-9122277, andrepascalkoch@web.de

Koch, Marcus Universität Heidelberg, Heidelberger Institut für Pflanzenwissenschaften, Biodiversität and Pflanzensystematik, Im Neuenheimer Feld 345, 69120 Heidelberg, Germany, mkoch@hip.uni-hd.de

Koch, Markus Institut für Biologie, Freie Universität Berlin, Königin-Luise-Str. 1-3, 14195 Berlin, Germany, Tel: +49 (0)30-83854893, mkoch@zoosyst-berlin.de

Koenemann, Stefan Institute for Animal Ecology and Cell Biology, University of Veterinary Medicine, Hannover, Büntgeweg 17d, 30559 Hannover, Germany, Tel: +49 (0)511-9538881, stefan.koenemann@tiho-hannover.de

Kohlbecker, Andreas Botanic Garden and Botanical Museum Berlin-Dahlem, Freie Universität Berlin, Königin-Luise-Str. 6-8, 14195 Berlin, Germany, Tel: +49 (0)30-83850292, a.kohlbecker@bgbm.org

Konstantinova, Nadezhda Polar-Alpine Botanical Garden-Institute of Kola SC RAS, Murmansk Prov., Kirovsk-6, Polar-alpine Botanical Garden, Laboratory of flora, Russia, Tel: +7 8153152340, nadya50@list.ru

Krak, Karol Institute of Botany, Academy of Sciences of the Cech Republik, Lesni 322, 252 43 Pruhonice, Czech Republic, Tel: +420 271015472, krak@ibot.cas.cz

Kramina, Tatiana Lomonosov Moscow State University, Higher Plants Department, Biological Faculty, Lomonosov Moscow State University, Leninskiye Gory, Moscow, 119991, Russia, Tel: +495 9391603, tkramina@yandex.ru

Krause, Stefanie Museum für Naturkunde der Humboldt-Universität zu Berlin, Invalidenstr. 43, 10115 Berlin, Germany, Tel: +49 (0)30-20938507, stefanie.krause@museum.hu-berlin.de

Kreier, Hans-Peter Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-395734, hkreier@uni-goettingen.de

Kremer, Philipp University of Heidelberg, Im Neuenheimer Feld 230, 69120 Heidelberg, Germany, Tel: +49 (0)6221-545659, Philipp.Kremer@urz.uni-hd.de

Kriegs, Jan Ole Institute of Experimental Pathology, University of Münster, Von-Esmarch-Str. 56, 48149 Münster, Germany, Tel: +49 (0)251-8352132, kriegs@uni-muenster.de

Kropf, Matthias Institute of Botany, University of Natural Resources and Applied Life Sciences, Vienna, Gregor Mendel-Str. 33, 1180 Vienna, Austria, Tel: +43 (0)47654-3156, matthias.kropf@boku.ac.at

Krüger, Jan Michael Universität Bonn, Endenicher Strasse 349, 53121 Bonn, Germany, Tel: +49 (0)228-6206739, janferious@gmx.de

Kück, Patrick Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany, patrick_kueck@web.de

Kücüködük, Mustafa Biology Department, Faculty of Art and Science, Selcuk University, 42031, Campus Konya, Turkey, Tel: +90 3322231879, mkucukoduk@selcuk.edu.tr

Kusber, Wolf-Henning Botanischer Garten und Botanisches Museum Berlin-Dahlem, ZE Freie Universität Berlin, Königin-Luise-Str. 6-8, Germany, Tel: +49 (0)30-83850177, w.h.kusber@bgbm.org

Lambertz, Markus Endenicher Allee 146, 53121 Bonn, Germany, Tel: +49 (0)176-21182412, lambertz@uni-bonn.de

Laschke, Corinna Department of Botany, University of Osnabrück, Barbarastr.11, 49076 Osnabrück, Germany, Tel: +49 (0)541-9692839, Laschke@biologie.uni-osnabrueck.de

Lázaro Iglesias, Eva Universitat de Barcelona, Facultat de Biologia, Dept. de Genètica, Av. Diagonal, 645, 08028 Barcelona, Spain, Tel: +34 934021647, evalazaro@ub.edu

Lehnert, Markus Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-3919364, mlehner1@uni-goettingen.de

Lenz, Sabine Botanic Garden and Botanical Museum Berlin-Dahlem (BGBM)/ FU Berlin, Königin- Luise-Str. 6-8, 14195 Berlin, Germany, Tel: +49 (0)30-83850151, s.lenz@bgbm.org

Letsch, Harald Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany, Tel: +49 (0)228-9122353, hletsch@freenet.de

Ley, Alexandra Institut für Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Schulstr. 47, 55124 Mainz, Germany, Tel: +49 (0)6131-3922877, aley@uni-mainz.de

Liede-Schumann, Sigrid Universität Bayreuth, 95440 Bayreuth, Germany, Tel: +49 (0)921-552460, sigrid.liede@uni-bayreuth.de

Lihová, Judita Institute of Botany, Slovak Academy of Sciences, Dúbravská cesta 14, 845 23 Bratislava, Slovak Republic, Tel: +421 259426148, judita.lihova@savba.sk

Linares-Palomino, Reynaldo Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, s460192@stud.uni-goettingen.de

Linder, Hans Peter University of Zurich, Institute of Systematic Botany, Zollikerstrasse 107, 8008 Zurich, Switzerland, Tel: +41 (0)44-6348410, plinder@systbot.uzh.ch

Ling, Chen National Natural Science Foundation of China, Department of Life Sciences, 83 Shuangqing Road, Haidian Beijing 100085, P. R. China, Tel: +86 01062326914, chenling@mail.nsfc.gov.cn

Liu, Yu Work Group Biosystematic Documentation, University of Ulm, Helmholtzstr. 20, 89081 Ulm, Germany, Tel: +49 (0)731 5031006, yu.liu@uni-ulm.de

Lo Presti, Rosa Maria Institute of Botany, University of Regensburg, Universitätsstr. 31, 93053 Regensburg, Germany, Tel: +49 (0)941-9433128, rosa-maria.lo-presti@biologie.uni-regensburg.de

Lohrmann, Volker Museum für Naturkunde der Humboldt-Universität zu Berlin, [c/o Michael Ohl], Invalidenstr. 43, 10115 Berlin, Germany, Tel: +49 (0)30-20938507, volker.lohrmann@smnk.de

Lohwasser, Ulrike Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), Abt. Genbank, Corrensstrasse 3, 06466 Gatersleben, Germany, Tel: +49 (0)39482-5282, lohwasse@ipk-gatersleben.de

López Sepulveda, Patricio Department of Systematic and Evolutionary Botany, Faculty Center of Botany, University of Vienna, Rennweg 14, 1030 Vienna, Austria, Tel: +43 (0)1-427754141, plopez@udec.cl

Lotfalizadeh, Hosseinali Department of Insect Taxonomy, Iranian Research Institute of Plant Protection, P. O. Box 19395-1454, Tehran, Iran, Tel: +98 9143923685, hlotfalizadeh2001@yahoo.com

