Genetic diversity within lichen photobionts of the Lecanora varia group (Lichenes, Ascomycota)

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Wien, 20. – 23. Februar 2007
Naturhistorisches Museum Wien

GfBS
Gesellschaft für
Biologische Systematik

9. Jahrestagung der Gesellschaft für Biologische Systematik (GfBS)

Programm
Kurzfassung der Vorträge (Abstracts) [1]
Kurzfassung der Posterbeiträge (Abstracts) [1]

Herausgeber: Naturhistorisches Museum Wien / Gesellschaft für Biologische Systematik (GfBS), Wien 2007
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Elisabeth Haring
Christoph Hörweg
Kriemhild Repp
Helmut Sattmann

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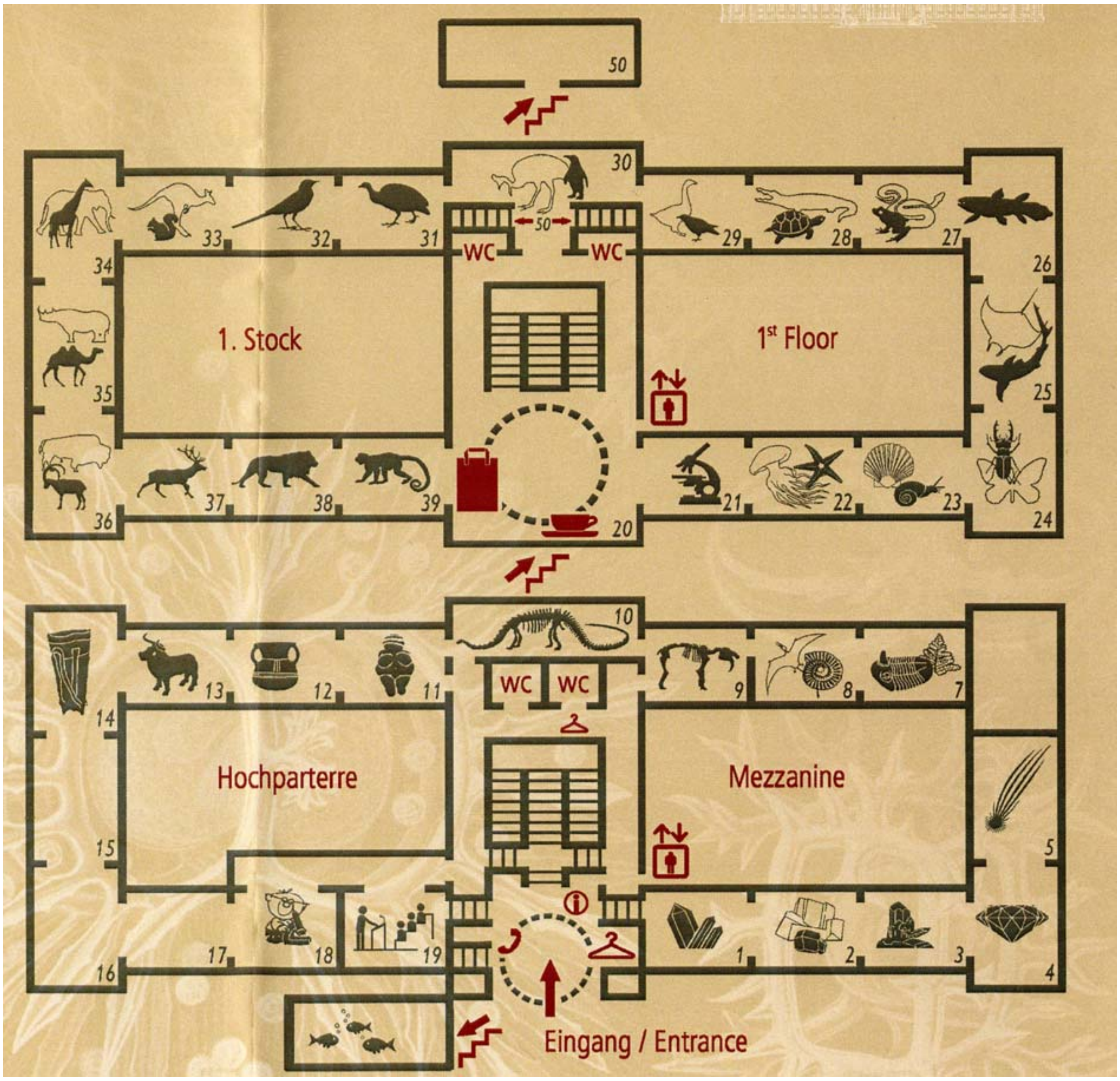
[1] Die eingelangten Kurzfassungen sind alphabetisch (Erstautor) geordnet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Eingang / Entrance

DIENSTAG, 20. FEBRUAR 2007

10.00 – 13.00 Vorstandssitzung GfBS

11.00 Uhr Öffnung des Tagungsbüros im NHM Wien, Eingangshalle
Bitte nutzen Sie diese Möglichkeit, um sich zu registrieren, Ihr Poster auszustellen und Ihren Vortrag aufzuspielen.

11.00 – 14.00 Führung in die Sammlung des Naturhistorischen Museums, Treffpunkt Seiteneingang NHM

14.00 – 18.00 **9. Kuratorentreffen** (Vortragssaal)

Moderation und Organisation: Marion Kotrba (Sprecherin der AG Kuratoren)

Begrüßung
Robert Huxley (The Natural History Museum, London): The SYNTHESYS Standards project: assessing European natural history collections and defining best practice for their access and management
Daniel Burckhardt (Naturhistorisches Museum Basel) & **Marion Kotrba** (Zoologische Staatssammlung München): Alkoholkonservierung: mehr Probleme als Lösungen?
Peter Giere (Museum für Naturkunde, Berlin): Die Embryonensammlung am Berliner Naturkundemuseum
Markus Thiem (Anton Paar GmbH): Vorstellung des Dichtemessgeräts DMA 35N zur Prüfung von Alkoholkonzentrationen.
Testzugang zur aktualisierten Version von **ZEFOD** (Zentralregister Biologischer Forschungssammlungen in Deutschland)

16.00 – 16.30 Kaffeepause

Carsten Lüter (Museum für Naturkunde, Berlin): Modernes Sammlungsmanagement in einem Denkmal. Planung eines neuen Alkoholmagazins im wiederaufgebauten Ostflügel des Berliner Naturkundemuseums.
Ernst Vitek (Naturhistorisches Museum Wien): Erfahrungen mit ehrenamtlichen Mitarbeitern in naturwissenschaftlichen Sammlungen
Wahl einer/eines neuen Sprecherin/Sprechers der AG Kuratoren
Diskussion

18.00 – 22.00 "Icebreaker" NHM Wien, obere Kuppelhalle
Begrüßung durch Generaldirektor Bernd Lötsch

MITTWOCH, 21. FEBRUAR 2007

08.00 Uhr Öffnung des Tagungsbüros im NHM Wien, Eingangshalle

VORTRAGSSAAL

08.30 – 09.00 **Begrüßung** durch
Wolfgang Wägele (Präsident der GfBS)
Ulrike Aspöck (Tagungspräsidentin, NHM Wien)

09.00 – 10.00 Plenarvorträge Naming & Ranking Zoologie / Botanik

Vorsitz: W. Wägele & R. Jahn
09.00 – 09.30 **W. Sudhaus**: Artbegriff in der Zoologie – theoretisch und pragmatisch
09.30 – 10.00 **S. Renner**: New developments in the implementation of phylogenetic naming

10.00 – 10.30 Kaffeepause und Postervorstellung 1-21 (1. Stock, Kuppelgang vor Saal 30)

10.30 – 12.30 Naming & Ranking Zoologie 1

Vorsitz: G. Haszprunar & G. Steiner
10.30 – 10.45 N. Brinkmann, **M. Glaubrecht**: Darwin's "competent systematists": species taxa and concepts in Australian thiarid gastropods
10.45 – 11.00 **A. Klussmann-Kolb**, Ch. Albrecht: New insights into the phylogeny of Euthyneura (Mollusca, Gastropoda)
11.00 – 11.15 **A. Dinapoli**, A. Klussmann-Kolb: Towards a molecular phylogeny of the Heterobranchia (Gastropoda, Mollusca) – preliminary results
11.15 – 11.30 **K. Jörger,** T.P. Neusser, M. Schrödl: "Mining deeper" - Additional characters for reconstruction of acochlidian phylogeny
11.30 – 11.45 **H. Wägele**, C. Avila: Gibt es eine Korrelation von Verteidigungsdrüsen und Sekundärmetaboliten mit der Phylogenie der opisthobranchiaten Schnecken?
11.45 – 12.00 **C. Todt**: Are acoel flatworms platyhelminths? - New comparative data on receptor cells and pharynx types
12.00 – 12.15 **M. Pfannkuchen**, J. Gugel, M. Meixner, T. Kupka, N. Hambsch, F. Bruemmer: Taxonomy and suitable markers in freshwater sponges
12.15 – 12.30 **M. Ohl**: Subjektivität und ihr Wert - Was können Linnaeische Kategorien?

12.30 – 14.00 Mittagspause, Treffen der Jungen Systematiker (Saal 21)

14.00 – 15.00 Plenarvorträge Naming & Ranking Protistologie / Ancient DNA

Vorsitz: J. Walochnik & L. Haring
14.00 – 14.30 **M. Schlegel**: Artbegriff und Protistenevolution
14.30 – 15.00 **L. Bachmann**: Genetic Variation in Holocene Bowhead Whales from Svalbard

15.05 – 15.20 Naming & Ranking Protistologie

Vorsitz: L. Bachmann & L. Haring
15.05 – 15.20 **J. Walochnik**, H. Aspöck: Phylogenie und Klassifikation der "Amöben": Ein Update

MITTWOCH, 21. FEBRUAR 2007

08.00 Uhr	Öffnung des Tagungsbüros im NHM Wien, Eingangshalle

SAAL 50

10.00 – 10.30	Kaffeepause und Postervorstellung 1-21 (1. Stock, Kuppelgang vor Saal 30)

10.30 – 12.30	**Naming & Ranking Botanik**
Vorsitz: S. Renner & E. Vitek	
10.30 – 10.45	**R. Jahn**, W.-H. Kusber: Naming and ranking in phycology
10.45 – 11.00	**E. Hörandl**: Paraphyletic vs. Monophyletic taxa - evolutionary vs. cladistic classifications
11.00 – 11.15	**S.R. Gradstein**, R. Wilson, J. Heinrichs, H. Schneider: Neotenic evolution and classification: the case of the Lejeuneaceae
11.15 – 11.30	**M. Achatz**: Interspecific hybridization and the taxonomy of Caiophora (Loasaceae)
11.30 – 11.45	C.J. Dixon, **P. Schönswetter**, G.M. Schneeweiss: Evolution and phylogeography of *Androsace* sect. Aretia (Primulaceae)
11.45 – 12.00	**N. Enke**, B. Gemeinholzer: First Insights into speciation processes in *Crepis* L. (Compositae)
12.00 – 12.15	**J. Buschbom**, D. Barker: The importance of realistic and balanced taxon samplings in model-based ancestral character state reconstructions
12.15 – 12.30	**K. Schulte**, G. Zizka: Phylogenetic relationships and evolutionary traits of Bromelioideae (Bromeliaceae): insights from plastid and nuclear DNA sequence data

12.30 – 14.00	Mittagspause, Treffen der Jungen Systematiker (Saal 21)

MITTWOCH, 21. FEBRUAR 2007

VORTRAGSSAAL

15.20 – 16.20 Ancient DNA

Vorsitz: L. Bachmann & L. Haring

15.20 – 15.35 **J. Burger**, A. Scheu, R. Bollongino: Can mitochondrial DNA sequences discriminate between wild and domestic populations?

15.35 – 15.50 **L.S. Epp**, M. Trauth, R. Tiedemann: Ancient African DNA: Insights Into the History of Kenyan Rift

15.50 – 16.05 **U. Joger**: Determining the phylogenetic position of *Mammuthus* versus *Elephas* and *Loxodonta* (Elephantidae) with mitochondrial genes: Why did it take so long?

16.05 – 16.20 **C. Schander**: Accessing DNA for molecular analyses from formalin fixed tissue

16.30 – 17.00 Kaffeepause und Postervorstellung 22-42 (1. Stock, Kuppelgang vor Saal 30)

17.00 – 18.00 Naming & Ranking Zoologie 3

Vorsitz: W. Wägele & D. Sperlich

17.00 – 17.15 **U. Aspöck**, H. Aspöck: Zur Systematisierung der Raphidioptera: Serendipity und Analyse

17.15 – 17.30 **D. Ahrens**, A.P. Vogler: Naming and ranking in chafers: using molecular phylogenies to stabilize nomenclature

17.30 – 17.45 **E. Dell´Ampio**, N. Szucsich, A. Carapelli, F. Frati, G. Steiner, G. Pass: Phylogenetic relationships among the basal hexapods: contribution from the rRNA 28S gene

17.45 – 18.00 **G. Purschke**, H. Hausen: Ultrastructure and phylogenetic importance of ciliary photoreceptors and pigmented eyes in errant polychaetes (Annelida)

18.00 – 19.30 Jahreshauptversammlung der GfBS (2. Stock, Saal 50)

19.30 – 19.50 Transfer zum Abendempfang mit Shuttle-Bussen;
Abfahrt vom Seiteneingang des NHM zwischen 19.30 und 19.50 Uhr (letzte Möglichkeit!!)

20.30 Uhr Abendempfang des Wiener Bürgermeisters beim Heurigen
"Fuhrgassl-Huber" in Neustift am Walde 68

Rückfahrt individuell !
Bus 35A Richtung Spittelau (Umsteigen zur U-Bahn U4/U6)
oder Aussteigen Döblinger Gürtel / Glatzgasse und Umsteigen zur Straßenbahn Nr. 37 und 38 (Station Nußdorfer Straße) Richtung Schottentor (U-Bahn U2, Anschluß an die Straßenbahn-Ringlinien 1 und 2 und Straßenbahn D)

MITTWOCH, 21. FEBRUAR 2007

SAAL 50

15.15 – 16.30	**Naming & Ranking Zoologie 2**
Vorsitz: D. Burckhardt & U. Aspöck	
15.15 – 15.30	**P. Feulner**, F. Kirschbaum, R. Tiedemann: Molecular phylogeny of African weakly electric fish (genus *Campylomormyrus*): Evidence for sympatric speciation
15.30 – 15.45	**J. Hoffmann**, C. Lüter: Unrecognised species complex of Thecidellina (Brachiopoda) in the Caribbean and the Atlantic
15.45 – 16.00	**S. Richter**: Eine kombinierte Analyse zur Aufklärung der phylogenetischen Verwandtschaftsbeziehungen der Branchiopoda (Crustacea)
16.00 – 16.15	**A. Bergter**, V. Hunnekuhl, M. Schniederjans, A. Paululat: Comparative analyses of patterns during myogenesis in clitellates - phylogenetic implications
16.15 – 16.30	**D.T. Tietze**, J. Martens: Acoustic and morphometric differentiation of treecreepers (Aves: Certhia)

16.30 – 17.00	Kaffeepause und Postervorstellung 22-42 (1. Stock, Kuppelgang vor Saal 30)

17.00 – 18.00	**Freie Themen Botanik**
Vorsitz: M. Steinhof & R. Jahn	
17.00 – 17.15	J.-M. Park, J.-F. Manen, **G.M. Schneeweiss**: Horizontal gene transfer of plastid genes in a group of non-photosynthetic parasitic plants
17.15 – 17.30	**H. Prillinger**, K. Lopandic, T. Sugita, M. Wuczkowski: *Asterotremella* gen.nov. *albida* a symbiontic tremelloid yeast isolated from the agarics *Asterophora lycoperdoides* and *A. parasitica*
17.30 – 17.45	**D.C. Albach**: The use of AFLP fingerprints in the analysis of hybrid complexes
17.45 – 18.00	**N.V. Tkach**, M. Röser, M.H. Hoffmann, K.B. von Hagen: Plant evolution in the Arctic: Hypotheses testing in multiple lineages of *Artemisia*

18.00 – 19.30	Jahreshauptversammlung der GfBS
19.30 – 19.50	Transfer zum Abendempfang mit Shuttle-Bussen; Abfahrt vom Seiteneingang des NHM zwischen 19.30 und 19.50 Uhr (letzte Möglichkeit!!)
20.30 Uhr	Abendempfang des Wiener Bürgermeisters beim Heurigen "Fuhrgassl-Huber" in Neustift am Walde 68 Rückfahrt individuell ! Bus 35A Richtung Spittelau (Umsteigen zur U-Bahn U4/U6) oder Aussteigen Döblinger Gürtel / Glatzgasse und Umsteigen zur Straßenbahn Nr. 37 und 38 (Station Nußdorfer Straße) Richtung Schottentor (U-Bahn U2, Anschluß an die Straßenbahn-Ringlinien 1 und 2 und Straßenbahn D)

DONNERSTAG, 22. FEBRUAR 2007

08.00 Uhr	Öffnung des Tagungsbüros im NHM Wien, 2. Stock gegenüber Saal 50

VORTRAGSSAAL

08.30 – 09.30	**Plenarvorträge Paläontologie / Koevolution**
Vorsitz: M. Harzhauser & H. Sattmann	
08.30 – 09.00	**J. Rust**: Der Beitrag der Paläontologie zur modernen Systematik
09.00 – 09.30	**H. Aspöck**, J. Walochnik: Die Parasiten des Menschen aus der Sicht der Koevolution

09.30 – 10.45	**Paläontologie**
Vorsitz: J. Rust & M. Harzhauser	
09.30 – 09.45	**A.N. Muellner**, D.D. Vassiliades: Biebersteiniaceae Endl.: status, position, origin, and revised age estimates for the families of Sapindales
09.45 – 10.00	**S. Wedmann**, S. Bradler, J. Rust: The first fossil walking leaf (Insecta: Phasmatodea) - an example of evolutionary stasis
10.00 – 10.15	**A. Staniczek**: Eintagsfliegen (Insecta: Ephemeroptera) aus der kreidezeitlichen Crato-Formation Nordost-Brasiliens
10.15 – 10.30	**J.T. Haug**, A. Maas, D. Waloszek: The One-eyed Sisters: *Cambropachycope clarksoni* & *Goticaris longispinosa*, Derivatives of the Stemlineage of Crustacea
10.30 – 10.45	**S. Klaus**, M. Groß: Palaeontology of the European freshwater crabs (Brachyura, Potamidae)

10.45 – 11.15	Kaffeepause und Postervorstellung 43-63 (1. Stock, Kuppelgang vor Saal 30)

11.15 – 12.30	**Koevolution**
Vorsitz: H. Aspöck & W. Sudhaus	
11.15 – 11.30	**D. Burckhardt**: Blattflöhe und Blütenpflanzen: ein Fall von Koevolution?
11.30 – 11.45	**D. Guicking**, H. Feldhaar, K. Weising, F.R. Blattner, B. Fiala: Coevolution in a tropical ant-plant association? The case of *Macaranga-Crematogaster*
11.45 – 12.00	**K. Händeler**, H. Wägele: Phylogenie der Sacoglossa (Gastropoda: Opisthobranchia)
12.00 – 12.15	**M. Herrmann**, W.E. Mayer, R.J. Sommer: The nematode genus *Pristionchus*: A model for cryptic speciation, Haldane's rule and species invasion
12.15 – 12.30	**M. Gottschling**, I.G. Bravo, A. Stamatakis, Á. Alonso, L. Gissmann, E. Stockfleth, I. Nindl: Phylogenomics of papillomavirus and the biological interpretations

12.30 – 14.00	Mittagspause

14.00 – 14.30	**Plenarvortrag – Anthropologie**
Vorsitz: M. Teschler-Nicola	
14.00 – 14.30	**J. Schwartz**: So Many Hominid Fossils but So Little Systematic Rigor

DONNERSTAG, 22. FEBRUAR 2007

08.00 Uhr Öffnung des Tagungsbüros im NHM Wien, , 2. Stock gegenüber Saal 50

SAAL 50

09.45 – 10.45	**Freie Themen Zoologie**
Vorsitz: U. Joger & K. Sefc	
09.45 – 10.00	**N. Rivera**, L. Heine, J. Heinze, C.D. Schubart: Genetic analyses of geographic structure, multiple paternity and brood parasitism in the Jamaican bromeliad crab *Metopaulias depressus* (Brachyura: Sesarmidae)
10.00 – 10.15	**T. Santl**, K.A. Crandall, C.D. Schubart: Witnessing species evolution? Genetic population structure of the Jamaican freshwater crab *Sesarma dolphinum* (Crustacea, Brachyura)
10.15 – 10.30	**H. Letsch**, B. Misof, R. Stocsits: Simultaneous Inference of RNA Structure and Multiple Sequence Alignment
10.30 – 10.45	B. Misof, **K. Meusemann**, J. Dambach: The Atelocerata: a vanishing hypothesis - molecular phylogeny of basal hexapods

10.45 – 11.15 Kaffeepause und Postervorstellung 43-63 (1. Stock, Kuppelgang vor Saal 30)

11.15 – 12.30	**Zoologie – Morphologie**
Vorsitz: G. Pass & E. Christian	
11.15 – 11.30	J. Willkommen, **T. Hörnschemeyer**: The flight apparatus of Ephemeroptera and the ground-pattern of insect flight
11.30 – 11.45	**C.S. Wirkner**, S. Richter: Evolutionary morphology of the circulatory organs in Peracarida
11.45 – 12.00	**P. Grobe**, T. Bartolomaeus: The Coelomic Origin and Phylogenetic Affinities of the Phoronida
12.00 – 12.15	**J. Zantke**, G. Scholtz: The first record of specific nerve dye in Tardigrada: notes on the general course of the CNS and the construction of the brain
12.15 – 12.30	**K. Edlinger**: Konstruktion und Morphologie - zur Frage der Lesrichtung in der Stammesgeschichte

12.30 – 14.00 Mittagspause

DONNERSTAG, 22. FEBRUAR 2007

VORTRAGSSAAL

14.35 – 15.10	**Anthropologie**
Vorsitz: J. Schwartz & M. Teschler-Nicola	
14.35 – 14.55	R.E. Green, **J. Krause**, S.E. Ptak, M. Lachmann, A. Briggs, M. Ronan, J.F. Simons, L. Du, M. Egholm, J. Rothberg, S. Pääbo: Neandertal Genomics
14.55 – 15.10	**P.R. Menke**, W. Henke: 3-d reconstruction of the hyo-laryngeal complex based on ontogenetic data: cladistic implications for primates and their relatives.

15.10 – 16.00	**Organellen DNA**
Vorsitz: G. Steiner & C. Schander	
15.10 – 15.30	H. Dreyer, **G. Steiner**: Mitochondrial genomes of molluscs: are sequence- and gene order phylogenies chaotic?
15.30 – 15.45	**C. Bleidorn**, I. Eeckhaut, L. Podsiadlowski, N. Schult, D. McHugh, K.M. Halanych, M.C. Milinkovitch, R. Tiedemann: Mitogenomics and nuclear data unravel phylogenetic relationships of Myzostomida
15.45 – 16.00	**L. Podsiadlowski**, G. Mayer, A. Braband: Mitochondrial genomes of Onychophora

16.00 – 16.30 Kaffeepause und Postervorstellung 64-83 (1. Stock, Kuppelgang vor Saal 30)

16.30 – 18.00	**Naming & Ranking Zoologie 4**
Vorsitz: A. Hundsdörfer & U. Fritz	
16.30 – 16.45	**S. Treplin**, R. Tiedemann: Chicken repeat 1 (CR1) retrotransposons as phylogenetic markers in passerine birds (Aves: Passeriformes)
16.45 – 17.00	**C. Pázmándi**: A phylogeny of blennioid fishes (Teleostei), based on 12S and 16S mtDNA, and its use to trace different degrees of morphological integration of their pectoral fins
17.00 – 17.15	**T. Kleinteich**, A. Haas: Cranial muscles in caecilian larvae: a contribution to the ground pattern of the Lissamphibia
17.15 – 17.30	**S. Bradler**, O. Mai: A phylogeny of stick and leaf insects (Insecta: Phasmatodea) with special emphasis on re-evolution events
17.30 – 17.45	**S. Koenemann**, T.M. Iliffe: Larval development of Remipedia (Crustacea)
17.45 – 18.00	**T. Stach**, J. Winter, R. Schnabel: The cell lineage of *Oikopleura dioica* (Appendicularia, Tunicata)

18.15 – 20.00 Ehrungen durch die Gesellschaft
Verleihung der Preise für die besten studentischen Beiträge
Verleihung des Bernhard-Rensch-Preises
Vortrag des Bernhard-Rensch-Preisträgers

DONNERSTAG, 22. FEBRUAR 2007

SAAL 50

14.45 – 16.00	**Biogeographie 1**
Vorsitz: P. Schönswetter & B. Misof	
14.45 – 15.00	**O. Niehuis**, B. Misof: Evolutionary history of the burnet moth genus *Zygaena*: phylogeny, host-plant association and historical biogeography
15.00 – 15.15	**J.C. Habel**, T. Schmitt, M. Meyer: Gene in Raum und Zeit: Phylogeographische Untersuchungen am *Melanargia galathea / Melanargia lachesis* - Artkomplex
15.15 – 15.30	**O. Schultz**, C. Hemp, W. Wägele: Hot Spot of Biodiversity: Molecular Phylogeny of endemic grasshoppers in the Eastern Arc range (Tanzania, East Africa)
15.30 – 15.45	**M. Husemann**, A. Hochkirch: Rapid radiation and colonization processes in the genus *Sphingonotus* FIEBER, 1852
15.45 – 16.00	**D. Nunes**: Worldwide survey of *Drosophila melanogaster* variability shows a contrasting pattern for nuclear and mitochondrial markers

16.00 – 16.30 Kaffeepause und Postervorstellung 64-83 (1. Stock, Kuppelgang vor Saal 30)

16.30 – 18.00	**Biogeographie 2**
Vorsitz: S. Weiss & W. Westheide	
16.30 – 16.45	**I. Richling**: The New Caledonian Helicinidae: Diversity, distribution pattern, and zoogeographic affinities in the Pacific (Mollusca: Gastropoda: Neritopsina)
16.45 – 17.00	**J. Sauer**, B. Hausdorf: Comparative analysis of land snail radiations on Crete
17.00 – 17.15	**T. von Rintelen**, F. Riedel, M. Glaubrecht, F. Köhler: Evolution and biogeography of Southeast Asian viviparids (Mollusca: Gastropoda: Caenogastropoda)
17.15 – 17.30	**C.D. Schubart**, L. Ragionieri, S. Fratini: Gene flow within the Indo-West Pacific: a genetic comparison of geographic structure in two common mangrove crabs (Brachyura: Sesarmidae & Gecarcinidae)
17.30 – 17.45	N. Rabet, **R. Scalone**: Widespread distribution of an American *Artemia* species in France (Crustaceae, Anostracea): Morphological, genetic and morphometric data
17.45 – 18.00	**S. Reuschel**, C.D. Schubart: *Palaemon elegans* Rathke (1837): variation of a marine littoral species across its native range

VORTRAGSSAAL

18.15 – 20.00 Ehrungen durch die Gesellschaft
Verleihung der Preise für die besten studentischen Beiträge
Verleihung des Bernhard-Rensch-Preises
Vortrag des Bernhard-Rensch-Preisträgers

FREITAG, 23. FEBRUAR 2007

VORTRAGSSAAL

09.00 – 11.00	**Datenbanken**
Vorsitz: E. Vitek & M. Kotrba	
09.00 – 09.10	**E. Vitek**: Impulsreferat
09.10 – 09.20	**L. Vogt**, P. Grobe: MorphDBase - a Morphological Description Database
09.20 – 09.30	C. Klingenberg, **M. Verhaagh**: Anttypes.org: a new online resource for modern ant taxonomy
09.30 – 09.40	**E. Geiser**, M. Malicky: Inwieweit kann man die Synonymisierung einer Biodiversitätsdatenbank überlassen - oder warum Carl von Linné kein Systematiker, sondern ein Informatiker war
09.40 – 11.00	Gemeinsame Diskussion
11.00 – 11.30	Kaffeepause

11.30 – 13.00	**Schaustellung versus Bewahrung**
11.30 – 11.45	**W. Wägele**: Impulsreferat
11.45 – 13.00	Allgemeine Diskussion
13.00 Uhr	Schlussworte von Wolfgang Wägele (Präsident der GfBS) Ende der Tagung

FREITAG, 23. FEBRUAR 2007

KURSSAAL

WORKSHOP: BAYESSCHE METHODEN IN DER PHYLOGENETISCHEN REKONSTRUKTION

Organisation: Gerhard Steiner (Universität Wien)

Bitte eigenen Laptop mitbringen!

09.00 – 10.00	Teil 1 - Theorie
10.00 – 10.20	Kaffeepause
10.20 – 12.50	Teil 2 - Praxis

VORTRAGSSAAL

13.00 Uhr	Schlussworte von Wolfgang Wägele (Präsident der GfBS) Ende der Tagung

POSTERBEITRÄGE

01-32 **Naming & Ranking Zoologie**
01 **F. Beck**, M. Heß, G. Haszprunar: The Microanatomy of *Leptogyra constricta* Marshall, 1988 and *Leptogyropsis kalinovoae* Marshall, 1988 (Gastropoda, Neomphalida)
02 **S. Brauer**, H. Hausen: Ultrastructure of nuchal organs and larval photoreceptors does not support a closer relationship of Cirratulidae and Spionidae (Annelida, Polychaeta)
03 **S. Brix**, C. Held, M. Raupach, A. Brandt: A secret of genes? The phylogeny of Desmosomatidae Sars, 1897
04 **K. Fahrein**, H. Hausen: Systematic significance of chaetal arrangement and prostomial sensory organ ultrastructure in Chaetopteridae (Annelida, Polychaeta)
05 S. Feistel, **G. Haszprunar**: Molecular Morphology of 18S rDNA of the Bivalvia
06 **J. Gugel**, F. Bruemmer, A. Jaklin: High Diversity in Populations of *Suberites* sp. near Rovinj (Croatia, northern Adriatic Sea)
07 **E. Haring**, K. Kvaløy, J.-O. Gjershaug, N. Røv, A.Gamauf: Phylogenetic analyses of the hawk-eagles (genus *Spizaetus*) based on mitochondrial markers: convergent evolution and paraphyly
08 **M. Helmkampf**, I. Bruchhaus, B. Hausdorf: Molecular phylogenetic analysis of Lophophorata and Chaetognatha
09 **T. Hülsken**, S. Schreiber, M. Clemmensen, M. Hollmann: Systematics and Biodiversity of the Caenogastropod family Naticidae
10 **S. Kaiser**, S. Brix, A. Brandt: A deep-sea systematic odyssey: a tale of two important isopod families
11 **B. Klee**, R. Heim, I.T. Hyman, G. Haszprunar: Species boundaries in *Limax* (Gastropoda: Stylommatophora): extreme colour variations in and between species
12 **S. Koblmüller**, B. Egger, C. Sturmbauer, K.M. Sefc: Molecular phylogeny of the Perissodini, Lake Tanganyika's scale eating cichlids: Incongruence with morphological data
13 **Markus Koch**, G.D. Edgecombe: Evolution of peristomatic structures in Lithobiomorpha (Chilopoda)
14 **Martin Koch**, M. Maderbacher, J. Herler, C. Bauer, C. Sturmbauer: Phenotypic and genetic distinctness of a natural hybrid population from its two parental populations in the Lake Tanganyika cichlid fish *Tropheus moorii*
15 **T. Kunze**, M. Heß, G. Haszprunar: The microanatomy of *Ventsia tricarinata* (Warén & Bouchet, 1993), a Skeneimorph Vetigastropod from Pacific Hydrothermal Vents (Mollusca)
16 **J. Lehrke**, T. Bartolomaeus: Ultrastructure in echiurid sperm: implications for ingroup relationships
17 **Y. Liu**, X. Hou, A. Maas, D. Waloszek: *Leanchoilia illecebrosa* and the Stemlineage of Chelicerate
18 **A. Meyer**, K. Streit, R.P. Kelly, D.J. Eernisse, B. Lieb**:** Hemocyanin as a promising molecular marker for phylogenetic analyses in chitons (Polyplacophora)
19 **S.V. Ober**, E.-G. Burmeister: The damselfly family Dicteriadidae: a phylogenetically interesting group of Odonata
20 **S. Simon**, S. Sagasser, H. Hadrys: Hemocyanin in Mantophasmatodea (Insecta, Pterygota): Restricted homology among pterygote orders?
21 **E. Speimann**, M. Heß, G. Haszprunar: The Microanatomy of *Xenoskenea pellucida* (Monterosato, 1874) (Gastropoda, Heterobranchia, Ectobranchia)

22 **T. Stach**: Phylogeny of extant Tunicata and its bearing on chordate evolution
23 **S. Tenner**, M. Glaubrecht, T. von Rintelen: Species delimitation and trophic specialization of Tylomelania (Caenogastropoda: Cerithioidea: Pachychilidae) in the Malili-System
24 **C. Todt**, M. Härlin, Y. Bertrand, Ch. Schander: DNA Barcoding, Species and Species Boundaries
25 **T. Töpfer**: Preliminary results of a comparative phylogeny of bullfinches (genus *Pyrrhula*) based on molecular data obtained from tissue samples and museum study skins
26 **B. Ullrich**, K. Reinhold, B. Misof: Tracing the evolutionary history of the bush cricket genus *Poecilimon* FISCHER, 1853
27 J. von Döhren, **T. Bartolomaeus**: Looking *Lineus viridis* (Nemertea: Heteronemertea) in the Eye: The Phylogenetic Implications of a Nemertean Photoreceptor
28 **B. von Reumont**, W. Wägele, D. Waloßek: Molecular phylogenetic analyses of lower crustaceans ("Entomostraca")
29 J. Waringer, **W. Graf**, S. Pauls: Morphology - Ethology - Genetics: Three Approaches, One Goal. A close-up of the genus *Drusus* (Insecta: Trichoptera) in Central Europe
30 **T.W. Wyrwoll**: Ein Vorschlag zur systematischen Bildung deutscher Tiernamen
31 **T.W. Wyrwoll**: Ordo Zoologiae contra Arbitratum Culturae Formarum - Ein Vorschlag zur wissenschaftlichen Benennung der Haustiere
32 **D. Zimmermann**, W. Klepal, U. Aspöck: Staubhafte Enthüllungen. REM-Untersuchung an zwei Spezies der Familie Coniopterygidae (Neuroptera)

33-36 Naming & Ranking Botanik

33 **K. Bardy**, D.C. Albach, P. Schönswetter, M.A. Fischer: Speciation on the Balkan Peninsula - three case examples from Veronica (Veronicaceae)
34 **L. Ferrufino**, W. Berendsohn, W. Greuter, J. Gómez-Laurito: Useful taxonomic characters in *Smilax* of Costa Rica
35 **M. Krummel**, B. Gemeinholzer, Ch. Beurton: Phylogenetic reconstruction of *Zanthoxylum* L. s.l. (Rutaceae) from the Greater Antilles
36 **B. Surina**, P. Schönswetter, G.M. Schneeweiss: Phylogeny and phylogeography of the genus *Edraianthus* (Campanulaceae): a preliminary report

37 Naming & Ranking Protistologie

37 **W.-H. Kusber**, C. Cocquyt, R. Jahn: Dissemination of historical biodiversity data from collections: East African Surirella-taxa (Bacillariophyta) as a pilot study

38-39 Ancient DNA

38 **A. Scheu**, S. Hartz, U. Schmoelcke, A. Tresset, J. Burger, R. Bollongino: Aurochs or domesticated cattle? Ancient DNA analysis of early animal husbandry in Rosenhof, Northern Germany
39 **K.M. Sefc**, R.B. Payne, M.D. Sorenson: Sequencing and microsatellite genotyping errors in PCR products from avian museum specimens

40-42 Paläontologie

40 **M. Harzhauser**, W.E. Piller, O. Mandic, A. Kroh, M. Reuter, B. Berning: Paleogeography versus Paleobiogeography: the rise of the western Indo-Pacific bioprovince predates the *Terminal Tethyan Event*

41 **A. Maas**, D. Waloszek, J. Haug: A Tiny 3d-preserved Nemathelminth Larva from the Cambrian 'Orsten'

42 **M.M. Solórzano Kraemer**: Die Mexikanische und Dominikanische Bernsteinfauna - Eine Paläobiogeographische Studie

43-45 Koevolution

43 **I. Burghardt**, H. Wägele: Investigations on the biology and ecophysiology of the symbiosis between the "solarpowered" species *Melibe engeli* Risbec, 1937 (Gastropoda, Nudibranchia, Dendronotoidea) and zooxanthellae (Dinophyceae)

44 **S. Pérez-Ortega**, U. Søchting, C. Printzen: Genetic diversity within lichen photobionts of the *Lecanora varia* group (Lichenes, Ascomycota)

45 **N. Reiff**, E. Schwabe: First record of free-living nematodes (Nematoda: Chromadorida) in the mantle cavity of a Chilean polyplacophoran (Mollusca)

46-64 Freie Themen Zoologie

46 **S. Affeld**, C. Avila, H. Wägele, G. König: Untersuchung von Sekundärmetaboliten der Cladobranchia (Nudibranchia, Opisthobranchia, Gastropoda)

47 **N. Brinkmann**, A. Wanninger: Neurogenesis in *Sabellaria alveolata* (Polychaeta: Sabellaridae) as inferred by immunolabelling and digital 3D reconstruction techniques

48 C. Franken, **G. Purschke**: Scanning and transmission electron microscopic observations on the development of the nuchal organs in *Platynereis dumerilii* (Annelida, Phyllodocida)

49 **A. Fürst von Lieven**: Can we homologize developmental stages? Instars and heterochrony, and heterochrony as a prerequisite for morphological diversity

50 **A. Gruhl**: Neuromuscular system of ctenostome bryozoan larvae and metamorphic stages examined by flourescence staining and cLSM

51 **Y. Grzymbowski**, I. Burghardt, H. Wägele: Chloroplasteneinlagerung und Photosynthese bei Sacoglossa (Opisthobranchia, Gastropoda)

52 **S. Hoffmann**, T. Bartolomaeus: The axocoel stone canal complex in the larva of Antedon bifida (Crinoida): a possible apomorphy of the Crinoida?