Luebert, Federico Institut für Biologie der Freien Universität Berlin - Systematische Botanik und Pflanzengeographie, Altensteinstraße 6, 14195 Berlin, Germany, Tel: +49 (0)30-83856645, fluebert@zedat.fu-berlin.de

Lüter, Carsten Museum für Naturkunde der Humboldt-Universität zu Berlin, Invalidenstraße 43, 10115 Berlin, Germany, Tel: +49 (0)30-20938529, carsten.lueter@museum.hu-berlin.de

Maas, Andreas Work Group Biosystematic Documentation, University of Ulm, Helmholtzstr. 20, 89081 Ulm, Germany, Tel: +49 (0)731-5031002, andreas.maas@uni-ulm.de

Mahelka, Václav Institute of Botany, Academy of Sciences of the Czech Republic, Zámek 1, 252 43, Průhonice, Czech Republic, mahelka@ibot.cas.cz

Mahfoud, Hafez Technische Universität Dresden, Institut für Botanik, Zellescher Weg 20b, 01062 Dresden, Germany, Tel: +49 (0)176-23915745, hafezmahfoud@yahoo.com

Mahr, Friederike Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany

Marhold, Karol Institute of Botany, Slovak Academy of Sciences, Dúbravská cesta 14, 845 23 Bratislava, Slovak Republic, Tel: +421 259426128, karol.marhold@savba.sk

Martin, Esra Selçuk University, Education Faculty, Biology Department, 42090 Meram, Konya, Turkey, Tel: +90 3323238220216, esramartin@gmail.com

Masoudian, Nahid Islamic azad university, Science and Research branch, Semnan province, Damghan, Islamic Azad university of Damghan, Department of Biology, postal code: 36716-39998, Iran, Tel: +98 2325237836, nahidmasoudian@yahoo.com

Mathieu, Guido Ghent University, K.L. Ledeganckstraat 35, 9000 GENT, Belgium, guido.mathieu@taxa.be

Mayland-Quellhorst, Eike Justus-Liebig-Universtität Giessen, Senkenbergstr. 19, 35390 Giessen, Germany, Tel: +49 (0)641-9935136, Eike.Mayland-Quellhorst@bot1.bio.uni-giessen.de

Mazooji, Ali Islamic Azad University- Rodehen Branch, No 29.2, Kajabadi St., Africa Ave., Tehran, Iran, Tel: +98 2122412500, amazooji@yahoo.com

Metzing, Detlev AG Biodoversität & Evolution der Pflanzen, Fak. V: IBU, Botanischer Garten, Universität Oldenburg, Philosophenweg 39, 26121 Oldenburg, Germany,
Tel: +49 (0)441-777654, detlev.metzing@uni-oldenburg.de

Meusemann, Karen Zoologisches Forschungsmuseum Alexander Koenig (ZFMK), Adenauerallee 160, 53113 Bonn, Germany, Tel: +49 (0)228-9122351, mail@karen-meusemann.de

Meve, Ulrich Dept. of Plant Systematics, University of Bayreuth, Universitätsstr. 30, 95440 Bayreuth, Germany, Tel: +49 (0)921-552452, ulrich.meve@uni-bayreuth.de

Meyer, Achim Institut für Zoologie, Johannes Gutenberg Universität, Müllerweg 6, 55128 Mainz, Germany, Tel: +49 (0)6131-3924654, meyera@uni-mainz.de

Meyer, Axel Lehrstuhl für Zoologie und Evolutionsbiologie, Universität Konstanz, Universitätsstr. 10, 78457 Konstanz, Germany, axel.meyer@uni-konstanz.de

Mika, Irma Forstwissenschaften, Georg-August-Universität Göttingen, Valentinsbreite 5, 37077 Göttingen, Germany, Tel: +49 (0)551-3072632, irmamika@aol.com

Mohr, Oliver Systematische Botanik und Pflanzengeographie, Freie Universität Berlin, Altensteinstr. 6, 14195 Berlin, Germany, Tel: +49 (0)30-83853159, more@zedat.fu-berlin.de

Moon, Hye-Kyoung Institute of Botany and Microbiology, K.U.Leuven, Laboratory of Plant Systematics, Kasteelpark Arenberg 31, P. O. Box 2437, 3001 Leuven, Belgium,
Tel: +32 16321535, hyekyoung.moon@bio.kuleuven.be

Morrison, David SWEPAR, Swedish University of Agricultural Sciences, Uppsala, Sweden, david.morrison@vmm.slu.se

Mosel, Silke Museum of Natural History Berlin, Department of Research, Invalidenstrasse 43, 10115 Berlin, Germany, Tel: +49 (0)30-20938614, silke.mosel@museum.hu-berlin.de

Mostafavi, Golaleh Islamic Azad University, 2045, Sobhan L Tower, Mirzapour Ave., Shariati St. Tehran, Iran, Tel: +98 (0)21 22681516, golaleh_m@hotmail.com

Mühlhausen, Andreas Universität Osnabrück, Botanik, Barbarastr.11, 49069 Osnabrück, Germany, Tel: +49 (0)541-9692838, andreas.muehlhausen@biologie.uni-osnabrueck.de

Müller, Kai Nees Institute for Biodiversity of Plants, University of Bonn, Meckenheimer Allee 170, 53115 Bonn, Germany, Tel: +49 (0)228-732683, kaimueller@uni-bonn.de

Mwinyi, Adina Freie Universität Berlin, Institut für Biologie (Zoologie), Königin-Luise-Straße 1-3, 14195 Berlin, Germany, +49 (0)30 838 569 95, adina.mwinyi@gmx.de

Naderpour, Mohammad Islamic Azad University of Damghan, Semnan province, Damghan, Department of Biology, postal code: 36716-39998, Iran, Tel: +98 (0)232-5237836, mohammad-naderpoor@yahoo.com

Nakonechnaya, Olga Institute of Biology and Soil Science, Far Eastern Branch Russian Academy of Sciences, IBSS, 159 Prospect Stoletiya, Vladivostok, 690022, Russia, Tel: +7 4232312129, markelova@biosoil.ru

Nebel, Martin State Museum of Natural History Stuttgart Rosenstein 1, 70191 Stuttgart, Germany, Tel: +49 (0)711-8936208, nebel.smns@naturkundemuseum-bw.de

Neinhuis, Christoph Technische Universität Dresden Helmholtzstr. 10, 01069 Dresden, Germany, Tel: +49 (0)351 46336032, christoph.neinhuis@tu-dresden.de

Nevill, Paul University of Melbourne, 25 Blanche Parade Mt Macedon Victoria, 3441, Australia, Tel: +61 (0)3-54263211, p.nevill@pgrad.unimelb.edu.au

Nguyen, Phi Nga Department of Forest Genetics and Forest Tree Breeding, Büsgenweg 2, 37077 Göttingen, Germany, Tel: +49 (0)551-399522, ngacuc1974@yahoo.com

Normann, Felix Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-3810525, FelixNormann@googlemail.com

Nürk, Nicolai M. Leibniz Institute of Plant Genetics and Crop Research (IPK), Department of Taxonomy and Evolutionary Biology, 06466 Gatersleben, Germany, Tel: +49 (0)39482-5730, nuerk@ipk-gatersleben.de