53 **U. Hörmann**, U. Aspöck, W. Klepal: Ich seh das Tier vor lauter Borsten nicht – Genitalsegmente ausgewählter Neuropterida im REM

54 **K.M. Jörger**, T.P. Neusser, M. Schrödl: Cilia patterns and pores: comparative external SEM examination of acochlidian opisthobranch gastropods

55 A. Kirbach, **T. Stach**: Comparative ultrastructure of larval musculature in tunicates and its phylogenetic implication

56 **A. Kleewein**, U. Aspöck: Abenteurer und genetzte Flügel - eine unendliche Romanze. Die Neuropterida-Sammlung des Naturhistorischen Museums Wien

57 **L. Kruckenhauser**, W. Pinsker, A.A. Bryant: Intraspecific microsatellite variation in the highly endangered Vancouver Island marmot (*Marmota vancouverensis*) and implications for conservation genetics

58 **R. Lamers**, A. Stein, T. von Rintelen, M. Glaubrecht: Thiarid tramps: how a species can dominate the snail world

59 T. Neusser, A. Martynov, **K. Jörger**, M. Schrödl: 3D microanatomy and sperm ultrastructure of the interstitial acochlidian gastropod *Asperspina murmanica* (Kundinskaya & Minichev, 1978)

60 **B. Pachner**, C. Guseck: Auswirkungen verschiedener Pflegemaßnahmen auf die Arthropodenfauna einer Heißlände (Obere Lobau) im Nationalpark Donauauen

61 **C. Pázmándi**: The morphospace of the fin-limb transition

62 **R.O. Schill**: Tardigrades - from biodiversity to biotechnology

63 **J. Winter**, T. Stach: Electron microscopic analysis of the ontogeny of the appendicularian *Oikopleura dioica* (Tunicata, Chordata)

64 **J.M. Ziermann**, O.R.P. Bininda-Emonds, L. Olsson: Identifying sequence heterochronies in Lissamphibia

65-69 Zoologie – Morphologie

65 **F. Anderle**, W. Klepal, U. Aspöck: Mordwerkzeuge höchster Präzision - Zur Evolution der larvalen Saugzange der Neuroptera

66 **K. Drilling**, K. Dettner, KD. Klass: Der Sensillenbesatz der Antennen als Merkmalsystem für die phylogenetische Analyse bei neopteren Insekten

67 **P. Giere**: The orbital mosaic of *Tenrec ecaudatus* (Tenrecidae, Mammalia): evidence against the Insectivora

68 **L. Hubweber**: Functional morphology of the genitalia in longhorn beetles (Coleoptera: Cerambycidae)

69 **E. Redl**, L. Salvini-Plawen: Nervensystem-Anatomie und Systematik bei Caudofoveata (Mollusca)

70-76 Biogeographie

70 **F. Brümmer**, R.O. Schill, M. Schopper, G. Falkner, H.-J. Niederhöfer: Molecular characteristics of European snail populations within the genus *Bythiospeum* (Mollusca)

71 **B. Egger**, S. Koblmüller, C. Sturmbauer, K.M. Sefc: AFLP markers reveal genetic cohesion within and hybridization among color morphs

72 **G.B. Fritz**, R.O. Schill, F. Brümmer: The question of dispersal and establishment of an aquatic non-indigenous species: *Craspedacusta sowerbii* Lankester, 1880

73 **D. Gassmann**: Studies on the historical biogeography of calicnemiine damselflies from New Guinea (Odonata, Platycnemididae)

74 **E. Haring**, A. Gamauf, A. Kryukov: Mitochondrial sequences reveal different phylogeographic patterns in widespread corvid birds

75 **André Koch**, W. Böhme, B. Misof, E.A. Arida: Wallacea & Warane (Squamata: Varanidae: *Varanus salvator*): Rekonstruktion der Besiedlungsgeschichte Sulawesis durch Großreptilien

76 **S. Schweiger**: Intraspecific genetic biodiversity of the Wall lizard, *Podarcis muralis*, in Austria - glacial refugia and postglacial colonisation routes

77 Anthropologie

77 **T.W. Wyrwoll**: Haratin - Ssandaui - Hottentotten. Die Ethogenese und Anthroposystematik der Khoiniden

78-81 Organellen DNA

78 **S. Bleidißel**, B. Misof, H. Wägele: Die Phylogenie der Aeolidoidea (Nudibranchia, Gastropoda) in Korrelation mit ihrer Nahrung

79 **S. Esch**, M. Haase, B. Misof: Morphological and genetic differentiation of the land snail *Arianta arbustorum* (Pulmonata: Helicidae) within the Alps

80 **F. Kilpert**, L. Podsiadlowski: Gene arrangements and other phylogenetic markers of isopod mitochondrial genomes

81 O. Paun, P. Schoenswetter, M. Winkler, **A. Tribsch**, IntraBioDiv-consortum: Evolutionary history of the *Ranunculus alpestris* group in the European Alps and the Carpathians

82-83	**Datenbanken**
82	W.G. Berendsohn, **B. Gemeinholzer**, G. Haszprunar, E. Stackebrandt, J.-W. Wägele: On the importance of DNA-Banks
83	**K.-H. Lampe**: Mapping of Knowledge in Biodiversity

The origin of novelty - hybridization and the systematics and taxonomy of the genus *Caiophora* (Loasaceae, Cornales)

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Loasaceae subf. Loasoideae contains 200 species in 14 genera. One of the largest genera is nearly exclusively high-Andean *Caiophora*, with an estimated 30—60 species. The genus is morphologically diverse and comprises annuals, perennial rosette or winding herbs and subshrubs, and includes a wide range of floral morphologies and pollination syndromes. Notwithstanding the morphological diversity of the genus, taxon delimitation at species and species group level is extremely difficult due to widely varying combinations of characters.

Previous studies indicated a) very low molecular divergence in the genus and b) relatively frequent incidences of natural hybridization. To investigate the possibility of interspecific hybridization and its consequences, experimental hybridiazation was carried out in the greenhouses, including taxa from 4 morphologically well-differentiated species groups.

All interspecific crosses resulted in the same or higher fruit and seed formation than intraspecific cross-pollination. F1 was vigorous and fully fertile and showed largely intermediate character expression (in morphology and nectar production). The F2 generation showed strong character segregation, leading to (compared to the parental taxa) novel character states in, e.g., floral morphology and growth habit, but especially in nectar production and concentration.

The results indicate that a) there are not barriers to interspecific hybridization even between morphologically highly divergent taxa, b) the offspring shows a strong heterosis effect, c) many of the taxonomic problems in *Caiophora* may result from hybridization and introgression and d) a range of entirely novel character states and combinations in floral morphology and function (nectar) can be generated from crosses even between taxa which have the same pollination syndrome and very similar nectar characteristics. Hybrization can thus be the source of novelty.

Naming and ranking in chafers: using molecular phylogenies to stabilize nomenclature

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The Sericini (Coleoptera: Scarabaeidae) are a group of ecologically and morphologically similar chafers, being related to may beetles, rose chafers, and dung beetles. They include about 3500 described species globally in more than 200 genera. Many species still remain to be discovered. Their high degree of endemism and the insufficient effort to explore their systematics and taxonomy resulted in the fact that most Sericini genera were established in studies mostly limited to local faunas. Some of these generic names are in use for more than a hundred years. Due to their uniform external morphology, reconstruction of their phylogenetic relationships becomes difficult because diagnostic characters (e.g. genital morphology) are limited given the high number of taxa. This creates problems when trying to redefine these genera around monophyletic groups since most available apomorphies that may support their monophyly are highly homoplastic and diagnostics of genera in a worldwide scale based just on morphology becomes almost impossible.

With the reconstruction of the Sericini phylogeny based on ribosomal and mitochondrial DNA sequences we attempt to link existing diagnostic morphological characters with tree topology to redefine monophyla that are diagnosable on a worldwide scale based on non-homoplastic characters with the aim to a) facilitate the identification of genera, b) to make nomenclature of genera and species more stable, and c) to make new taxa of poorly studied or unexplored geographical regions easily assignable to an extant genus concept.

This work is highly relevant for the application of Linnaean names and will hopefully accelerate biodiversity exploration.

The use of AFLP fingerprints in the analysis of hybrid complexes

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The applicability of AFLP fingerprints in phylogenetic and phenetic analyses has been debated due to the difficulty in assessing homology of AFLP bands. But even assuming homology analyses of AFLP become challenging in the presence of hybrids.

Here, I investigate differences between various methods in the presence of multiple polyploid hybrid taxa sharing one parent, the worst-case scenario. Numerous methods (Neighbor-joining, UPGMA, parsimony, likelihood) have been employed in the past.

Here, I show that even subtle differences in these methods can lead to drastically different conclusion, which should be a warning against analyzing a complex marker system such as AFLP fingerprints using only one of these methods.

For example, standard parsimony analysis may be misleading, because character-state weighting leads to stronger support for the clustering of hybrids with their parent having more markers with increasing weight for losses of AFLP markers. Similarly, Bayesian analyses with fixed priors for character state changes can mimic results in parsimony analyses with character state weighting.

Finally, differences between distance measures (Jaccard versus Nei-Li) can lead to different results. Theoretically, both should lead to the same results for polyploids when both parents contribute equally to the number of AFLP bands in a polyploid.

However, unequal contribution of AFLP bands to a hybrid genome can lead to decisive differences between neighbor-joining analyses using one or the other distance measure. Therefore, in the absence of independent knowledge on the parentage quantitative analysis of taxon-specific AFLP markers is superior to other methods.

Die Parasiten des Menschen aus der Sicht der Koevolution

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In der Medizin versteht man unter Parasiten (aus Gründen der Tradition) alle Erreger und Überträger, die nicht zu den Viren, Bakterien oder Pilzen zählen, also alle im oder am Menschen parasitierenden Protozoen, Helminthen und Arthropoden. Das ist ein außerordentliches systematisches Sammelsurium biologisch völlig unterschiedlicher Organismen mit den entsprechend vollkommen verschiedenen Formen der Wirt-Parasit-Beziehung.

Koevolution im strengen Sinn ist die wechselseitige Anpassung zweier miteinander (meist stark) interagierender Spezies zur Optimierung oder gar Sicherung ihrer Existenzgrundlagen. Als Paradebeispiele für Koevolution gelten Blütenpflanzen und deren Bestäuber und Parasiten und deren Wirte. Die Situationen und Strategien der Evolution sind dabei aber außerordentlich verschieden. Im ersten Fall wird eine für beide Seiten a priori oder zumindest sehr früh vorteilhafte Interaktion immer weiter verbessert, bis solche Phänomene wie die 30 cm langen Sphingiden-Rüssel und die entsprechend langen Nektarsporne der besuchten Blüten entstehen. Bei den Parasiten und ihren Wirten geht es hingegen um eine Auseinandersetzung unter primär negativen Vorzeichen, die gelegentlich als „evolutionäres Wettrüsten“ bezeichnet wird. Dieses Schlagwort wird indes der sehr komplexen und sich im Verlauf der Evolution eines Wirt-Parasit-Verhältnisses ändernden Situation nur zum Teil gerecht, weil in der Auseinandersetzung zwischen Parasit und Wirt nicht nur die Strategien des Angriffs, sondern noch mehr die des Schutzes, letztlich – bemerkenswerter Weise – vor allem (aber nicht nur) des Parasiten vor dem Wirt (Evasionsmechanismen), mit denen er den Abwehrmechanismen unspezifischer und spezifischer Art (Immunsystem) zu entkommen sucht, von essentieller Bedeutung sind. Letztlich „zielt alles darauf ab“ (richtiger natürlich: führt im optimalen Fall dazu), dass einerseits der Parasit im Wirt möglichst wenig beeinträchtigt seine Entwicklung fortsetzen, sich (in diesem Wirt oder anderswo) vermehren kann und durch den Wirt in seiner Verbreitung nicht behindert wird, sondern im Gegenteil möglichst eine Verstärkung der Ausbreitung erfährt, und dass auf der anderen Seite der Wirt (in diesem Fall also der Mensch) keine Minderung seiner Reproduktionskapazität erfährt. (Wenn er eine Beeinträchtigung seiner Lebensqualität durch eine parasitäre Erkrankung erleidet und/oder früher stirbt, als es seiner Lebenserwartung entspricht, ist dies aus der Sicht der Evolution von durchaus untergeordneter Bedeutung – wenn nur solche Ereignisse erst nach der Fortpflanzungsperiode eintreten.) Ein Mechanismus hat sich möglicherweise aus der Koevolution der Parasiten und des Menschen ergeben, der zu Vorteilen für den Wirt geführt hat: die Reduktion von Allergien und bestimmten Autoimmunerkrankungen durch Immunmodulation.

Es gibt knapp 100 Protozoen, mehr als 350 Helminthen und viele 100 Arthropoden, die als Parasiten des Menschen fungieren können. Der Mensch ist der Organismus mit den meisten Parasiten, was darauf zurückzuführen ist, dass diese euryöke, außerordentlich erfolgreiche Spezies *Homo sapiens* in geradezu alle Ökosysteme der Erde direkt oder indirekt eingedrungen und daher mit Parasiten zahlreicher anderer Metazoen in Kontakt gekommen ist. Daher sind auch die weitaus meisten beim Menschen nachgewiesenen Parasiten-Spezies das Resultat mehr oder weniger zufälliger Begegnungen, die selbstverständlich von jeglichen Überlegungen von Koevolution ausgeklammert werden können.

Immerhin verbleibt eine erstaunlich hohe Zahl von anthropostenoxenen Parasiten, ca. 35 – etwa 10 Protozoen-, 18 Helminthen- und 6 Arthropoden-Spezies –, die in ihrer Existenz auf den Menschen angewiesen sind, mit dem sie durch eine lange gemeinsame Evolution, also Koevolution, verbunden sind. Faktoren, die für das Verständnis der Interaktionen bedeutsam sind, sind die Bifurkation Hominini-Panini vor 6-7 Mio. Jahren in Afrika, die Entstehung des aufrechten Ganges (wahrscheinlich in engem Zusammenhang mit dem Leben der frühen Hominini am Wasser), die Herbivorie und Piszivorie der frühen Hominini und die Entwicklung der Karnivorie vor vielleicht 2,5 Mio. Jahren, der Verlust des Haarkleids und (viel später) die Erfindung der Bekleidung, die zahlreichen Migrationen und schließlich unter bestimmten Gesichtspunkten auch relativ junge Ereignisse wie Domestikation von Tieren, Sesshaftwerdung und Entwicklung des Ackerbaus.

Auf der Grundlage dieser Faktoren wird die Koevolution des Menschen mit Parasiten an einigen konkreten Beispielen (Plasmodien, Taenien, Läusen u.a.) erläutert.

Zur Systematisierung der Raphidioptera: Serendipity und Analyse

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Sie infiltrieren unser Leben seit über 40 Jahren, wir kennen ihre Biologie, ihre glazialen Refugien, ihre Beinaheauslöschung durch den KT Impakt. Wir haben sie auf der Kontinentaldrift begleitet und konnten dennoch ihren Verwandtschaftscode nicht knacken, obwohl oder eben weil es sich um eine reliktäre Gruppe mit nur 2 Familien, Inocelliidae (6 Genera, 23 Arten) und Raphidiidae (26 Genera, ca.190 Arten) handelt.

Die Raphidiidae haben wir – ganz pragmatisch – in 7 hypothetisch monophyletischen Gruppen gebündelt. Eine jüngst entdeckte mexikanische Art des Genus *Alena* (Subgenus *Aztekoraphidia*) induziert eine männchengenitalmorphologische Neuinterpretation der bisherigen Hypovalva (9. Gonapophysen) als Amalgam von Hypovalva + Parameren (10. Gonapophysen) für *Alena* (Mexiko und südliche USA) und auch für die paläarktischen Genera *Hispanoraphidia* (Iberische HI) und *Harraphidia* (Iberische HI und Nordafrika).

Die Hypothese einer Synapomorphie würde die Position von *Alena* als Schwestergruppe aller übrigen Raphidiidae zugunsten eines atlantikübergreifenden Monophylums falsifizieren. Die neue Interpretation von *Hispanoraphidia* und *Harraphidia* – bisher Taxa der Gruppe II – könnte auch für andere Genera dieser Gruppe gelten und hätte paraphyletischen Status der Gruppe II zur Folge. Auch *Agulla* (Nearktis) – bisher Adelphotaxon von Gruppe II wäre involviert.

Drei weitere Genera der Gruppe II, *Puncha* (Mitteleuropa), und die auf der südlichen Apenninen-Halbinsel endemischen Genera *Italoraphidia* und *Calabroraphidia* bilden zwar ein Monophylum, sind aber symptomatisch für lange isolierte, und was ihre Herkunft betrifft, enigmatische monotypische Raphidiiden-Taxa – letzte Boten einer viel artenreicheren Vergangenheit. Vollends rätselhaft ist auch die Genese der heterogenen isolierten Gattung *Mongoloraphidia* (Zentral- und Ostasien) (Gruppe VI) für deren Eigenständigkeit und Diversifizierung nicht nur die ehemalige Turgai-Senke, sondern auch die mächtigen Gebirgsauffaltungen viel zu jung erscheinen ...

Bald wird sich zeigen, ob die derzeit laufenden morphologischen und molekularsystematischen Analysen Licht in die Phylogenie der Kamelhalsfliegen bringen können – die letzten Rätsel werden sie aber bestimmt nicht lösen.

Genetic Variation in Holocene Bowhead Whales from Svalbard

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Bowhead whales (*Balaena mysticetus*) are distributed in the Arctic in five putative stocks. All stocks have been heavily depleted due to centuries of exploitation. We determined the nucleotide sequence variation of the mitochondrial control region from bone remains of 99 bowhead whales from Svalbard and confirmed the authenticity of the data. The bones ^{14}C dated from recent to more than 50,000 years B.P. and are expected to relate to ancestors of the today nearly extinct Spitsbergen stock of bowhead whales.

Fifty-eight haplotypes were found, a few being frequent but many only found in one individual. The most abundant haplotypes of the Spitsbergen stock are the same as those most abundant in the extant Bering-Chukchi-Beaufort (BCB) Seas stock of bowhead whales.

Nucleotide diversity and haplotype diversity showed only minor differences between the Spitsbergen and BCB stocks. F_{ST} and K_{ST} indicate a very low genetic differentiation between the Spitsbergen and the BCB stocks that was not considered informative due to the very high levels of genetic diversity of mtDNA haplotypes in both bowhead whale stocks.

The data suggest that the historic Spitsbergen stock - before the severe bottleneck caused by whaling - did not have substantially more genetic variation than the extant BCB stock. The similar haplotypes of the Holocene Svalbard samples and the current BCB stock indicate significant migration between these two stocks and question the current designation of five distinct stocks of bowhead whales in the Arctic.

Comparative analysis of patterns during myogenesis in clitellates - phylogenetic implications

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An outer layer of circular and an inner layer of longitudinal muscles was generally considered to represent the basal somatic muscle pattern in annelids. The view of this clitellate-like muscle arrangement as the plesiomorphic condition in annelids has been challenged by recent investigations of polychaete muscle organization.

Substantial cell lineage studies on oligochaetes and leeches provide deep knowledge and a valuable basis to study developmental processes in those species. However, muscle formation in clitellates has been scarcely investigated. Direct comparison of potential homologous muscles between these annelid groups is hampered thereby.

In our work, body-wall muscle differentiation was monitored during embryogenesis of several annelid species by phalloidin staining. Our findings show that comparative studies on myogenesis during clitellate embryogenesis are a promising approach to uncover new information on annelid muscle arrangements.

Therefore those morphological studies will be an important contribution to the discussion on the plesiomorphic annelid muscle system and provide new insights about the direction of evolutionary changes in annelid body wall musculature.

Mitogenomics and nuclear data unravel phylogenetic relationships of Myzostomida

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Myzostomida are marine worms associated with echinoderms which show a puzzling body plan consisting of a mixture of lophotrochozoan characters. Their phylogenetic placement is highly disputed among systematists and recent molecular systematic analyses consistently grouped Myzostomida outside annelids.

Here we present the first nearly complete mitochondrial genome of a myzostomid. Additionally we sequenced nuclear genes. We show re-analyses of previous molecular datasets using updated data and methods, and analyse the new sequence data, as well the gene order data.

Our analyses robustly support an annelid origin of these enigmatic worms. This result is congruent with morphological investigations and we hypothesize that myzostomids evolved from a segmented annelid-like ancestor which gained its derived anatomy due to its long adaptation to echinoderm hosts.

A phylogeny of stick and leaf insects (Insecta: Phasmatodea) with special emphasis on re-evolution events

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Phylogenetic work in the Phasmatodea has been essentially lacking for a long period of time. A recent phylogenetic analysis based on three nuclear genes has led to the surprising assumption that the ancestral phasmatodean was apterous and that wings were regained several times independently. This scenario of reverse evolution has received exceedingly controverse attention.

Here we present the first comprehensive cladistic analysis based on morphological and behavioural characters of a representative number of taxa (70 genera covering all major phasmatodean lineages).

The results demonstrate that the Phasmatodea are monophyletic and *Timema* is the sister group of the Euphasmatodea. The data also support the monophyly of Neophasmatidae, Aschiphasmatinae, Phylliinae, Heteropteryginae, Pseudophasmatinae *s. str.* (excl. *Agathemera*, incl. *Prisopus*), the Lanceocercata and the Eurycanthomorpha (incl. monophyletic Eurycanthinae).

The remaining, often species-rich taxa traditionally referred to as families resp. subfamilies appear to be polyphyletic. On the basis of these relationships and the position of the wingless taxa at the base of the phasmatodean topology, the most parsimonious assumption supports the hypothesis of ancestral loss and multiple reacquisitions in wing evolution. The absence of wings in females is a possible character that phasmatodeans share with their putative sister group, the webspinners (Embioptera). Mushroom sensillae on the prothorax which are present in numerous subordinate phasmatodeans are most likely another case of reverse evolution, as might be the reappearance of the tibial area apicalis and the male postgenital clasper, the vomer.

Darwin's "competent systematists": species taxa and concepts in Australian thiarid gastropods

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250 years after Carl von Linné and 150 years after Charles Darwin systematists and evolutionary biologists alike are still left with three "*Darwinian mysteries*", viz. (i) the question how many species exist on earth, (ii) what the exact nature of species is, and (iii) how species evolve. Irrespective of the many fruitful attempts to solve these fundamental biological questions, all three remain largely unanswered. In order to accomplish modern systematists' tasks, i.e. for quantifying, biodiversity, establishing phylogenies and understanding the evolutionary process of speciation and radiation several prerequisites are indispensable, albeit neglected even in many modern systematic approaches. For example, persisting misconception as to the nature and importance of species, in particular the permanent confusion of *species taxon* with *species concept*, hampers both biodiversity research and understanding evolution. Some of the pertinent problems with merely artifical deliniation and naming of species will be discussed using viviparous Australian freshwater gastropods of the Thiaridae as exemplars. On this long isolated continent, where according to Darwin apparently "two distinct creators must have been at work", the creation of monotypical genera and the naming of more than a dozen species have helped to cloud both the phylogenetic and the biogeographical relationships with other pantropical Thiaridae as well as any insight into the evolution of the Australian taxa. Based on type material, museum collection as well as field work in various parts of Australia we have utilized morphological and molecular sequence data (500 bp of 16S) for developing a preliminary phylogeny of Australian thiarids, identifying ten distinct evolutionary lineages. We will discuss the taxonomical, systematical and biogeographical implications of this first phylogenetical hypothesis and attempt to correlate current thiarid distribution (ranging from continent-wide to drainage-based pattern) with reproductive features and life history strategies. Finally, we will develop an evolutionary scenario for the colonization of Australia by these freshwater gastropods, concluding why typology and earlier practise of naming and ranking was misleading in case of these truly Darwinian snails.

Psyllids (Insecta, Hemiptera) and angiosperms: a case of coevolution?

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Jumping plant-lice constitute a small group of some 3000 described species of highly host specific plant sap-sucking insects. They are mostly associated with dicotyledonous plants, and related psylloid species tend to develop on related plant taxa. This makes psylloids an interesting model taxon for coevolutionary studies. In the case of cospeciation, congruent host and parasite trees are expected.

Examples from the Neotropical Region show that present day psyllid diversity is only partly explained by cospeciation with their host plants and that other factors are more important. Host shifts are relatively frequent and biogeographic vicariance is possibly the main force driving species diversification in psyllids. Many psylloid species induce galls on their host, which are very diverse in shape and position on the plant.

In an example of psyllids associated with *Schinus* (Anacardiaceae) it is found that the specificity is higher in gall formers than in free living forms. Shape and position of the galls are more consistent with host rather than parasite phylogeny. Pit galls on leaves are primitive, nipple galls on leaves define a monophyletic group, and galls on branches and inflorences constitute a parallelism.

Can mitochondrial DNA sequences discriminate between wild and domestic populations?

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Since 1989 prehistoric DNA (ancient DNA or aDNA) from skeleton finds has contributed to the resolution of numerous systematic and palaeontological problems. Research with aDNA has yielded significant new discoveries, above all in the field of animal phylogeny, primarily with extinct species (e.g. Burger et al. 2004; Krause et al. 2006; Noonan et al. 2006). Here, we address the population genetic processes that can be observed when wild animal populations become domestic. We therefore refer mainly to mitochondrial DNA data from populations of extinct and extent animals produced in our lab (e.g. Bollongino 2005). In theory, ancient DNA analysis provides us with a direct horizontal line to the past. However, the case is rarely that clear-cut, and limited sample sizes as well as their chronological scatter patterns present enormous limitations to its efficacy. We will use selected examples from cattle and horse to show the extent to which molecular genetic analysis of archaeological skeleton finds nonetheless represents a significant step forward for the systematic identification of wild and domestic populations.

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The importance of realistic and balanced taxon samplings in model-based ancestral character state reconstructions

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Investigations into the evolutionary history of molecular and phenological characters shed light onto evolutionary trends and mechanisms. While tests of the distribution of character states within a group of organisms provide insight into the genetic basis underlying the studied character, reconstructions of character states at ancestral nodes within a phylogeny further elucidate the transition system between the character states and the direction of evolution taken within the group.

Model-based maximum likelihood and Bayesian approaches to ancestral character state reconstructions provide the advantage that here the transition model does not need to be fixed a priori but is optimized based on the data and to return reconstruction results that are associated with estimates of their likelihood. Specifically Bayesian reconstruction methods account for uncertainty present in evolutionary relationships and transition model in a statistically rigorous manner. They, thus, provide results that are independent of any specific phylogeny or transition model chosen. The centrepiece of model-based reconstructions is the likelihood function, which is calculated taking into account the whole phylogeny. It has been proposed that this requires the investigated taxon sampling to represent adequately the group under consideration and especially for large clades of taxa constant with regard to character state to be represented realistically.

The importance of a balanced and realistic taxon sampling is shown in a study of the evolutionary history of reproductive modes in a group of lichen-forming ascomycetes. Besides demonstrating the impact of taxon sampling, the study, furthermore, suggests that the likelihood surface is not easily interpolated, that is, that intermediate taxon samplings do not necessarily provide intermediate reconstruction results. Taking taxon sampling into account, it is possible to draw conclusions about the evolutionary history of vegetative reproduction in the investigated group of lichenized ascomycetes.

Phylogenetic relationships among the basal hexapods: contribution from the rRNA 28S gene

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In the past few years a number of molecular analyses using both nuclear and mitochondrial markers have been performed to shed light on the relationships among the orders of basal hexapods.

Despite the large amount of data available, some topics still remain a matter of debate such as the monophyletic status of Diplura and the relationships among Protura, Collembola, Diplura and Insecta *s.str.*.

To clarify these questions we used the almost complete sequence of the nuclear gene encoding for the rRNA 28S which has recently proved its efficiency in resolving deep phylogenetic relationships among Ecdysozoa.

Representatives of all four major arthropod groups were chosen to generate conclusions on the relationships of Hexapoda in a broad context. Phylogenetic trees were reconstructed using both Maximum Likelihood and Bayesian approaches, as well as Maximum Parsimony.

Our results give unambiguous corroboration to the Pancrustacea-concept. A sistergroup relationship of Myriapoda and Pancrustacea (Mandibulata-hypothesis) is preferred to a sister group relationship of Myriapoda and Chelicerata (Paradoxopoda- or Myriochelata-hypothesis).

The Crustacea appear to be paraphyletic with respect to the Hexapoda. Regarding the monophyly of the Hexapoda a cluster made up of Protura and Diplura (Nonoculata) do not unite with Collembola and Insecta *s.str.*, but in some analyses it clustered with Branchiopoda.

Towards a molecular phylogeny of the Heterobranchia (Gastropoda, Mollusca) – preliminary results

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Many questions regarding gastropod phylogeny have not been answered yet like the molecular confirmation of the Heterobranchia concept based on morphological studies from HASZPRUNAR (1985). This taxon contains the Pentaganglionata HASZPRUNAR, 1985 (with the Opisthobranchia and Pulmonata) and the "Triganglionata" HASZPRUNAR, 1985 (with several "primitive" or "basal" members united as "Allogastropoda" HASZPRUNAR, 1985).

Phylogenetic relationships of subgroups of Heterobranchia have not been resolved satisfactorily and monophyly of some taxa within Heterobranchia (e.g. Opisthobranchia) are questionable.

In order to resolve phylogenetic relationships within the Heterobranchia we perform a molecular systematic approach by sequencing and analysing a variety of genetic markers (e.g. nuclear 28S rRNA + 18S rRNA or mitochondrial 16S rRNA + COI).
First results including representatives of all major subgroups will be presented.

We also tested the utility of H3 gene sequences for phylogenetic reconstruction within the Heterobranchia because many markers have problems particularly in solving deeper nodes. Partial fragments of the gene coding for the extremely conservative H3 protein were used. Unfortunately Histone H3 alone provides no new marker for studying molecular evolution of the Heterobranchia because of the high grade of conservation and the low phylogenetic signal.

Evolution and phylogeography of Androsace sect. Aretia (Primulaceae)

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Due to historical climatic factors, and the scattered distribution of mountain ranges, alpine plants in Europe often have distributions which are on some scale disjunct, either between mountain ranges, or within a larger mountain range. Simple geographical arguments have often been used to suggest that current patterns of disjunction match the former locations of refugia during the ice ages. While this may hold true for narrow endemic taxa, found only in one small area, it need not be so for more widely distributed taxa. We studied intraspecific genetic variation in *Androsace* section Aretia to probe the causes of patchy distributions in alpine plants. This European-centred group contains species with disjunctions at all ranges from a few tens of kilometres to several hundred, but which are otherwise similar in floral syndrome and apparent dispersal abilities. Our results show that, even if the current disjunct distributions coincide with potential glacial refugia, more recent dispersal between areas is a better explanation in many cases, and that other biological factors such as hybridisation, extinction and cryptic speciation can further disrupt our ability to draw conclusions simply from cartographical data.

Mitochondrial genomes of molluscs: are sequence- and gene order phylogenies chaotic?

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Published data of molluscan mitochondrial genomes have limited power of phylogenetic resolution and yield several nonsense-clades. Why is that so? Whereas the in arthropods and vertebrates mitochondrial genomes are highly conserved in gene order, the arrangement of the genes in molluscs is highly variable. Changes in gene order often involve changing the strand the genes are encoded on, i.e. genes move from the heavy to the light strand or *vice versa*. These changes influence the A and T and the G and C skews of their genes. This results in inhomogeneous model parameters for phylogenetic reconstructions and, thus, in unreliable and wrong trees.

A putative plesiomorphic gene order is described for the polyplacophoran *Katharina tunicata*, the gastropod *Haliotis rubra* and the cephalopods *Octopus ocellatus* and *Octopus vulgaris.* However, gene order varies among cephalopods and among gastropods. In scaphopods and bivalves no plesiomorph gene order is published so far.

We show the first near-plesiomorphic gene order in a bivalve and in an aplacophoran mollusc. In addition, we report eight other unpublished molluscs genomes and discuss the phylogeny of molluscs inferred from the complete mitochondrial genomes.

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Konstruktion und Morphologie - zur Frage der Lesrichtung in der Stammesgeschichte

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Die in den vergangenen Jahren zunehmend in die biologische Systematik und Verwandtschaftsforschung eingeführten chemischen Methoden brachten einerseits große Fortschritte in der Erhellung von Verwandtschaftsverhältnissen zwischen verschiedenen Gruppen und auch Arten, andererseits werfen sie das Problem der stammesgeschichtlichen Rekonstruktion auf.

Diese hat nicht nur die Erhellung von Verwandtschaftsverhältnissen zu leisten, sondern auch die Rekonstruktion des stammesgeschichtlichen Wandels.

Dieser Wandel besteht nicht nur in Veränderungen auf der biochemischen Ebene der Organismen, sondern auch und vor allem in Umgestaltungen ihrer Gesamtkonstruktion.

Die Frage der Erklärung morphologischer Merkmale durch wissenschaftlich stringente Begründungen verbindet sich so mit dem Problem der phylogenetischen Veränderung.

Diese kann nur über jeweils funktionsfähige Zwischenstadien begründet und erklärt werden.

Eines der größten Probleme dabei ist die Richtung der Veränderung und der Kriterien, die bei ihrer Eruierung angewandt werden.

Bei der Erstellung von Lesrichtungskriterien des stammesgeschichtlichen Wandels liefern konstruktions- und funktionsmorphologische Untersuchungen und Theorien wertvolle Hilfe.

Organismen werden in ihrer Merkmalsausbildung als hydraulische Systeme verstanden, deren Formbildung sich aus physikalischen Prozessen verstehen lässt. Formbildung und –erhaltung sind dabei immer als Energie wandelndes Geschehen zu verstehen.

Die Ausbildung von Subsystemen ist findet im Rahmen der organismischen Gesamtkonstruktion statt.

Die Konstruktionsmorphologie erlaubt es, Organismen in ihrer Gesamtheit und in den Interdependenzen ihrer verschiedenen Teilsysteme bzw. Merkmale zu betrachten, während die Funktionsmorphologie Hinweise auf Vorteile organismischer Konstruktionen bei der Nutzung und Erschließung von Lebensräumen und Ressourcen liefert. Ein wichtiges Kriterium dabei ist die Zunahme der Ökonomie des Bauplans bzw. der Konstruktion, die als Energiewandler verstanden wird.

Durch verschiedene Ableitungsmodelle, für die der fossile Befund als ergänzende Begründung dienen kann, ist es möglich, nicht nur die Großgruppen des Pflanzen- und des Tierreichs, sondern auch kleinere systematische Einheiten phylogenetisch abzuleiten.

Dies wird an ausgewählten Beispielen von Molluskenphylogenesen aufgezeigt.

First insights into speciation processes in *Crepis* L. (Compositae)

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Babcock (1947) revised the approximately 200 species of Crepis L. (Compositae) arranging them into 27 sections based on morphological and karyological traits. He proposed hypotheses about character evolution and speciation processes, stating that species formation in *Crepis* was caused primarily by changes in chromosome structure and number leading to intra- and interspecific sterility and only secondarily by interspecific hybridisation. To reinvestigate these hypotheses molecular tools were applied to reconstruct a phylogeny for comparison with karyological and morphological traits. The nuclear ITS spacer region and plastid marker *mat*K were sampled from 67 species covering most of Babcocks sections.