Nuroniah, Hani Sitti Departments of Forest Genetics and Forest Tree Breeding, Büsgen Institute, Georg-August University of Göttingen, Büsgenweg 2, 37077 Göttingen, Germany, Tel: +49 (0)551-393539, hnuroni@gwdg.de

Oelschlägel, Birgit Technische Universität Dresden, Plant Phylogenetics & Phylogenomics Group, TU Dresden, Institut für Botanik, 01062 Dresden, Germany, Tel: +49 (0)351-46336032, b.oelschlaegel@gmx.de

Ogunwenmo, Kayode Babcock University, Ilishan-Remo, PMB 21244, Ikeja, Lagos 100 001, Nigeria, Tel: +234 7033149933, ogunwenmo@yahoo.com

Ohl, Michael Museum für Naturkunde der Humboldt-Universität zu Berlin, Invalidenstraße 43, 10115 Berlin, Germany, Tel: +49 (0)30-20938507, michael.ohl@museum.hu-berlin.de

Olsson, Sanna Technische Universität Dresden, TUD, Institut für Botanik, 01062 Dresden, Germany, Tel: +49 (0)1520-3600341, sanna.olsson@helsinki.fi

Oltmann, Gabriele Institut für Paläontologie, Universität Bonn, Nussallee 8, 53115 Bonn, Germany, Tel: +49 (0)228-734843, goltmann@uni-bonn.de

Osterholz, Martin German Primate Center, Kellnerweg 4, 37077 Göttingen, Germany, Tel: +49 (0)551-3851110, mosterh@gwdg.de

Othman, A. Sofiman Universiti Sains Malaysia, School of Biological Sciences, Universiti Sains Malaysia, 11800 Penang, Malaysia, Tel: +60 46433888 4019/3905/3503, sofiman@usm.my

Oyama, Ryan Ludwig-Maximilians University, Menzinger Str. 67, 80638 München, Germany, Tel: +49 (0)89-17861194, royama@lrz.uni-muenchen.de

Oyelana, Olatunji Babcock University, Ilishan-Remo, PMB 21244, Ikeja, Lagos 100 001, Nigeria, Tel: +234 8055213933, oyelana2@yahoo.com

Öztürk, Meryem Selçuk University, Education Faculty, Biology Department, 42090 Meram, Konya, Turkey, Tel: +90 3323238220225, mrym_ztrk@yahoo.com

Paetsch, Ricarda Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany

Papenbrock, Jutta Universität Hannover, Institut für Botanik, Herrenhäuserstr. 2, 30419 Hannover, Germany, Tel: 49 (0)511-7623788, Jutta.Papenbrock@botanik.uni-hannover.de

Paule, Juraj Heidelberg Institute of Plant Science, Abteilung 1, Im Neuenheimer Feld 345, 69120 Heidelberg, Germany, Tel: +49 (0)6221-544619, jpaule@hip.uni-heidelberg.de

Paun, Ovidiu Jodrell Laboratory, Royal Botanic Gardens Kew, Richmond TW9 3AB, United Kingdom, Tel: +44 208-3325378, O.Paun@kew.org

Perseke, Marleen Universität Leipzig, Fakultät für Biowissenschaften, Pharmazie und Psychologie, Institut Biologie II, AG Molekulare Evolution & Systematik der Tiere, Talstraße 33, 04103 Leipzig, Germany, Tel: +49 (0)341-9736743, perseke@rz.uni-Leipzig.de

Peters, Jule University of Kassel, Abt. Morphologie & Systematik der Pflanzen Heinrich-Plett-Str. 40, 34132 Kassel, Germany, Tel: +49 (0)561-8044204, jule-peters@gmx.de

Pick, Kerstin Courant Research Center Geobiology, Geoscience Center Göttingen, Georg-August-Universität Göttingen, Goldschmidtstr.3, 37077 Göttingen, Germany,
Tel: +49 (0)551-397903, kpick@gwdg.de

Pihu, Silvia University of Tartu, Institute of Ecology and Earth Sciences, Lai 40, 51005, Tartu, Estonia, Tel: +372 7376258, silvia.pihu@ut.ee

Pirie, Michael D. Institute for Systematic Botany, University of Zurich, Zollikerstrasse 107, 8008 Zurich, Switzerland, Tel: +41 (0)44-6348430, michael.pirie@systbot.uzh.ch

Pleines, Thekla Leibniz-Institut für Pflanzengenetik und Kulturpflanzenforschung (IPK), Corrensstraße 3, 06466 Gatersleben, Germany, Tel: +49 (0)39482-5269, pleines@ipk-gatersleben.de

Podlacha, Kathrin Museum für Naturkunde der Humboldt-Universität zu Berlin, Invalidenstraße 43, 10115 Berlin, Germany, Tel: +49 (0)30-20938488, kathrin.podlacha@museum.hu-berlin.de

Podsiadlowski, Lars Freie Universität Berlin, Inst. Für Biologie / Zoologie, Königin-Luise Straße 1 – 3, 14195 Berlin, Germany, Tel: +49 (0)30-83854692, podsi.lars@t-online.de

Pohl, Hans Institut für Spezielle Zoologie und Evolutionsbiologie mit PhyletischemMuseum, Friedrich-Schiller-Universität Jena, Erbertstrasse 1, 07743 Jena, Germany, hans.pohl@uni-jena.de

Preisfeld, Gela Bergische Universität Wuppertal, Fachbereich C Biologie, Gaussstr. 20, 42097 Wuppertal, Germany, Tel: +49 (0)202-4392815, apreis@uni-wuppertal.de

Prinz, Kathleen Universität Kassel, Universität Kassel, FB 18 Systematik und Morphologie der Pflanzen Heinrich-Plett-Straße 40, 34132 Kassel, Germany , Tel: +49 (0)561-8044322, kathleenprinz@freenet.de

Purschke, Günter Universität Osnabrück, Fachbereich Biologie/Chemie, Zoologie, Barbarastrasse 11, 49069 Osnabrück, Germany, Tel: +49 (0)541-9692857, purschke@biologie.uni-osnabrueck.de

Quandt, Dietmar TU Dresden, Institut für Botanik, Plant Phylogenetics and Phylogenomics Group 01062 Dresden Germany, Tel: +49 (0)351-46334070, dietmar.quandt@tu-dresden.de

Rastegar Pouyani, Eskandar Sabzevar University, Iran, Department of Biology, Faculty of science., Teacher Training University of Sabzevar, Sabzevar, P.O.Box. 397, Iran, Tel: +98 5714411040, Eskandar.Rastegar-Pouyani@urz.uni-heidelberg.de, E-rastegar@sttu.ac.ir, Erastegar@yahoo.com

Rastegar-Pouyani, Nasrullah Department of Biology, Faculty of Science, Razi University, 67149 Kermanshah, Iran, Tel: +98 8314274545, nasrullah.r@gmail.com

Raupach, Michael Zoologisches Forschungsmuseum Alexander Koenig, Adenauerallee 160, 53113 Bonn, Germany, Tel: +49 (0)228-9122242, m.raupach.zfmk@uni-bonn.de, michael.raupach@rub.de