There is a clear discrepancy between taxonomic groups recognized by morphological characters and those resulting from molecular analysis. The chromosome numbers are highly variable both within and between clades which leads to the conclusion that karyotype alterations can not be used to explain the natural groups derived from molecular phylogenies. Therefore Babcock’s initial hypothesis about chromosome change being the driving force of speciation has to be rejected. Our results suggest frequent hybridisation and introgression as a primary source of speciation within *Crepis*.

Ancient African DNA: Insights into the History of Kenyan Rift Lakes

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Ancient DNA research, especially that of environmental samples, has to date focused on samples obtained from colder regions. We are characterizing present-day and historical planktonic communities in Kenyan Rift Lakes with the use of molecular genetic methods, focussing on rotifer and diatom assemblages. Within the eastern branch of the East African Rift System there are a series of shallow lakes in close proximity, yet with strikingly different hydrological and geological features. Between 15 and 5 kyrs ago the rift comprised several large lakes that were fresh and several 100's of meters deep. Tectonically separated, these lakes underwent a tremendously different development in the course of a trend towards a drier climate since 6,000 years ago. Today the 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. A combination of geological and molecular genetic methods will reveal time and mode of the response of limnic organismic assemblages to fluctuating and diverging environmental conditions in the course of climate change. This approach will enable a detailed analysis of present day and historical connectivity of plankton assemblages and populations in the different lake basins, allowing 1) inferences about the size and degree of connectedness of former lakes and 2) insights into the history and evolution of taxa in the lakes. Apart from presenting tools to assess the presence and dominance of taxa meaningful for ecological reconstructions, molecular markers provide the opportunity to investigate intraspecific variability and phylogenetic affiliations of members of the limnic communities.

Molecular phylogeny of African weakly electric fish (genus *Campylomormyrus*): Evidence for sympatric speciation

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The endemic African mormyrids comprise the single largest group of electric fishes worldwide. While their phylogenetic position within Osteoglossomorpha is well settled, relationships within mormyrids are not resolved yet, especially at and near the species level. This is particularly true for the genus *Campylomormyrus*, which included over the years from three up to 16 species. To shed light on the entangled systematics of this genus, we have sampled 106 individuals near Brazzaville (Congo Basin). We adopted a multidisciplinary approach, combining a variety of molecular markers with geometric morphometrics, and monitoring of ontogenetic diversification in the electric organ discharge (EOD) waveforms to build up the first convincing phylogenetic hypothesis for *Campylomormyrus*. Sequences of mitochondrial and nuclear genes consistently identified at least five reciprocally monophyletic clades occurring in sympatry. Assignment tests and pairwise F_{ST} values based on 16 microsatellite loci corroborated these results. Morphometric analyses showed that the major source of differentiation among clades resides in traits correlated with the feeding ecology. These results, along with those on adult EODs, suggest that *Campylomormyrus* underwent an adaptive radiation, possibly in sympatry. This was triggered by sexual selection via assortative mating due to differences in EODs and was associated with divergent selection of ecologically important morphological traits. Genetic and morphometric data, taken altogether, allowed us to revise the current systematics of this speciose genus.

Inwieweit kann man die Synonymisierung einer Biodiversitätsdatenbank überlassen – oder warum Carl von Linné kein Systematiker, sondern ein Informatiker war

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Synonyme, also die unterschiedlichen wissenschaftlichen Namen für ein und dieselbe Art, verursachen bei artbezogener Datenspeicherung und Auswertung in Biodiversitätsdatenbanken erhebliche Probleme. Die Autoren haben ein Verfahren ausgearbeitet und in der Datenbank ZOBODAT implementiert, das die Zuordnung von Synonymen zum jeweils gültigen Namen ganz oder teilweise automatisiert und dennoch eine korrekte artbezogene Datenspeicherung und Auswertung mit minimalem Aufwand gewährleistet.

Carl von Linné hat vor über 250 Jahren die binäre Nomenklatur eingeführt, um Arten mit einer möglichst kurzen Zeichenkette eindeutig zu kennzeichnen und um die bis dahin herrschende Begriffsverwirrung zu beenden. Es war keineswegs die Absicht von Linné, die binäre Nomenklatur dazu zu verwenden, um phylogenetische Zusammenhänge abzubilden, wie das heute etwa bei der Zuordnung von Gattungsnamen ganz selbstverständlich gefordert wird. Das Verfahren von Linne ist dem Konzept des Primärschlüssels in einer relationalen Datenbank informationstheoretisch äquivalent.

Um den enorm hohen Arbeitsaufwand des Synonymisierens bei der Verarbeitung artbezogener Daten zu reduzieren, haben die Autoren zunächst ein Anforderungsprofil für eine Lösung zusammengestellt. Anschließend wurden die Synonymieprobleme am Beispiel der Chrysomeliden (Blattkäfer) Mitteleuropas acht verschiedenen Kategorien zugeordnet und für jede Kategorie eine Lösung erarbeitet, die die Anforderungen ganz oder so weit wie möglich abdeckt. Die Häufigkeitsverteilung der Synonymieprobleme bezogen auf die Artenzahl ergibt, dass bei 84 % der Arten mit Synonymen deren Handhabung vollständig algorithmierbar und bei weiteren 10 % immerhin teilweise algorithmierbar ist. Diese Zahlenverhältnisse treffen in der Größenordnung auf die meisten mitteleuropäischen Insektenarten zu. Das Verfahren liefert auch klare Kriterien, für welche Schritte und in welchen Fällen man Spezialisten direkt oder für die Supervision von Nichtspezialisten braucht.

Phylogenomics of papillomavirus and the biological interpretations

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The rapid increase of published sequence data challenges classic evolutionary approaches for the reconstruction of the tree of life. The individual choice of the taxon sampling, the specific genomic segments, and the methodology for phylogenetic reconstruction have a tremendous impact on tree topologies and their biological interpretation. The circular double-stranded DNA genome of papillomaviruses (PVes) (total 8 kb) consists mainly of four large genes E1, E2, L2, and L1. Approximately, 150 viral genomes have been completely sequenced to date. We analyzed a representative sample of 56 PV genomes, using Maximum Likelihood, Bayesian inference, Maximum Parsimony, and distance-based methods on nucleotide as well as on amino acid alignments by deploying high performance computing methods. When the four genes were analyzed separately, amino acid-based phylogenies contradicted each other less than did nucleotide-based trees (judged by partition homogeneity tests). Especially the L2 gene generated significant incongruence ($p < 0.001$). Combined analyses of the remaining genes E1-E2-L1 (3.7 kb) produced a well-supported phylogeny including supertaxon $\beta+\gamma+\pi+\xi$-PVes (infecting Carnivora, Lagomorpha, Primates, and Rodentia) and supertaxon $\kappa+\lambda+\mu+\nu+\sigma$-PVes (infecting Artiodactyla, Carnivora, Primates, and Rodentia). Based on the tree topology, host-linked evolution appears plausible at shallow, rather than deeper, taxonomic levels. Diversification within PVes may also involve adaptive radiation into different niches (within a single host species) and recombination events (within single host cells). Heterogeneous groups of closely related PVes infecting, for example, humans and domestic animals such as hamster, dog, and cattle suggest multiple infections across species borders. The molecular data globally supports a complex evolutionary scenario for PVes, which is driven by multiple mechanisms, rather than solely by host-parasite co-evolution. Apart from PVes, our approach using both a maximum of reliable genetic information and the battery of phylogenetic tools currently available might also be suitable to other pathogens with small genomes.

Neotenic evolution and classification: the case of the Lejeuneaceae

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It is often assumed that neoteny has played an important role in the morphological evolution of plants but few attempts have been made to assess the classifications of these neotenic organisms using modern phylogenetic methods.

We have assessed the relationships and classification of neotenic taxa in the family Lejeuneaceae (Marchantiophyta) using chloroplast DNA sequences and morphology. Lejeuneaceae are a highly diverse group of tropical rain forest organisms and possess several unique neotenic features that probably evolved as adaptations to ephemeral substrates. Three different types of neoteny occur in this family, protonemal, primary and secondary neoteny. Primary and secondary neoteny occur in hundreds of species, in about ten genera, whereas protonemal neoteny is extremely rare and only known in the enigmatic *Metzgeriopsis pusilla*, hitherto classified as a separate subfamily or even family.

Our analysis indicates that this protonemal neotenic taxon has evolved from a primary neotenic ancestor. Moreover, primary and secondary neoteny apparently originated by multiple heterochronic events. Dating of the molecular tree using penalized likelihood suggests that these evolutionary events are of relatively recent date and occurred since the Mid-Tertiary.

The consequences of these findings for the classification of the neotenic members of Lejeuneaceae and of other neotenic taxa of Marchantiophyta are discussed.

The Coelomic Origin and Phylogenetic Affinities of the Phoronida

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The horse-shoe worms (Phoronida) comprise 11 exclusively marine species. They are sessile inside a chitinous tubes and feed on suspended organic matter, they is filtered from the water with their perioral tentacles. The tentacles originate from a slightly horseshoe-shaped ridge, the lophophor. Tradionally phoronids are grouped with Brachiopoda and Bryozoa, comprising the Lophophorata. The pelagic phoronid larva, the actinotrocha, is planktotrophic and has a distinct epi- and hyposphere and numerous tentacles. In contrast to the remaining phoronids, *Phoronis ovalis* Wright, 1856 has a lecithotrophic, slug-like larva that ones hatched from the parental tube, crawls on the substrate using a distinct ventral rim surrounding the mouth pore. No tentacles or body regions can be detected. In order to find shared characters of this larva and the lecithotrophic larvae of Brachiopoda, the *P. ovalis* larva was studied ultrastructurally in terms of coelomogenesis and mesoderm differentiation. Prior to gastrulation the first mesodermal cells delaminate from the vegetal ectoderm of the blastula into the blastocoelic space. After gastrulation a compact strand of mesodermal cells forms that surrounds the archenteron. Later, the strand becomes divided into two parts, an anterior and a smaller posterior one. The latter encircles the major portion of the intestine. Both compartments become double layered and the coelomic cavities are formed by fluid accumulation. According to our cladistic analyses *P. ovalis* is the sister taxon to the remaining Phoronida. Among Brachiopoda the Craniida have a lecithotrophic larva, in contrast to the larvae of the remaining articulate brachiopods. Distinct correspondences in the formation of the coelom in the craniid larva and the *P. ovalis* larva indicate that a lecithotrophic larva represents the primary type of larva in Phoronida in Brachiopoda. It remains to be shown whether this indicates a common ancestry of Phoronida and Brachiopoda, probably in the sense of an intregration of the Phoronida into the Brachiopoda (Cohen & Gawthrop 2005: ODE 5:253-273), or a plesiomorphy of the Lophorata or even the Radialia or Lophotrochozoa.

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Coevolution in a tropical ant-plant association? The case of *Macaranga-Crematogaster*

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One of the most species-rich ant-plant mutualisms worldwide consists of the palaeotropical pioneer tree genus *Macaranga* (Euphorbiaceae) and its manifold associations with ants from the genus *Crematogaster* (Myrmicinae), mainly of the subgenus *Decacrema*. About 30 *Macaranga* species in South East Asia are associated with at least ten *Crematogaster* and a few *Camponotus* species. Phylogenetic studies suggest that myrmecophytism has evolved several times independently in *Macaranga*. In these obligate relationships the plants provide food and nesting space in exchange for protection by their ant partners. *Macaranga*-associated *Decacrema* species have not yet been found outside their host-plants, and 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. The obligatory symbiosis may reduce gene flow among populations and may lead to a close co-evolution between ants and plants, even though dispersal modes are quite different. Whereas the ants disperse through the flight capability of the queen, the plants are mainly dispersed via thrips (pollen) and birds (seeds). A good congruence between the phylogenies of the two partners was indeed found at the level of species groups, where major groups of ants were specifically associated with the main myrmecophytic lineages in *Macaranga*. Within these groups, however, no strict co-cladogenesis was observed. Furthermore, ecological studies have shown that most *Decacrema* morphospecies colonize not a single but several host-plant species. These data suggest that local adaptations to specific host plants are uncommon, whereas host-shifts or host-expansion are common, and that phylogenetic relationships and co-speciation are probably not the major factors shaping the *Macaranga-Crematogaster* associations. The limited dispersal ability of the ants and different selection pressures exerted by alternative hosts in the same habitat patches may enhance diversification processes. To investigate how the interdependence of ants and plants may influence patterns of geographic substructuring, we compared phylogeographic and population genetic data of the two symbiotic partners across Borneo. In those cases where both data sets are congruent, we hypothesize that the mutual interactions may promote co-diversification.

Gene in Raum und Zeit: Phylogeographische Untersuchungen am *Melanargia galathea* / *Melanargia lachesis* – Artkomplex

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Die klimatischen Schwankungen während des Pleistozän prägten die aktuelle genetische Textur von Organismen in Europa. Der Wechsel von Warm– und Kaltzeiten führte zu einer Verschiebung der Verbreitungsgebiete von Arten. Insbesondere thermophile Arten starben während der Eiszeiten in Mitteleuropa aus und überdauerten in Refugialgebieten südlich der großen europäischen Gebirge (Pyrenäen, Alpen, Karpaten). Während der häufig über hunderttausend Jahre andauernden Kaltzeiten differenzierten sich genetische Linien innerhalb einer Art und es entwickelten sich neue Arten. Die postglazialen Wiederbesiedlungsmuster Mittel- und Nordeuropas wurden von zahlreichen Biogeographen an unterschiedlichen Organismen beschrieben. An der Gattung *Melanargia* (Lepidoptera: Satyrinae) konnten wir mit Hilfe allozymelektrophoretischer Analysen genetische Muster detektieren; auf deren Grundlage lässt sich die nacheiszeitliche Wiederbesieldung sowie potentielle Differenzierungszentren während der Glaziale feststellen. Neben einer vollständigen Differenzierung in die Art *M. lachesis* in Spanien konnten wir innerhalb der Art *M. galathea* eine westliche und eine östliche genetische Linie als Folge der Isolation während der Eiszeiten nachweisen. Die Art überdauerte das Würm-Glazial in Italien und am Balkan. Außerdem konnten wir eine genetische Strukturierung des südosteuropäischen Differenzierungszentrums in drei Subzentren (i) südlich dem Schwarzen Meer, (ii) die heutige griechische Küste und (iii) die Ex-Jugoslavische Küstenregion, nachweisen. Die Analyse von Proben aus Nordafrika (Atlasgebirge) zeigt eine deutlich höhere genetische Diversität und eine starke genetische Differenzierung der einzelnen beprobten Lokalpopulationen auf einem relativ kleinen Areal und für Nordafrika endemische Allele. Diese Befunde belegen ein nordafrikanisches Artbildungs- und Ursprungszentrum von *M. galathea*. Es ist anzunehmen, dass die Art Europa während der letzten Warmzeit (Eem-Warmzeit) vor ca.130.000 Jahren besiedelte. Da zu diesem Zeitpunkt die Iberische Halbinsel bereits von der Schwesterart *M. lachesis* besiedelt war, erfolgte die Kolonisierung Europas von *M. galathea* vermutlich ausschließlich über Sizilien / Italien.

Phylogenie der Sacoglossa (Gastropoda: Opisthobranchia)

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Die erste Phylogenie der Sacoglossa wurde 1996 von K.R. Jensen präsentiert. Sie basierte auf morphologischen Daten und umfasste ca 30 Gattungen. Ihre Verwandtschaftshypothese zeigt zwei klar getrennte evolutive Linien: die Placobranchacea mit den monophyletischen Schwestergruppen Placobranchoidea und Limapontioidea, und die Oxynoacea. Letztere vereint die beschalten Sacoglossen. Bereits Jensen weist auf die wenig aufgelösten Verwandtschaftsverhältnisse innerhalb der Untergruppen hin. Wir untersuchen die Phylogenie der Sacoglossen mit Hilfe zweier molekularer Marker des mitochondrialen Genoms (jeweils ein partieller Abschnitt des 16S-rDNA Gens und des COI-Gens), wobei wir insbesondere von den sehr artenreichen Taxa (z.B. Elysia und Thuridilla) mehr Arten aufnehmen konnten.
Die Ergebnisse werden im Zusammenhang mit den (soweit bekannten) Futteralgen diskutiert und die Hypothese von Jensen (1997) zur Co-Evolution der Algen überprüft.

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The One-Eyed Sisters: *Cambropachycope clarksoni* & *Goticaris longispinosa*, Derivatives of the Stem Lineage of Crustacea

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The two Upper Middle Cambrian (approx. 505 Ma) ‚Orsten' euarthropods *Cambropachycope clarksoni* and *Goticaris longispinosa* are sister species sharing, besides other characters, a large single and anteriorly projecting compound eye. Moreover, these eyes are extended into a pointed end distocaudally and bear a small hook ventrally. The two taxa were described already in 1990 and were recognised as derivatives of the stem lineage towards the Eucrustacea. In the original description at least three different larval stages were mentioned for *G. longispinosa*, but not explained in detail. Due to new material at hand, we could recognise larval series for both species embracing no less than five succesive stages each using the morphogenesis of structural details. All instars have been reconstructed as 3d computer models for a better visualisation and comparability of morphological structures. Ontogeny of early fossil taxa, as exemplified by *C. clarksoni* and *G. longispinosa*, turns out to be an important tool and data set aiding to improve our knowledge about the early evolution of Crustacea.

The nematode genus *Pristionchus* : a model for cryptic speciation, Haldane´s rule and species invasion

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Diplogastrid nematodes of the genus Pristionchus are associated with beetles - not being parasitic or phoretic but necromenic. That means they rest on their beetle host until it dies and then start to grow and reproduce feeding on the bacteria and fungi growing on the carcass.

In a large scale field study we could find 18 Pristionchus species in different parts of the world on many beetle species- mostly members of the superfamily Scarabaeoidea. Because of high phenotypic plasticity, species identification of the nematodes by morphological measurements was not applicable. We therefore established a method of determination of species by sequencing the small subunit of the ribosomal RNA (SSU) in the first place. The results were then confirmed by mating experiments with reference strains.

Sometimes two close related species (P. aerivorus and P. pseudaerivorus n. sp.) occured on the same beetle. Mated with each other they give infertile offspring that follows Haldane´s rule in that males are highly underrepresented or absent.

Finally, one species (Pristionchus uniformis) occurs both in the United States of America and Western Europe on the Colorado potato beetle. Given the introduction of the Colorado potato beetle to Europe in 1877, our results suggest that P. uniformis was introduced together with its beetle vector.

Paraphyletic vs. monophyletic taxa - evolutionary vs. cladistic classifications

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The criteria for classification of organisms are still under intensive debate. Phylogenetic methods and Hennigian principles of classification are nowadays routinely used in systematics, and monophyly is widely accepted as the only criterion for grouping of taxa. On the other hand, facing an accumulation of phylogenetic classifications that are in strong conflict with traditional taxa, proponents of paraphyletic taxa request a consideration of evolutionary processes for classification.

A basic problem of cladistic classifications is the assumption that evolutionary processes always result in a dichotomous split of taxa, ie., an extant taxon cannot be at the same time the progenitor of another taxon. By reviewing several evolutionary processes such as budding, anagenetic speciation, and hybridization, I will demonstrate that non-dichotomous branching processes are common in evolution, resulting frequently in the synchronous existence of progenitors and derivatives. If such groups of taxa are analyzed using cladistic tree-building methods, the progenitors, although previously monophyletic, are automatically turned into a paraphyletic group. If clades are taken directly as a basis for classification, this results in large inhomogeneous taxa or misconceptions of “older” natural taxa. Such taxa fail to reflect evolutionary processes and are therefore regarded as unsatisfactorily by proponents of evolutionary classifications (e.g., Mayr & Bock, J. Zool. Syst. Evol. Research 40: 169–194 (2002); Hörandl, Taxon 54: 564-570 (2006).

Possible solutions of the problems are (1) integration and further development of alternative phylogenetic methods (e.g., network and patristic methods) for a better understanding and visualization of evolutionary processes, (2) a more comprehensive sampling of markers and characters that reflect evolutionary processes, and (3) a consideration of paraphyletic taxa if (1) and (2) are not yet available for the classification of a certain group.

Unrecognised species complex of *Thecidellina* (Brachiopoda) in the Caribbean and the Atlantic

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Recent thecideide brachiopods are sessile filter-feeders belonging to two subfamilies, Thecidellininae and Lacazellinae. Whereas the Lacazellinae comprises four genera, the Thecidellininae include only one Recent genus, *Thecidellina*. The representatives of this genus live in cryptic habitats of coral reefs and are known for their unique brood care. To date, only six species of *Thecidellina* have been described worldwide. Samples of this genus were often left undescribed or uncritically assigned to one of the six available species, either depending on their geographical provenance or macroscopic resemblance. The rarity of obvious diagnostic and discriminating characters within the genus led to the small number of species descriptions within *Thecidellina*, despite its worldwide distribution.

In this study we investigate the peculiar case of the distribution of the Atlantic thecideide species *Thecidellina barretti* (Davidson,1864), the type species of *Thecidellina*, originally described from Jamaica, Caribbean.

Over the last few decades, specimens of *Thecidellina* have been collected from other locations within the Caribbean, e.g. the Bahamas, Curaçao, Cayman Islands, and Cape Verde. With genetic studies still to come, we - as a first step – here re-examined the skeletal structure of *Thecidellina* specimens from these additional localities by scanning electron microscopy.
Surprisingly, there is a high morphological diversity of *Thecidellina* within the Caribbean, suggesting an unrecognised species complex. The internal structures offer a set of valuable discriminating characters providing a basis for new species descriptions. However, there is no obvious correlation between the geographic distribution and the occurrence of distinct morphs.

As a next step we will compare the results of our morphological analyses with molecular data to figure out whether there is a cryptic speciation or a high morphological variability of *Thecidellina* in the Caribbean and the Atlantic.

Rapid radiation and colonization processes in the genus *Sphingonotus* FIEBER, 1852

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The Mediterranean region is one of the worldwide hotspots of biodiversity, with a high number of species and endemics to several islands or peninsulas. The genus *Sphingonotus* FIEBER, 1852 is one of the largest grasshopper genera, containing more than 100 species, which occur throughout the Mediterranean, Central Asia and East Asia. Most of the species are confined to semi-desert or desert habitats. Although many *Sphingonotus* species are rather common in northern Africa, the genus is still taxonomically insufficiently studied. Here, we present a phylogenetic analysis of the West Mediterranean species of the genus *Sphingonotus*. The aim of our study was to resolve speciation and colonization patterns of the Canarian and West Mediterranean species.

We sequenced a mitochondrial gene fragment (ND5) and the nuclear gene fragment (ITS2) of 94 individuals belonging to 21 species and subspecies. The resulting dataset was analysed using six different methods of phylogenetic inference (Maximum Parsimony, Maximum Likelihood, Minimum Evolution, Bayesian Inference, UPGMA and Neighbour Joining).

Our data suggest that the oldest taxa evolved during the Pliocene, about 4.1 million years ago. The phylogenetic relationships suggest that the genera *Sphingonotus, Pseudosphingonotus* and *Wernerella* are polyphyletic. Hence the two latter genera have to be synonymized with *Sphingonotus*. A high number of young species belong to two recent radiations (*S. caerulans*- and *P. azurescens*-group). The speciation process of these taxa is still not completed and the taxonomic status of some species is rather dubious. The origin of these lineages dates back about 200.000 years ago.

Our data does not support a stepping-stone model for the colonisation of the Canary Islands, but suggests multiple colonization and extinction events. These colonization events differ strongly in time, including palaeoendemics (*W. guancha, W. picteti, W. rugosa*) as well as neoendemics (*W. pachecoi, S. sublaevis, S. willemsei*). Populations of *W. pachecoi* from Fuerteventura are genetically distinct, indicating the presence of a cryptic species.

S. caerulans from northeastern Europe are related to some band-winged relict populations from the Sierra Nevada in Spain, which have usually been misidentified as *S. azurescens*. The western European lineage of *S. caerulans* is related to the more widespread bluish-winged Spanish populations. *S. rubescens* is a young sister species of *S. caerulans*, which colonized parts of southern Europe, northern Africa and the Canary Islands rapidly. Many of the older lineages are endemic to small geographic regions (*P. airensis*: Air mountains, *P. candidus lusitanicus*: southern Portugal). The taxonomic status of many younger species and subspecies needs further investigation, including more sensitive genetic methods (e.g. Amplified Fragment Length Polymorphism) and bioacoustic investigations.

Naming and ranking in phycology

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Phycology is dealing with algae, i.e. organisms which are doing predominantly the job of a plant in a water ecosystem. Therefore, phycology is a discipline of botanical research. Historically, especially the flagellated species have been treated either as plants because of photosynthesis or as animals because of their movement. These biregnal taxa, which can be treated by the rules of two different codes (International Code of Botanical Nomenclature, Vienna Code, ICBN 2006 versus International Code of Zoological Nomenclature, ICZN, 1999), are a serious problem in science when conflicting rules are used for one single taxon. These problems occur in the Cryptophyceae, Dinophyceae, Euglenophyceae and additionally in the Bacillariophyceae, Chrysophyceae and Chlorophyceae, when dealt with in historical works.

In the euglenoids, for example, several single species have different names under different codes; e.g. well established taxa below the subspecies rank, valid according to the ICBN, are unavailable under the ICZN. A complete change of organism clades from the responsibility of the ICBN into the responsibility of the ICZN or vice versa would cause an extreme instability of names which is against the preambles of the ICBN and the ICZN, respectively. To make things even more complicated, in the current phylogenetic discussion the algae are classified within at least four different kingdoms. Does this imply that more specialized Codes are needed?

A solution might be the implementation of the universal BioCode, which was discussed in the 1990s and was supposed to go into effect in 2000. But the drafted BioCode has been put on ice as was the registration of botanical names in databases as a prerequisite for valid publication. We think, the time is ready for a single BioCode encompassing all organisms!

„Mining deeper“ – additional characters for reconstruction of acochlidian phylogeny

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The phylogeny and evolution of the enigmatic Acochlidia, a comparably small group of opisthobranch gastropods with 27 valid species, remains unresolved, due to a lack of reliable primary data and a generally poor set of valuable characters for taxonomic and phylogenetic analyses. In order to enhance the quality and quantity of primary data, current studies focus on a detailed (re-)description of phylogenetic important acochlidian species, including the 3-dimensional reconstruction of their anatomy using AMIRA software, scanning electron microscopical (SEM) examinations of radulae, calcareous parts and external characters of the body wall, as well as transmission electron microscopical (TEM) investigations of sperm and spermatophores.

In order to gain further phylogenetically informative character sets, these morphological studies are exemplarily supplemented by investigations on the ontogenetic development of muscle and nervous patterns by means of immunocytochemistry combined with confocal laserscanning microscopy, with a special focus on the innervation pattern of cephalic sensory organs, difficult to reveal with traditional histological methods. To approach an acochlidian phylogeny with molecular methods, a set of molecular data consisting of mitochondrial genes (16S, COI) and nuclear ribosomal DNA (18S and 28S) is tested for its phylogenetical information content. Preliminary results support pervious morphologically-based trees. Secondary rRNA (18S, 28S, 16S) structures of available acochlidian and other euthyneuran taxa are exemplarily analysed and compared. This “molecular-morphological” dataset offers promising additional characters for phylogenetical analyses at different taxonomic levels.

Future studies aim to reconstruct acochlidian phylogeny and evolution based on a combined analysis of the collected morphological, molecular and “molecular-morphological” data.

Determining the phylogenetic position of *Mammuthus* versus *Elephas* and *Loxodonta* (Elephantidae) with mitochondrial genes: Why did it take so long?

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The first ancient DNA sequences from Woolly mammoth (*Mammuthus primigenius*) genes were published in 1994. The primary goal was to solve a very simple 3-taxon problem: Which 2 out of the 3 genera, *Elephas*, *Loxodonta* and *Mammuthus*, are sister taxa? Regardless of many attempts in the following 11 years, it took till 2005 to solve the question. KRAUSE et al. (2006) sequenced the complete mitochondrial genome of *Mammuthus primigenius* and found strong evidence for a clade *Elephas-Mammuthus*. The only paper that produced a similar clear evidence for *Elephas* as sister taxon of *Mammuthus* was the one by JOGER & GARRIDO (2001) using control region sequences of 8 *Mammuthus* individuals. Studies using cytochrome b (cyt b) sequences (including our own) produced ambiguous and unreliable results. But why?

A closer look on the particular regions of the *Mammuthus* cyt b gene studied by different authors revealed that one region of the gene in deed shows more common bases with *Loxodonta* cyt b than with *Elephas* cyt b, whereas another region of the same gene has more similarities with *Elephas* cyt b and a third region would favour even an *Elephas*-*Loxodonta* sistership. Studies using the whole cyt b gene were not able to find enough support for any of the alternatives. The lack of a suitable outgroup such as other extinct proboscideans contributed to this failure.

Other problems with earlier studies include very low sample size (single individuals) and high sequence variability between individuals. The question must be asked whether this variability is real or due to degraded DNA or amplification errors.

The experiences gained with such studies can teach us lessons which are useful for future work on ancient or degraded DNA.

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Palaeontology of the European freshwater crabs (Brachyura, Potamidae)

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Freshwater crabs represent one of the most diverse groups of brachyuran crustaceans. In the recent past, they were object of intense research concerning their taxonomy, phylogeny and population biology. In contrast, the freshwater crabs' fossil record remains poorly known, although several studies on freshwater crabs use palaeontological data to approach divergence times or to evaluate hypotheses on their historical biogeography.

To close this gap, we recorded all taxonomic data on the fossil freshwater crabs of the European Neogene and propose a revised taxonomy. We recognise six species of fossil freshwater crabs, that we assign to the genus *Potamon*. Therefore we contradict former assumptions on a relationship with African or Southeast Asian freshwater crabs and argue for these fossil freshwater crabs to belong to the stem-group of the modern European potamids.

Current excavations in the vicinity of Lake Constance (Höwenegg, south Germany) and Graz (Gratkorn, Austria) yielded new specimens and indicate that freshwater crabs occur more frequently in the miocene freshwater deposits of Central Europe than previously thought.

Cranial muscles in caecilian larvae: a contribution to the ground pattern of the Lissamphibia

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According to the Batrachia-Hypothesis, caecilians (Gymnophiona) are considered to be in a sister-group relationship to the Batrachia, i.e. frogs (Anura) plus salamanders (Caudata). Thus, knowing the Gymnophiona is essential in reconstructing amphibian evolution. Free living larvae, that pass through a metamorphosis to the adult, are present in the Anura, Caudata, and Gymnophiona. The cranial musculature in larvae of frogs and salamanders was used in previous studies for the reconstruction of amphibian evolution. However, the cranial musculature in caecilians has been neglected until recently. This study examines the head-muscles in larvae of the caecilian species *Epicrionops bicolor*, *E. petersi*, and *Ichthyophis kohtaoensis*. Homologies of cranial muscles in the different groups of the extant amphibians (Lissamphibia) are proposed. Most of the muscles in caecilians are also present in salamanders and frogs and can be assigned to the lissamphibian ground pattern. The muscles that transform to the m. depressor mandibulae in adults (m. depressor mandibulae group) differ in frogs as compared to caecilians and salamanders. Based on the Batrachia-Hypothesis, the condition of the m. depressor mandibulae group in caecilians and salamanders is plesiomorphic and part of the ground pattern of the Lissamphibia; the condition in frog tadpoles is derived. Within the three extant amphibian lineages, the m. levator quadrati and the m. pterygoideus are unique to the Gymnophiona; the presence of these muscles in larvae of the common lissamphibian ancestor remains to be resolved.

Anttypes.org: a new online resource for modern ant taxonomy

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Progress in ant taxonomy is still hampered by lack of easy access via internet to well documented and researchable museum collections including their type specimens. German natural history museums hold a number of medium-sized collections of international importance (e.g. coll. Roger, Seifert, Stitz, Viehmeyer, part of Forel etc.). However, only incomplete information about ant collections in Germany exists and only few type catalogues of ants in German museums have been published [e.g. www.senckenberg.de; www.zsm.mwn.de/wiss_start.htm]. In this context, the FoCol-project as part of the German Global Biodiversity Information Facility program [www.gbif.de] focuses on ant collections in Germany and their primary type specimens. All types are characterised in detail in the following way: original name, author and year of description, citation, currently recognised taxonomical status, type locality, collection date and collector, digital photos of the pin and labels and of frontal, lateral and dorsal views of the ants. For the digital photos a high-resolution camera and the software package AutoMontage® is used [www.syncroscopy.com] to produce a series of in-focus images from which a single image with extended focus is calculated. The dataset will be finished during 2007 and will include then about 3000 entries of some 1500 type taxa and more then 17.000 photos.

All data including the photos will be available via the GBIF portal [www.gbif.org] using the internet database SysTax [www.biologie.uni-ulm.de/systax] and the newly created ant type portal “Anttypes” [www.anttypes.org]. Besides photographs and taxonomic information the site offers contact data and direct links to the collections where the types are hosted, and a continuously updated and extended link list on myrmecological topics. The internet-based documentation makes a time-consuming search for ant types unnecessary and allows a rapid type examination for most purposes. In most cases travelling to museums or mailing of types become unnecessary, thus reducing budgets and time required for taxonomic investigations. By minimizing physical handling, the database also will help to conserve the types for the future.

New insights into the phylogeny of Euthyneura (Mollusca, Gastropoda)

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The Euthyneura, including Opisthobranchia and Pulmonata, comprise a rather diverse group of higher Gastropoda inhabiting marine, limnic and terrestrial habitats. Due to their different life histories they display a heterogeneous array of morphological characters rending reconstruction of evolution and phylogeny based on morphology difficult. Molecular systematic approaches including euthyneuran gastropods of all major taxa have been very sparse and have not satisfactorily resolved phylogenetic relationships within Euthyneura.

We performed a comprehensive molecular systematic study of more than 50 euthyneuran taxa based 18S-, 28S- and 16S rRNA as well as CO1 sequences (more than 4000bp in total). Bayesian inference methodologies as well as supertree approaches were conducted. We will present results on the phylogenetic relationships within Euthyneura and discuss the systematic status (monophyly versus paraphyly) of the major euthyneuran subgroups. Moreover we will shed light on questions regarding macro-evolution of Euthyneura, as e. g. invasion of limnic and terrestrial habitats.

Larval development of remipede crustaceans

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During diving expeditions to the Bahamas in March and August 2006, we collected 14 crustacean larvae that could be identified as belonging to the Remipedia. Previously, practically nothing was known about the mode of development in this group of hermaphroditic crustaceans. All larvae were collected from anchialine cave systems below the halocline. The collection consists of two orthonauplii, 11 metanauplii, and one postnaupliar specimen that exhibits distinct transitional developmental features between naupliar and adult morphology. Based on this series of different larval stages, it is possible for the first time to reconstruct the early development of remipede crustaceans.

Neandertal Genomics

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Neandertals are a hominid group that is morphologically distinct from modern humans. They appeared in the European fossil record around 400.000 years ago and disappeared around 30.000 years ago and are believed to be our closest extinct relatives. Although Neandertals and modern humans overlapped in certain regions in time and geographic range, the relationship between us and them is unclear and contentious. Genetic comparisons between modern humans and Neandertals could both address this relationship between us and them and offer the possibility to identify genetic changes that happened specifically on the human lineage.

We extracted DNA from a 38,000 year old Neandertal fossil found to be exceptionally free of modern human contaminating sequence. Direct sequencing using the 454^{TM} sequencing platform from this extract yielded nearly one megabase of hominoid DNA sequence. Several lines of evidence, including comparison to a modern human sample sequenced in a similar way, indicate that the fossil extract sequence is of Neandertal origin. Comparison to the human and chimpanzee genomes reveals that modern human and Neandertal DNA sequences diverged on average about 500,000 years ago and the effective size of the ancestral population of the two groups was similar to the effective population size of modern humans. Extrapolating from this study, we conclude that the existing technology and fossil resources are sufficient to begin a Neandertal complete genome sequencing project.

Simultaneous Inference of RNA Structure and Multiple Sequence Alignment

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One of the crucial, if not the most important step of molecular phylogenetic inference is the alignment of the sequence data. Several recent investigations show that the choice of alignment approaches is more important than tree reconstruction methods. The goal of an accurate multiple sequence alignment is to find homologous positions, as only those can provide reasonable markers of genealogical descent. One approach to improve the accuracy of a multiple sequence alignment is to take into account prior knowledge about the examined sequences. For ribosomal RNA this knowledge mainly depends on the functional secondary and/or tertiary structures of these genes. Here we represent a new computer based method for a simultaneous alignment of ribosomal RNA sequences and their corresponding structures. A preliminary multiple alignment of the examined rRNA sequences is compared with a known structure of the appropriate ribosomal gene. Matching structure information is evaluated by searching for conserved motifs in the alignment. In the next step, patterns of co-variation are located via consistent and compensatory substitutions. The resulting structure skeleton is taken as a constraint for individual sequence folding of the highly variable regions by predicting minimum free energy structures. This leads to a complete structure for each sequence. The final alignment of the combined sequence/structure elements is done by taking both structure and sequence information for each position into account. The resulting alignment can now be used as an input for several phylogenetic reconstruction programs, like PAUP*, MrBayes or PHASE.