Rebernig, Carolina Anna University of Vienna, Department of Systematic and Evolutionary Botany, Rennweg 14, 1030 Vienna, Austria, Tel: +43 (0)1-427754163, carolin.anna.rebernig@univie.ac.at

Reich, Mike Geowissenschaftliches Zentrum der Universität Göttingen, Museum, Sammlungen & Geopark, Goldschmidtstr. 3-5, 37077 Göttingen, Germany, Tel: 49 (0)551-397998, mreich@gwdg.de

Reiner-Drehwald, Maria Elena Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-397861, mreiner@uni-goettingen.de

Renner, Susanne University of Munich, Menzingerstr. 67, Germany, renner@umsl.edu

Renner, Swen State Museum of Natural History Stuttgart, Rosenstein 1, 70191 Stuttgart, Germany, Tel: +49 (0)711-8936172, renner.smns@naturkundemuseum-bw.de

Reuscher, Michael University Heidelberg, Friedensstr. 3, 69198 Schriesheim, Germany, Tel: +49 (0)6203-65797, Michael.Reuscher@gmx.net

Rex, Martina Molecular Systematics, Dept. of Sciences, University of Kassel, Heinrich-Plett-Str. 40, 34132 Kassel, Germany, marta.rex@gmx.de

Richter, Christian Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Neurobiologie, Universität Göttingen, Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-3991186, Richter-Ch@web.de

Ricroch, Agnes University of Orsay, Bat 360. Labo ESE. F-91405 Orsay cedex, France, Tel: +33 169155665, agnes.ricroch@u-psud.fr

Riehl, Torben ZIM, Uni Hamburg, c/o AG Brandt, Biozentrum Grindel, Martin-Luther-King Platz, 20146 Hamburg, Germany, Tel: +49 (0)40-428385642, t.riehl@gmx.de

Riemann, Ole Carl von Ossietzky Universität Oldenburg Institut für Biologie und Umweltwissenschaften (IBU), 26111 Oldenburg, Germany, Tel: +49 (0)441-1817054, o1Riemann@gmx.net

Riutort, Marta Universitat de Barcelona, Dpt. de Genètica. Edifici annex., Av. Diagonal, 645, 08028 Barcelona, Spain, Tel: +34 934035432, onaalvarez@ub.edu

Rodrigues de Moraes, Pedro Universidade Estadual de Feira de Santana, BR116 Km3 Campus Universitário. Feira de Santana - BA, CEP 44031-460, Brazil, Tel: +55 1934272055, pedro.moraes@pq.cnpq.br

Ronse De Craene, Louis Royal Botanic Garden Edinburgh, 20A Inverleith Row, Edinburgh EH3 5LR, United Kingdom, Tel: +44 1312482804, l.ronsedecraene@rbge.ac.uk

Röser, Martin Institut für Biologie, Neuwerk 21, Germany, Tel: +49 (0)345-5526218

Rossina, Valentina Paleontological Institute of Russian Academy of Science, Prophsouznaya str., 123, Moscow, Russia 117997, Russia, Tel: +7 4953398900, ros@paleo.ru

Rothe, Birgen Holger Evolutionsbiologie Abt.2, Fak. Biologie, Universität Bielefeld, Morgenbreede 45, 33615 Bielefeld, Germany, Tel: +49 (0)521-1062820, birgenrothe@lycos.de

Rudolph, Barbara Biocenter Klein Flottbek, Ohnhorststr. 18, 22609 Hamburg, Germany, Tel: +49 (0)40-42816405, b.rudolph@botanik.uni-hamburg.de

Rust, Jes Institute of Palaeontology, University of Bonn, Nussallee 8, 53115 Bonn, Germany, Tel: +49 (0)228-734842, jrust@uni-bonn.de

Sack, Peter Heidelberger Institut für Pflanzenwissenschaften (HIP) Abt.1: Biodiversität und Pflanzensystematik, Im Neuenheimer Feld 345, 69120 Heidelberg, Germany, Tel: +49 (0)6221-544618, psack@hip.uni-heidelberg.de

Saleh, M. Nazre Herbarium, Faculty of Forestry, Universiti Putra Malaysia, Universiti Putra Malaysia, 43400 UPM Serdang, Selangor, Malaysia, Tel: +603 89467196, nazre@putra.upm.edu.my

Salimpour, Fahimeh Islamic Azad University- North Branch of Tehran, No 29.2- Kajabadi St.- Africa Ave., Tehran, Iran, Tel: +98 2122044631, fahimeh48@yahoo.com

Samadi, Leyli Emerging focus, Department of Evolutionary Biology, Faculty of Life Sciences, University of Vienna, Althanstraße 14, 1090 Vienna, Austria, Tel: +43 (0)1-427754453, leili.samadi@univie.ac.at

Samain, Marie-Stephanie Departemeent of Biology, Research Group Spermatophytes, K.L. Ledeganckstaat 35, 9000 Gent, Belgium, Tel: +32 (0)9-2645058, MarieStephanie.Samain@Ugent.be

Şanda, Murad Aydin Selçuk University, Faculty of Arts and Sciences, Department of Biology, Campus, 42075, Selçuklu, Konya, Turkey, Tel: +90 3322231879, maydin@selcuk.edu.tr, muradsanda@gmail.com

Sauer, Jan University Hamburg Zoological Institute & Museum, University Hamburg, Biozentrum Grindel, Marthin-Luther-King Platz 3, 20146 Hamburg, Germany, Tel: +49 (0)40-428383876, Ja_Sa@web.de

Scalone, Romain Institut für Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Bentzelweg 9a, 55099 Mainz, Germany, Tel: +49 (0)6131-3922928, scalone@uni-mainz.de

Schäferhoff, Bastian Nees-Institut für Biodiversität der Pflanzen, Universität Bonn, Meckenheimer Allee 170, 53115 Bonn, Germany, Tel: +49 (0)228-732123, schaeferhoff@uni.bonn.de

Schanzer, Ivan Main Botanical Garden of Russian Ac. Sci, Botanicheskaya Str. 4, 127276 Moscow, Russia, Russia, Tel: +7 4959778444, ischanzer@mail.ru

Schardt, Lavinia Spezielle Botanik, Johannes Gutenberg Universität Mainz, Spezielle Botanik, Johannes Gutenberg Universität Mainz Bentzelweg 9a, 55099 Mainz, Germany, Tel: +49 (0)6131-3924342, Lavinia.Schardt@gmx.de

Scheriau, Charlotte Heidelberg Institute of Plant Sciences, Biodiversity and Plant Systematics, University of Heidelberg, Im Neuenheimer Feld 345, 69120 Heidelberg, Germany, Tel: +49 (0)6221-544618, cscheriau@hip.uni-heidelberg.de

Scheunert, Agnes LMU München, Department Biologie I, Institut für Systematische Botanik, Menzinger Straße 67, 80638 München, Germany, Tel: +49 (0)89-17861199, Agnes.Scheunert@stud.uni-muenchen.de