3-d reconstruction of the hyo-laryngeal complex based on ontogenetic data: cladistic implications for primates and their relatives

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Concerning the topic of primate supraordinal relationships, there exists a major incongruence: molecular biologists usually favour the Euarchontoglires-grouping, which consists of the Euarchonta (= Primates + Dermoptera + Scandentia) and the Glires (= Lagomorpha + Rodentia). However, many morphologists still adopt the Volitantia hypothesis, a clade defined by the sister-groups Dermoptera (flying lemurs) + Chiroptera (bats). Actually, these two orders represent the core of the traditional superorder Archonta. As many key characters are concluded from highly-adapted postcranial data, the presented approach considers the 3-d reconstruction of the hyo-laryngeal complex - an anatomical region that might be named as a cladistic “terra incognita” and could serve as a window on primate origins. In the context of a dissertation, two other morphological sections have also been investigated in order to enlarge the amount of character states: the (1) dentition and (2) tarsal region. Finally, some methodological remarks on the phenomenon of intersubjectivity are made.

The Atelocerata: a vanishing hypothesis - molecular phylogeny of basal hexapods

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This project is designed to be integrated into the SPP 1174 "Deep Metazoan Phylogeny - Stammesgeschichte der Grossgruppen der Tiere" (DFG). In this project we will contribute data from basal hexapod lineages and myriapods. The contribution of these two arthropod groups will be important in clarifying long still insufficiently resolved phylogenetic questions concerning the evolution of arthropods. Besides contributing data for the metazoan tree, the project will focus on two pieces of detailed work: a) a basal phylogeny of hexapod lineages, in coordination with projects of the SPP 1174 on pterygote insects and b) on a phylogeny of the myriapods. The sequencing efforts refrain from sequencing mostly easily accessible mitochondrial genes, but instead will rely on EST analyses which will deliver many new gene targets for these phylogenetic reconstructions. Together with sequencing of more traditional genetic markers, both subprojects can be expected to deliver new insights into the evolution of hexapods and myriapods. Robust phylogenetic relationships among arthropod groups, and in particular among hexapod and myriapod lineages, will help to improve our interpretation of assumed ground plan body patterns and evolution of arthropod terrestrial life. It can be expected, that the published results from these analyses will foster new molecular investigations in various fine scaled phylogenetic analyses of arthropod groups by profiting from the comparative EST data.

Biebersteiniaceae Endl.: status, position, origin, and revised age estimates for the families of Sapindales

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Biebersteinia is a genus of perennial herbaceous plants distributed in temperate mountainous regions from China in central Asia to Greece in southeastern Europe. Phylogenetic affiliations of the genus were unclear from the beginning of its taxonomic history as the combination of morphological characters provided insufficient or conflicting evidence for its placement. In spite of its small size, no previous study included all species of the genus. In the present investigation we report on a phylogenetic study of *Biebersteinia* based on plastid *rbc*L data covering all species and the genus' whole geographical range, and including all its phylogenetically closest relatives among flowering plants. Together with information on fossils and the extant distribution of species in the genus, we focus on the following topics: (1) family status of Biebersteiniaceae; (2) resolution of its phylogenetic position relative to Sapindales as well as to other related orders; and (3) temporal and (4) geographical origin of the genus. (5) In addition we use our phylogenetic and temporal framework to provide a revision of age estimates for the families of Sapindales. The comparison of age estimates by previous authors to our estimates shows that former calculations underestimated the ages of several divergence events in Sapindales by up to more than 50%. This asks for caution of calibrating phylogenetic trees on a higher taxonomic level with low sampling of taxa at generic level and highlights the importance of corroboration of results not only by a single calibration point but several independent lines of fossil evidence. "Model systems" in parts of plant phylogeny with a relatively rich fossil record, like Sapindales and its families, could be used as testbeds for emerging procedures to estimate divergence time in the future. Cross-validation using multiple fossils (rather than more sequences) may pave the way for evaluating progress in methodology within these more empirically rich taxa.

Evolutionary history of the burnet moth genus *Zygaena*: phylogeny, host-plant association and historical biogeography

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Burnet moths of the genus *Zygaena* are a striking group of primarily diurnal Lepidoptera displaying an exceptional phenotypic plasticity. Previous attempts to elucidate the phylogenetic history of the group had been confounded by a perplexing pattern of characters or insufficient taxon sampling. We inferred a phylogeny of the genus *Zygaena* by analysing 5.4 kilobases of their nuclear and mitochondrial DNA. 84 of the 98 currently recognised species in this genus are considered, including representatives of all described species groups. RNA coding sequences were aligned with reference to zygaenoid moth specific secondary structure models of corresponding molecules. We conducted phylogenetic analyses within a Bayesian framework applying partition specific substitution parameters; co-variation of paired sites in RNA gene sequences was accommodated by using doublet substitution models. Our data revealed that a considerable number of currently recognized species groups in *Zygaena* are not monophyletic. The traditional subgeneric classification proved to be artificial, too; *Agrumenia* and *Zygaena* (sensu stricto) are polyphyletic. Only the subgenus *Mesembrynus* was confirmed as a monophyletic species cluster. Contrary to previous assumptions, optimisation of larval host-plant associations on sampled trees of the Bayesian analyses suggests a shift from cyanogenic to acyanogenic host-plants within the genus and not the other way around. Our results challenge the classic assumption that early species diversification in *Zygaena* took place in the Irano-Turkestanian region. Rather, the molecular data point to the western Mediterranean area as the geographical origin of the group.

Worldwide survey of *Drosophila melanogaster* variability shows a contrasting pattern for nuclear and mitochondrial markers

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Despite its popularity in functional genetics and population genetics, the global pattern of neutral variation has not yet been comprehensively described in *Drosophila melanogaster*. For the first time, we combine a global survey of neutral microsatellite variability with pattern of mitochondrial sequence variation. 35 populations originating from five continents were compared. In agreement with previous microsatellite studies, sub-Saharan African populations were most variable. The remaining populations contained a subset of the African variation, most likely reflecting a single 'out of Africa' habitat expansion event. While the African populations also contained most mtDNA haplotypes, European/Mediterranean region harbored, the more divergent haplotypes and a higher haplotype diversity. In the light of the well-established African origin of *D. melanogaster*, our results clearly show that mtDNA is not well-suited to infer biogeography in *Drosophila*.

Subjektivität und ihr Wert – Was können Linnaeische Kategorien?

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Eine der zentralen Schwierigkeiten in der Diskussion um die Bedeutung der Linnaeischen Kategorien in der modernen Biosystematik sind grundsätzliche Mißverständnisse und eine dadurch ausgelöst Überbeanspruchung des Kategorien-Konzepts.

Linnaeische Kategorien bezeichnen hochgradig heterogene Klassen, deren Elemente nur eine verbindene Eigenschaft besitzen, nämlich ihre relative, hierarchische Position. So bezeichnet eine Kategorie diejenige Hierarchie-Ebene in einer Systematisierung, die definitionsgemäß zwischen zwei bestimmten anderen Kategorien steht.

Darüberhinaus sind Kategorien und den von ihnen bezeichneten Hierarchie-Ebenen keine weiteren, grundsätzlich gültigen Eigenschaften zuweisbar. Gegensätzliche Bemühungen, wie z.B. die Definition der Kategorien als Ausdruck des geologischen Entstehungsalters der von ihnen bezeichneten Taxa, sind vergebliche Versuche ihrer "Objektivierung". Die Zuweisung der Kategorien zu Hierarchie-Ebene ist dagegen inhärent subjektiv und spiegelt zeitlich-begrenzte Konventionen innerhalb eines gewählten phylogenetischen Bereichs wider. Innerhalb dieses klar zu umreissenden Bereichs einer Systematisierung sind Kategorien ein freiwilliges, sprachliches Instrument, dem spezifische, wenn auch limitierte Aufgaben in der Rede über den phylogenetischen Gegenstand zukommen.

Horizontal gene transfer of plastid genes in a group of non-photosynthetic parasitic plants

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Plastid sequences are among the most widely used in phylogenetic and phylogeographic studies in flowering plants, where they are usually assumed to evolve like non-recombining, uniparentally transmitted, single-copy genes. Among others, this assumption can be violated by intracellular gene transfer (IGT) within cells or by the exchange of genes across mating barriers (horizontal gene transfer, HGT). We report on HGT of a plastid region including *rps2*, *trnL-F*, and *rbcL* in a group of non-photosynthetic flowering plants. Species of the parasitic broomrape genus *Phelipanche* harbor two copies of *rps2*, a plastid ribosomal gene, one corresponding to the phylogenetic position of the respective species, the other being horizontally acquired from the related broomrape genus *Orobanche*. While the vertically transmitted copies probably reside within the plastid genome, the localization of the horizontally acquired copies is not known. With both donor and recipient being parasitic plants, a possible pathway for the exchange of genetic material is via a commonly attacked host.

A phylogeny of blennioid fishes (Teleostei), based on 12S and 16S mtDNA, and its use to trace different degrees of morphological integration of their pectoral fins

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Blennioidei (Teleostei) comprise six families of small, primarily bottom dwelling fishes occuring in coastal habitats in temperate and tropical regions. A cladistic analysis of phylogenetic relationships within Blennioidei based on 12S mt DNA sequence data by Stepien et al. (1997) combined three families into a monophyletic group, but rendered one family, Labrisomidae, paraphyletic within it. Part of my doctoral thesis was the establishment of a phylogeny based on 16 S mt DNA for the family Blenniidae, which strongly supported several clades within Blenniidae. One them consists of species with mostly eulittoralic habitats, possessing a higly differentiated pectoral fin used for seal-like locomotion in shallow water. The phylogenies mention above enable to track character evolution and the evolution of character correlations within the pectoral fin. Evolutionary correlations of certain characters within the pectoral fin are stronger if the individual characters show a higher degree of complexity.

Stepien C.A., A.K. Dillon, M. J. Brooks, K.L. Chase and A. N. Hubers (1997): The evolution of blennioid fishes based on an analysis of mitochondrial 12S rDNA. Pp.245-270 in: Molecular Systematics of Fishes. Edited by T. Kocher and C.A. Stepien. Academic Press, San Diego and London.

Taxonomy and suitable markers in freshwater sponges

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Freshwater sponges exclusively belong to the suborder Spongillina, which comprises 7 families (Spongillidae, Lubomirskiidae, Malwispongiidae, Metaniidae, Metschnikoviidae, Palaeospongillidae, Potamolepidae) and 45 genera.

An increasing number of sampled freshwater sponges cannot be classified unambiguously due to the lack of important morphological characters given in the determination keys commonly used. Given as an example: some *Ephydatia* species do not build gemmules and thus lack gemmuloscleres which are important characters for their identification which also holds true for many freshwater sponges. Since the first descriptions of freshwater sponges, e.g. Linnaeus 1758, Systema Naturae or Lamarck 1816, their taxonomy and phylogeny are revealed from morphological characters like body size, external shape, consistency, colour, skeletal architecture and scleres (shapes, dimensions and distribution or situation). But depending on the employed marker and method even antithetic results are revealed. Therefore we here discuss the limits and possibilities of already employed and possible markers or better character sets. The synthesis of all possible character sets at a weighted balance produces the most reliable data in taxonomy as well as phylogeny. Such “syntaxonomic” data sets result from morphological matrices as well as DNA-sequence alignments. We compare the resulting phylogenies and evaluate possible molecular markers for taxonomic purposes. For molecular as well as for morphological characters we found some to be not useful (e.g. ITS or colour) and some to be very suitable (e.g. 28S rDNA or scleres) for taxonomic and thus phylogenetic analysis.

Mitochondrial genomes of Onychophora

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Onychophorans play a crucial role in actual discussions of arthropod phylogeny. The ongoing Articulata – Ecdysozoa debate is in need for well supported hypotheses about ground pattern characters for Arthropoda (incl. Onychophora). As well Onychophora is an important outgroup taxon for resolving the euarthropod relationships, no matter whether morphological or molecular data are in use. Up to now there was a noticeable lack of mitochondrial genome data from onychophorans. Here we present the first two complete mitochondrial genome sequences from members of both major subtaxa, Peripatidae (*Epiperipatus biolleyi*) and Peripatopsidae (*Metaperipatus* sp.nov.). There are several special features in the two genomes. Both show an extreme degree of genome shuffling, which led to strong differences in gene order between both taxa and also in comparison to other arthropods. The *Metaperipatus* sp. nov. gene order is easily derivable from a tandem duplication of the complete genome and random-loss of genes. The *E. biolleyi* sequence lacks 9 tRNA genes usually present in bilaterian mitochondrial genomes (and present in *Metaperipatus* sp. nov.). All of these reduced tRNAs have anticodon sequences to fourfold degenerated codons, while all 13 tRNAs with anticodons to twofold degenerated codons persisted in the mitochondrial genome. Sequence based phylogenetic analysis of euarthropod relationships yielded support for Mandibulata and Pancrustacea / Tetraconata.

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Asterotremella gen.nov. *albida* a symbiontic tremelloid yeast isolated from the agarics *Asterophora lycoperdoides* and *A. parasitica*

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Using a genotypic approach (PCR-fingerprinting, DNA/DNA reassociation, partial sequences of the 26S rDNA gene, complete sequences of the 18S rDNA gene, and sequences of the internal transcribed spacer) five tremelloid yeast isolates from the agarics *Asterophora lycoperdoides* and *A. parasitica* were shown to be conspecific with *Cryptococcus ramirezgomezianus.* It was not possible to distinguish the yeast strains from *A. lycoperdoides* and *A. parasitica* using sequences from the intergenic spacer (IGS1). Phylogeny based on the 26S rDNA (D1/D2-domain) and 18S rDNA demonstrated that *C. ramirezgomezianus* is closely related to several additional *Cryptococcus* species (*C. humicola, C. longus, C. musci, C. pseudolongus*) within the Trichosporonales. A new genus, *Asterotremella*, and a new family, Asterotremellaceae were introduced for *Cryptococcus* species clustering within the Trichosporonales having an ubiquinone Q-9. *Cryptococcus ramirezgomezianus* is a synonym o*f Asterotremella albida.*

Ultrastructure and phylogenetic importance of ciliary photoreceptors and pigmented eyes in errant polychaetes (Annelida)

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The evolution of photoreceptor cells and eyes in Metazoa is far from being resolved although recent developmental and structural studies gave strong evidence for a common origin of photoreceptor cells and existence of sister cell types in early metazoans. These are rhabdomeric and ciliary photoreceptor cells depending on which part of the cells is involved in photoreception proper. However, a crucial point in understanding eye evolution is the explanation of the enormous structural diversity in terms of photoreceptor cells and visual systems in the view of a general molecular conservation of the photoreceptor cells proper. One example for such diversity can be observed in Annelida. The ultrastructure of the cerebral ciliary and rhabdomeric sense organs in various species of errant polychaetes (Aciculata) was investigated to elucidate whether they provide any phylogenetic signal either for evolution of visual systems within Annelida or for metazoan phylogeny in general. The investigations show that ciliary photoreceptor-like sense organs composed of one or a few ciliary sensory cells and an unpigmented supportive cell are generally present in species of Aciculata. These organs clearly belong to two different types one of which most likely is restricted to Phyllodocida, a subgroup of the former. In addition, Aciculata is the only group of polychaetes possessing true multicellular eyes which are composed of numerous rhabdomeric sensory cells and pigment supportive cells forming a continuous epithelium in which the two cell types intermingle. Certain structural peculiarities most likely represent evolutionary novelties for certain subgroups. The findings are discussed with respect of conflicting phylogenetic hypotheses explaining annelid phylogeny.

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Widespread distribution of an American *Artemia* species in France (Crustaceae, Anostracea): Morphological, genetic and morphometric data

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New parthenogenetic and sexual populations of *Artemia* were found along the French Atlantic and Mediterranean coasts.
In order to determine the relationship of these new populations, we present a genetic study using the variability of the caudal gene in these populations. In addition, a morphological study of the frontal knob and penis of the male specimens using scanning electronic microscopy (SEM) was conducted to support the molecular data. The usefulness of a third morphological trait (the ratio of spine clusters on the frontal knobs) for the determination of the species is discussed in the light of a statistical analysis using a morphometric approach.

This study reveals that all French sexual populations of *Artemia* belong to *A. franciscana* from the New World and not to *A. salina* accepted as the only sexual native species in Europe. The progressive replacement of the parthenogenetic (*A. parthenogenetica*) local French species by a sexual species coming from North America is fast and concerns all of Western Europe and the Mediterranean region. These results provide another example for a decrease of European biodiversity through an American invasive species introduced by human.

New developments in the implementation of phylogenetic naming

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My talk will provide an update on the efforts to implement phylogenetic naming, the strongest movement in the history of systematics to advocate doing away with ranks. The starting date for the PhyloCode is now scheduled to coincide with the publication of the "First Book of Phylogenetically Defined Names," which will provide phylogenetic definitions for many widely used names. (The latest PhyloCode leaves the regulation of species names to the rank-based codes; the genus portion of species binomina will, of course, not imply a rank.) A contract has been signed with U. of California Press for the simultaneous publication of the Code and the "First Book," and 86 authors from 18 countries are currently working on name definitions. Among botanists, well-known contributors include P. Cantino, M. Donoghue, J. A. Doyle, S. Graham, W. Judd, D. Olmstead, and D. and P. Soltis, and I shall present examples from their work. As stated in the PhyloCode, its "intent is not to replace existing names but to provide an alternative system for governing the application of both existing and newly proposed names." Many doubt that this can work (see Dubois, MPE 42, 2007). A sometimes overlooked difference btw. the PhyloCode and the Botanical Code is mandatory name registration (other Codes also require registration, but not the ICBN; the ICBN also still requires Latin). Clearly, registration is desirable, and it has been suggested that the most important role of the PhyloCode may be to govern the link between names and their definitions in an electronic age. Unexpectedly (or perhaps not), name registration, which requires an oversight committee, sufficient permanence of software, hardware, and staffing, as well as database development, is turning into another obstacle for phylogenetic naming. This is because phylogenetic definitions rely on references to published phylogenies plus clade apomorphies or extant or extinct specifiers. Permitting queries about the synonymy of such names requires sophisticated informatics because synonymy will depend on the reference phylogenies, which will need to be represented and compared mathematically. Since the registration database, RegNum, for its phylogenies depends on external sources, such as TreeBase or TreeOfLife, which so far are not laid out for comparing trees, this presents a technical hurdle. Information retrieval experts also point to a risk of confusion of nomina used under the Phylocode and other Codes (consider the different meanings of the genus name/rank; above).

Given these obstacles, I am not optimistic that phylogenetic naming will soon replace existing conventions of botanical naming, especially since botanists active in nomenclature are of a remarkably conservative mindset as illustrated by 2005 movements against name registration and against the use of English in descriptions. I believe it would benefit botany if we took serious the view expressed in the Preamble of the ICZN (2000) that "The conventional Linnaean hierarchy will not be able to survive alone...The Linnaean tradition will be supplemented, but not replaced, by new semantic and lexical tools." I think that should be our goal.

Palaemon elegans Rathke (1837): variation of a marine littoral species across its native range

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The common rock prawn *Palaemon elegans* Rathke (1837) is distributed in the Atlantic Ocean from Scotland and Norway to Mauritania including the Azores, Madeira and Canary Islands. It is furthermore common in the Baltic Sea, Mediterranean Sea, Black Sea, Caspian Sea and Lake Aral. This geographical region was strongly affected by well documented Pleistocene glaciations possibly acting in addition to contemporary oceanographic boundaries. The opening and closing of the Strait of Gibraltar has made the Mediterranean a region of high endemism and a generator of diversity. The biogeographic history could have influenced the population structure of *P. elegans* across its native range. To detect this influence with population genetics we used the two mitochondrial genes 16S rRNA and COI for a population genetic comparison and included the following animals of *P. elegans*: Canary Islands, Portugal, North Sea and Baltic Sea coasts of Germany and Poland from the Atlantic Ocean; and Spain, Croatia, Greece, Italy and Corsica from the Mediterranean Sea in addition to specimens from the Black Sea and the Caspian Sea. Our study revealed a surprisingly high population structure. Three main groups of haplotypes can be clearly separated, one from the Atlantic Ocean (Atlantic type) and two from the Mediterranean Sea (Mediterranean type and Black Sea type) with extended zones of overlap.The Atlantic type and the Mediterranean type overlap at the the Almeria-Oran-oceanographic front, a well-defined hydrographic boundary between Atlantic and Mediterranean surface waters. It is possible that the third group of haplotypes, the Black Sea type, goes back to the Messinan Crisis. It often occurs sympatrically with the Mediterranean type.

The New Caledonian Helicinidae: Diversity, distribution pattern, and zoogeographic affinities in the Pacific (Mollusca: Gastropoda: Neritopsina).

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Based on recent comprehensive collections assembled between 1978-1989 by scientists and collaborators of the Muséum National d' Histoire Naturelle de Paris it was for the first time possible to revise the representatives of the operculate land snail family Helicinidae in the biodiversity hot spot area of New Caledonia and the adjacent Loyalty Islands. In combination with historical material the study is mainly founded on shell morphology and anatomy.

In a rather conservative approach 17 species were recognised as valid, among them 3 new species. All species are endemics with a more or less restricted distribution. The three species inhabiting the Loyalty Islands are local endemics while the smaller northern and southern adjacent islands of New Caledonia (Îles Belep, Île des Pins etc.) share their one or two species with the main island. The highest diversity with eight species is found in the southern third of Grande Terre.

On account of similarities in the female reproductive system all New Caledonian helicinids were included into the single genus *Sturanya* WAGNER 1905. Despite the similarities, two subgroups were recognised on Grande Terre which are readily distinguished by the surface sculpture of the early postembryonic whorls. The significance of this characters is evidenced by the resulting consistent pattern of distribution revealing a northern and a southern radiation with the latter being more diverse and reaching further north due to a share of small-sized species with a wider distribution.

Although zoogeographical inferences are hampered by the absence of similarly detailed studies in neighbouring areas, superficial resemblance and the geological history of New Caledonia render Australian species the most likely candidates of origin. The younger Loyalty Islands were obviously colonised from different sources with one species originating from the southern radiation on Grande Terre while the other two species show affinities to Vanuatu, and several north-eastern archipelagos such as Vanuatu, Fiji, Tonga, and Samoa respectively.

Eine kombinierte Analyse zur Aufklärung der phylogenetischen Verwandtschaftsbeziehungen der Branchiopoda (Crustacea)

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Die phylogenetischen Verwandtschaftsbeziehungen der Kiemenfüßer (Branchiopoda, Crustacea) werden mit Hilfe einer kombinierten Analyse auf der Grundlage von 65 morphologischen Merkmalen und sechs molekularen Loci (18S rRNA, 28S rRNA, 12S rRNA, 16S rRNA, COI, EF 1alpha) untersucht. Zentrale Aspekte der Analyse sind die Verwendung des Direct optimization Verfahrens (Kombination von Alignierung und phylogenetischer Analyse in einem Schritt) sowie die Verwendung von 20 Parametersets, die jeweils unterschiedliche Gewichtungen für Insertions-/ Deletionsereignisse bzw. Transitionen/ Transversionen berücksichtigen. Der Beitrag der morphologischen Daten wird kritisch diskutiert. Die Verwendung eines möglichst großen Spektrums aus dem theoretisch unendlichen Parameterraum stellt ein besonders strenger Test der der Stabilität des Datensatzes dar. Anhand des vorgestellten Beispiels werden einige generelle Anmerkungen über das Publizieren molekularer Verwandtschaftsanalysen gemacht und die Bedeutung einer für morphologischen Analysen entwickelten Terminologie kritisch hinterfragt.

Genetic analyses of geographic structure, multiple paternity and brood parasitism in the Jamaican bromeliad crab *Metopaulias depressus* (Brachyura: Sesarmidae)

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The Jamaican bromeliad crab *Metopaulias depressus* (Rathbun 1896) is unique in its habitat preferences and the resulting social behaviour. The crabs live in water-filled leaf axils of bromeliads as family colonies, and older siblings probably help their mother with the brood care for the latest offspring. This brood care is very cost-intensive, consisting of regulation of pH, calcium content, and oxygen in the nursery axil. The offspring also has to be defended against predators and food has to be provided. The high efforts a mother has to invest into her offspring as well as the recent finding that mother crabs cannot distinguish smaller crabs as own or foreign until these have reached a certain size, enables the occurrence of brood parasitism. We addressed this question with genetic markers, including the mitochondrial genes NDH1 and COI and nuclear microsatellites. Our results suggest that brood parasitism occurs in *M. depressus*. The crabs only leave their bromeliad in order to find a mate or an unoccupied bromeliad to start their own colony. It is not known how far they can migrate, but during their migration they are endangered by predators and dehydration. The mitochondrial markers COI and NADH1 revealed a restricted gene flow of the species throughout its range. An as yet not exactly determined barrier separates the populations into a western and an eastern group. This finding suggests that the species is experiencing an ongoing separation, which in future research needs to be confirmed with a nuclear marker.

Der Beitrag der Paläontologie zur modernen Systematik

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Zusammenfassung

Den Ausgangspunkt für phylogenetische Verwandtschaftsanalysen bilden heute in der Regel die rezenten Organismen, während die Fossilien erst nachträglich als Stammlinienvertreter berücksichtigt werden. Dennoch sind die Fossilien für die Stammesgeschichtsforschung unverzichtbar, da ihr Ziel die Rekonstruktion der phylogenetischen Beziehungen *aller* Organismen ist, egal ob sie rezent oder fossil sind. Der Fossilbericht ist für sehr viele Taxa vollständig genug, um zahlreiche phylogenetische Fragestellungen beantworten zu können. Von besonderer Bedeutung sind Fossilien nach wie vor für die Eichung molekularer Uhren. Während in manchen Fällen noch erhebliche zeitliche Diskrepanzen zwischen molekularen Aufspaltungsaltern und ältesten Fossilnachweisen bestehen, wurden beide Datensätze in anderen Fällen bereits weitgehend angenähert. Fossilien können auch für die Rekonstruktion der Verwandtschaftsbeziehungen der rezenten Organismen von Bedeutung sein, etwa bei der Bewertung des Status eines Merkmals, bei der Klärung der Verwandtschaft hochgradig abgeleiteter rezenter Taxa oder durch den Nachweis von heute unbekannten Merkmalskombinationen. Wichtig sind sie ferner für die Analyse der sequenziellen Chronologie der Evolution komplexer Merkmale. In der stratigraphischen Abfolge des Erscheinens fossiler und rezenter Taxa steckt ein unabhängiger Datensatz, der für phylogenetische Rekonstruktionen genutzt werden kann. Die dafür notwendigen methodischen und theoretischen Grundlagen sind aber noch Gegenstand zukünftiger Forschung. Die Zukunft der Phylogenie wird maßgeblich von der Annäherung ihrer verschiedenen Teildisziplinen profitieren. Dabei werden morphologische Merkmale von rezenten und fossilen Organismen zusammen mit genetischen und molekularen Daten gemeinsam eine tragende Rolle spielen.

Abstract

Usually, modern taxa are the starting point in phylogenetic reconstructions, while fossils can be placed only subsequently on a stem lineage. Nevertheless, fossils are of great importance for phylogeny because the main aim of phylogeny is the reconstruction of the phylogenetic relationships of *all* organisms, wether they are extant or fossil. For many taxa the fossil record is complete enough for answering numerous questions in phylogeny. Fossils are also of crucical importance for the calibration of molecular clocks. While in some cases there are still considerable discrepancies between molecularly determined splitting ages and the oldest fossil record of a taxon, there is a marked agreement of both data sets in other cases. Fossils are also of importance for phylogenetic hypotheses founded solely on recent organisms. Examples are assessments of character states, clarification of the phylogenetic relationship of highly derived living taxa, and the detection of character combinations unknown today. Additionally, they are of importance for the reconstruction of the time sequence of character evolution. The stratigraphic sequence of the appearance of fossil and modern taxa is an independent data set, that can be used for phylogenetic reconstructions, but the required methodological as well as theoretical foundations still have to be established. In the future, phylogeny will greatly benefit from the integration of its subdisciplines. The combination of morphological characters of living and fossil organisms together with molecular and genetic data will play a significant role.

Witnessing species evolution? Genetic population structure of the Jamaican freshwater crab *Sesarma dolphinum* (Crustacea, Brachyura).

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The island of Jamaica plays a special role among the Greater Antilles. Its different geological history produced a unique environment and facilitated several adaptive radiations. One of those adaptive radiations is the one of the Jamaican freshwater crabs, which resulted in at least 12 species belonging to the family Sesarmidae. In our study, we looked at the genetic population structure of *Sesarma dolphinum*, a recently described species from the western part of the island. Specimens from 14 sampling spots were analysed using the two mitochondrial markers CO1 and NADH1. From these data statistical parsimony networks were constructed. Based on those networks, we then performed a nested clade analysis to investigate the population history of *S. dolphinum*. In addition we also used the nuclear gene complex ITS1-5.8SrRNA-ITS2, for which we obtained over 220 clones from 32 specimens. To test if genetic differences already is reflected in phenotypic manifestations we conducted a morphometric analysis using 50 individuals covering the whole range of the species. The mitochondrial data indicate that *S. dolphinum* consists of two main population complexes, which is supported by the morphometric data. The ITS dataset shows the same separation into two groups, but also indicating a certain level of hybridisation. These results give us some evidence of initial steps of differentiation in a species which is in the process, or at least has strong probabilities, to evolve into two separate species.

Comparative analysis of land snail radiations on Crete

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To investigate the causes for the land snail radiations on Crete we studied the systematics and phylogeny of the radiation of the genus *Xerocrassa* on Crete using morphological characters, mitochondrial (*cox1*, 16S rDNA) and nuclear (ITS2) DNA sequences and AFLP markers. About 20 *Xerocrassa* species occur on Crete the half of which has not been described so far. Distribution maps of these species were based on almost 3000 records. With these data and corresponding data on other Cretan land snail radiations, especially of the genera *Albinaria* and *Mastus*, we tested the hypothesis that these radiations were the result of a fragmentation of Crete into several paleoislands during the late Miocene and Pliocene. Contrary to the predictions of this hypothesis, the phylogenies of the radiations do not reflect a common pattern and Monte Carlo simulations showed that the distribution areas of the Cretan endemics are not significantly clustered. These results indicate that the land snail radiations on Crete were not caused by a common sequence of vicariance events. Probably stochastic events like chance colonization of isolated habitats and peripatric speciation were more important in the origin of the mostly allopatric and apparently non-adaptive land snail radiations on Crete.

Accessing DNA for molecular analyses from formalin fixed tissue

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Obtaining material for studies of phylogeny, systematics and phylogeography is often a laborious and costly business, and key species are often excluded due to lack of material. In the course of the increasing destruction of habitats and the accompanying loss of biodiversity, specimens in museum collections often become irreplaceable when the populations and species they came from are extinguished. Such specimens may then represent the last and only sources for molecular data. Given this situation, the need to access formaldehyde-fixed samples is all the more critical, making the use of archival collections increasingly important. Much of this material has been fixed in formaldehyde for other purposes limiting its utility for DNA studies.

Initial attempts to use formaldehyde-fixed material for molecular studies were made in the medical field to study genetic diseases. The yields of DNA in the early attempts were generally low, and the conclusion was that the results were largely dependent on fixation time and type of storage (Schander & Halanych 2000, 2003). Several protocols for the extraction of DNA has since been suggested, but it has also been suggested that the critical part may not be the extraction, but the actual problems may lay in the PCR step (Skage & Schander, submitted). Several repair kits and enzymes are currently available on the market, but their effectiveness has not been fully investigated.

Possible alternative paths that may be taken were discussed at a workshop in Washington DC in 2006 (Tang 2006). These include improved extraction, repair, alternative sequencing methods and bioinformatics methods. Some of these methods will be addressed in this talk.

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The species concept and protist evolution

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The biological species concept as coined by Ernst Mayr is not applicable to many protists which reproduce by inbreeding or asexually. An extended concept supplementing the biological species concept was suggested by T. M. Sonneborn after intensive studies on differently reproducing species of the *Paramecium aurelia* complex. In his concept, based on the hypothesis that inbreeding or asexually reproducing taxa also evolve as discrete units, he suggested that a species should be recognized as an evolving entity that has undergone a threshold of minimum evolutionary divergence. However, Sonneborns´ idea was poorly received. I examine different morphological and molecular characters discovered and applied in taxonomy since Sonneborn developed his hypothesis. I conclude that there is now an abundance of objective characters to arrive at sound judgement to delimit species in Sonneborn´s sense when the biological species concept is not applicable. In addition, combined morphological and molecular studies reveal that, although many free-living protists may be globally distributed, geographical patterns with locally restricted distribution of species also occur.

Gene flow within the Indo-West Pacific: a genetic comparison of geographic structure in two common mangrove crabs (Brachyura: Sesarmidae & Gecarcinidae)

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The two tropical crab species *Neosarmatium meinerti* (de Man, 1887) and *Cardisoma carnifex* (Herbst, 1796) are widespread throughout the Indo-West Pacific and mainly associated with the mangrove ecosystem. Both live in the upper mangrove zone, and release the larvae during spring tides. The larvae spend about four weeks in the open water and then the megalopae settle in the mangrove habitat. We studied the genetic structure of several populations along the East African coast, from the Seychelles and neighbouring islands, and from a number of other localities throughout the Indian Ocean and the western Pacific by sequencing 633 basepairs of the mitochondrial DNA corresponding to the cytochrome oxydase subunit 1 gene (COI). We observed clearcut differences in the genetic differentiation of the two species. In *Cardisoma carnifex*, there is only weak intraspecific geographic structure in populations separated by several thousand kilometres (East Africa versus French Polynesia). In contrast, in *Neosarmatium meinerti* there is already a marked genetic separation between the four East African populations and the populations from the Seychelles and nearby islands (Mauritius, Aldabra and Rodriguez). The genetic differentiation increases when including individuals from Sri Lanka, Thailand, Indonesia, Taiwan and Australia. This separation was confirmed by additional sequences from the large ribosomal subunit (16S rRNA) mtDNA. Overall, four geographically and genetically defined subunits can be clearly separated within *Neosarmatium meinerti*, which are here proposed to represent cryptic species.

Phylogenetic relationships and evolutionary traits of Bromelioideae (Bromeliaceae): insights from plastid and nuclear DNA sequence data

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Bromeliaceae (Poales) are a large neotropical family of flowering plants, comprising more than 2,600 species in 56 genera, and are extraordinarily rich in epiphytes (SMITH & TILL 1998). Bromeliads are renowned for their high morphological as well as ecological plasticity allowing them to occupy a great variety of terrestrial as well as epiphytic habitats. Phylogenetic relationships and character evolution within subfamily Bromelioideae are only poorly understood.

Recent studies of Bromelioideae phylogeny only included DNA-data from the plastid genome. The low sequence variability of the plastidary markers investigated resulted in a low resolution within Bromelioideae, especially in the group of *Aechmea* and allied genera. The establishment of a variable nuclear marker for Bromeliaceae has been a desideratum for a long time.

We investigated partial sequences of the nuclear gene phosphoribulokinase (PRK) using primers designed for Bromeliaceae by BARFUSS et al. (University of Vienna). With those primers multiple copies of the gene were retrieved thus requiring the development of specific primers for one of the paralogues. Cloning was necessary in many taxa due to slight allelic sequence variation (point mutations and indels). Sequence variation of the investigated paralogue between the clones was lower than between taxa thus making the marker well applicable for the phylogenetic reconstruction of the subfamily. Thus for the first time nuclear sequence data could be included in a detailed phylogenetic analysis of Bromelioideae.

The variablity of PRK-sequences in Bromeliaceae is considerably higher than that of the up to now investigated plastidary markers. Parts of the intron regions were highly variable. They could not be aligned reasonably for the whole species set and therefore were excluded from the analysis. For a group of more closely related bromelioid genera (mainly core Bromelioideae) sequence divergence was not as high and a reasonable alignment including the intron regions was possible. For those taxa a separate analysis was conducted.

The topology of the phylogenetic reconstruction based on nuclear data alone is principally congruent with the results obtained from plastidary data (SCHULTE et al. 2005. Senck. Biol. 85(1): 113-125) but exibits a higher resolution. Basal groups of Bromelioideae can be identified as well as smaller clades within the core Bromelioideae. Nevertheless, within the latter resolution still is unsatisfying, this pointing to a young and rapid radiation of this group which centres principally in SE-Brazil. The evolution of selected characters is discussed in the light of the combined phylogeny.