Schmickl, Roswitha University of Heidelberg, Heidelberg Institute of Plant Science, Department Biodiversity and Plant Systematics, Im Neuenheimer Feld 345, 2nd floor, 69120 Heidelberg, Germany, Tel: +49 (0)6221-544619, rschmickl@hip.uni-heidelberg.de

Schmidt, Marco Forschungsinstitut Senckenberg, Abt. Botanik & molekulare Evolutionsforschung, Forschungsinstitut Senckenberg, Senckenberganlage 25, 60325 Frankfurt am Main, Germany, Tel: +49 (0)69-970751615, marco.schmidt@senckenberg.de

Schmidt, Sabrina Universität Hamburg Biozentrum Klein Flottbek, Ohnhorststr. 18, 22609 Hamburg, Germany, Tel: +49 (0)40-42816399, sabalexaschmidt@yahoo.de

Schmidt-Lebuhn, Alexander Abt. Pflanzenökologie, Institut für Biologie / Geobotanik, Martin-Luther-Universität Halle-Wittenberg, Am Kirchtor 1, 06108 Halle, Germany, Tel: +49 (0)172-4151802, schmidtleb@yahoo.de

Schmidt-Rhaesa, Andreas Zoological Museum Hamburg, Martin-Luther-King-Platz 3, 20146 Hamburg, Germany, Tel: +49 (0)40-428383921, andreas.schmidt-rhaesa@uni-hamburg.de

Schmitz, Jürgen University of Münster, Institute of Experimental Pathology, Von-Esmarch-Str. 56, 48149 Münster, Germany, Tel: +49 (0)251-8352133, jueschm@uni-muenster.de

Schneider, Julia Institut für Biologie, Spezielle Botanik, Martin-Luther-Universität Halle-Wittenberg, Neuwerk 21, 06099 Halle, Germany, Tel: +49 (0)345-5526245, julia.schneider@botanik.uni-halle.de

Schneider, Harald Department of Botany, Natural History Museum, Cromwell Road, London SW7 5BD, United Kingdom, Tel: +44 (0)2079426058, h.schneider@nhm.ac.uk

Schoenwitz, Roswitha Deutsche Forschungsgemeinschaft, Kennedyallee 40, 53175 Bonn, Germany

Schorr, Gertrud Institut für Spezielle Botanik der Johannes Gutenberg-Universität Mainz, (Department of Ecology & Evolution, UNIL Lausanne, CH), Bentzelweg 9a, 55099 Mainz, Germany, Tel: +49 (0)6131-3922928, schorrg@uni-mainz.de

Schulte, Katharina Forschungsinstitut Senckenberg & J.W. Goethe-Universität Frankfurt/M., Senckenberganlage 25. 60325 Frankfurt am Main, Germany, Tel: +49 (0)69-970751184, katharina.schulte@senckenberg.de

Schultze, Hans-Peter Museum für Naturkunde der Humboldt-Universität zu Berlin, Institut für Paläontologie, 10099 Berlin, Germany, hp1937@ku.edu

Schulz, Joana FU-Berlin, Institut für Biologie, Systematische Botanik und Pflanzengeographie, Altensteinstr. 6, 14195 Berlin, Germany, Tel: +49 (0)172-953273, joana.schulz@fu-berlin.de

Schulze, Corinna Institute for Ecology, Evolution and Diversity – Phylogeny and Systematics J.W. Goethe-Universität, Siesmayerstr. 70, 60054 Frankfurt am Main, Germany, Tel: +49 (0)69-79824918, schulze.anderhufe@arcor.de

Schulze, Arne Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie, Universität Göttingen, Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395463, thamnopsis@arcor.de

Schulz-Mirbach, Tanja Ludwig-Maximilians-University Munich, Department of Earth and Environmental Sciences, Section Palaeontology, Richard-Wagner-Str. 10, 80333 Munich, Germany, Tel: +49 (0)89-21806618, t.schulz-mirbach@lrz.uni-muenchen.de

Schütz, Nicole Universität Kassel, Heinrich-Plett-Straße 40, 34132 Kassel, Germany, Tel: +49 (0)561-8044204, nschuetz@uni-kassel.de

Schwarzer, Christian FU Berlin - Institut für Biologie - Systematische Botanik und Pflanzengeographie, Altensteinstr. 6, 14195 Berlin, Germany, Tel: +49 (0)179-4546293, schwarzer.one@web.de

Seiml-Buchinger, René AG Evolutionsbiologie, Institut für Biologie/Zoologie, FU-Berlin, Königin-Luise-Str. 1-3, 14195 Berlin, Germany, Tel: +49 (0)30-83853917, rseimlbuchinger@yahoo.de

Shahsavari, Abbas Bu-Ali Sina University, Department of Biology, Bu-Ali Sina University, Hamedan, Iran, Tel: +98 8118257402, shah_hend@yahoo.de

Simon, Sabrina Stiftung Tierärztliche Hochschule Hannover, ITZ, Ecology & Evolution, Bünteweg 17d, 30559 Hannover, Germany, Tel: +49 (0)511-9538571, sabrina.simon@ecolevol.de

Sinitsyna, Tatiana All Russian N.I.Vavilov Research Institute of plant industry, 190000 Saint-Petersburg, B.Morskaya str., 42., Russia, Tel: +8 9062632166, t.sinitsyna@list.ru

Smith, James F. Department of Biology, Boise State University, 1910 University Drive, Boise, ID, 83725-1515, USA and Idaho Botanical Research Foundation, 637 Warm Springs, Boise, ID, 83712, USA, jfsmith@boisestate.edu

Söhner, Sylvia Martin-Luther-Universität Halle-Wittenberg, Neuwerk 21, 06108 Halle (Saale), Germany, Tel: +49 (0)345-5526245, sylvia_soehner@yahoo.de

Solórzano, Kraemer Mónica Morayma, Institut für Paläontologie, Universität Bonn, Nussallee 8, 53115, Bonn, Germany, Tel: +49 (0)228-734843, msolorzanokraemer@gmail.com

Sommer, Sabine Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie, Universität Göttingen, Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395463, gudrid@freenet.de

Soria Auza, Rodrigo Wilber Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-395716, wilbersa@armonia-bo.org

Sporn, Simone Goda Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-392014, godaSporn@web.de

Sradnick, Jan Georg-August-Universität, Göttingen, Johann-Friedrich-Blumenbach-Institut für Zoologie und Anthropologie, Berliner Str. 28, 37073 Göttingen, Germany, Tel: +49 (0)551-392135, Jan.Sradnick@web.de

Staubach, Sid Institute for Ecology, Evolution and Diversity – Phylogeny and Systematics, J. W. Goethe-University, Siesmayerstraße 70, 60054, Frankfurt am Main, Germany, Tel: +49 (0)69-79824701, Staubach@bio.uni-frankfurt.de

Stech, Michael Nationaal Herbarium Nederland, Universiteit Leiden branch, P.O. Box 9514, 2300 RA Leiden, The Netherlands, Tel: +31 715274730, stech@nhn.leidenuniv.nl

Steger, Gerhard Institut für Physikalische Biologie, Heinrich-Heine-Universität Düsseldorf, 40225 Düsseldorf, Germany, steger@biophys.uni-duesseldorf.de