Hot spot of Biodiversity: Molecular Phylogeny of flightless endemic grasshoppers in the Eastern Arc Range (Tanzania, East Africa)

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From the African continent several of the world´s most important hotspots of biodiversity and endemism are known. One of these areas are the Eastern Arc Mountains and the volcanoes in East Africa, extending from southeastern Kenya through most Tanzania. Due to the high accumulation of endemic species and the isolated, island-like tropical mountainforests, this region is called *"the Galápagos of Africa"*.

To investigate dispersion- and radiation events in this region, the phylogeny of selected grasshopper taxa were analysed. The observed animals are flightless endemics in the Eastern Arc range and extremely adapted to the humid montane forest habitats. They show an restricted geographic distribution and presence of closely related species on neighbouring, but isolated mountain ranges. This leeds to the assumption that episodic migration and geographic isolation caused speciation and the evolution of endemics.

By means of molecular-genetic investigations the phylogeny of endemic grasshopper species will be analysed to gain more knowledge about the dispersal into this unique and sensitive tropical region and to take a closer look at the origin of speciation and evolution !

So Many Hominid Fossils but So Little Systematic Rigor

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Probably most paleoanthropologists are unaware that their discipline's history does not derive from, but is quite different than the history of non-hominoid systematics and paleontology. While, because of Steno, Great Chain of Being taxonomists of the late 17th century could embrace fossils as representatives of once-living plants and animals, they believed that humans could not be antedilvuian. Thus, given the mixed acceptance of the Feldhofer Grotto Neanderthal as an ancient human, it was not until the late 19th century, with the unquestionable association of the Spy Neanderthals with bones of extinct animals, that a broader appreciation of human antiquity gained a foothold. Once it did, however, the quest for human fossils took off, with discoveries in Southeast Asia and then in Africa and China keeping apace with those in Europe. Unfortunately, in the mid-20th century, Dobzhansky and Mayr used their clout as founders of the evolutionary synthesis to impose a scheme of unilinear transformation upon the interpretation of the hominid fossil record. The result was the same as with the synthesis: They squelched alternative thinking. Here I shall demonstrate with multiple examples that it is no longer possible to deny that the human fossil record presents a diversity of taxa. It is time that paleoanthropologists shed the blindfold that has kept them from seeing it and join the ranks of serious systematists.

The cell lineage of *Oikopleura dioica* (Appendicularia, Tunicata)

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Utilizing four-dimensional differential interference microscopy the cell lineage of the appendicularian *Oikopleura dioica* from fertilization to hatching was documented for the first time. In combination with transmission electron microscopy of complete serial sections of a newly hatched animal this technique allowed for the determination of the cell lineage and fate map in unprecedented detail. As in other deuterostomes, the first cleavage separates blastomeres from prospective left and right body sides, the second anterior from posterior, and the third animal from vegetal. Endomesoderm and notochord derive entirely from the vegetal quartet of cells at the eight-cell stage while epidermis derives exclusively from the animal quartet. Both, tail muscle cells and cells of the nervous system derive from both sources. Prospective tail muscle cells (b6.5 and b6.5) derived from the animal quartet of the embryo are internalized at a later stage during gastrulation at the 62-cell stage (80 min pf) compared to prospective tail muscle cells that derive from the vegetal quartet (B7.6 and B7.6; 60 min pf). Nervous system derives also from both halves of the 8-cell stage, from the vegetal cells A5.2 and A5.2 and the animal cells a6.6 and possibly a6.6. Neurulation occurs as the internalization of a single row of cells at the prospective dorsal, predominantly anterior side of the embryo at the 62-cell stage (75 min pf). Lineage and fate map of *O. dioica* closely resemble those of *Halocynthia roretzi*, an ascidian tunicate, suggesting common ancestry not shared by other chordates. However, development is considerably faster and fate restriction in certain identifiable cell lines absolutely and relatively earlier in *O. dioica* compared to *H. roretzi* and even more so if compared to other deuterostomes. These facts support the hypothesis that Appendicularia is a derived taxon within Tunicata in concordance with numerous morphological characters (e.g., u-shaped gut, horizontal tail orientation, reduction of the serotonergic nervous system, functional and structural differentiation of adult and larval tunic, late origin of ecm during ontogeny) and molecular characters (e.g., disintegration of the Hox-gene cluster, minute genome, unique histone organization). In respect to the evolution of the high-ranking chordate taxa, the interpretation of these facts supports the traditional Notochordata-hypothesis and rejects the recently proposed Olfactores-hypothesis.

Eintagsfliegen (Insecta: Ephemeroptera) aus der kreidezeitlichen Crato-Formation Nordost-Brasiliens

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Die Crato-Formation aus der unteren Kreide Brasiliens stellt eine der weltweit bedeutsamensten kreidezeitlichen Fossillagerstätten dar, deren Bedeutung vor allem von einer reichhaltigen Überlieferung fossiler Insekten herrührt. Besonders Eintagsfliegen (Ephemeroptera) sind aus Crato in großer Individuendichte erhalten. Eine Revision der Ephemeropteren aus Crato erbringt unter anderem neue Erkenntnisse zur Verwandtschaft der Hexagenitidae, ein fossiles monophyletisches Taxon, dessen Stellung im System der Eintagsfliegen bisher ungeklärt war. Der erstmals beschriebene Feinbau der larvalen Tracheenkiemen von *Protoligoneuria limai* (Hexagenitidae) läßt auf eine nähere Verwandtschaft der Hexagenitidae mit den Heptagenioidea + Oligoneurioidea schließen. Eine kritische Nachuntersuchung weiterer aus Crato benannter Vertreter der Hexagenitidae wirft das Problem der mangelhaften Beschreibung oder Erhaltung mancher Taxa auf. Schließlich mündet die Revision der Ephemeropteren aus Crato im ersten kreidezeitlichen Nachweis der bisher fossil nur aus Baltischem Bernstein bekannten Baetiscidae. Im Zusammenhang damit werden auch alte Beschreibungen fossiler Ephemeropteren als wahrscheinliche Vertreter der Baetiscidae interpretiert.

Artbegriff in der Zoologie – theoretisch und pragmatisch

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Biologische Aussagen sind generalisierte Aussagen über Arten, die zunächst an wenigen untersuchten Individuen einer Population gewonnen wurden, aber an anderen Individuen überprüfbar sind, die als artzugehörig erkannt werden können. Dies bestimmt das vorrangige Interesse an der Identifikation von Arten. In der lokalen Fauna und Flora ist dies für den Kenner einer Organismengruppe unter Verwendung verschiedenster Hilfsmittel und Berücksichtigung des vielfältigen Wissens über diese Arten in den allermeisten Fällen problemlos. Die fachliche Diskussion wird dagegen von den wenigen Problemfällen beherrscht, die sich aus Bastardierung, der Existenz von ökologischen Rassen und Zwillingsarten sowie unerforschter Variabilität bei Agamospezies ergeben. Probleme beim richtigen Zuordnen der Individuen zu Arten in bisher nicht untersuchten Lebensgemeinschaften ergeben sich wegen deren zunächst unbekannter Vielgestaltigkeit in Ontogenese oder Generationenfolge, durch Polymorphismus/-phänismus, bei fehlender Unterscheidungsmöglichkeit kryptischer Arten und in der Frage der Artgleichheit allopatrischer Populationen. Zur Klärung dieser Probleme reicht nicht der Analogievergleich aus dem schon Bekannten, sondern detaillierte Studien zu Lebensweise, Ökologie und Verhalten sind notwendig!

An all diesen Fragen entzündete sich die Diskussion um den Artbegriff. Eine biologische Art als natürliche Klasse von Organismen mit großteils übereinstimmenden Eigenschaften der Morphologie, des Verhaltens und der ökologischen Ansprüche lässt sich über mehrere Aspekte charakterisieren. Evolutiv bedingt (ultimat) ist sie als ökologische Einheit (Ökospezies) durch die Realisierung ihrer ökologischen Nische (Gesamtheit der Wechselbezüge ihrer Individuen mit deren Umwelt). Ihre Anpassungen daran werden bei Organismen mit Fremdbefruchtung durch proximat wirkende Partnererkennungsmechanismen geschützt, die genetisch isolierend wirken (Biospezies). Anpassungen an die Ökonische, die meistens zweielterliche Fortpflanzung sowie interne Stabilisierung bedingen eine übereinstimmende Merkmalsausstattung von der Molekül- bis zur Verhaltensebene (Aspekt der Morphospezies). Die historische Abgrenzung der Art mit nicht willkürlichem Anfang und Ende führt zur Auffassung als Chronospezies, die sich zwischen zwei direkt aufeinander folgenden Speziationsereignissen evolutiv ändert. Durch den Speziationsprozess gibt es in Raum und Zeit fließende Grenzen, die nur eine injunktive Erfassung der Art zulassen.

Acoustic and morphometric differentiation of treecreepers (Aves: *Certhia*)

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Treecreepers (*Certhia*) make up a morphologically extremely homogeneous and, consequently, clearly defined group of passerine birds. They are confined to tree bark as their habitat and adapted to the niche performed by tree trunks by long and curved bill, long hind-claw, stiff rectrices and camouflaging plumage. Consequently, within-group differentiation as regards outer appearance is mostly weak. In order to shed light on *Certhia* evolutionary history, we present a molecular phylogeny, which comprises all described species and a representative number of subspecies from all over the Holarctic distribution range of the genus. We detected several differentiation levels and thereby uncovered (at least) two cryptic species. In a second step, we adopt the findings of a bioacoustic analysis to the molecular phylogeny on the one hand and to the distribution patterns of certain taxa on the other hand. *Certhia* species with simpler trill-like songs represent more basal taxa in the phylogeny and have smaller distribution areas. They are restricted to the transition zone between Palaearctic and Indomalayan Realms, whereas species with more complex songs are phylogenetically derived and spread recently over large parts of the northern hemisphere. Based on a total of 16 acoustic traits, a phylogenetic signal can be detected in *Certhia* song. This allows us to affiliate taxa which were not incorporated into the molecular analyses to one of the nine species. This is done through principal-component analyses of parameters obtained from sonagrams of song verses. Finally, we demonstrate by which characters the postulated cryptic species can be separated from their closest relatives by outer morphology. We describe geographic variation of measurements within species with large distribution ranges. – This project has been supported by the Evangelisches Studienwerk Villigst e. V. as well as by the Feldbausch- and the Wagner-Stiftung at the Fachbereich Biologie of Mainz University.

Plant evolution in the Arctic: Hypotheses testing in multiple lineages of *Artemisia* (ASTERACEAE)

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Arctic plants seem to been a precedence for allopolyploidy and other connections to alpine temperate habitats. We study on the example of the rich species genus *Artemisia* L. (Asteraceae) whether these long standing hypotheses are also true for multiple closely related lineages which have colonized arctic habitats at different times and can be subjected to statistical tests. *Artemisia* with 36 species occurring in arctic habitats is among the most diverse genera of the Arctic. We sampled 133 taxa including all but two of the arctic species, sequenced the parts of 3'ETS and ITS region, and produced a molecular phylogeny. Additional we collected data on karyology, morphology, distribution range, and ecological preferences from the literature. We found, that arctic habitats were colonized repeatedly and independently from many different geographical source areas. Also sistergroups of the arctic lineages were quite heterogeneous with respect to their distribution, habitat occupancy, and life form. There were proportionally no more polyploids in arctic lineages than in other habitats or in their respective sistergroups, but their flowering heads were significantly larger. We conclude, that better pollinator attraction in *Artemisia* replaces the formation of permanent heterozygosity by a allopolyploidisation usually found in other arctic taxa.

Are acoel flatworms platyhelminths? – New comparative data on receptor cells and pharynx types

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Acoels are small, aquatic, soft-bodied worms inhabiting predominantly marine habitats. Due to their apparent simplicity, particularly their lack of body and digestive cavities and - in most cases – lack of a muscular pharynx, they have repeatedly been in the center of interest in discussions about the starting point of a phylogenetic tree of triploblastic bilaterian animals. Based on ultrastructural characters, it was proposed that the Nemertodermatida, sister group to the Acoela with an entirely epithelial digestive tract, appear more primitive, thus rendering the syncytial digestive parenchyma of acoels a derived feature. Much controversy, however, remains concerning the relationship of the Acoelomorpha (Acoela and Nemertodermatida) to other bilaterians, placing them either as one of the major clades of the Platyhelminthes or as basal bilaterians not related to other flatworms.

Here, I compare receptor cell types associated with the mouth, pharynx, and the anterior body tip in acoels, including the presumably primitive Solenofilomorphidae and Hofsteniidae, with receptors known from other flatworms. Special focus thereby is set on the so-called collar receptors, which are described not only in a large number of Platyhelminthes but also in various other invertebrates. According to my results, however, collar receptor-like sensory cells are present in the Acoela in the more derived taxa, only, but the ultrastructure of pharynx receptor cells in Solenofilomorphidae and Hofsteniidae points to a closer relationship between these two "primitive" taxa.

The second character considered is the muscular pharynx itself, which is present in all major taxa of free-living platyhelminths but only in a few acoel taxa. The homology of pharynges within the Acoela and even the basic question of whether a pharynx is a primitive trait within the Acoela and is homologous to the pharynx of other turbellarians has been a matter of discussion for decades. My study included representatives of Solenofilomorphidae, Hofsteniidae, and Proporidae – the major acoel taxa with a pharynx – as well as Convolutidae bearing a simple mouth tube. There is a great variability in muscle systems associated with the mouth and pharynx among these taxa and there are no close similarities between the muscle systems of the investigated acoel pharynges and of pharynges in other primitive flatworms, such as the Catenulida.

In conclusion, neither receptor cell fine structure nor pharynx muscle patterns provide inambiguous indications for nesting Acoela within the Platyhelminthes.

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Chicken repeat 1 (CR1) retrotransposons as phylogenetic markers in passerine birds (Aves: Passeriformes)

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The by far largest avian taxon comprising more than a half of all living birds are the passerine birds (Passeriformes) which form a morphological very homogenous group. Due to their tremendous and rapid radiation during the early Tertiary their phylogenetic relationships have been the subject of many debates. Since the first extensive study on avian systematics based on DNA-DNA hybridization analyses several approaches of nucleotide sequence data tried to elucidate passerine phylogeny during the last six years. Although those studies brought some new cognitions which partly were conflicting with the first hypotheses, some phylogenetic questions remained unanswered. Most publications delt with more or less similar datasets and the same genes as phylogenetic markers. We present the totally different and first approach of retrotransposon insertion as a phylogenetic marker in passerine birds. Retrotransposons are mobile genetic elements which are integrated in the genome via RNA intermediates. Whereas SINE insertions are well established as molecular markers and have shown to be reliable for phylogenetic inference studies, the use of non-LTR retrotransposons is not common yet. With estimated up to 100.000 copies in the chicken genome the chicken repeat 1 (CR1) is the most important non-LTR retrotransposon in birds. We present two CR1 loci in passerine birds not only found in representatives of the Corvinae (Jays, Crows and allies) but also in the West-African *Picathartes* species which give new evidence for a deeper relationship of these species than usually believed.

Morph·D·Base – a Morphological Description Database

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Our overall objective with Morph.D.Base, an online relational data base for storing morphological descriptions and graphical material, is to provide a convenient tool for recording and managing all kinds of data on organisms, including media files, specimen and taxon information, data on general biology, morphological descriptions, literature and a glossary of various terms and concepts of organismic biology. Currently, four modules are online. You can enter data referring to the particular Specimens you are working with and specify e.g. their sex, sampling data, museum collection information and more. Specimens are linked to the Morph.D.Base taxonomy which is based on the ITIS taxonomy and nomenclature (http://www.itis.usda.gov). You can add new Taxa to the Morph.D.Base taxonomy if it is incomplete. Furthermore, you can upload Media files (bitmap, vector graphics, audio, and movie files) and classify them into general categories such as CLSM, diagram, drawing and others. If the file refers to a Morph.D.Base specimen or taxon entry, you can also link it to this entry. The Biogeography module has Google Maps implemented, which provides a convenient tool for illustrating the sampling locations of those specimen entries that have the locations specified. We work on further developing Morph.D.Base to become a mediating tool between data representation and phylogenetic inference therewith closing the methodological gap between data production and tree evaluation. Herein, a biological ontology will take in a central function and enable intelligent data management, inference and querying. Morph.D.Base is online (http://www.morphdbase.de) since 25th of September 2006.

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Evolution and biogeography of Southeast Asian viviparids (Mollusca: Gastropoda: Caenogastropoda)

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Viviparids are a widely distributed group of freshwater gastropods, which serve as important intermediate hosts for human trematode infections in tropical regions. The group is particularly speciose in continental and insular Southeast Asia, and the species of that region have been assigned to at least ten different genera. Minor radiations have been reported from ancient lakes in Myanmar and Sulawesi. In this study we have used mitochondrial DNA sequences from a wide range of viviparid species from Thailand, Indochina, Indonesia, the Philippines and Australia (1) to test the monophyly of previously established genera, (2) to investigate biogeographical relationships in the region, and (3) to gain insights into the nature of the alleged ancient lake radiations. The molecular phylogeny indicates that the current morphology-based viviparid taxonomy does not reflect phylogenetic relationships among taxa. The data also support a distinct origin of species from Sulawesi, and a derivation of Australian taxa from the Southeast Asian mainland. Low genetic differences among the species or populations from the ancient lakes of both Myanmar and Sulawesi do not support the assumption of intralacustrine radiations in these lakes.

Gibt es eine Korrelation von Verteidigungsdrüsen und Sekundärmetaboliten mit der Phylogenie der opisthobranchiaten Schnecken?

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Umfangreiche histologische Untersuchungen haben gezeigt, dass die Opisthobranchia zahlreiche unterschiedlichste Drüsentypen aufweisen, die sehr wahrscheinlich der Verteidigung dienen. Literaturdaten zu nachgewiesenen Sekundärmetaboliten bei diesen Schnecken zeigen, dass bestimmte Stoffe vermehrt bei einzelnen Opisthobranchia-Taxa auftreten. Häufig wird dies mit der Nahrung korreliert. Neuere phylogenetische Untersuchungen zeigen, dass zumindest einige Drüsentypen und auch bestimmte Sekundärmetabolite bestimmten Opisthobranchia-Taxa zugeordnet werden können.

Es wird hier versucht, eine Korrelation zwischen der Phylogenie und bisherigen Daten zu Verteidigungsdrüsen und Sekundärmetaboliten zu erstellen.

Phylogenie und Klassifikation der „Amöben“: Ein Update

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Die Amöben wurden lange Zeit als eine monophyletische Gruppe, Rhizopoda, angesehen und in fünf Taxa unterteilt: Amoebida, Eumycetozoa, Foraminifera, Heliozoa und Radiolaria.

In den letzten Jahren wurde allerdings immer deutlicher, dass dem Begriff „Amöbe“ keinerlei systematische Bedeutung zukommt. Die amöboide Fortbewegung kommt nicht nur bei zahlreichen Protozoen, sondern auch bei verschiedenen Zellen der Wirbeltiere vor und ist in der Evolution mehrmals und unabhängig voneinander entstanden. Durch das Aufkommen elektronenoptischer und molekularbiologischer Techniken haben sich schließlich in der Klassifizierung der Amöben insgesamt grundlegende Veränderungen ergeben. Früher für taxonomische Zwecke genutzte auffällige Merkmale, wie die Mitochondrienlosigkeit oder die Fähigkeit zur Fruchtkörper- oder Geißelbildung, werden nun als Ergebnis konvergenter Entwicklungen oder als plesiomorphe Merkmale angesehen. Die alten Amöben wurden auf drei der derzeit insgesamt sechs eukaryotischen Phyla aufgeteilt: auf die Amoebozoa, die Excavata und die Rhizaria. Die Amoebozoa, zu denen u. a. die Gattung *Amoeba*, die Akanthamöben, die Entamöben und die Schleimpilze gezählt werden, gelten als Schwestergruppe der Opisthokonta. Während die früher mit den Akanthamöben als „Limax-Amöben“ vereinten Näglerien heute zu den Excavata in die Verwandtschaft der Euglenozoa gestellt werden. Die Foraminiferen, Radiolarien und Heliozoen bilden gemeinsam mit u. a. den Cercozoa die Rhizaria.

Insgesamt bleibt allerdings festzuhalten, dass in der Systematik und Evolution der Amöben noch immer viele Fragen unbeantwortet sind, und dass in den nächsten Jahren noch erhebliche Veränderungen in der Klassifikation der Amöben zu erwarten sind. Aus der Schwierigkeit der Anwendung des Konzepts der biologischen Art bei den meisten Amöben ergeben sich zudem erhebliche Probleme der Nomenklatur, für deren Lösung mehrere Möglichkeiten diskutiert werden. Die Charakterisierung und Differenzierung der „Spezies“ (Stämme, Genotypen,...) ist nicht zuletzt auch von medizinischem Interesse, weil einigen Vertretern der „Amöben sensu classico“ erhebliche humanmedizinische Bedeutung zukommt, wie *Entamoeba histolytica*, dem Erreger der Amöbenruhr, und den ansonsten freilebenden Amöben *Acanthamoeba*, *Balamuthia*, *Sappinia* und *Naegleria*, den Erregern der *Acanthamoeba*-Keratitis, der Granulomatösen Amöbenenzephalitis und der Primären Amöbenmeningoenzephalitits.

The first fossil walking leaf (Insecta: Phasmatodea) - an example of evolutionary stasis

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Phasmid insects mainly exhibit a stick-like habitus. Only 37 described species pertain to the walking leaves or Phylliinae which are impressive leaf imitators. Here we present the first record of specialized angiosperm leaf mimicry in a fossil walking leaf. The fossil originates from 47-million-year-old deposits of Grube Messel in Germany. It has the same size and foliaceous appearance as extant male walking leaves. Thus, this fossil is an example of stasis in the evolution of cryptic morphology and it gives evidence that angiosperm leaf mimicry had evolved at least by the middle Eocene. The exquisite preservation of the fossil specimen allows the determination of its phylogenetic position among Phylliinae and permits an assessment of the temporal sequence of character transformation that led to the extant crown-group. Presumably its morphological resemblance to leaves was perfected by a special behaviour, e.g. the ability to remain perfectly still for long periods or imitating a leaf swaying in the wind at perturbation. This type of camouflage must have been caused by vigorous selection pressure through visually oriented predators. Potential predators reported from the Eocene are birds, early primates and bats. At present, the species of walking leaves are distributed primarily in south-east Asia and adjacent regions. The fossil record from the lower Tertiary of Germany shows that their former geographical range was distinctly larger and that today the walking leaves only have a relict distribution.

The flight apparatus of Ephemeroptera and the ground-pattern of insect flight

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Ephemeroptera are usually seen as the most ancient flying insects (Pterygota). For example, they are the only extant Insects that moult in a winged stage. The flight musculature and the sclerites of the wing base of Ephemeroptera are distinctly different from that of the remaining Pterygota. Until now there is no generally accepted hypothesis about the evolution of the different forms of the flight systems of Ephemeroptera, Odonata and Neoptera from a common winged ancestor.

In this context we did a comprehensive investigation of the thoracic musculature and the wing base sclerites of Ephemeroptera and Plecoptera. In addition to dissections and serial sectioning, we used high resolution X-ray tomography to be able to study as many species as possible. Our survey shows that the flight musculature of Ephemeroptera is highly specialised. Nevertheless, it is possible to homologise the wing base sclerites of Ephemeroptera and Neoptera and to reconstruct a possible ground pattern for the wing base of the Pterygota. This ground pattern probably was much more similar to the wing base of extant Neoptera than to extant Ephemeroptera.

Evolutionary morphology of the circulatory organs in Peracarida

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The Peracarida comprise taxa such as the marine planctontic Mysidacea, limnic or amphibic Amphipoda and also partly terrestrial living Isopoda. This great diversity lead to a continued controversy on the phylogeny of peracarid taxa. To assess peracarid phylogeny and to analyse the evolution of their circulatory system in particular, we studied 22 species, representing all the peracaridan high rank taxa (including Thermosbaenacea) by means of several morphological techniques such as serial Semi-Thin-Sectioning, Corrosion Casting, SEM and Micro-Computer-Tomography.

Features of the vascular systems vary between peracaridan groups, ranging from an elongated tubular heart in combination with an elaborate arterial system to systems consisting “only” of a shortened heart together with some arterial structures in the cephalothorax.

Characters such as extension and position of the heart, number of ostia, presence / absence and number of lateral cardiac arteries are conceptualised for all terminals. A total of 24 characters of the circulatory system are analysed with 88 other morphological characters in a cladistic analysis. Finally, results are discussed along different phylogenetic hypotheses from functional morphological and evolutionary points of view.

The first record of specific nerve dye in Tardigrada: notes on the general course of the CNS and the construction of the brain

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Tardigrades – also known as water bears – are tiny protostomes that live in freshwater, marine and terrestrial environments. The phylogenetic relationships of Tardigrada are unsolved and have always been controverversially discussed. However, it is currently more generally accepted that tardigrades belong to the arthropods. The advent of the Ecdysozoa hypothesis allows to interpret the tardigrade organisation as kind of intermediate between that of nemathelminths and of arthropods.

The analysis of the nervous system of tardigrades always played an important role in the discussion of the phylogenetic affinities of the group. For Tardigrada essential elements of a ladder-like nervous system with commissures, connectives, a dorsal cerebral ganglion, circumoesophageal connectives and four pair ventral trunk ganglia have been described. In particular the tripartite organisation of the brain has been related to the three sections of the euarthropod brain, namely the proto-, deuto-, and tritocerebrum.

We investigated the structure of the nervous system of *Macrobiotus hufelandi* C.A.S Schultze, 1833 for the first time by means of modern morphological techniques such as fluorescence microscopy, confocal-laser-scanning-microscopy, and computer-aided 3D reconstruction. It appears that the central nervous system of *M. hufelandi* corresponds with the current statements. However, the results reveal new data concerning the connection of the brain to the ventral chain of ganglia, the existence of a "real" suboesophageal ganglion, and the fact that no commissures exist between the ganglia of the ventral nerve cord. Furthermore, it is proposed that ganglia and neuropils of the tardigrade brain form a complex structure but that there is no indication for a tripartite brain comparable to that of euarthropods.

Which phylogenetic implications let derive from our study of tardigrade neuroanatomy?

NOTIZEN

Untersuchung von Sekundärmetaboliten der Cladobranchia (Nudibranchia, Opisthobranchia, Gastropoda)

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Cladobranchia sind marine Gastropoden, die eine vollständige Reduktion der Schale aufweisen. Damit einher ging die Entwicklung neuer Verteidigungsstrategien. Dazu gehören Mimese, die Aufnahme und Einlagerung von Cnidocysten (Aeolidoidea) und die Verwendung von Sekundärmetaboliten als Fraßschutz.

Viele Opisthobranchia erhalten einen chemischen Schutz, indem sie Sekundärmetabolite aus den Nahrungsorganismen aufnehmen (z.B. Vertreter der Porifera, Ascidiacea oder Cnidaria). Einige Arten sind sogar in der Lage, die aufgenommenen Stoffe chemisch zu modifizieren und damit deren Wirksamkeit zu erhöhen. Andere synthetisieren ihre chemischen Abwehrstoffe *de novo*.

Während einige opisthobranchiate Gruppen mittlerweile sehr gut auf Sekundärmetabolite untersucht sind, fehlen solche Untersuchungen weitgehend bei den Cladobranchiern.

Unsere vorläufigen Untersuchungen zu dieser Gruppe zeigen, dass in vielen Cladobranchiern kein ausgeprägtes Spektrum von Sekundärmetaboliten nachweisbar ist, allerdings kommt häufig Homarin (N-Methylpyridin-2-carboxylat) vor. Diese Substanz ist unter marinen Organismen weit verbreitet, ist aber bei den anderen von uns untersuchten Opisthobranchiern nicht nachweisbar. Homarin konnte auch in einigen Nahrungsorganismen der Cladobranchier (Vertreter der Hydrozoa und Octocorallia) nachgewiesen werden. Bei dem Aeolidier *Phyllodesmium lizardensis*, der sich von Weichkorallen der Gattung *Xenia* ernährt, fehlt das Homarin. Es konnten allerdings 3 Sesquiterpene isoliert werden: das bereits bekannte (+)-α-Murrolen sowie zwei Derivate. Diese sind ebenfalls in der Weichkoralle vorhanden.

Mordwerkzeuge höchster Präzision – Zur Evolution der larvalen Saugzange der Neuroptera

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Die Neuropterida umfassen die Ordnungen Megaloptera und Raphidioptera, deren Larven beißend-kauende Mundwerkzeuge besitzen, sowie die Neuroptera, deren larvale Mundwerkzeuge zu komplexen Sauginstrumenten – spektakulärste Autapomorphie dieser Ordnung – modifiziert sind. Trotz der großen Vielfalt an Formen (stilettartig zugespitzt, nadelförmig verlängert, zangen- oder hauerartig gekrümmt) liegt eine gemeinsame, unter den Insekten einzigartige Konstruktion zugrunde: Mandibel und Teile der Maxille sind miteinander verfalzt und bilden so den Nahrungskanal, der Giftkanal verläuft innerhalb der Maxille – eine raffinierte Funktionseinheit zur Lähmung, Tötung und extraintestinalen Verdauung. Übergangsstadien zwischen beißend-kauenden Mundwerkzeugen und den Saugzangen fehlen, auch werden die maxillären Bestandteile der Saugzange immer noch sehr kontrovers diskutiert. Da bei den Larven der Megaloptera und Neuroptera die Cardines in die Kopfkapsel integriert wurden – eine der Voraussetzungen zur Bildung einer Saugzange –, während sie bei Raphidioptera terminal stehen, erscheint die Hypothese, dass die Saugzangen auf einen gemeinsamen Vorfahren der Megaloptera + Neuroptera zurückgehen, plausibel. Verlängerte Stipites bei Megaloptera lassen die Hypothese einer Verlängerung der Stipites bei einem gemeinsamen Vorfahren der Megaloptera und Neuroptera wahrscheinlicher erscheinen als eine Ableitung vom plesiomorphen Zustand, den wir von Raphidioptera kennen. Morphologische und histologische Untersuchungen sowie REM-Analysen an larvalen Mundwerkzeugen aller drei Ordnungen laufen ...

Speciation on the Balkan Peninsula – three case examples from *Veronica* (Veronicaceae)

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With more than 6500 species of native seed plants the Balkan Peninsula is richer than any comparable area in Europe; presumingly because it has acted as a refugial area for many plant species during the ice ages. Despite being a source for the recolonization of Europe, the Balkan Peninsula was a place for further diversification and formation of new species given its richness in endemic species – summing up to almost one third of its flora.

Up to now, our knowledge of the phylogeographic history of plant taxa of the Balkan Peninsula is predominantly based on the study of tree species. However, most of the species richness of the Balkan Peninsula is due to herbaceous species such as the genus *Veronica*. Information on different aspects of the biology of the genus *Veronica* combined with its available phylogenetic framework makes the genus an excellent model taxon for our study. We focus on species from three different subgenera: subgenus *Stenocarpon* – growing in alpine habitats – subgenus *Pseudolysimachion* – occurring on open meadows – and subgenus *Chamaedrys* – mainly inhabiting forests. Using genome size estimation, AFLP fingerprints, cpDNA markers and nuclear low-copy DNA sequence data we address the following main questions: 1) Which taxa form well-defined taxonomical units? 2) How are the phylogeographical patterns of these taxa on the Balkan Peninsula? 3) What are the differences between ecologically different (alpine vs. open meadow vs. forest) taxa?

The Microanatomy of *Leptogyra constricta* Marshall, 1988 and *Leptogyropsis kalinovoae* Marshall, 1988 (Gastropoda, Neomphalida)

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The helicoid microgastropods (1-2 mm shell diameter) *Leptogyra constricta* and *Leptogyropsis kalinovoae* from sunken wood off New Zealand (depth about 1000 m), have been originally classified among the poorly defined Skeneidae (Vetigastropoda, Trochoidea) based on shell characters, external morphology and radula fine-structure. To scrutinize the systematic placement we investigated the microanatomy and histology of the two above mentioned species by means of serial semithin sectioning followed by computer-aided 3D-reconstruction (software AMIRA™).

The soft body of *Leptogyra constricta* is characterized as follows: Blunt snout; round propodium with short lateral outgrowths; four head appendages: penis, accessory penis and two laterally placed, smooth cephalic tentacles; several smooth epipodial tentacles; single pedal gland; single bipectinate gill with skeletal rods; single (left), kidney; monotocardian heart bypassed by rectum; hermaphroditic genital system with separated receptaculum; rhipidoglossate radula with a bifid radular caecum; one pair of radular cartilages; two digestive glands; hypoathroid and streptoneurous nervous system; no eyes; a single (left) osphradium; statocysts with a single statolith inside.

All examined specimens of *Leptogyropsis kalinovoae* were females with simple oviduct and separated receptaculum seminis. This species resembles the former in most anatomical characters, differences are a single digestive gland, asymmetrically orientated radular cartilages, oesophageal papillae and a pair of reduced eyes.

The anatomical data clearly exclude *Leptogyra constricta* and *Leptogyropsis kalinovoae* from the Trochoidea - Skeneidae and the Vetigastropoda as a whole, but strongly suggest a systematic position among the likewise rhipidoglossate Neomphalida, where the small, helicoid *Melanodrymia* shows most similarities. Preliminary data on shell structure (Steffen Kiel pers.comm.) and molecular studies (Yasunori Kano pers.comm.) confirm this result. The “sunken wood habitat” might have served as an ecological bridge between the ancestral regular deep benthos and the hydrothermal vent habitat otherwise typical for Neomphalida.

On the importance of DNA-Banks

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DNA-Banks are technically optimized service facilities for long term storage of well documented DNA or small pre-prepared tissue samples. The declared purpose is to enhance taxonomic, systematic, genetic and evolutionary studies world-wide by providing (1) at-cost availability of DNA material for further, complementary or corroborating studies, subject to the recipient's compliance according to the articles of the Convention on Biological Diversity (2) permanent storage of DNA material on which molecular studies have been performed, so that results can be corroborated and complemented in the future (3) full documentation of each sample, in a database accessible online, with the provenance of the original material, the place of deposit of voucher (ideally with digital images accessible online), DNA extraction techniques and links to extant molecular data (when published).

Several quality standards for long term DNA or tissue storage have to be met, concerning laboratory handling, the technical infrastructure, documentation, standardization, open access, public awareness, and sustainability. In times of increased staff fluctuation in the institutions, the current practice of storage left to the individual researcher must be replaced by services offered in central storage facilities. Depositing material should become common practice for any scientist and should be incorporated in the "Proposal for safeguarding good scientific practice".

Die Phylogenie der Aeolidoidea (Nudibranchia, Gastropoda) in Korrelation mit ihrer Nahrung

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Die Phylogenie der Aeolidoidea wurde mit zwei molekularen Markern aus dem mitochondrialen Genom untersucht (partielle Bereiche des 16Sr RNA und des COI Gens). Während die Ergebnisse des 16S Gens durch bereits bekannte morphologische Daten gestützt werden, erscheinen die Ergebnisse des COI Gens zu variabel um die phylogenetischen Beziehungen der verschiedenen Familien innerhalb der Aeolidoidea zu untersuchen. Nur die Ergebnisse des 16SrRNA Gens werden hier dargestellt.

Informationen über die bevorzugte Nahrung der verschiedenen Aeolidoidea Arten (aus der Literatur bzw. aus eigenen Beobachtungen zusammengetragen) werden in Korrelation zur Phylogenie der Aeolidoidea gebracht und diese wiederum in Bezug zu aktuellen Ergebnissen der Cnidaria Phylogenie (Collins et al. 2006) diskutiert.

Collins A.G., Schuchert, P., Marques, A.C., Jankowski, T., Medina, M. & Schierwater, B. 2006. Medusozoan phylogeny and character evolution clarified by new Large and Small Subunit rDNA data and an assessment of the utility of phylogenetic mixture models. Syst. Biol. 55: 97-115.

Ultrastructure of nuchal organs and larval photoreceptors does not support a closer relationship of Cirratulidae and Spionidae (Annelida, Polychaeta)

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The systematic position of Cirratulidae within Polychaeta is controversially discussed by molecular and morphological reasons. Traditionally Cirratulidae were often placed close to Spionidae, but clear evidence for this hypothesis is lacking. In order to test such an interrelationship we investigated those characters of the cirratulid *Cirriformia tentaculata,* which show a specific structure in Spionidae and relatives: the apical cover of the nuchal organs and certain ciliary sensory organs in the prostomium of the larvae. The cuticle of the nuchal organs is in Spionidae and several related taxa overlain by a paving stone like arrangement of microvilli, which emerge from the supportive cells and penetrate the cuticle. Beside ordinary rhabdomeric pigment cup ocelli are unpigmented, but nevertheless most probably light sensitve, ciliary sensory organs present in the larval prostomium of Spionidae, Poecilochaetidae and Trochochaetidae. The sensory cilium of a single monociliated receptor cell protrudes into a cavity of one supporting cell and branches into numerous microvilli-like projections. Receptor and supportive cell are surrounded by several non penetrative bipolar, flask shaped sensory cells.

Neither the nuchal organ structure nor the organisation of the larval photosensitive organs in *Cirriformia tentaculata* supports a close relationship of Cirratulidae and Spionidae. The microvilli of the nuchal organ supporting cells do not show any modification in comparison to the microvilli of epidermal cells like it is known in many other polychaete groups. No paving stone like cover is present above the cuticle like in Spionidae and relatives. The prostomial photoreceptors in larvae of *Cirriformia tentaculata* consist of three cells. Each of the two receptor cells bears microvilli and a long cilium. The microvilli protrude in an apical open cup, which is formed by a pigmented supportive cell and which is directly covered by the cuticle. The cilia run over a long distance between cuticle and epidermal cells. They give rise to several microvilli like processes. The investigated organs share no specific features with photoreceptors of Spionidae or any other polychaete subgroup. Alternative hypotheses on the systematic position of Cirratulidae have to be proofed.

Neurogenesis in *Sabellaria alveolata* (Polychaeta: Sabellaridae) as inferred by immunolabelling and digital 3D reconstruction techniques

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Recent phylogenetic studies often reveal incongruencies between morphological and molecular data. Modern morphological techniques such as confocal laser scanning provide new characters for comprehensive comparative analyses. These techniques in concert with 3D reconstruction programs allow us to look at animal structures from a new perspective. Although there is both a growing interest and the accumulation of data in this field of immunocytochemistry research, only few studies focus on developmental stages of lophotrochozoan taxa. Therefore, in our study the larval nervous system in the polychaete *Sabellaria alveolata* (Linnaeus, 1767) was investigated by using fluorescence-coupled antibodies against the neurotransmitters serotonin and FMRFamide. The first neurons are visible at the early trochophore stage with the serotonergic fibres arising first in close proximity to the chaetal sacs at around 34 hours after fertilisation. The FMRFamidergic signal appears later on in the anterior region of the larva. Within the next 24 hours the larval neuronal system is fully developed and consists of two subunits, of which one is associated with the digestive tract and the other innervates the prototroch and the apical organ. Basal features for Trochozoa such as two ventral nerve cords are expressed and the adult nervous system begins to form in late larval stages. A comparison with other recent studies on larvae of *Phyllodoce maculata* and *Pomatocerus lamarckii* show similar results, thus challenging earlier hypotheses that proposed formation of early larval neural elements in strict anterior-posterior direction. Moreover, apparently there is a smooth transition from larval to adult characters in the nervous system.

A secret of genes? The phylogeny of Desmosomatidae Sars, 1897

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The existing system of the deep-sea family Desmosomatidae Sars, 1897(Crustacea: Isopoda) is discussed and brought up to date in a phylogenetic analysis based on morphological and molecular data. In the morphological analysis, a total of 107 species and 129 characters were included. All characters were discussed in detail sensu Hennig (1966, Wägele 2004). Describing new species helped to clarify relationships indicated by intermediate forms. The morphological study yields the taxonomic background for molecular analyses of deep-sea Desmosomatidae. Five (new) subfamilies are defined, which are supported by the result of the phylogenetic analysis (consensus trees). Using molecular methods seems to be necessary to access a better understanding of the relationships in Desmosomatidae. The aim of the present study is to compare results of a molecular analysis with the phylogenetic ideas obtained out of the morphological analysis of the family Desmosomatidae.

The international project CeDAMar (Census of the Deep Abyssal Marine Life) was created to gain a more detailed picture about benthic life in the deep sea. DIVA (DIVersity of the Atlantic benthos) and ANDEEP (ANtarctic benthic DEEP-sea biodiversity, colonization history and recent community patterns) are two of the projects under the umbrella of CeDAMar. Yet, the molecular work depends on fresh material for DNA extraction. This could be gained during the ANDEEP cruises with RV Polarstern and DIVA-2 with RV Meteor in 2005. Sequences of new species of Desmosomatidae could be gained for the 18s gene and CO I. Preliminary results are presented.

Molecular characteristics of European snail populations within the genus *Bythiospeum* (Mollusca)

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Over 65 taxa of the stygobiont genus *Bythiospeum* BOURGIGNAT 1882 (Family Hydrobiidae TROSCHEL 1857) occurs in central Europe (France, Germany, Switzerland, Austria, Hungary). The shells are between 1 to 5.5 mm long. However, the variability of morphological characters like shell and anatomy is not well studied. Although shells have been studied, live collected specimens are rare.

In cooperation with cave divers (Arbeitsgemeinschaft Blautopf) living animals and their behaviour, e. g. while feeding, could be observed and documented for the first time in situ. Mitochondrial gene, cytochrome c oxidase I (COI), and a fragment of the 18S ribosomal RNA was studied from two populations of the Danube system in Baden-Württemberg, Germany. These nucleotide sequences have been shown to be useful in resolving taxonomic relationships among closely-related taxa and we utilized them to clarify genetic variability within one river system. To find out genetic differences on species level, we compared the two populations from the Danube with a distant population of the Rhine system (Ruhr valley in Nordrhein-Westfalen, Germany).

Up to now, genetic information is only available for a *Bythiospeum*-population from the Rhône system, France (WILKE et. al. 2001). Little is known about stygobiont mollusc of the Danube and the Rhine system. The present findings reveal that this morphological and molecular study of the genus *Bythiospeum* raises more questions in understanding the separation of aquatic populations and speciation.

Investigations on the biology and ecophysiology of the symbiosis between the “solarpowered” species *Melibe engeli* Risbec, 1937 (Gastropoda, Nudibranchia, Dendrontoidea) and zooxanthellae (Dinophyceae)

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For the first time, several specimens of a dendronotoid species housing zooxanthellae (*Symbiodinium* sp.) were cultivated for more than 9 months and the efficiency of the mutualistic symbiosis investigated by measuring photosynthesis under varying conditions. This species obtains its symbionts not by feeding on zooxanthellate prey, but, as a singularity within Nudibranchia, as a bycatch when browsing the watercolumn for potential food (mainly crustaceans). Specimens kept under starvation conditions survived the whole period, grew to a modest size and were able to lay eggs continuously. Other specimens which were fed additionally with crustaceans and turbellarians grew to a much bigger size and laid more eggs, implying a higher fecundity compared to the starving specimens. Photosynthetic activity was always high, independant on cultivation conditions. Morphological structures housing the zooxanthellae are described for the first time for this species.

Der Sensillenbesatz der Antennen als Merkmalssystem für die phylogenetische Analyse bei neopteren Insekten

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Ziel dieser Arbeit war die Erschließung des Sensillenbesatzes der Antennen als neues Merkmalssystem für die phylogenetische Analyse bei neopteren Insekten. Die Antennen von mehreren Vertretern der einzelnen Stammlinien der Neoptera (exkl. Zoraptera) wurden dazu rasterelektronenmikroskopisch untersucht, die Verteilung der Sensillen an homologisierbaren Skleriten (Scapus und Pedicellus) der Antennen sowie deren phylogenetische Information diskutiert; diese Arbeit schloss ebenfalls die jüngst entdeckte Ordnung der Mantophasmatodea ein. Für zwei Arten dieser Ordnung (*Hemilobophasma montaguensis, Austrophasma caledonensis*) wurde exemplarisch die Verteilung der Sensillen entlang des Flagellums beschrieben; auch auf die mögliche Natur der autapomorphen „dark spots“ im distalen Teil der Antenne wurde eingegangen.

Auf Ordnungsebene untermauert dieses neue Merkmalssystem die Monophylie der Neoptera sowie der Plecoptera; ein Hinweis auf ein mögliches Schwestergruppenverhältnis zwischen den Plecoptera und Dermaptera konnte ebenfalls aufgezeigt werden. Bei Ausweitung der Taxonauswahl könnte dieses Merkmalssystem auf niedrigerem systematischen Niveau allerdings die Verwandtschaftsbeziehungen innerhalb der Ordnungen und Familien weiter aufhellen.

AFLP markers reveal genetic cohesion within and hybridization among color morphs

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Tropheus display high levels of population structure across very short geographic distances, and gradual among-population differences in color pattern generally increase with geographic distance between populations, whereas major habitat barriers often separate phenotypically highly distinct morphs. Nevertheless, mitochondrial phylogenetic reconstructions of *Tropheus* populations are in several instances inconsistent with the geographic distribution of populations and with color pattern similarities among populations, which has been ascribed to migration events in the course of lake level fluctuations and to incomplete lineage sorting in the identified population clades. In contrast, phylogenetic reconstructions based on AFLP data are largely congruent with phenotypic similarities, and in many cases also with the current geographic distribution of populations. We conclude that mitochondrial phylogeographic patterns still bear the signal of large-scale migration events during major lake level fluctuations, whereas the genetic cohesion among geographic groups of populations indicated by AFLP data results from gene flow between adjacent populations triggered by relatively frequent minor lake level fluctuations. Additionally, AFLP data revealed potential cases of hybrid origin of certain color morphs, and introgression between morphs. The inclusion of a hybrid taxon into a phylogeny constructed from multiple unlinked nuclear loci introduces homoplasy (reflected e.g. in low bootstrap values), and removal of the hybrid taxon results in increased statistical support for clades that contain hybridization partners (Seehausen 2004). Such an effect was observed upon removal of several taxa from the dataset, e.g. a newly described morph (New Kirschfleck), the yellowish morphs occurring around the Lufubu River estuary, and the samples from the Livua population. Our results suggest that lake level fluctuations drive diversification not only by fragmenting populations, but also by promoting hybridization that may generate stable novel morphs.

Morphological and genetic differentiation of the land snail *Arianta abustorum* (Pulmonata: Helicidae) within the Alps

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Arianta arbustorum is a polymorphic, wide-spread and common land snail occurring in the low lands and mountains of Europe except for the southern peninsulas. It has been suggested that its Pliocene ancestor had a depressed shell adapted to mountainous, steep, rocky habitats. According to this hypothesis the most common globular shell morph would be derived and the extant flat-shelled populations relics. The alternative view suggests that flat-shelled populations evolved locally in the Alps and Pyrenees descending from the wide-spread globular form.

However, previous investigations based on sequence data and a rather gross sampling design across Europe did not allow for unambiguous conclusions, but indicated, that *A. arbustorum* must have survived the Pleistocene glaciations in northern, possibly even Alpine refugia. In order to shed more light on shell evolution and the question of Pleistocene survival and postglacial expansion we analysed the genetic variation of populations from the Gesäuse mountains and the Totes Gebirge and their surroundings. Both massifs in the Austrian Alps harbour depressed shelled populations.

Our analyses across morphotypes were based on variation of a fragment of the mitochondrial cytochrome oxidase subunit I and one very variable microsatellite locus. The genetic data were complemented by a morphological analysis using geometric morphometrics. The aim of our study was the reconstruction of the dynamic picture of population genetic and evolutionary processes of an organism with low potential for active dispersal within an Alpine setting.

Systematic significance of chaetal arrangement and prostomial sensory organ ultrastructure in Chaetopteridae (Annelida, Polychaeta)

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Chaetopteridae were traditionally placed within Spionida, whose members bear one pair of peristomial palps. Though these palps are meanwhile assumed to be plesiomorphic for spionid taxa, monophyly of Spionida is supported by recent morphological analyses. The two crucial characters are, however, homoplastic (anterior sterile nephridia) or disputable in case of Chaetopteridae (form of nuchal organs). The only hint on the existence of nuchal organs in Chaetopteridae is based on an external and insufficient description of *Spiochaetopterus costarum*.

In order to test, whether nuchal organs structure is a suitable character to infer chaetopterid phylogeny, we examined prostomia of *Spiochaetopterus costarum* by light, scanning and transmission electron microscopy. No nuchal organs were found. Unspecific single sensory cells are distributed all over the epidermis like in many polychaetes. Grooves in front of the palps basis show an accumulation of sensory cells, but do not exhibit the fine structure, which is typical for nuchal organs. Neither an olfactory chamber, a retractory muscle, a modified cuticle nor distinct multiciliary supportive cells are present. Furthermore, the sensory cells do not project to the dorsal root of the circumoesophageal commissure.

In search of other characters supporting the presumed closer relationship of Spionidae and Chaetopteridae we investigated the arrangement of chaetae in *Spiochaetopterus costarum* and *Chaetopterus variopedatus*. Spionidae and related taxa possess like many other polychaetes transverse rows, which are twisted around 90 degree along the proximo-distal axis. The ventral chaetae shift to a posterior position inside the tissue in notopodia. A second formative site forms longitudinal rows ventral in neuropods resp. dorsal in notopods. Chaetal arrangement in both investigated chaetopterid species differs in several aspects. No second chaetal formative site is present. Anterior neuropodia are lacking and the notopodial transverse rows are twisted in the opposite direction as in Spionidae and relatives. The ventral chaetae shift to an anterior position inside the tissue.

Obviously neither nuchal organ structure nor chaetal arrangement supports a closer relationship of Chaetopteridae to Spionidae and related taxa. A close position is also rejected by recent molecular analyses of polychaete relationships. Further comparitive investigations are necessary to reveal the systematic position of Chaetopteridae.

Molecular Morphology of 18S rDNA of the Bivalvia

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The phylogeny of bivalves (Mollusca), consisting of about 20.000 species, is still uncertain und controversally discussed. Up to now comparative morphology and sequence analyses have not provided conclusive results beyond the four subtaxa Protobranchia, Pteriomorpha, Heterodonta and Schizodonta. This study is concentrated on the folding patterns of slowly evolving 18S rDNA molecules in expectation of finding “deep phylogenetic” information, i.e. early Paleozoic structural signatures.

126 sequences of 18S rDNA with lengths of about 1800 base pairs each, available from Genbank, have been studied, covering all four subtaxa (Protobranchia 13 OTUs, Pteriomorpha 63 OTUs, Schizodonta 10 OTUs, Heterodonta 40 OTUs).

With standard software, 3D molecular structures were created from the primary sequences und subsequently mapped into 2D patterns. The 2D/3D structures are known to be more conservative than the primary structure (the linear base sequence). Their morphological characters were detected, quantified and homologized for the generation of a character matrix. A first phylogram has been constructed by means of the parsimony method. The method is described in detail and preliminary results are discussed. Next streps are the integration of the new character set with morphological as well as molecular sequence data in order to reach a “total evidence” approach.

Useful taxonomic characters in *Smilax* of Costa Rica

(Caracteres utiles para identificar las especies de Smilax, un caso en Costa Rica)

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The genus *Smilax* (Smilacaceae) consists of approximately 300 species in temperate and tropical areas in both hemispheres. It is well known for its use in folk medicine. In the past its economic significance was much larger and its roots were widely exported from the Neotropics to treat syphilis. Until now it is unclear which species contain the active components, because many species show a great phenotypic plasticity and the delimitation of most species in the Neotropics is still poorly understood.

A morphological analysis was carried out of the species occurring in Costa Rica, based on herbarium specimens deposited in USJ, CR, INB and MO. Traditionally, up to 14 species were accepted. Our research demonstrated the presence of only 7 species: *Smilax domingensis*, *S. mollis*, *S. panamensis*, *S. spinosa*, *S. spissa*, *S. subpubescens* and *S. vanilliodora*. The following names are treated as synonyms: *Smilax engleriana* and *S. kunthii* of *S. domingensis*; *S. hirsutior*, *S. angustiflora* and *S. candelariae* of *S. mollis*, and *S. chiriquensis* of *S. vanilliodora*.

Taxonomically useful characters were found in the rhizomes, the shape of the stems and the prickles, the size of the tepals and the change in color of the berries during their development. The color and shape of the rhizomes are of particular interest for the identification of the commercially important species. Traded are two types of roots, called “cuculmeca” and “sarsaparilla” in Central America and Mexico. The first comprises tuberous, white and red rhizomes. The species featuring these characters are: *Smilax domingensis*, *S. panamensis* and *S. spissa*. The second concerns elongated rhizomes as occur in *Smilax vanilliodora*, *S. spinosa*, *S. subpubescens* and *S. mollis*.

Scanning and transmission electron microscopic observations on the development of the nuchal organs in *Platynereis dumerilii* (Annelida, Phyllodocida)

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Nuchal organs are generally regarded as chemosensory organs usually visible as a pair of densely ciliated areas at the posterior edge of the prostomium in adult polychaetes. Due to previous studies it is thought that they develop from the episphere and are thus prostomial in origin. Thus far no ultrastructural studies on their development have been carried out to date. In the present study the development of nuchal organs has been observed in the scanning and transmission electron microscope in *Platynereis dumerilii* starting with early trochophores (24h) and ending with adult (atokous) individuals. The nuchal organs of the adults are situated just behind the brain at the border between pro- and peristomium. They are structurally similar to those of other polychaetes and consist of ciliated supportive cells, primary bipolar uniciliated sensory cells and a retractor muscle. The sensory processes are located in a subcuticular olfactory chamber bordered by pillar-like extensions of the supportive cells. In the TEM the first anlagen are detectable in metatrochophores not earlier than after 60h after fertilization (20^0 C). At this stage these anlagen are still invisible under the SEM. With SEM the earliest stages may be found after 68h and after 72h they are clearly recognizable as well. The nuchal organs develop from cells located just behind the prototroch cells and, therefore, they are hardly distinguishable from the latter in early stages. While the prototroch disappears the nuchal organs become more prominent and distinct. The developing nuchal organs consist of supportive and sensory cells while the retractor muscle is formed somewhat later on. The number of cells increases continuously and an olfactory chamber is formed at the 68-72h stage. Developing stages of 96h and older possess nuchal organs similar in structure to those of the adults mainly differing in the number of cells. Thus, nuchal organs most likely represent solely adult structures. Since they develop behind the prototroch cells at the level and in close vicinity to the first pair of tentacular cirri, their supposed prostomial origin may be questionable.

The question of dispersal and establishment of an aquatic non-indigenous species: *Craspedacusta sowerbii* Lankester, 1880

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The freshwater jellyfish, *Craspedacusta sowerbii*, Lankester 1880, was discovered in 1880 in London, England. Originating from the Yangtze-kiang River in China, it spread throughout world's temperate areas and is now found on all continents except Antarctica. Although it is known from many locations, reports increased over the past years in Germany. This could be due to multiple factors including i) increasing summer temperatures facilitate the development of the easily detectable medusa stage, ii) after sporadic occurrences the jellyfish is spreading more rapidly during the past two decades, and iii) increasing recreational aquatic activities, increase the number of observations. Any combination of factors could lead to an answer. Although not exactly an invasive species, also influences on zooplankton compositions have been shown, it is also an important example of the unnoticeable spread of a non-native species, whose polyp stage is cryptic, due to its size and benthic, submerged habitat, and long-lived; and the medusa, although very conspicuous to divers, occurs only for a short period of time in warm summers. In combination with other factors, such as there are so far only single sex populations found and therefore sexual reproduction almost impossible, *C. sowerbii* seems to exhibit an interesting dispersal pattern. New distribution maps of the medusa have been compiled over the past two years, giving a new insight in the actual dispersal dimension. In addition, we were able to keep the polyps ex situ, thus, creating the basis for genetic work on population level. Combining broad-scale observations on the occurrence of *Craspedacusta* medusa, surveys on the so far ignored *in situ* presence of the polyp stage, successful ex situ maintenance as well as modern molecular techniques to determine population dynamics, this research is intended to improve the understanding of the dynamics and ecology of a non-indigenous, sometimes cryptic, sometimes conspicuous aquatic species.

Can we homologize developmental stages? Instars and heterochrony, and heterochrony as a prerequisite for morphological diversity

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Developmental stages as "embryo" or juvenile stages in moulting organisms like J1, J2... are defined as periods of time between certain developmental events and are called instars whereas other stages as e.g. "tadpole stage" in nematodes refer to characters (like "having the shape of a tadpole"). As the concept of homology can only be applied to characters and not to periods of time, only character defined stages can be homologized between species. Nematodes usually go through 4 juvenile instars before they reach the adult stage. It seems straightforward to regard the corresponding j1 – j4 instars as comparable stages between different nematode species. Problems arise when comparing with species showing only 3 postembryonic instars as in diplogastrids where the first moult occurs within the egg. The embryonic j1 in diplogastrids corresponds with the postembryonic j1 of other nematodes, but some events occur in the diplogastrid j1 that correspond with events in the embryo of other nematodes, like stoma morphogenesis. (The j1 in diplogastrids does not need a stoma as it dwells in the egg.) Likewise the first division of the somatic gonad founder cells that usually occurs in J1, occurs in J2 in diplogastrids. These instances of heterochrony show that, when seeking for comparable developmental stages, we must focus on developmental events one by one and not on instars that are periods between noticeable events like first and second moult (second juvenile instar). Hence naming instars is only useful for superficial description of life histories but not for finding homologous entities in development. Heterochrony not only causes terminological problems when describing development but also provides possible explanations for how alterations in ontogeny create freedom for the evolvution of new morphological characters: In diplogastrids the biological relevance of the heterochronic shift of the first moult into the egg period is the possibility to omit secretion of the J1 stoma and pharynx cuticle as the diplogastrid J1 does not feed. Thereby the time slot for stoma morphogenesis that must be finished before cuticle deposition is prolonged. Within Diplogastridae this time slot facilitated the evolution of a tremendous diversity of complex stoma morphologies that is unique for rhabditid nematodes and reflects the diverse feeding habits in this group. As opposed to rhabditids that feed on bacteria, Diplogastrids are also herbi-, fungi-, carni-, or omnivores.

Studies on the historical biogeography of calicnemiine damselflies from New Guinea (Odonata, Platycnemididae)

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During the last years, comprehensive studies on the taxonomy, phylogeny and biogeography of the tropical damselfly subfamily Calicnemiinae (Odonata, Platycnemididae) have been carried out. Taxonomic revisions of genera and species-groups from New Guinea and the Philippines, combined with phylogenetic analyses, have broadened our knowledge of the complex biogeography of the region. The calicnemiine fauna of New Guinea belongs to the most enigmatic and most diverse assemblages of tropical Platycnemididae. The apparent affinities of taxa from the central ranges of New Guinea with those from the Philippine island of Palawan are particularly intriguing. Distribution areas of almost all New Guinean species of Calicnemiinae closely match the postulated existence of formerly separated geological terranes. Traditional concepts of areas of endemism in the region, however, have to be modified, since the recent discoveries of new species indicate that the pattern of endemism in New Guinea has to be dealt with on a much smaller scale than previously thought.

The orbital mosaic of *Tenrec ecaudatus* (Tenrecidae, Mammalia): evidence against the Insectivora

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The relations of the bones in the mammalian orbita have long been used for mammalian systematics in various taxa. In the Insectivora (Erinaceidae, Soricidae, Talpidae, Solenodontidae, Tenrecidae, Chrysochloridae), the absence of a contact between two of orbital elements, the frontal and the palatine, have long been regarded as autapomorphic. However, since the proposal of the Afrotheria (including Tenrecidae and Chrysochloridae, formerly classified as members of the Insectivora) in 1998, the weak morphological evidence for the Insectivora have been under increased scrutiny.

In a postnatal ontogenetic study, the orbital mosaic of *Tenrec ecaudatus*, was examined and the relations especially of the frontal and palatine bones were documented. It was found that besides a small area of visible contact of the orbital wing of the palatine with the orbital wing of the frontal, there is a much larger contact concealed medial of the maxillary. Since this contact is also present in the Chrysochloridae, it is suggested that the absence of the fronto-palatine contact is an autapomorphy of the core insectivores or Eulipotyphla (Erinaceidae, Soricidae, Talpidae, Solenodontidae) rather than for the Insectivora.

Neuromuscular system of ctenostome bryozoan larvae and metamorphic stages examined by flourescence staining and cLSM

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Bryozoans possess pelagic larvae that undergo a cataclysmic metamorphosis after settling on the substratum. Various former studies dealt with this (eg. Reed 1984: Acta Zool 65(4): 227-238), but focussed mainly on topological changes of the different larval tissues by ultrathin and semithin sectioning techniques.

Phalloidin staining of larvae of *Flustrellidra hispida* (Fabricius, 1780) and *Alcyonidium gelatinosum* (L., 1761) reveals a rather complex system of muscular filaments, which is apparently of no use during the short pelagic life of these lecithotrophic larvae, as their locomotion is largely mediated by ciliary bands. Part of the muscles act prior to metamorphosis, during the so-called „snuffling stage“, when the larva inspects the substrate in a creeping manner. Here the pyriform organ, a glandular and sensory structure situated at the frontal side of is escpecially involved. Further groups of muscles cause the eversion of the larval internal sac, which is the adhesive structure for settlement. After the settlement rapid muscle-mediated morphogenetic movements rearrange the larval tissues. Detailed illustrations and descriptions of these processes are given.

Simultanous antibody stainings against serotonin 5-HT and FMRFamide show basic resemblance to previous results on cheilostome bryozoan larvae provided by Wanninger et. al. (2005: Zoomorph. 124(4): 161-170). However, especially *F. hispida* shows a much more complex nervous system with an increased number of serotonergic neurons. Labelling of microtubules with antibodies against acetylated-α-tubulin indicates that large portions of the larval nervous system are neither serotonergic nor FMRFamidergic.

Further comparison of neuromuscular systems of different bryozoan larve could provide new insights into the the still unresolved question of the evolution of larval types within Bryozoa.

Chloroplasteneinlagerung und Photosynthese bei *Sacoglossa* (Opisthobranchia, Gastropoda)

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Das monophyletische Taxon *Sacoglossa* weist zahlreiche Autapomorphien auf. Eine ist das Vorkommen einer Radula nur mit Rhachiszähnen, die dolchartig zugespitzt sind. Mit Hilfe dieser Zähne stechen die Sacoglossen die Zellwand ihrer Futteralge (zumeist syncytiale Chlorophyta) an und saugen die Zellflüssigkeit aus. Aufgenommene Chloroplasten werden häufig in der stark verzweigten Mitteldarmdrüse des Verdauungstraktes angereichert. Dies hat zur Folge, dass die Tiere meist die Färbung ihrer Futteralge annehmen und kryptisch werden. Für einige Formen ist bekannt, dass die eingelagerten Chloroplasten weiterhin photosynthetisch aktiv bleiben und zur Ernährung der Schnecke beitragen.

In unseren Langzeit-Untersuchungen gehen wir der Frage nach, ob und wie lange die Chloroplasten in den verschiedenen Schnecken-Arten gehältert werden, photosynthetisch aktiv sind und somit zum Metabolismus der Schnecken beitragen. Messungen mit einem „Pulse Amplitude Modulated Fluorometer“ (PAM) in Frankreich, Spanien und Australien konnten zeigen, dass viele Sacoglossa Arten, die auf Grund ihrer Färbung für photosynthetisch aktive Formen gehalten wurden, nur eine sehr geringe bis gar keine Ausbeute der Photosyntheseaktivität erzielten. Es gibt aber auch Arten, wie *Placobranchus ocellatus,* die mehrere Monate ohne zusätzlich Nahrung überdauern können und ihren Energiebedarf ausschließlich aus der Photosyntheseaktivität der Chloroplasten decken.

High Diversity in Populations of *Suberites* sp. near Rovinj (Croatia, northern Adriatic Sea)

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The sponge species *Suberites dommuncula* (Porifera, Demospongiae, Hadromerida, Suberitidae) is very widespread and common in eastern Atlantic and Mediterranean waters. But this well-known "species" seems to represent a complex of several similar species.
In eastern Atlantic waters *S. ficus* (truly sessile, never in association with hermit crabs), *S. suberia* (mobile sponge, usually in association with hermit crabs) and *S. domuncula* (mobile sponge, usually in association with hermit crabs) of the above mentioned species-group are found.
In the Mediterranean Sea the situation is a bit more complicated: Recorded without doubt is only *S. domuncula*. Several times mentioned is *S. ficus*, most probably these records refer to *S. suberia*, indeed *S. ficus* seems to lack in the Mediterranean Sea. Several records of *S. domuncula* seem to refer to *S. suberia*.
Up to date the species are mainly distinguished on the basis of differences in their siliceous spicules. A morphological analysis of 14 specimens of the above characterized species group including preparations from the Neotype of *S.domuncula* was performed focusing on the skeleton and the spicules. Slight differences between the species could be detected beyond the known differences in the spicules. Most of the records (10) turned out to be *S. domuncula*, two specimens belonged to *S. suberia,* one specimen belonged probably to a new species in the Genus *Suberites*.
Many authors follow Burton (1953) and others, who synonymize at least *S. domuncula* and *S. suberia* under the name of the former.
The present results indicate that all three species are valid. Differences among these species can definitely be seen, lacking for the moment are investigations with molecular biological methods, which might help in clarifying the taxonomic problems. These investigations are planned by our group.

Mitochondrial sequences reveal different phylogeographic patterns in widespread corvid birds

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We analysed several widespread Palearctic corvid taxa with respect to their phylogeographic patterns using the mitochondrial (mt) control region as a molecular marker. In the DNA based trees a deep split into two lineages was observed in five cases: Within *Corvus corone*, *Corvus frugilegus*, and *Pica pica* as well as between the species pairs *Corvus monedula - Corvus dauuricus* and *Cyanopica cyanus - C. cooki.* Interestingly, in these five examples the genetic pattern and level of divergence between clades are rather similar, although the respective taxa display a variety of distribution patterns from disjunct to para/allopatric and continuous. In contrast, no differentiation into clearly divergent lineages was detected in three taxa: *Corvus corax*, *Perisoreus infaustus*, and *Nucifraga caryocatactes*. To explain these two types of phylogeographic pattern found in corvid birds (designated East-West pattern and single group pattern, respectively) one has to take into account the ecological conditions which may have accompanied the climatic changes during the Pleistocene. A prominent factor influencing the pattern of genetic differentiation seems to be the preference for either open to semi-open habitats (East-West pattern) vs. forest dominated habitats (single group pattern).

Phylogenetic analyses of the hawk-eagles (genus *Spizaetus*) based on mitochondrial markers: convergent evolution and paraphyly

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We analysed the phylogenetic relationships of New and Old World hawk-eagles (genus *Spizaetus*; Aves: Accipitridae) using mitochondrial DNA sequences. Besides 48 specimens representing all *Spizaetus* species and most of the currently distinguished subspecies, 12 other booted and non-booted “eagle“ genera were included. The basal ramifications could not be resolved with the two markers used (*cytochrome b*, control region). Nevertheless, the trees clearly show that the hawk-eagles represent a paraphyletic assemblage and therefore their external similarities can be ascribed to convergent evolution. The members of the genus *Spizaetus* are grouped according to geographic affiliations: The New World taxa cluster together, yet the South American species *Oroaetus isidori* is also embedded within this group. The Asian taxa form a clearly separated monophyletic group, which is further divided into two subgroups. The only African representative of the genus, *Spizaetus africanus*, is found in a mixed cluster consisting of members of the genera *Aquila* and *Hieraaetus*. Our findings are in accordance with several previous studies of other authors based on various molecular markers and different sets of taxa, but do not agree with current taxonomy. Several taxonomic consequences arising from the phylogenetic relationships as revealed by molecular traits are discussed.

Paleogeography versus Paleobiogeography: the rise of the western Indo-Pacific bioprovince predates the *Terminal Tethyan Event*

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During the Palaeogene the (Neo)Tethys connected the two major oceanic realms, the Atlantic and the Pacific. Throughout the latest Cretaceous to the Early Eocene marine benthic invertebrate faunas in this area are characterised by a large number of taxa showing a wide geographic distribution. Affinities between east and west were even larger than between the northern and southern coast. The Terminal Tethyan Event, which resulted in the disconnection of these two oceanic realms and brought about the "birth" of the Indian Ocean and the Mediterranean, changed this situation. From the Late Eocene to Early Oligocene onwards affinities between European/North African and West Indian/East African faunas began to decline. Although the precise dating of the disconnection and when it started to affect faunal migration is still under discussion most authors agree that with the beginning of the Middle Miocene each region had developed its own distinct biota.

The knowledge of the Oligocene and early Miocene European mollusc faunas of the Western Tethys Region is relatively extensive. Hardly any information, however, is available about coeval faunas from the southern shelf of the Western Tethys. The current project attempts to extend our understanding of the assemblages along the eastern coast of the Sultanate of Oman on the Arabian Peninsula. There, a mollusc fauna was collected in shallow water carbonates of the Dhofar Group (Shuwayr Formation) and the Fars Group (Warak and Ghubbarah Formations) in the area of Madrakah and Duqm. These Omanian faunas are expected to be keystones for the reconstruction of paleobiogeography in the eastern Western Tethys.

The fauna displays a high degree of endemism, comprising 42% of species unknown from other localities. This endemism has to be put into the perspective of the poor state of knowledge about coeval faunas of the eastern and northern African coast. Their absence in the much better studied Mediterranean-Iranian Province (MIP) in the west and the Western Indian Province (WIP) in the north and northeast, however, suggests the existence of a discrete biogeographic entity called the Eastern-African-Arabian Province (EAAP). The influence from adjacent bioprovinces is documented by an uneven proportion of shared species. The strongest links are present with the MIP (40%), whereas the connections with the WIP and PIPP faunas are surprisingly low. These data imply that, during the Oligocene and Aquitanian, the exchange between the MIP and PIPP faunas was quite low along the southern coast of the Tethys. In contrast, the WIP faunas, described by VREDENBURG (1925, 1928), suggest a much higher influx from the eastern faunas along the northern coast of the Tethys. Hence, during the considered time interval, the gastropod fauna of the Arabian shelf contributed to a discrete biogeographic province, which was still part of the Western Tethys region. This pattern indicates that the core of the Neogene western Indo-Pacific bioprovince was already at the Paleogene/Neogene boundary predating the paleogeographic *Terminal Tethyan Event* by about 5 ma.

Molecular phylogenetic analysis of Lophophorata and Chaetognatha

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Despite significant advances in the field of molecular phylogeny, the interrelations among many metazoan phyla remain uncertain. In the present study we focus on lophophorates and chaetognaths which received relatively little attention in recent publications, even though they might hold key positions for our understanding of the early evolution of bilaterian animals.

Lophophorate animals include bryozoans, brachiopods and phoronids. Based on morphological data, these taxa were traditionally thought to form a monophyletic entity related to deuterostomes. In contrast, molecular phylogenetic analyses consistently place all three taxa in the protostome superclade Lophotrochozoa. While most molecular studies further indicate that lophophorates are polyphyletic, their relative positions within Lophotrochozoa are still unresolved. Bryozoans are of particular interest for understanding metazoan phylogeny as they have been proposed to occupy a basal position within Lophotrochozoa.

The phylogenetic affinities of chaetognaths are even more elusive. Often allied to Deuterostomia on the basis of morphological data, several molecular analyses suggest placing them at positions pivotal to metazoan phylogeny, including the basis of Lophotrochozoa plus Ecdysozoa, or the basis of all bilaterians.

Here we present phylogenetic analyses based on concatenated amino acid sequences of seven nuclear gene fragments, including parts of the elongation factor 1 alpha, catalase and fructose bisphosphate aldolase. Our taxon sampling comprises the bryozoans *Alcyonidium* (Gymnolaemata, Ctenostomata), *Flustra* (Gymnolaemata, Cheilostomata) and *Plumatella* (Phylactolaemata), the brachiopods *Novocrania* (Inarticulata) and *Terebratulina* (Articulata), the phoronid *Phoronis* and the chaetognath *Sagitta.* The data were analysed by employing both Maximum Likelihood and Bayesian phylogenetic inference methods. In addition, we also present results obtained from examining several thousand expressed sequence tags (EST) of the bryozoan *Flustra foliacea.*

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Ich seh das Tier vor lauter Borsten nicht – Genitalsegmente ausgewählter Neuropterida im REM

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Die Genitalsegmente erweisen sich für die Taxonomie und Systematik der Neuropterida als sehr wichtig. Für (bisher vernachlässigte) Studien der Genitalsegmente mit dem Rasterelektronenmikroskop wurden drei Arten herangezogen: aus der Ordnung der Megaloptera *Sialis lutaria* (Linnaeus, 1758), sowie aus der Ordnung der Neuroptera *Sisyra nigra* (Retzius, 1783) und *Osmylus fulvicephalus* (Scopoli, 1763). Die Genitalsegmente und angrenzenden Segmente der Abdomina von Männchen und Weibchen dieser Arten wurden sowohl nach Standardfixierung, als auch nach einem von uns entwickelten Quellungsverfahren betrachtet.