Steiner, Gerhard University of Vienna, Dept. Evolutionary Biology, Althanstr. 14, 1090 Vienna, Austria, Tel: +43 (0)1-427754450, Gerhard.steiner@univie.ac.at

Steinhof, Monika Überseemuseum Bremen, Bahnhofsplatz 13, 28195 Bremen, Germany, Tel: +49 (0)421-1603841, m.steinhof@uebersee-museum.de

Steudel, Bastian Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, BastianSteudel@aol.com

Stöger, Isabella Zoologische Staatssammlung München, Münchhausenstraße 21, 81247 München, Germany, Tel: +49 (0)89-8107124, Isabella.Stoeger@zsm.mwn.de

Struck, Torsten Department of Zoology, Faculty of Biology, University of Osnabrück, Barbarastr. 11, 49069 Osnabrück, Germany, Tel: +49 (0)541-9693450, struck@biologie.uni-osnabrueck.de

Stuessy, Tod Institute of Botany, University of Vienna, Rennweg 14, 1030 Wien, Austria, Tel: +43 1427754 140, tod.stuessy@univie.ac.at

Symmank, Lars Technische Universität Dresden, TU Dresden, Fakultät Mathematik und Naturwissenschaften, Fachrichtung Biologie, 01062 Dresden, Germany, Tel: +49 (0)351-46339548, Lars.Symmank@tu-dresden.de

Szövényi, Péter Duke University, Duke University, Durham, North-Carolina, 27708, 139 Biological Sciences Bldg. Box 90338, USA, Tel: +1 9196137453, pis@duke.edu

Tavakkoli, Solmaz Department of Plant Biology -Faculty of science- Tarbiat Modares University-Tehran, Iran, Tel: +98 2188011001, Narsisusa@yahoo.com

Teege, Patrick Institut für Spezielle Botanik, Johannes Gutenberg-Universität Mainz, Bentzelweg 9a, 55099 Mainz, Germany, Tel +49 (0)6131-3922624, teege@uni-mainz.de

Theißen, Günter Friedrich-Schiller-Universität Jena, Lehrstuhl für Genetik, Philosophenweg 12, 07743 Jena, Germany, Tel: +49 (0)3641-949550, guenter.theissen@uni-jena.de

Thell, Arne The Biological Museums, Östra Vallgatan 18, 22361 Lund, Sweden, Tel: +46 462228978, Arne.Thell@botmus.lu.se

Thiv, Mike Staatliches Museum für Naturkunde Stuttgart, Rosenstein 1, 70191 Stuttgart, Germany, Tel: +49 (0)711-8936205, thiv.smns@naturkundemuseum-bw.de

Tkach, Natalia Institute of Biology, Department of Geobotany and Botanic Garden, Martin-Luther-University Halle Wittenberg, Neuwerk 21, 06099 Halle, Germany, Tel: +49 (0)345-5526249, natalia.tkach@botanik.uni-halle.de

Troitsky, Aleksey A.N.Belozersky Institute of Physicochemical Biology, M.V.Lomonosov Moscow State University, Leninskie Gory. Moscow, 119991, Russia, Tel: +7 499-1934171, bobr@genebee.msu.su

Tröster, Gert Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie, Universität Göttingen, Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395524, gtroest@gwdg.de

Tschan, Georg Florian Department of Palaeobotany, Swedish Museum of Natural History / Stockholm University, P. O. Box 50007, 10405 Stockholm, Sweden, Tel: +46 851954087, Georg.Tschan@nrm.se

Tugay, Osman Selçuk Universty Selçuk University, Faculty of Arts and Sciences, Department of Biology, Campus, 42075, Selçuklu, Konya, Turkey, Tel: +90 (0)332-2231271, otugay@selcuk.edu.tr

Turini, Florian LMU München, Department Biologie I, Systematic Botany, Menzinger Str. 67, 81638 München, Germany, Tel: +49 (0)89-17861199, Florian.Turini@lrz.uni-muenchen.de

Tyson, Bernadette Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-395732, sysbot@uni-goettingen.de

Ullrich, Esther Freie Universität Berlin, Institut für Biologie (Zoologie), Königin-Luise-Straße 1-3, 14195 Berlin, Germany, Tel: +49 (0)30-83856996, eullrich@zoosyst-berlin.de

Vidalis, Amaryllis A. Department of Forest Genetics and Forest Tree Breeding, University of Göttingen, Büsgenweg 2, 37077 Göttingen, Germany, Tel: +49 (0)551-393539, avidali@gwdg.de

Vilnet, Anna Polar-alpine Botanical Garden-Institute of Kola SC RAS, Murmansk Prov., Kirovsk-6, Polar-alpine Botanical Garden, Laboratory of flora, Russia, Tel: +7 (0)815-3152742, anya_v@list.ru

Vogel, Gisela Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie, Universität Göttingen, Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395463, gvogel1@gwdg.de

Vogler, Alfried P. Department of Entomology, The Natural History Museum London, Cromwell Road, London, SW7 5BD, United Kingdom, Tel: +44 (0)207-9425613/5016, a.vogler@nhm.ac.uk

Vogler, Catherine Courant Research Center Geobiology, Geoscience Center Göttingen, Georg-August-Universität Göttingen, Goldschmidtstr.3, 37077 Göttingen, Germany, Tel: +49 (0)551-397903, cvogler@gwdg.de

Vogt, Lars Freie Universität Berlin, Königin-Luise-Str. 1-3, 14195 Berlin, Germany, Tel: +49 (0)30-83851567, lars.vogt@zoosyst-berlin.de

Voigt, Oliver Courant Research Center Geobiology, Geoscience Center Göttingen, Georg-August-Universität Göttingen, Goldschmidtstr.3, 37077 Göttingen, Germany, Tel: +49 (0)551-397903, ovoigt@gwdg.de

von Döhren, Jörn Freie Universität Berlin, Institut für Biologie, Königin-Luise Straße 1 – 3, 14195 Berlin, Germany, Tel: +49 (0)30-83856995, jdoehren@zoosyst-berlin.de

von Hagen, Bernhard Institut für Biologie, Universität Halle, Neuwerk 21, 06099 Halle, Germany, Tel: +49 (0)345-5526284, VONHAGEN@botanik.uni-halle.de

von Reumont, Björn M Zoologisches Forschungsmueum Alexander Koenig, Bonn, Adenauerallee 160, 53113 Bonn, Germany, Tel: +49 (0)228-9122351, bmvr@arcor.de

von Rintelen, Kristina Museum für Naturkunde, Humboldt-Universität zu Berlin, Invalidenstr. 43, 10115 Berlin, Germany, Tel: +49 (0)30-20938488, kristina.rintelen@museum.hu-berlin.de

von Rintelen, Thomas Museum für Naturkunde, Humboldt-Universität zu Berlin, Invalidenstr. 43, 10115 Berlin, Germany, Tel: +49 (0)30-20938404, thomas.rintelen@museum.hu-berlin.de

Wägele, Heike Institut für Evolutionsbiologie, Rheinische Friedrich-Wilhelms-Universität Bonn, An der Immenburg 1, 53121 Bonn, Germany, Tel: +49 (0)228-735159, hwaegele@evolution.uni-bonn.de