In der Arbeit wurden die mannigfaltigen Oberflächenstrukturen (Fransen, Borsten, campaniforme Sensillen, Cuticularkämme, Leisten, Noppen), hinsichtlich Aussehens, Größe, Verteilung und Anordnung erläutert und in Form von Bildern, Grafiken und Diagrammen dargestellt. Standardfixierte Abdomina wurden mit gequollenen verglichen, wobei bei letzteren die Segmente je nach Stärke der Quellung nahezu vollständig untersucht werden konnten. Schließlich soll versucht werden, auf der Basis rasterelektronischer Merkmale zur Konfliktlösung vorliegender diskrepanter morphologischer und molekularsystematischer Stammbäume beizutragen.

The axocoel stone canal complex in the larva of *Antedon bifida* (Crinoida): a possible apomorphy of the Crinoida?

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Until today no information is available on the ultrastructure of the cystidean and pentacrinoid stage of comatulids. Recent studies on comatulid larval development refer to the development of embryonic stages, the larval epidermis of free-swimming stages as well as to the formation of the skeleton of cystidean and pentacrinoid stages. However, present knowledge of crinoid coelomic development after hatching goes mainly back to studies carried out in the nineteenth century using histological sections. According to these studies, the archenteron first divides into an enterohydrocoel and a somatocoel, which subsequently separates into a left and a right somatocoel. Left hydro- and left axocoel then bud successively from the enteric sac. Later the axocoel gains contact to the exterior via the hydropore, and the hydrocoel successively establishes the pentaradial symmetry of the water-vascular system. The primary stone canal connects hydrocoel and axocoel.

In the present study, several cystidean and pentacrinoid stages of *Antedon bifida* were examined by serial semithin sections. They show that both the hydrocoel and the somatocoel are connected to the environment via the hydroporus. Such a condition is neither known for larvae of hemichordates nor for those of other echinoderm groups. Therefore, it is to be assumed that this connection represents an apomorphic condition for the Crinoida or at least for one of their subtaxa which include *A. bifida.* Since no autapomorphic characters are known for Crinoida, further studies have to show whether this clearly derived condition is found in other crinoid taxa.

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Functional morphology of the genitalia in longhorn beetles (Coleoptera: Cerambycidae)

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Genitalia of beetles, especially male genitalia, are often used as characters in articles on taxonomy and phylogeny, because of their complex structure and divergent evolution. Very curious is the fact that there are almost never hypotheses concerning the function of the different elements. In my ongoing PhD-project I try to close this gap. After describing different methods of collecting beetles in copula and dissecting them, I will give an introduction on the complexity and terminology of genitalia, followed by some ideas on the possible function of different structures such as the internal sac and tegmen. The tegmen consists of a tegminal strut and parameres. These parameres can be quite variable in appearance, but there are many unsolved questions on their function. The internal sac or endophallus is the intromittent organ in cerambycids, everted during copulation. Therefore, it comprises different sclerites for distinct functions.

Systematics and biodiversity within the caenogastropod family Naticidae

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An estimated 260-270 Recent and more than 2500 fossil species in the family Naticidae are currently known. The Naticidae arose during the mid-Mesozoic 200-250 million years ago and are classified into the group Neomesogastropoda within the Caenogastropoda. The Naticidae are a cosmopolitan family of carnivorous prosobranch snails found in tropical, temperate as well as arctic waters. They live chiefly within the intertidal region between shallow water and 20 meters depth and their greatest diversity is found in tropical waters. Different arrangements of the genera of the Naticidae have been proposed over time as reviewed by Kabat in 1991. Recent classifications distinguish between four subfamilies, namely Naticinae, Polinicinae, Sininae, and Ampullospirinae. While a world-wide review of the families has not been attempted in well over 100 years, several excellent regional or stratigraphical reviews of Recent and fossil species illustrate the controversial discussion of the phylogenetic derivation and evolutionary history of the Naticidae. Kabat (1996) as well as Riedel (2000) suggested that only the Naticinae represent a monophyletic clade, while the Polinicinae are a grade and the extant species and genera of the Polinicinae should either be placed with the Naticinae or with the Sininae. Currently, evolutionary classification within the Naticidae is based on morphological characters, particularly shell morphology. This analysis suggests polytomic clades due to unspecific morphological characters which have been formed convergently and which appear to be only specific for genera. For example, Popenoe et al. (1987) noted that the umbilical area is formed convergently in the different groups of Naticidae and cannot be used for differentiation among the subfamilian groups. These groups are solely separated by the material and size of their opercula. It is unclear at present whether these characters will suffice to affirm the evolution of the Naticidae plausibly. For a more detailed investigation sequence analysis of the mitochondrial 16S rRNA gene (16S), the cytochrome oxidase subunit I gene (COI), the 18S rRNA gene (18S) and the Histone 3 gene (H3) shall help to reconstruct the phylogenetic relationship of the different groups within the Naticidae and may highlight the position of this poorly investigated species group within the Gastropoda. The molecular data shall also help to examine the validity of the presently postulated genera whose distinctions are merely based on morphological shell characteristics. Additionally, the sequence analyses are used for species separation. For instance, two different forms of Neverita duplicata (Say, 1822) showing different umbilical characters can be separated from each other (Hülsken 2006) as *Neverita duplicata* and the reestablished taxon *Neverita delessertiana* (Recluz, 1843) which previously had been synonymized due to their similar morphological appearance (Tryon 1886, Kabat 1997). Research on the biodiversity of the Naticidae can be extended by comparing sequence data from egg clutches collected directly from the sand bottom with sequences from adult species.

Cilia patterns and pores: comparative external SEM examination of acochlidian opisthobranch gastropods

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Acochlidians are a morphologically and biologically extremely diverse group of opisthobranch gastropods. Only limited information is available for the 27 valid species, concerning their anatomy, biology and reproduction, while their external morphology is fairly well described. Pervious scanning electron microscopical (SEM) examinations of some acochlidian species however indicated that external morphology still offers a variety of new characters for phylogenetic and taxonomic analyses.

SEM-examinations of several individuals of 8 marine and 2 limnic acochlidian species revealed a series of interspecific characters on the body wall, valuable for description and separation of species: 1) the general pattern of distribution of bundles of cilia on the head-foot complex and visceral hump; 2) the presence/absence, number and development of ciliary bands on the head appendages; 3) ciliated areas associated with the gonopore and 4) the distribution, size and amount of pores of epidermal gland cells. Each of the examined species exhibits a specific pattern of distribution of bundles of cilia on the body wall. Even though the density of cilia bundles and the length of cilia may vary between adult specimens, as well as between juveniles and adults, a species specific pattern is always present.

Suggested functions of the observed external characters are discussed and compared in the light of the inhabited ecological niches. A sensoric function of the ciliary bands on the head appendages is likely, while the ciliated areas associated with the gonopores probably serve a reproductive function in transportation of eggs or sperm.

A deep-sea systematic odyssey: a tale of two important isopod families

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Taxa linking shelf to abyss, poles to tropics and old to young sea floor are crucial for evolutionary and ecological studies but pinpointing phylogenetic resolution is vital. The relationship of two ubiquitous isopod families, the Desmosomatidae Sars, 1897 and Nannoniscidae Hansen, 1916 have been a much discussed puzzle, especially the enigmatic genus Pseudomesus Hansen, 1916. The link between the two families has long been unclear yet with resolution they could provide fascinating insights into many deep-sea patterns. Pseudomesus´ own tale reflects the very difficulties in ”lumping” or “splitting” of the two families. Combining molecular and morphological techniques has given taxonomists a powerful match. A close analysis of desmosomatid and nannoniscid characters using evidence from these traditional and new methods has solved a 100 year problem and opened the floor to evolutionary ecologists. The evidence to date, suggests that two should become one, and that one family should be called the Desmosomatidae. These relationships within this family, in themselves, provide an intriguing story to answer questions about faunistic colonization of deep- and shelf-sea floors.

Gene arrangements and other phylogenetic markers of isopod mitochondrial genomes

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Beside plain sequence data mitochondrial genomes offer additional genome-level features which have been proven useful for solving phylogentic relationships. The most promising characters are gene arrangements which allow to infer gene translocation events which can be used as apomorphic characters. However, due to their relative rare appearance a good phylogenetic resolution is limited to lineages with increased variation in gene order. Within isopods we determined numerous mitochondrial genome rearrangements. Using a PCR approach, partial genomes containing sequences ranging from *cob* to *cox1* were obtained from five species comprising Asellota, Oniscidea, Valvifera and Cymothoidea. A translocation of the adjacent genes *nad5* and *trnF* is shared by the oniscidean, valviferan and cymothoidean species studied, but was not found in Asellota. As well a reversed strand bias of nucleotide frequencies, evidence for a reversed origin of replication, is a common feature of the oniscidean, valviferan and cymothoidean species. A translocation of *trnV* is shared by both analysed oniscidean species. Other translocation events were detected for single species. Five translocation events (also including the control region) are assumed to have evolved before isopods got split into major groups. None of them is shared with other malacostracan crustaceans studied so far. Other features like unusual secondary structures of tRNA genes and repetitive sequences could probably gain phylogentic importance when data of more species become available.

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Comparative ultrastructure of larval musculature in tunicates and its phylogenetic implication

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Phylogenetic relationships of higher tunicate taxa is still controversial. During ontogeny of the phlebobranch ascidian *Ecteinascidia turbinata* the tail rotates through 90 degrees to the left. As a result fin blades are oriented horizontally, a situation not found in other Phlebobranchiata but similar to Appendicularia and Aplousobranchiata. To test the hypothesis that a horizontal tail orientation in *E. turbinata* arose convergently, we examined the larval tail organization in *E. turbinata* and seven other tunicate species representing four of the five higher taxonomic groups. The sarcotubular system was examined by electron microscopy of serial sections and 3D-reconstructions. Four types of organization occur in tunicates. In Aplousobranchiata and Appendicularia invaginations of the sarcolemma consist of flat tubules and some aplousobranch ascidians are reported to possess tubular invaginations. In Phlebobranchiata and Stolidobranchiata laminar invaginations exist. In all taxa muscle cells without invaginations can be found. A similar character distribution exists in the number of muscle cells per cross section. Aplousobranchiata and chordate outgroups possess more than six muscle cells whereas Phlebobranchiata, Stolidobranchiata, and Thaliacea possess six. Thus, laminar invaginations of the sarcolemmata and a constant number of six muscle cells can be hypothesized as apomoph for a taxon consisting of Phlebobranchiata, Stolidobranchiata, and Thaliacea. This implicates a convergent evolution of the horizontal orientation of the tail of *E. turbinata* compared to Aplousobranchiata and Appendicularia.

Species boundaries in *Limax* (Gastropoda: Stylommatophora): extreme colour variations in and between species

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Biodiversity research needs taxonomic expertise in a broad variety of organisms. Most scientists working in the creation of species inventories are not specialists in every investigated group, so reliable species identification is one of the major problems. Working on the terrestrial slug genus *Limax*, we recognized that specimens from many species, even common ones, are often misidentified in checklists or collections. Juvenile animals are even more difficult to assign to a species.

In the current study we compare three species, all of which show extreme variation in their external appearance. Two of these species, *Limax maximus* and *Limax cinereoniger*, are very widely distributed in Central Europe. The third (undescribed) species, *Limax* sp., is endemic to the south–western Central Alps. In all three species, body colour ranges from black to pale yellow or cream, with patterning ranging from absent to variable black stripes or spots. It is usual to find more than one colour variant in a population and extraordinary exceptions in colouration also exist.

Our preliminary molecular phylogeny of *Limax* has shown that these three species can clearly be distinguished using the mitochondrial gene cytochrome oxidase subunit I. These results agree with conventional characters such as penis morphology and copulation behaviour. We have been able to use these results to reassess the external appearance characters, and have found that in combination, colour and pattern may be used for identification of adults. The most important characters include the colour and pattern of the sole and the pattern on the mantle.

Abenteurer und genetzte Flügel – eine unendliche Romanze Die Neuropterida-Sammlung des Naturhistorischen Museums Wien

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Die Neuropterida-Sammlung des Naturhistorischen Museums Wien gehört zu den bedeutendsten der Welt. Im Kontext eines Typenkatalogs mit vollständiger Dokumentation der Etiketten, Angaben zur Synonymie und zum taxonomischen Status der Arten wird besonders das kulturhistorische Ambiente der Neuropterida-Sammlung ausgelotet. Die ältesten Typen stammen aus dem Jahre 1846. Die große Ära der Expeditionen - so z.B. in Brasilien und Mexiko - begann schon zu Zeiten der Monarchie. Die wohl spektakulärste Expedition aus dieser Zeit – sie stand unter dem Schutz der Kriegsmarine – ist die Novara-Expedition (1857-1859), die wissenschaftliches Material von unschätzbarem Wert erbrachte. Die berühmtesten Persönlichkeiten, die wesentlich zur Bereicherung der Sammlung und ganz besonders zur Kenntnis und Systematik der Neuropterida beigetragen haben, sind Friedrich Moritz Brauer (1832-1904) und Anton Handlirsch (1865-1935). Unter dem Kustodiat der bedeutenden Wissenschaftler Max Beier (1903-1979) und Alfred Kaltenbach (1920-2005) wurden die Neuropterida in der Folge hervorragend betreut. Seit 1986 (Kustodiat U. Aspöck) setzen Expeditionen (Mediterraner Raum, Vorderasien, Zentralasien, Südafrika und Australien) biogeographische und taxonomisch/systematisch neue Akzente für morphologische und molekularsystematische Analysen.

Die „Vereinigten k.k. Naturalien-Cabinete“ waren von Anbeginn Forschungsinstitute. Die programmatische Widmung am Haupteingang des 1891 eröffneten Naturhistorischen Museums Wien „Dem Reiche der Natur und seiner Erforschung“ ist aktueller denn je.

Molecular phylogeny of the Perissodini, Lake Tanganyika's scale eating cichlids: Incongruence with morphological data

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Although Lake Tanganyika is not the most species-rich of the Great East African Lakes it comprises by far the greatest diversity of cichlid fishes in terms of morphology, ecology and breeding styles. Unlike the mono- or diphyletic speciec flocks of Lakes Malawi and Victoria, the Lake Tanganyika cichlid species flock is a polyphyletic conglomerate of several distinct lineages. Our study focuses on the Tanganyikan cichlid tribe Perissodini, which exhibits one of the most peculiar feeding strategies found in cichlids – scale-eating. Their evolutionary history was reconstructed from 1416 bp DNA sequences of two mitochondrial genes (partial control region and ND2) and from 612 polymorphic AFLP markers. We confirm the inclusion of the zooplanktivorous genus *Haplotaxodon* in the tribe of the scale-eaters, and support the species status of the recently described *H. trifasciatus*. Moreover, our data do not support the currently valid morphology-based subdivision of the scale-eating species into the genera *Perissodus*, *Plecodus* and *Xenochromis*, thus indicating the need for a taxonomic revision. Both, mitochondrial and nuclear data suggest a period of rapid cladogenesis at the onset of the diversification of the Perissodini. The major lineages emerged within a short period roughly 1.5 - 2 million years ago, which makes their radiation slightly younger than that of other Tanganyikan cichlid tribes. All species except *Perissodus microlepis* and *Plecodus straeleni*, which diverged relatively recently (~0.36 million years ago), have existed for more than one million years. Most scale-eaters evolved in deep-water habitat, perhaps associated with the previously documented radiations of other deep-water dwelling cichlid lineages (increasing food supply for scale-eaters), and colonized the shallow habitat only recently.

Wallacea & Warane (Squamata: Varanidae: *Varanus salvator*): Rekonstruktion der Besiedlungsgeschichte Sulawesis durch Großreptilien

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Sulawesi liegt im Zentrum des Malaiischen Archipels zwischen den biogeographischen Großregionen der Orientalis und der Australis, also inmitten einer zoogeographischen Übergangszone, die als Wallacea bekannt ist. Aufgrund der langen geologischen Isolation seit über 40 Mio. Jahren ist diese Insel durch einen hohen Endemismus charakterisiert; über 75% der nachgewiesenen Amphibienarten sind hier endemisch. Dennoch gab es für Tiere in der Vergangenheit mehrfach Möglichkeiten Sulawesi über Inselketten zu besiedeln - niedrige Meeresspiegel bedingt durch weitreichende Vergletscherungen während des Pleistozäns erleichterten die Besiedlung.

Verschiedene Studien über unterschiedliche Organismen (v.a. über Sulawesis Affen der Gattung *Macaca*) haben gezeigt, dass eine signifikante Korrelation zwischen der Verbreitung nahe verwandter Taxa und dem wiederholten Wechsel des Meeresspiegels besteht. Diese Makaken leben mit mehreren parapatrischen Populationen auf der Insel. Eigene Untersuchungen zur Morphologie der Bindenwarane (*Varanus salvator* Komplex) Sulawesis konnte dieses Phänomen bestätigen. Ferner soll die Analyse der unterschiedlichen Haplotypen helfen, die geologische Geschichte dieser Region zu rekonstruieren und die bestehenden Szenarien zur Besiedlung der Insel durch ihre Herpetofauna überprüfen.

Ein zweiter Aspekt betrifft die generelle Erforschung der Herpetofauna Sulawesis, da diese in der Vergangenheit stark vernachlässig wurde. So sind z. B. nur 40 Amphibienarten von Sulawesi bekannt, während es für Borneo 140 sind. Deshalb stellt sich die Frage, ob Sulawesis Herpetofauna tatsächlich eine derart verarmte Diversität aufweist oder ob dieses lediglich ein Artefakt der ungenügenden Bearbeitung darstellt. Daher soll das Projekt eine detaillierte Revision eines Teils der Sulawesischen Herpetofauna darstellen. Um dieses Ziel zu erreichen, wurde ein kombinierter Ansatz aus molekularen (Warane) und morphologischen Methoden (Warane und übrige Herpetofauna) gewählt.

Evolution of peristomatic structures in Lithobiomorpha (Chilopoda)

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A comparative survey of the epipharynx and hypopharynx of lithobiomorph centipedes by light and scanning electron microscopy contributed several informative new characters for the phylogeny of the Lithobiomorpha. Distinctive bottle-shaped glandular structures situated between the labral and clypeal parts of the epipharynx are consistently present in all 18 species studied so far, but are absent in all non-lithobiomorph centipedes. Monophyly of the Lithobiomorpha is further supported by a characteristic transverse bulge on the epipharynx, a distinctive shape of the hypopharynx, and a group of spines set beside a cluster of sensilla immediately behind the mouth on the hypopharynx. Within Lithobiomorpha, the high-ranking subgroups are distinguished by the presence of paired spine rows on the clypeal part of the epipharynx, which are restricted to and apomorphic for the Lithobiidae. Monophyly of the mostly southern temperate clade Henicopidae does not receive unique support from the peristomatic structures although two homoplastic characters (convergent within Lithobiidae) contribute to this node. Within Lithobiidae, most of the shortest cladograms identify Pseudolithobiinae as sister to other lithobiids, whereas members of the Ethopolyiinae nest within the Lithobiinae. The genus *Lithobius* proved to be polyphyletic, with different species being most closely related to such genera as *Australobius*, *Hessebius* and *Pleurolithobius*. Within Henicopidae, the high-ranking subgroups Anopsobiinae and Henicopinae differ in the structure of epipharyngeal spine fields within the clypeal part. A field of grooves on the medial labral part of the epipharynx favours the recently described genus *Dzhungaria* being more closely related to Henicopinae than to Anopsobiinae. Cladistic analysis of 11 characters of the peristomatic structures together with 29 additional morphological characters serves as the basis for interpreting the evolution of the lithobiomorph peristomatic structures. Rooting of the cladogram with Scutigeromorpha is facilitated by hypotheses of homology between the main sclerotized bars, spine clusters, and sensilla clusters in scutigeromorphs and lithobiomorphs.

Phenotypic and genetic distinctness of a natural hybrid population from its two parental populations in the Lake Tanganyika cichlid fish *Tropheus moorii*

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Biodiversity hot spots are of special interest to evolutionary biologists. Cichlid fishes of the East African Great Lakes offer special opportunities to study divergence of allopatric populations, ultimately leading to new species. Lake Tanganyika, with an age of about 20MYR, harbors the eco-morphologically most complex species assemblage with more than 200 endemic species. Diversification most likely followed the allopatric model of speciation, by which divergence is believed to be driven by the interaction of extrinsic factors of the ecosystem in combination with intrinsic biological characteristics of the evolving organisms. The genus *Tropheus* – with about 120 distinct populations and six nominal species described so far – is perhaps the best example for this phenomenon. The evolutionary history of the genus has been shaped by numerous lake level fluctuations, causing phases of isolation and secondary admixis. So far it has been assumed that the morphology of color morphs is highly similar and constrained by stabilizing selection, but no systematic survey was attempted to date. Here we analyze two genetically distinct populations of *T. moorii* and their contact zone during the latest period of low lake level (12-14 KA), in which a small natural hybrid population exists. We characterize these three populations by means of neutral nuclear markers and comparative morphological methods. Thereby we show that even in terms of morphology and genetics populations are significantly differentiated from each other and that the hybrid population clearly appears as intermediate. Population specific morphological differences are concentrated on the cranial morphology. However, population discriminating variables were not significantly correlated between morphological and genetic data sets. These results demonstrate decoupled evolution of microsatellite loci and adaptive morphological characters, a precondition to assess selection-driven evolution of traits. The identified morphological traits will be used in artificially crossed hybrid populations as well as for future QTL mapping experiments.

Intraspecific microsatellite variation in the highly endangered Vancouver Island marmot (*Marmota vancouverensis*) and implications for conservation genetics

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Among the 14 extant species of the genus *Marmota* the Vancouver Island marmot (*Marmota vancouverensis*) is the most endangered one. In 2005 only as few as 35 individuals were left in the wild, while the captive population has increased to 123 individuals. For the breeding program a large microsatellite analysis was carried out. 29 different primer pairs were tested in 30 individuals. Only nine of these loci proved to be polymorphic and were subsequently analysed in 105 samples representing almost the total remaining population of *M. vancouverensis*. Intraspecific variation measured as average expected heterozygosity (H_e) is low compared to other mammals: between 10% and 23% within colonies. Genetic distances between the colonies show that the 11 individuals from the Mt. Washington area are highly differentiated (D values ranging from 0.37 to 0.47) from the Nanaimo lake colonies (94 individuals) in the South of Vancouver Island. Among the Nanaimo Lake colonies the genetic distances are about three times lower (D values from 0.02 to 0.14). For the genetic management of the species it was important to decide, if the two populations should be managed as discrete units. The Mt. Washington population is threatened by extinction due to its small population size and low heterozygosity. Therefore it is advisable to neglect possible local adaptations in favour of the overall genetic variation of the species and to crossbreed marmots from different areas.

Phylogenetic reconstruction of *Zanthoxylum* L. s.l. (Rutaceae) from the Greater Antilles

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Zanthoxylum L. s.l. (Rutaceae) is a genus of about 200 species of prickly evergreen or deciduous trees and shrubs with small dioecious or polygamous flowers. The genus has its centre of diversity in tropical and subtropical areas. In the Greater Antilles 35-40 species are present, of which the phylogeny of selected taxa has been reconstructed using sequence data of the nuclear ITS and the plastid *trn*L-F spacer region. The molecular data revealed *Zanthoxylum* s.l. to be monophyletic which is also supported by morphological data. Molecular divergence into two sister clades is morphologically characterized by the number of flower parts (perianth and stamen: 3 or 4(-5) versus 5(-4)) and fruit morphology (length of ventral suture). Additional synapomorphic features within each clade supporting the molecular data are the degree of connation of sepals, the presence or absence of phyllodes and (again) the number of perianth parts and stamen, rejecting Engler's earlier classification of *Zanthoxylum* (Engler 1931). As result of our molecular analysis the Asian uniseriate species of *Zanthoxylum* form a monophyletic clade within the species group with 5(-4) flower parts from the Greater Antilles so the development of uniserate flowers has been of multiple origin within this genus. We also have to reject Engler's hypothesis of *Zanthoxylum* s.str. comprising the species with uniseriate perianth which he thought to be basal within *Zanthoxylum.* The molecular analysis supports the unification of the genus *Fagara* and *Zanthoxylum* s.str. into one genus *Zanthoxylum* s.sl. and the classification into two main clades, which has already been proposed earlier based on morphological findings (Beurton 1994,1996).

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The Microanatomy of *Ventsia tricarinata* Warén & Bouchet, 1993, a Skeneimorph Vetigastropod from Pacific Hydrothermal Vents (Mollusca)

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The family Skeneidae (Mollusca: Vetigastropoda) is currently regarded as a polyphyletic lumping pot for small (max. 3 mm), rhipidoglossate gastropods showing signs of internal fertilisation. Recent methodological progress including serial semithin sectioning combined with computer-aided (software AMIRA) 3D-reconstruction enables the detailed anatomical investigation of such small, helicoid gastropods. Here we describe the microanatomy of the small (max. 2.5 mm) hot-vent inhabitant *Ventsia tricarinata* Warén & Bouchet, 1993 from the Lau Basin, Fiji (1800 m depth) and discuss its phylogenetic affinities.

The presence of papillate cephalic and epipodial tentacles, a ctenidium with skeletal rods and bursicles, a papillary left excretory organ, a papillary anterior oesophagus, and statocysts with several statoconia all strongly suggest a position inside the Vetigastropoda. This is further strengthened by a ventricle encircling the rectum and a right kidney with large volume and a urinogenital opening.

The remaining characteristics of *Ventsia* show a unique mosaic of plesiomorphic and apomorphic characters, which do not fit in any known vetigastropod subclade: The distinct appearance of epipodial tentacles and separate tentacular epipodial sense organs argues against an inclusion into the Trochoidea and thus Skeneidae, where combined epipodial tentacles are always present. Apomorphies like the single (left), monopectinate ctenidium, the presence of organs for inner fertilisation (penis or receptaculum seminis), a monotocardian heart and the lack of a right renopericaridal duct all are known to be homoplastic characters within basal gastropod groups.

Lacking autapomorphies of all existing vetigastropod subclades the skeneimorph *Ventsia tricarinata* cannot be classified in the present system but deserves at least its own family. However, since most skeneimorph microgastropods await microanatomcial as well as molecular studies, it seems premature to establish a new superior taxon prior to a thorough phylogenetic analysis. At present, *Ventsia* seems best classified as “Vetigastropoda *incertae sedis*“.

Dissemination of historical biodiversity data from collections: East African *Surirella*-taxa (Bacillariophyta) as a pilot study

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During the 19th and early 20th century scientists such as C.G. Ehrenberg and Otto Müller studied African algal samples, described new species and depicted their findings by line drawings. Later authors, however, regarded these early African taxa often as synonyms or as varieties or formas of European species. Beside these early studies, published in journals and books not well accessible today, there is a range of publications dealing with African micro-algae using, besides line drawings and LM photographs, also more advanced techniques (e.g. SEM). In the early 1990s a checklist on African Great Lakes algae was compiled and some distributed spotlights on biodiversity can be found but an overview on all African algal biodiversity is missing.

For all questions concerning inventorying, monitoring, as well as for studying biodiversity changes in Africa (and elsewere), a solid baseline of data is needed. To evaluate whether taxa are acceptable or synonyms of older ones, nomenclatural types have to be checked. In some cases only drawings exist, but many type specimens as well as other original material in public herbaria (e.g. B, BM, BR, BRM, etc.) are still available for re-evaluation. For African diatom species, *Surirella* taxa have been chosen as a pilot study, not only because they are a typical component of African aquatic environments, but also because a great number of them are endemic especially to the East African Great Lakes area.

Our working strategy is to publish our results, such as lectotypes, epitypes, etc., in international journals and to use additional methods for further dissemination of this information. An example is the AlgaTerra Information System [www.algaterra.org] which has been recently developed and is kept updated by the BGBM. A second example is the disseminating of picture data of types and typical specimens within a joint project (National Botanic Garden of Belgium, BGBM, and DH Environmental Consulting, Helderberg, South Africa) funded by the Andrew Mellon-Foundation.

Thiarid tramps: how a species can dominate the snail world

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Knowledge about the biology of particular species helps to understand and not to underestimate the way in which species spread around the world and at the same time displace the indigenous fauna.

Within the typical freshwater-snails species of the *Tarebia granifera* complex Adams & Adams (1854) act as a tropical invader in recent years. This group comprises about 60 morphospecies, all with only slightly different shells. All of the species are parthenogenetic and viviparous. They follow a K-strategy with a complete development of the juveniles to a shelled stage in the broodpouch. Using the phenotypical variability and the geographical distribution allows to distinguish four taxa within the species-complex *Tarebia.*

One of the species, *T. granifera* (Lamarck, 1822) is distributed from Southeast Asia to Fiji and Vanuatu and it invade the Caribbean Islands and just recently South Africa presumably via the aquarium trade. We found that these allochthonous populations have a higher percentage of fertile females and carry significantly more eggs than shelled juveniles within the broodpouch, while in autochthonous populations it is the other way round. Therefore they are producing embroys in fast sequences. As a consequence the reproduction rate of allochthonous populations is accelerated compared to autochthonous populations. *T. granifera* behaves like a highly invasive species, like a tramp, outside its natural occurrence, because the allochthonous populations follow a r-strategy with many eggs and only few shelled juveniles and can therefore reproduce „like hell“.

Mapping of Knowledge in Biodiversity

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Information integration supports the creation of knowledge. Information is modelled here with an ontology based on the CIDOC-Conceptual Reference Model (ISO 21127). In informatics, ontology is a formal specification of semantic concepts. As to be specified with some realistic examples taken from the field of biodiversity (collecting-, determination-, type creation-, expedition-, observation events, etc.) the formal specification of semantic concepts makes scientific activities commonly understandable. Ontologies not only allow one to describe the results of scientific activities, such as a description of a biological species, but they can help to clarify the path by which the goal was reached. In particular, they provide a high-level, uniform representation of transdisciplinary research activities and results. Ontologies as knowledge representation tools will therefore have strong impact on methodological questions and research strategies for different disciplines such as biology, archaeology, art history, socio-economy, etc. They can be regarded as semantic glue between and within scientific and scholarly disciplines.

Ultrastructure in echiurid sperm: implications for ingroup relationships

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Echiura is a small taxon of about 150 species of unsegmented, coelomate marine worms. According to morphological character distribution they are regarded as sister taxon of the Annelida, respectively Articulata. Molecular data, however, indicate that Echiura are the sister taxon of the Capitellida and thus a subordinate taxon within the Annelida. Presently no morphological characters are known that support this hypothesis. One of the reasons for the lack of morphological evidence is the fact that the internal relationships of the Echiura are unresolved. Thus, those characters and character states which can be assumed for the stem species of Echiura are unknown. Within a larger project to unravel the internal relationships of Echiura, we here analysed the sperm ultrastructure and compared it to other echiuran characters. These data were complemented with own data on the fine structure of spermatozoa in *Thalassema thalassemum* (Pallas, 1766) and *Echiurus echiurus* (Pallas, 1767). The comparison provided 10 characters with different character states. We included 8 further characters from the general morphology and implemented a Maximum Parsimony Analysis in Paup4.0b on the species level using *Capitella* sp. (Eckelbarger & Grassle, Mar Biol 95: 415-429) as outgroup species. Our combined analysis supports a taxon consisting of the bonellids *Bonellia viridis* Rolando, 1821 and *Hamingia arctica* Danielssen & Koren, 1881. The sperm of these two species show highly derived features which separates them from the rest. The study, thus, confirms the traditional view that the Bonellidae are monophyletic. It is the only taxon with sexually dimorph species among the Echiura. The data also reveal a clade consisting of *Ikedosoma gogoshimense* (Ikeda, 1904), *Listriolobus pelodes* Fisher, 1946, *Thalassema thalassemum*, *Ochetostoma caudex* (Lampert, 1883), *Echiurus echiurus* and *Urechis caupo* Fisher & MacGinitie, 1928. But, presently the relationships among these species can not be specified in further detail. However, the analysis of sperm structures only, indicates a common stem lineage for *Urechis caupo* and *Echiurus echiurus*, but displays no bootstrap values.

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Leanchoilia illecebrosa (Hou, 1987) and the stem-lineage of Chelicerata

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Leanchoilia illecebrosa (Hou, 1987) is one of the Lower Cambrian (530 Ma) 'great-appendage' arthropods from the Chengjiang biota, China. These arthropods, at least the ones having a short, claw-like 'great appendage' (corresponding to the first appendage of Arthropoda s. str.) are considered to be derivatives of the stem lineage toward the crown group of Chelicerata. Reinvestigation of *L. illecebrosa* led not only to a new model of the feeding mode of this animal but also brought up new features expanding our knowledge of the ground pattern of Chelicerata and even Euarthropoda. One feature is that the endopod of post-'great appendage' limbs has up to nine podomeres, more than previously thought. Another feature is that the exopod comprises two portions which are connected by a transverse fold, apparently enhancing flexure. Endopod and exopod, however are partly connected with each other. This discrepancy may be explained in a way that the endopod could flex in the anterior stroke at the basipod endopod joint (and using the fold within the exopod) pulling the whole exopod down and backwards in order to reduce the dragging forces (exopod following passively). In this functional model, no special musculature was necessary to operate the exopod. The evolutionary implications of this are briefly discussed.

A tiny nemathelminth larva from the Cambrian 'Orsten'

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A 120 µm long fossil in 'Orsten'-type three-dimensional preservation from Middle Cambrian limestones collected in Australia shows characters that point to nemathelminth affinities. These features include a ring-shaped terminal mouth with pharyngeal teeth and a body subdivided into an annulated anterior part and a posterior part with scale-like sclerotisations, from which caudally pointing hooks arise. The tail end is bifid, similar to that of gastrotrichs and kinorhynchs. This mixture of features is discussed in the light of the morphology of extant nemathelminth taxa.

Hemocyanin as a promising molecular marker for phylogenetic analyses in chitons (Polyplacophora)

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Native Molluscan hemocyanin molecules are formed from 10, 20 or more identical subunits of which each possesses a molecular mass of 350 - 400 kda. The subunits show a repetitive structure of either 7 (a-g) or 8 (a-h) functional units. In contrast to the situation in gastropods, bivalves and cephalopods, where paralogs of the entire gene region are observed, chitons possess only one type of hemocyanin. We analysed the phylogenetic utility of two protein coding hemocyanin domains (partial subunit f and g) separated by an ancient intron of variable size (157bp to 1297bp).

Depending on which data were used for our analyses (*exon*/*intron*/*exon*, *exon*/*exon* or *amino acids*) we obtained rather well supported clues for the phylogenetic relationship of the Polyplacophora at different taxonomic levels. Although, more sequences and more taxa are needed to robustly resolve the basal split of the Chitonina and Acanthochitonina, our preliminary results show a strong tendency towards this bipartition of the Chitonida and furthermore detect the Lepidopleurida as a third major group of the Polyplacophora. These findings were consistent with expectations for high-level relationships based on recent morphological and molecular studies. Additionally, our data suggest the paraphyletic relationship of the Ischnochitonidae. The analysis of several species of the genus *Lepidozona* failed to reveal phylogeographic structure of all studied specimens, but was very effective in resolving species relationships within this genus.

3D microanatomy and sperm ultrastructure of the interstitial acochlidian gastropod *Asperspina murmanica* (Kundinskaya & Minichev, 1978)

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Acochlidia are amazing opisthobranch gastropods with several aberrant morphological and biological features. Most of the 27 species are marine mesopsammic, inhabiting interstitial spaces of coastal sands worldwide. The acochlidian phylogeny is still not resolved and cladistic analyses are hardly feasible due to, amongst others, little detailed structural information and incorrect anatomical data from older species descriptions.

This study aims to re-examine in detail the microanatomy of the poorly-known species *Asperspina murmanica* (Kundinskaya & Minichev, 1978), in order to improve the quality of primary data.

Several specimens were collected at the type locality in the Barents Sea, Russia. Histological semi-thin serial sections were prepared and a computer-based three-dimensional reconstruction of all major organ systems was made using AMIRA software. For the first time, the sperm ultrastructure of a member of the Asperspinidae was examined by transmission electron microscopy (TEM).

Our results show various differences to the original description: the reproductive system is well-developed, comprising an ampulla and female glands; the nervous system shows paired rhinophoral and gastrooesophageal ganglia and large aggregations of precerebral accessory ganglia, whereas the presence of a genital ganglion could not be confirmed. But the major discrepancy refers to the absence of a mantle cavity. The gonopore, anus and nephropore open dextrolaterally to the exterior.