Wägele, Wolfgang Zoologisches Forschungsmuseum Alexander Koenig und Lehrstuhl für Spezielle Zoologie, Rheinische Friedrich-Wilhelms-Universität Bonn, Adenauerallee 160, 53113 Bonn, Germany, Tel: +49 (0)228-9122200, w.waegele.zfmk@uni-bonn.de

Wagenitz, Gerhard Systematische Botanik, Albrecht-von-Haller-Institut, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-395731, Gwageni@gwdg.de

Wagner, Natascha Universität Kassel, Heinrich-Plett Str. 40, 34132 Kassel, Germany, Tel: +49 (0)561-8044651, nataschawagner@gmx.de

Wahrmund, Ute Universität Bonn, IZMB, AG Molekulare Evolution, Kirschallee 1, 53115 Bonn, Germany, Tel: +49 (0)228-736523, wahrmund@uni-bonn.de

Waloszek, Dieter Biosystematische Dokumentation, Universität Ulm, Helmholtzstraße 20, 89081 Ulm, Germany, Tel: +49 (0)731-5031001, dieter.waloszek@uni-ulm.de

Wanke, Stefan TU Dresden, Institut für Botanik, 01062 Dresden, Germany, Tel: +49 (0)351-46334281, stefan.wanke@tu-dresden.de

Wanntorp, Livia Swedish Museum of Natural History, Box 50007, 104 05 Stockholm, Sweden, livia.wanntorp@botan.su.se

Wedmann, Sonja Forschungsinstitut Senckenberg, Forschungsstation Grube Messel, Markstr. 35, 64409 Messel, Germany, Tel: +49 (0)6159-91633214, sonja.wedmann@senckenberg.de

Weigelt, Patrick Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-3815439, patrickweigelt@gmx.de

Weising, Kurt Plant Molecular Systematics, Dept. of Sciences, University of Kassel, Heinrich-Plett-Str. 40, 34132 Kassel, Germany, Tel: +49 (0)561-8044601, weising@uni-kassel.de

Werner, Olaf Universidad de Murcia, Facultad de Biología, Departamento de Biología Vegetal (Botánica), Campus de Espinardo, E-30100 Murcia, Spain, Tel: +34 968364989, werner@um.es

Wicke, Susann Universität Wien, Institut f. Botanik – Dept. Biogeographie, Rennweg 14, 1030 Wien, Austria, Tel: +43 (01)-427754158, susann.wicke@univie.ac.at

Wieland, Frank Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie, Universität Göttingen, Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395391, fwielan@gwdg.de

Wilkens, Verena Universität Osnabrück, Barabarastraße 11, 49076 Osnabrück, Germany, verena.wilkens@biologie.uni-osnabrueck.de

Will, Maria Spezielle Botanik, Johannes Gutenberg Universität Mainz, Bentzelweg 9a, 55099, Germany, Tel: +49 (0)6131-3924279, willm@uni-mainz.de

Willmann, Rainer Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie, Universität Göttingen, Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395441, rwillma1@gwdg.de

Wilson, Rosemary Department of Systematic Botany, Albrecht von Haller Institute of Plant Sciences, University of Göttingen, Untere Karspüle 2, 37073 Göttingen, Germany, Tel: +49 (0)551-392269, rwilson@uni-goettingen.de

Wimmer, Ernst Dept. of Developmental Biology, Johann-Friedrich-Blumenbach Institut, Universität Göttingen, Justus-von-Liebig-Weg 11, 37077 Göttingen, Germany, Tel: +49 (0)551-392888, ewimmer@gwdg.de

Winterfeld, Grit Institute of Biology, University of Halle-Wittenberg, Neuwerk 21, 06099 Halle, Germany, Tel: +49 (0)345-5526227, GWinterfeld@gmx.net

Wipfler, Benjamin Johann Friedrich Blumenbach Institut für Zoologie & Anthropologie, Abteilung Morphologie, Systematik und Evolutionsbiologie, Universität Göttingen, Berliner Straße 28, 37073 Göttingen, Germany, Tel: +49 (0)551-395463, bwipfle@gwdg.de

Wissemann, Volker Justus Liebig Universität Giessen, Heinrich-Buff-Ring 38, 35392 Giessen, Germany, Tel: +49 (0)641-9935170, volker.wissemann@bot1.bio.uni-giessen.de

Worberg, Andreas Nees-Institut für Biodiversität der Pflanzen, Universität Bonn, Meckenheimer Allee 170, 53115 Bonn, Germany, Tel: +49 (0)162-1816773, worberg@uni-bonn.de

Wörz, Arno Staatliches Museum für Naturkunde, Rosenstein 1, 70191 Stuttgart, Germany, Tel: +49 (0)711-8936212, awoerz@gmx.de

Yildiztugay, Evren Selçuk University, Faculty of Arts and Sciences, Department of Biology, Campus, 42075, Selçuklu, Konya, Turkey, Tel:+90 (0)533-2538226, eytugay@selcuk.edu.tr

Yousofi, Mehdi Payam Noor University, No. 16, Alley 14th, Freiburg Northern Ave. Mardavij, Esfahan, postal code: 816877451, Iran, Tel: +98 9131311731, muosofi@yahoo.com

Zakrzewski, Anne-C. Freie Universität Berlin, Institut für Biologie, Chemie, Pharmazie – Zoologie – Evolution und Systematik der Tiere, Königin-Luise-Str. 1-3, 14195 Berlin, Germany, Tel: +49 (0)30-83856996, anne.zak@web.de

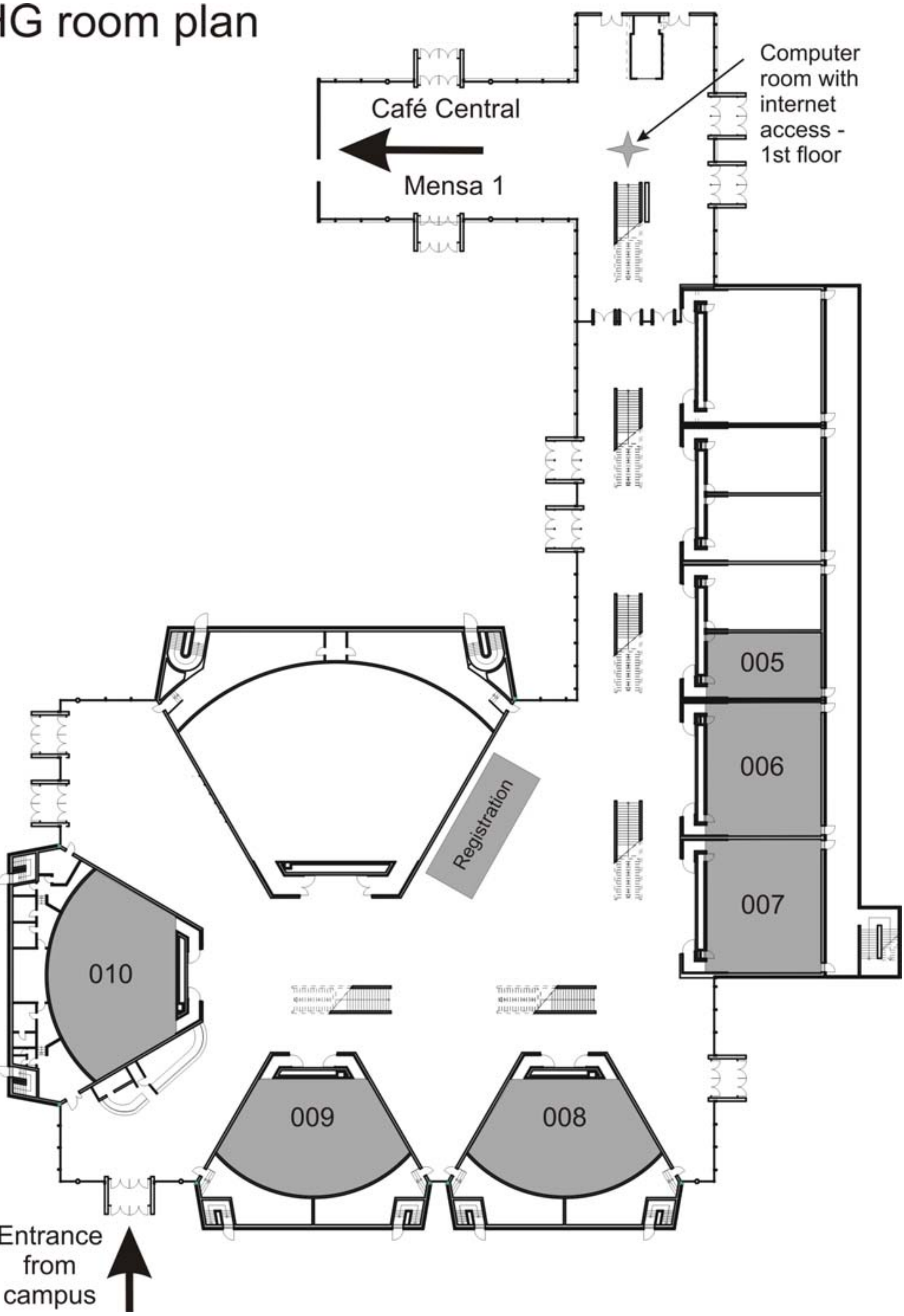
Zantke, Juliane Molecular Phylogenetics, Dept. of Evolutionary Biology, University Vienna, Althanstrasse 14, 1090 Vienna, Austria, Tel: +43 (0)1-427754453, juliane.zantke@univie.ac.at

Zetzsche, Holger Botanischer Garten und Botanisches Museum Berlin-Dahlem (BGBM), Freie Universität Berlin, Königin-Luise-Straße 6-8, 14195 Berlin, Germany, Tel: +49 (0)30-8385039, h.zetzsche@bgbm.org

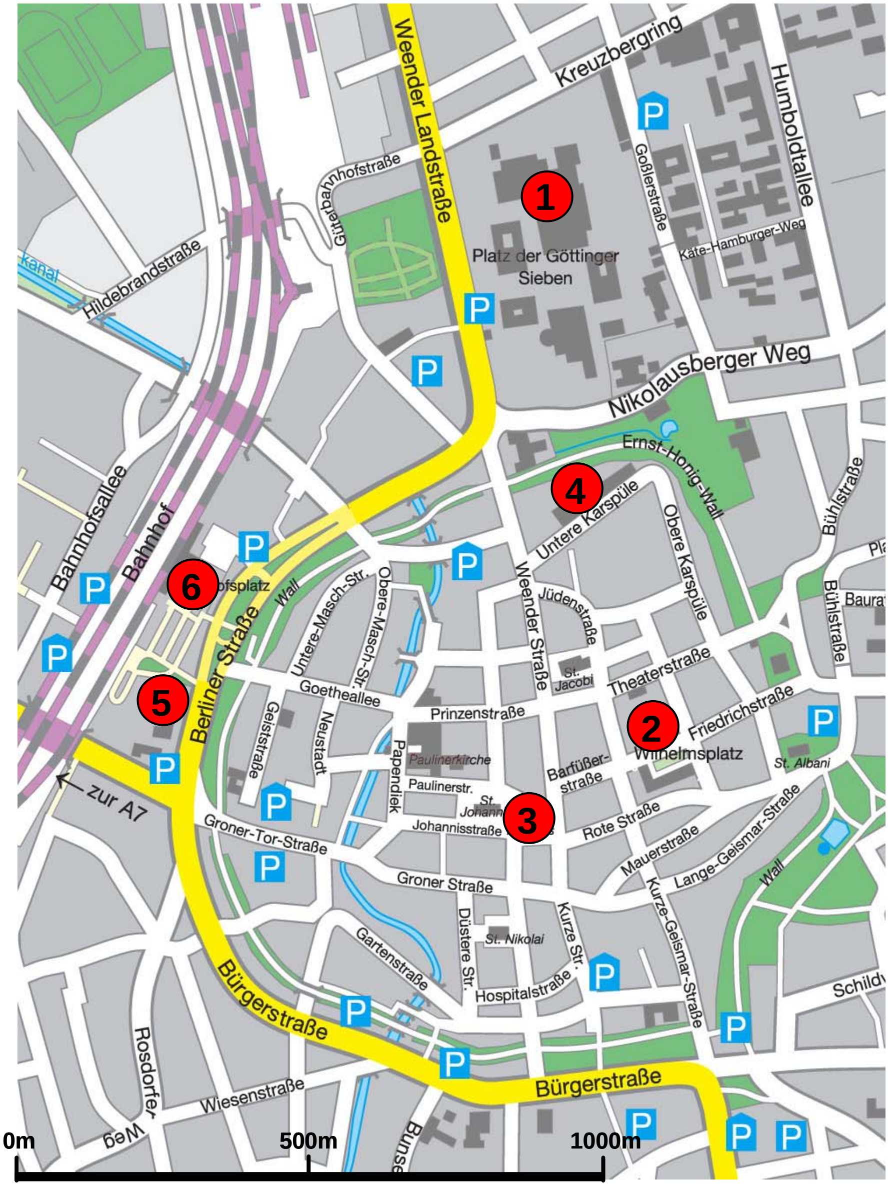
Zimmermann, Jonas Botanisches Museum und Botanischer Garten, Freie Universität Berlin, Königin-Luise-Str. 6-8, 14195 Berlin, Germany, Tel: +49 (0)1-3083850100, j.zimmermann@bgbm.org

Zimmermann, Dominique Naturhistorisches Museum Wien, Burgring 7, 1010 Wien, Austria, Tel: +43 (0)1-52177316, dominique.zimmermann@nhm-wien.ac.at

ZHG room plan



Göttingen town centre



1 Central Lecture Hall (ZHG) and Mensa 1

2 Wilhelmsplatz: University Aula and Mensa 2

3 Old Town Hall (Altes Rathaus and Rathskeller)

4 Albrecht von Haller Institute of Plant Sciences and Botanical Garden

5 Johann Friedrich Blumenbach Institute of Zoology and Zoological Museum

6 Train station

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