The damselfly family Dicteriadidae: a phylogenetically interesting group of Odonata

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With only two medium sized species, the Dicteriadidae are one of the smallest dragonfly families of the world. Both species, *Dicterias atrosanguinea* and *Heliocharis amazona*, inhabit small to large, moderately flowing watercourses of Neotropical rainforests. While *D. atrosanguinea* is restricted to the Brazilian Amazon basin, the larger *H. amazona* is much more widespread in tropical South America. Adults of the former species are brightly red in both sexes. Males of the latter species have a mainly blue abdomen and an olive green thorax; females are completely green. In comparison to *D. atrosanguinea*, *H. amazona* shows very high intraspecific variation in venation characters. This variation is greater than in any other odonate species and a primary reason for the high number of synonyms of *H. amazona*. Both species are characterised mainly by the large, movable hooks on each side of the mouthparts and by the long, thin legs which lack the two rows of small spines typical for all other dragonflies. These unique features are a reason for the isolated systematic position of the family, which is discussed in detail. In recent morphological studies the family is placed between Polythoridae and Amphipterygidae, between Polythoridae and Calopterygidae or as closely related to Chlorocyphidae or Megapodagrionidae. Results of a molecular analysis place the family together with Amphipterygidae and Polythoridae as sistergroup to Calopterygoidea. Morphological features of the larva of *H. amazona*, and also most probably of the unknown larva of *D. atrosanguinea*, are inconsistent with the molecular classification. The bare and slender legs as well as the long antennae and very long paraprocts are more similar to the corresponding features in Calopterygidae or Megapodagrionidae.

Auswirkungen verschiedener Pflegemaßnahmen auf die Arthropodenfauna einer Heißlände (Obere Lobau) im Nationalpark Donauauen

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Da Heißländen in Ausystemen, aufgrund ihrer geringen Wasserhaltekapazität und außergewöhnlichen Vegetationszusammensetzung, besondere Standorte darstellen, wird versucht durch verschiedene Maßnahmen wie Mahd, Beweidung und Entbuschung die Flächen zu erhalten.

Für die Arbeit wurden vier unterschiedliche Flächen herangezogen, die im Laufe der vergangenen Jahre unterschiedlich behandelt worden sind.

Aufgrund dieser ökologischen Umstände, wird versucht anhand spezieller Indikatorgruppen (Laufkäfer, Bodenlebende Spinnen) die bestmögliche Pflege der Flächen herauszufinden.

Ziel dieser wissenschaftlichen Untersuchung ist es ökologisch interessante Pflanzen- und Tierarten langfristig in ihrem Bestand zu erhalten.

Evolutionary history of the *Ranunculus alpestris* group in the European Alps and the Carpathians

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Phylogeographic and phylogenetic analyses on AFLPs and *matK* sequence variation of cpDNA were used to asses the evolutionary history of alpine *Ranunculus alpestris* s.l. (including the closely related endemics *R. bilobus* and *R. traunfelneri*) in the European Alps and Carpathians. Analyses of AFLP data split the 90 populations studied in three groups. The endemic species, both restricted to Southern Alps, together with south-eastern-most populations of *R. alpestris* formed one group, while the rest of the later species was split in a western and an eastern group (including the Carpathian populations). Chloroplast DNA sequences showed substantial intraspecific variation and confirmed the split of the endemics from *R. alpestris* s.s., tentatively estimated to have happened ca. 2.3 million years ago. The low divergence between the two endemics suggests ongoing speciation, while the lack of a synapomorphic 6 bp deletion in the *trnK* intron (flanking the *matK* region) in an accession of *R. bilobus* might indicate that *R. traunfelneri* has evolved from within *R. bilobus*. Despite the clear high level of variation in AFLPs, there is no divergence of cpDNA between western and eastern *R. alpestris* s.s.

The morphospace of the fin – limb transition

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Shubin et al. (2006) published a detailed description of *Tiktaalik roseae*, a fossil sarcopterygian whose pectoral appendage combines features of fins and limbs. I used their cladogram of lower vertebrates along the fin-limb transition series to explore the morphospace of this transition, using the computer simulation program FRONTERA. Producing known and unknown pectoral appendage forms along this transition, the morphospace seems to widen as it reaches into tetrapod limbs. However, the sarcopterygian morphospace with regards to pectoral fins is rather narrow, facilitating parallelisms in evolution. In turn, sarcopterygian pectoral fin morphospace is less constrained but less than its actinopterygian equivalent. Actinopterygians constitute the vast majority of fishes, yet none of their subgroups successfully conquered land beyond coastal habitats. Vice versa, the sarcopterygian lineage leading over *Tiktaalik* to tetrapods shows an increased variational freedom along with an increased morphological and functional complexity of the pectoral appendages.

Shubin, N.H., E. B. Daeschler and F. A. Jenkins (2006): The pectoral fin of Tiktaalik roseae and the origin of the tetrapod limb. Nature 440: 764 – 771.

Genetic diversity within lichen photobionts of the *Lecanora varia* group (Lichenes, Ascomycota)

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Lichens are symbiotic organisms, where a fungus–generally a member of the Ascomycota – and a photobiont – generally a green algae – interact closely in a widespread life form strategy.

Recently, numerous studies have focused on the genetic diversity and phylogenetic relationships of the fungal partner of the symbiosis. Meanwhile, knowledge about photobiont diversity and the degree of photobiont selectivity of the fungus have been lacking behind. The *Lecanora varia* group is a set of species within the genus *Lecanora* defined by the presence of an amphitecial cortex along with the presence of usnic acid as secondary metabolite. We have focused on a small group of three species, namely *L. varia*, *L. burgaziae*, and *L. densa* which share very similar anatomical and morphological characters and an identical chemistry, with psoromic and 2-O-demethylpsoromic acids in addition to usnic acid. We have collected populations of these three species from various localities within their distributional range: *L varia* (Spain, Austria, Sweden, Czech Republic, western Siberia); *L. burgaziae* (Spain) and *L. densa* (North America and Spain). Subsequently, we sequenced the internal transcribed spacer (ITS) region of the nuclear ribosomal DNA to assess the degree of genetic variability within the phobobionts present.

A high degree of variability was found among the photobionts of sampled specimens. Not only different lineages but also different photobiont species were detected. No correlation between lichen species and photobiont lineages was found. However, there is a high correlation between the geographical origin of samples and the photobiont lineages.

Nervensystem-Anatomie und Systematik bei Caudofoveata (Mollusca)

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Die Caudofoveata sind eine rein marine, grabend in schlammigem Sediment lebende Gruppe der Mollusken. Sie besitzen einen drehrunden, wurmförmigen Körper und sind primär schalenlos, d.h. der Mantel scheidet eine Cuticula und kalkige Sklerite ab. Da nun die Untersuchung ebendieser Sklerite und der Radula für eine Artbestimmung ausreicht, ist der Aufbau der übrigen Organsysteme teilweise sehr wenig untersucht. Dementsprechend basiert auch die Systematik auf Gattungs- und Familienniveau hauptsächlich auf der Morphologie des Radulaapparates. Merkmale aus der Anatomie des Weichkörpers, die zur Überprüfung und eventuellen Weiterentwicklung des Systems herangezogen werden könnten, sind nur wenige bekannt.

Im Rahmen der vorzustellenden Studie wurden mittels Rekonstruktionen von Schnittserien detaillierte vergleichend-anatomische Untersuchungen am Nervensystem der folgenden vier Arten aus allen drei Familien durchgeführt: *Scutopus ventrolineatus* SALVINI-PLAWEN, 1968 (Fam. Limifossoridae), *Prochaetoderma californicum* SCHWABL, 1963 (Fam. Prochaetodermatidae) sowie *Falcidens gutturosus* (KOWALEVSKY, 1901) und *Falcidens crossotus* SALVINI-PLAWEN, 1968 (Fam. Chaetodermatidae). Die Ergebnisse dieser Studie und eine Zusammenfassung der bereits (vor allem in älterer Literatur) publizierten Daten ermöglichen es, sowohl für das Gattungs- als auch das Familienniveau Merkmale oder Merkmalskomplexe mit potentiell systematischem Wert zu nennen.

Hierzu gehören die Anatomie des Cerebralganglions, die Innervierung der Buccalhöhle, der Ursprung und Verlauf der Buccalkonnektive, die Lage der lateralen Nervenstränge sowie die Ausbildung des Nervensystems am Hinterende des Körpers. Die Anzahl der Präcerebralganglien bzw. der Ganglien und Kommissuren im buccalen Nervensystem dürfte jedoch kein gutes Merkmal darstellen, da hier möglicherweise eine hohe Variabilität auf dem Art-Niveau (bei den Präcerebralganglien eventuell sogar innerhalb der Art) vorhanden ist.

First record of free-living nematodes (Nematoda: Chromadorida) in the mantle cavity of a Chilean polyplacophoran (Mollusca).

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Nematodes of the generally non-parasitic orders Monhysterida and Chromadorida have been reported up to now from the gill chambers of different crustaceans, inside of sponges, in and on annelids, and on the baleen-plates of whales.
This is the first record of free-living nematodes colonizing polyplacophorans.

Two different nematode species belonging to the order Chromadorida were found in a cyst in the mantle cavity of a *Chiton magnificus* Deshayes, 1827 collected in Comau Fjord, Chile:
Two females (length > 2 mm) possibly belong to the genus *Euchromadora*; the other smaller specimens (one female and 6 juveniles) are probably also members of the family Chromadoridae.

An actualized overview of members of the orders Chromadorida and Monhysterida living epibiotically or parasitic in or on other invertebrates given is relevant also in the light of recent molecular studies that group together Chromadorida and Monhysterida with mainly parasitic Secernentea.

Aurochs or domesticated cattle? Ancient DNA analysis of early animal husbandry in Rosenhof, Northern Germany

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For several hundred years beginning in approximately 5450 BC, the Mesolithic Ertebølle/Ellerbek culture in the Southwest Baltic region coexisted with adjacent Neolithic cultures to the south and east of the river Elbe. During this time of coexistence, acculturation processes led to the adoption of Neolithic elements by the Mesolithic population of East Holstein. Recovered artifacts evidence regular contact with farming cultures and archaeo-palynological analyses show that agriculture may even have been practiced on a small scale. This assumption is supported by archaeo-zoological analyses showing that Mesolithic bone samples from the Rosenhof LA 58 site are from fully domesticated cattle. However, skepticism of these results has often resulted from the professed diagnostic problem of overlap in size between small female aurochs and large male cattle. In addition, morphological analyses can give no unequivocal information on whether the presumed cattle are the result of independent domestication of indigenous aurochs populations, or domesticated animals introduced through direct contact with Neolithic settlers.

To contribute to clarification of these questions, we analyzed ancient mt- and ncDNA of several presumed domesticated cattle from the site Rosenhof LA 58. In addition to haplotype determination on the basis of the HVR I region within the mitochondrial d-loop, we successfully amplified parts of zinc finger genes on the X- and Y-chromosomes for sexing.

The results show that all bone samples stem from female individuals. However, only one of these samples revealed the lineage that appears in imported domesticated cattle with Near Eastern origin. The lineages of the other samples turned out to be typical for the European aurochs. In our poster we will expound the possibilities and problems of discriminating between wild and domesticated bovines on the basis of molecular genetic methods. Afterwards we will point out the influences our data will have on further morphological distinctions between aurochs and domesticated cattle. Finally we will introduce our results to the long-standing debate concerning early domestication of bovines in Northern Germany.

Tardigrades - from biodiversity to biotechnology

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Most of the 959 known tardigrade species are well-known cosmopolitan species. 799 limno-terrestrial species live in moist environments that facilitate the animal's gaseous exchange and avoid desiccation. However, such habitats frequently undergo seasonal changes that impact animals, but they are able to survive these periods of adverse conditions due to the ability to enter a cryptobiotic state. They have the remarkable ability to circumvent such problems and are able to survive almost complete dehydration and freezing. The aim of the project FUNCRYPTA, a tardigrade project funded by the BMBF Framework Programme „Biotechnologie - Chancen nutzen und gestalten", „QuantPro - Quantitative Analyse zur Beschreibung dynamischer Prozesse in lebenden Systemen", is the characterisation and quantification of molecular mechanisms of tolerance that enable tardigrades to survive in cryptobiosis. For this purpose, the expression of genes, induction of proteins, as well as metabolic products will be investigated. With the consortium of four academic research institutions, and one company it will be possible to gain more information about the dynamic processes in cells from a living active state to a cryptobiotic state, and vice versa in tardigrades. A better understanding of the survival mechanisms in cryptobiotic organisms will lead to the development of new methods for preserving biological materials *in situ*, macromolecules and cells from non-adapted organisms which would be of great benefit to tissue engineering, cell transplantation, individual medicine, cryo-preservation, other areas of biotechnology, and *ex situ* collection in the frame work of biodiversity research. The results will be obtained by modern approaches of (i) genomics to identifiy expressed genes, (ii) proteomics to identify induced proteins, (iii) physiological investigations to validate and quantify identified genes and proteins, (v) bioinformatics to drawing up mathematical models to predict dynamic cellular changes between the active and cryptobiotic stages of tardigrades, and of the interdisciplinary data from the FUNCRYPTA consortium.

Intraspecific genetic biodiversity of the Wall lizard, *Podarcis muralis*, in Austria - glacial refugia and postglacial colonisation routes

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In the course of the present study the intraspecific diversity of the Common Wall lizard (*Podarcis muralis*) was analysed. The distribution area of this warm adapted species ranges from Spain up to north-western Turkey. In Austria autochthonous populations are restricted to Carinthia, the eastern border of the Alps, and the Inn valley in Tyrol. Genetic analyses were performed including samples from the whole area of the species. A segment of the mitochondrial cytochrom b gene (878 bp) was PCR amplified and sequenced.

The haplotypes fall into 21 clearly separated clades constituting four main clades. While two main clades are restricted to small areas in Italy and southern France, the two other have northwestern and southeastern distributions covering the major part of the distribution range of the species. Genetic distances within this species exceed clearly the distances between some recognised species of the same genus. Nevertheless, colour and pattern proof that hybridisation occurs broadly on contact areas.

Three of the 21 haplotype groups were found in Austria: one belongs to the southeastern main clade and occurs in Carinthia and at the eastern border of the Alps. The other two are members of the northwestern main clade. One occurs in the Inn valley, and the other one in an isolate in the Erlauf valley in Lower Austria. These haplogroups correspond to those found in the east Adriatic area, northwestern Italy, and the central Balkans, repectively, indicating that the glacial refuges of the Austrian populations were located in these areas. In addition to the autochthonous populations there are some additional populations in Austria, which originated from human introduction.

Key words: *Podarcis muralis*, Austria, intraspecific diversity, mitochondrial genes, glacial refugia

Sequencing and microsatellite genotyping errors in PCR products from avian museum specimens

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Museum specimens are valuable sources of DNA whenever sampling of fresh tissue is not possible, but low concentration and quality of DNA can make genotyping of such samples difficult. Recently, considerable attention has been paid to the error-proneness of microsatellite genotypes from hair and fecal samples, whereas concerns about the accuracy of DNA sequencing have been raised mainly in relation to ancient or formalin-fixed tissues, where miscoding lesions in template DNA leading to artifact base changes in sequences have been well documented.

We observed similar types of PCR errors in sequencing mtDNA from relatively recent (≤ 35 years) avian museum specimens. Single base errors were confirmed by replicate sequencing and included both double peaks and artifact substitutions at rates of $\sim 3 \times 10^{-4}$ and $\sim 1 \times 10^{-4}$ per base-pair, respectively, resulting in one or more errors or ambiguities in an 1100 base pair sequence in 21% of 219 samples. Most errors involved C→T changes on the L-strand, presumably due to deamination of cytosine in the template. Additional artifacts were G→A transitions and C→A and G→T transversions.

In microsatellite genotyping from the same set of DNA extracts, complete amplification failure and the “dropout” of one allele from heterozygous genotypes were the predominant problems encountered. While negative PCRs are a nuisance and increase the effort required to obtain data, allele dropout presents a more severe problem as it may lead to the scoring of false homozygotes. The amplification of artifact bands was less frequent.

The frequencies of both sequencing artifacts and microsatellite genotyping errors increased with length of the amplified region and decreased with the concentration of template DNA.

Following our experience, we advocate heightened awareness of the potential for sequencing and genotyping errors and greater efforts to verify data in studies utilizing potentially problematic material. A posteriori evaluation of data and replicate reactions are effective measures to increase the quality of datasets obtained from suboptimal material.

Hemocyanin in Mantophasmatodea (Insecta, Pterygota): Restricted homology among pterygote orders?

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Here we report on newly identified coding regions for the hemocyanin subunit 2 from the recently established insect order Mantophasmatodea (*Mantophasma zephyra*) (Klass et al. 2002). Since the phylogenetic position of Mantophasmatodea among pterygote insects is still controversely discussed we focus on hemocyanin as a potential marker to clarify their phylogenetic position including Mantophasmatodea, Plecoptera, Caelifera, etc.

Hemocyanins are oxygen binding respiratory proteins of molluscs and arthropods. In insects a loss of the respiratory proteins has been related to the development of a direct gaseous oxygen transport by the tracheal system. However, here we present analysis of hemocyanin sequences from Mantophasmatodea in order to (i) evaluate their phylogenetic value for insect systematics and (ii) provide further information on the phylogenetic position of the new insect order Mantophasmatodea.

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Die Mexikanische und Dominikanische Bernsteinfauna. - Eine Paläobiogeographische Studie

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Die Untersuchung der Arthropodenfauna des mexikanischen und dominikanischen Bernsteins liefert neue Daten, die den Ursprung und die große Diversität der Arthropoden in Zentralamerika und den Karibischen Inseln besser verstehen helfen.

Die systematische Untersuchung der fossilen Fauna des mexikanischen Bernsteins zeigt eine Zusammensetzung aus überwiegend tropischen Elementen, deren heutige Vertreter hauptsächlich in Zentral- und Südamerika leben. Nur einige dieser fossilen Gattungen sind heute noch auf den Karibischen Inseln zu finden und nur ganz wenige Gattungen kommen bis in den Süden von Nordamerika vor.

Der Vergleich der Bernsteinfauna aus dem mittleren Miozän Mexikos mit der dominikanischen Bernsteinfauna, zeigt, mit einer Übereinstimmung von mehr als 30% der vorkommenden Gattungen, eine deutliche Beziehung zwischen Hispaniola und dem Süden Mexikos. Die Erklärung einer solchen heutigen Verbreitung und die Ähnlichkeit zwischen beiden Bernstein –Vorkommen kann man durch die Theorie einer Landbrücke zwischen Südamerika und die Karibische Insel und Insel nah mit einander zwischen Honduras, Jamainka und Haiti während des Oligozäns und Miozäns erklären. Die paläogeographische Position der Insel Hispaniola zu dieser Zeit hat vermutlich dann diesen Faunenaustausch ermöglicht.

The Microanatomy of *Xenoskenea pellucida* (Monterosato, 1874) (Gastropoda, Heterobranchia, Ectobranchia)

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Until recently the classification of most microgastropods has been based on shell characters, radula details and external morphology. Nevertheless, the vetigastropod family Skeneidae (type species *Skenea serpuloides* Clark, 1851) has often been suspected to represent a polyphyletic assemblage. Based on its heterostrophic apex the skeneimorph microgastropod (1.6 mm) *Xenoskenea pellucida* (Monterosato, 1874) has been transferred to basal Heterobranchia. Herein, we describe the detailed morphology and anatomy of this species based on computer-aided (software AMIRA) 3D-reconstructions from semi-thin section series.

Xenoskenea pellucida is characterised as follows: hyperstrophic larval shell; elongated snout with small appendages; smooth cephalic and no epipodial tentacles; a second posterior food gland; a single bipectinate, ciliated gill with two retractor muscles but lacking bursicles and skeletal rods; a single, left, pallially situated kidney; a monotocardian heart with passing rectum; a truly hermaphroditic genital system adapted for internal fertilisation; a rhipidoglossate radula but lack of radular cartilages; an epiathroid nervous system; statocysts containing a single statolith.

This character-set as a whole reflects basal heterobranch conditions and in particular affinities to ectobranch (valvatoidean) taxa such as *Hyalogyra* and *Hyalogyrina*. Accordingly, *Xenoskenea pellucida* should be transferred from Vetigastropoda – Skeneidae to Ectobranchia-Hyalogyrinidae. Further studies (in progress) on other hyalogyrinid species are necessary to clear up the specific position within this basal heterobranch family. The presence of the rhipidoglossate radula in the ectobranch Hyalogyrinidae makes it likely that the origin of Heterobranchia as a whole lies in the rhipidoglossate level of gastropod evolution.

Phylogeny of extant Tunicata and its bearing on chordate evolution

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Tunicata are a diverse group of marine invertebrates that are traditionally believed to be the sister group to Notochordata, which consist of Craniota plus Acrania. In contrast, recent molecular data suggest that Tunicata are the sister taxon to Craniota ("Olfactores-hypotheis"). In order to compare this proposal with results derived from a different set of data, the phylogenetic analysis of morphological characters is presented. Based on this analysis the interrelationships of higher tunicate taxa are resolved and a detailed reconstruction of the groundplan of the Tunicata is presented. Ascidiacea is found not monophyletic, with Appendicularia probably constituting the sister taxon to aplousobranch ascidians. The position of the Thaliacea remains problematic, although no morphological argument could be found to reject the molecular systematic hypothesis that Thaliacea is the sister taxon to phlebobranch ascidians. Rather, the reduced number of muscle cells found in the larval tail could be a synapomorphy of a taxon comprising phlebobranch and stolidobranch ascidinas and the planktonic thaliaceans. Based on these findings, it is suggested that the last common ancestor of Tunicata had a biphasic life-cycle with a sessile adult stage. The implication of these results for the interpretation of the evolution of the Tunicata and Chordata are discussed. The morphological data matrix supports the traditional view, the "Notochordata-hypothesis" and is therefore in conflict with interpretation of the molecular data.

Phylogeny and phylogeography of the genus *Edraianthus* (Campanulaceae): a preliminary report

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DNA sequence data from the plastid genome and AFLP fingerprinting data were used to establish a molecular based phylogeny and phylogeography of the genus *Edraianthus* (Campanulaceae), with majority of taxa being distributed on the Balkans. Preliminary results were generally congruent with classical systematic treatises, although several taxa (subsequently described in the 1970's and 80's) were not confirmed, and some new (cryptic) were detected. The most widespread and polymorphic taxon *E. graminifolius* s. lat., currently distributed disjunctly in mountain ranges of the Balkan Peninsula, the SW Carpathians, and the Apenninian Peninsula (as well as Sicily), appear to be differentiated into three groups of populations: (a) a NW and central Balkan – Apenninian (Sicilian) group, (b) a SW Carpathian group, and (c) a SE Balkan group. Phylogeographic analyses may indicate range expansion of *E. graminifolius* from the Balkans to the mountains of the Apenninian Peninsula and to Sicily, probably over the "Gargano" bridge during the glaciation periods.

Species delimitation and trophic specialization of *Tylomelania* (Caenogastropoda: Cerithioidea: Pachychilidae) in the Malili-System

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Lacustrine radiations in ancient lakes are ideal model systems for the study of speciation and diversification processes in general. We here examine the ecological context of species and speciation by the exemplary investigation of habitat preferences and (trophic) morphology in an ancient lake gastropod species flock on the Indonesian island Sulawesi. The five lakes of the Malili system harbour 25 species of the viviparous pachychilid *Tylomelania* (Caenogastropoda: Cerithioidea: Pachychilidae), which show a remarkable degree of inter- and intraspecific morphological differentiation. Within this system, comparatively small Lake Mahalona occupies a central position between two major lakes, and contains seven sympatric species of *Tylomelania*, which have formed the focus of this study.

We used predominantly shell and radula characters to delineate species. All seven taxa studied have characteristic shells, radulae and vary in the number of juveniles they carry. In addition, all species show a clear substrate preference, even though some taxa may occur on several substrates, such as rock and wood, or gravel and mud. The correlation between radula from (i.e. trophic morphology) and substrate is less clear. While four species occur almost exclusively on one substrate and show no significant variation in their radula, the remaining taxa present a more complicated and contrasting pattern. One species e.g. has a rather distinct radula form irrespective of substrate, and the other two species have a highly variable shell and trophic morphology even within populations on the same substrate. In the latter case, polymorphism or incipient speciation might both explain the data. We have applied mtDNA data and AFLPs to test these hypotheses. Simple models of diversification seem not sufficient to explain the observed diversity in this ancient lake species flock.

DNA Barcoding, Species and Species Boundaries

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DNA barcoding (also known as biological barcoding) has within just a few years become a well known and widely used technique for the identification of species. Among the advantages of this technique is that all life stages of a species can be identified and that species identifications in difficult groups can also be carried out by the non-expert.

The problem, however, is that the concept of species, despite having a long and important history in biology, is still ambiguous. This fact is often simply overlooked by the proponents of DNA barcoding, or presented in a very simplified form that most closely resembles phenetics and is a very ahistoric approach. This is unfortunate since new developments on individuality and natural kinds in philosophy of biology are likely to influence how DNA barcodes can and should be interpreted within biological systematics. As we see it, both the issue of concept and the issue of ontology are theoretical aspects that have bearing on more practical approaches when it comes to quantifying biodiversity. This becomes clear when we want to allocate a specimen to a species (or other taxon). Furthermore, the generalizations that can be made based on DNA barcodes are highly dependent on the ontological status of the entities subject to these generalizations.

Yet another central part of the practice of DNA barcoding is the deposition of vouchers at a public institution. The formal status of these vouchers have however rarely been discussed. This is also true for their relation to "types" of the biological codes. DNA barcoding has so far mainly been promoted by ecologists and not by taxonomists and systematisists which may explain why this issue so far has been totally ignored.

We here aim to shed light on the ontological status of "species" and its relation to DNA barcoding. We also discuss some of the potential problems with DNA barcoding and vouchers in relation to the biological codes, especially the phylocode.

Preliminary results of a comparative phylogeny of bullfinches (genus *Pyrrhula*) based on molecular data obtained from tissue samples and museum study skins

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The purpose of this project is to analyse the intrageneric phylogenetic relationships of bullfinches (Pyrrhula), using a comparative methodological approach. The genus Pyrrhula comprises 26 taxa, currently divided into six species. Combining classic and modern methods of phylogenetic research, the relationships between the Pyrrhula taxa are being examined by means of morphology, bioacoustics and molecular genetics.

The molecular part of the project comprises the reconstruction of a molecular phylogeny using a mitochondrial cytochome-b fragment of 924 bp length. According to availability, tissue or blood samples were obtained from our own collections or from other institutions. Using food pad tissue of study skins as a source for DNA, it is required to complete the whole sequence information from at most four overlapping partial sequences of about 300 bp length. Currently about one third of all sequences included in the analysis originate from museum skin DNA.

In general, the molecular results confirm the predictions of former morphology-based phylogenies. The Brown Bullfinch Pyrrhula nipalensis and the Philippines Bullfinch P. leucogenis are often regarded as the most primitive forms on grounds of morphology. According to the molecular data, these taxa take basal positions as well. A very close relationship between the Central Asian Beavan’s Bullfinch P. erythaca and Red-headed Bullfinch P. erythrocephala is also supported both by morphology and molecular genetics. Nonetheless, there is still more information needed to understand the status of the Azores Bullfinch P. murina and Grey Bullfinch P. p. cineracea.

The preliminary results show that DNA samples from study skins provide reliable genetic information that is of equal value for molecular phylogenies compared to buffer-stored blood or tissue samples. Apart from the laborious and time-consuming technological effort (cloning) there is no disadvantage in using study skin-based sequence information, particularly, if fresh material of rare taxa is not available. Furthermore, the respective voucher specimen allows a countercheck of morphological and molecular data.

Tracing the evolutionary history of the bush cricket genus *Poecilimon* FISCHER, 1853

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The acquisition of reproductive isolation remains one of the major challenges in evolutionary biology. In the present project, we try to elucidate the evolutionary mechanisms that were responsible for speciation in the bush cricket genus *Poecilimon*. We combine a phylogenetic analysis with experimental work to infer the possible forces behind the acquisition of reproductive isolation in this taxon. Our phylogenetic analysis includes the majority of described species in the genus *Poecilimon* and is based on mitochondrial and nuclear sequences as well as AFLP data. The phylogeny will provide us with information on the sister group relationships, which we need for the subsequent experimental work. The experiments are designed to measure type and strength of isolation mechanisms by examining female preferences of inter- or intraspecific males, efficiency of sperm transfer, hatching rates, sterility, and survival to adulthood.

Looking *Lineus viridis* (Nemertea: Heteronemertea) in the Eye – The Phylogenetic Implications of a Nemertean Photoreceptor

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Nemerteans are a comparatively uniform group of organisms which undisputedly form a monophylum that belongs to the Spiralia. Furthermore, the closer relationships of this taxon have so far not been resolved. The apparently acoelomate organisation hints at a relationship with the platyhelminths, whereas the blood-vascular system has been interpreted as an equivalent to coelomic cavities of annelids, making nemerteans the closest relatives to this taxon. In order to contribute to clarifying this matter we studied the ultrastructure and formation of the eyes of *Lineus viridis* (Müller, 1774), because annelids and patyhelminths differ significantly in this regard. In the latter the first pair of eyes that occur during development forms subepidermally as cerebral derivative, whereas in the former it develops out of modified epidermal cells. In the heteronemertean *L. viridis* the inverse eyes are located deeply underneath the epidermis and consist of a few pigmented cells that form a cup like structure with interdigitating processes that contain numerous pigment granules. The optical cavity contains processes of 12 sensory cells, each bearing a single cilium and various microvilli. The perikarya of these cells are dislocated distally from the pigment cup and connect to their processes via slender, neurite like structures that penetrate the pigment cell layer. Analysing various developmental stages, we found no evidence for an epidermal origin of the eyes. Instead, eye formation resembles that described in platyhelminths. Provided that ultrastructure and formation of the eyes in *L. viridis* is characteristic for nemerteans, our study allows two alternative explanations: (1) The mode of eye formation is derived and nemerteans and platyhelminths share a common ancestor. (2) The mode of eye formation is plesiomorphic for spiralians. Thus, nemerteans would be sister to trochozoans who then would show a derived condition of eye development. Although a final decision on this issue cannot be made at present, our results show that nemerteans can hardly be members of the trochozoans.

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Molecular phylogenetic analyses of lower crustaceans ("Entomostraca")

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We want to contribute crustacean sequences for the final analyses of all data compiled within the „Schwerpunktprogramm“ SPP 1174. To test with new information the Ecdysozoa-hypothesis versus the Articulata (e.g. controversy Zrzavy et al. 1998 vs. Waegele and Misof 2001), to test the Tetraconata or Pancrustacea and Myriochelata -hypotheses (e.g. Richter 2002, Pisani et al. 2004) versus the Mandibulata, it is essential to have data of lower crustaceans and of Malacostraca, because the place in the arthropod tree where the insects and myriapods branch off might be within Crustacea.

New sequence data of lower crustaceans will be obtained by DNA and EST sequencing, focusing on representatives of all major groups of crustaceans.

Combining these data with those from other arthropods (obtained by other teams) we will be able to test if Crustacea are paraphyletic with respect to insects and/or myriapods. Furthermore, we want to resolve the phylogeny within Crustacea (or Pancrustacea, if Tracheata branch off within the crustacean tree). To test the obtained phylogenies we want to compare the results of the molecular analyses with studies of morphological data.

Morphology – Ethology – Genetics: Three Approaches, One Goal. A close-up of the subfamily *Drusinae* (Insecta: Trichoptera) in Central Europe.

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Based on morphological characteristics, molecular genetics (nuclear sequence data) and feeding ecology (functional mouthpart anatomy) we investigate Drusinae larvae in order to construct a phylogenetic tree, to test contemporary species grouping concepts and to describe the hitherto unknown larvae of the 24 Central European species. So far, 21 species are known; *Drusus alpinus*, *D. franzi*, *D. melachaetes*, *D. muelleri* and *D. nigrescens* have been newly described in the project so far, whereas *D. chapmani*, *D. improvisus* and *D. noricus* still remain unknown. The larvae were either identified by rearing eggs of previously identified egg-laying females in the laboratory or through molecular based associations of unknown larvae with field collected adults. Associations are based on sequence data from the mitochondrial cytochrome oxidase I region (mtCOI).

With respect to mouthpart anatomy, three distinct species groupings exist in Central European Drusinae: in *Cryptothrix nebulicola*, *Drusus chrysotus*, *D. discolor* and *D. muelleri*, mandibles with teeth around edges are present; this, together with additional setae on the legs and with long filtering bristles at the first abdominal sternum, identifies this group as carnivorous filterers. In *D. franzi* and *D. alpinus*, mandibles with teeth around edges are present, but additional filtering bristles on legs and the first abdominal sternum are lacking, which is typical for omnivorous generalists. In the remaining 15 species, a spoonshaped mandible without teeth is present and additional setae and bristles are lacking, identifying this species group as scrapers feeding mainly on epilithic algae. A molecular phylogenetic hypothesis was formulated for the group based on sequence data from three gene regions: mtCOI, mitochondrial ribosomal DNA (mtLSU), and nuclear wingless (nuWG). With exception of the placement of *C. nebulicola* the grouping in those species with filtering bristles and a group lacking these bristles is well supported by the molecular data. This suggests that the development from scraper to generalist/filterers occurred at least twice in the group: once in the *discolor/chrysotus/muelleri/alpinus/franzi* clade and once in *Cryptothrix nebulicola*.

Electron microscopic analysis of the ontogeny of the appendicularian *Oikopleura dioica* (Tunicata, Chordata)

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The phylogenetic position of Appendicularia is still an unresolved riddle, although they play an important role in the consideration of tunicate and chordate evolution. For a better understanding of the ontogeny of *Oikopleura dioica*, a complete series of ultrathin sections of a four hours old larva was investigated by means of TEM and detailed 3D-reconstruction. In the four hours old larva, the tail is straight, similar to other chordate embryos. It can be divided into trunk and tail and is covered with a bi-layered, extracellular tunic that forms finlets on both sides of the tail like in solitary ascidian larvae. A floating extension is present at the posterior tip of the tail. The tail is rotated through 90 degrees to the left, compared to the plesiomorphic chordate condition. Tissues in the tail which are used for locomotion are already well differentiated. Similar to other tunicate larvae the central notochord consists of a single row of cells as does the right sided endodermal strand. Dorsally and ventrally the notochord is flanked by a row of staggered muscle cells. The nervous system consists of a dorsal prospective brain in the anterior part of the trunk that is connected by a nerve to the left sided nerve cord in the tail. In the present study we describe the first time two rows of ten cells that are situated between the muscle cells and the epidermis. The ventrally situated endoderm at the anterior end of the trunk possesses a gut-like lumen. Between anterior endoderm and endodermal strand in the tail a mass of undifferentiated cells occurs. These cells are the Anlagen of the future intestine and mesodermal pericard. The cells of all tissues contain a large nucleus without condensed chromatin and numerous large mitochondria. All cells are associated with each other by gap junctions. Apart from the notochord no other organ or tissue is delimited by an ecm. These findings may be a result of an accelerated development in the ontogeny of *O. dioica*. The early stages of *O. dioica* consist of a mosaic of advanced and primitive features. Furthermore the present study supports the hypothesis that appendicularia were derived from an ascidian-like ancestor via neoteny.

Ein Vorschlag zur systematischen Bildung deutscher Tiernamen

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Während im fachbiologischen Sprachgebrauch die Verwendung wissenschaftlicher bzw. „lateinischer" Namen üblich ist, konnten sich diese aufgrund ihrer formalen Fremdartigkeit v.a. im außerbiologischen Sprachgebrauch i.d.R. nicht durchsetzen. Auch der systematisch arbeitende Biologe kommt daher oftmals nicht umhin, nationalsprachliche (= n.) Taxanamen zu verwenden. Bei bekannten Arten mit i.w. unproblematischer systematischer Stellung und nur einer geläufigen Bezeichnung ergibt sich dabei kein Problem. Anders verhält es sich bei jenen Organismen, die bisher nie oder nicht nachvollziehbar n. benannt worden, und bei solchen mit einer Vielzahl unterschiedlicher Volks- und Büchernamen. Bei ersteren sieht sich der Biologe genötigt, neue Bezeichnungen oft *ad hoc* zu kreieren, während er bei letzteren eine Auswahl zu treffen oder einen vermeintlich „besseren" Namen zu schaffen hat. Derartige n. Taxanamen sind daher oft voneinander verschieden und erweisen sich nicht selten als miß- oder sogar völlig undeutbar. Dies behindert die Verständigung und führt in der Öffentlichkeit zu einem Reputationsverlust der Biosystematik. Eine geregelter Gebrauch n. Taxanamen erscheint daher erforderlich.

Eine solche Regelung für das Deutsche sollte jedes Taxon mit nur *einem Namen* bezeichnen (Mononomie), der auf den Rang der Form bezogen, nach einheitlich Kriterien aufgebaut, praktisch gut anzuwenden, sprachlich nicht irreführend und bei Vorliegen von Volks- oder Büchernamen möglichst an diesen sowie ihrer Verwendungshäufigkeit orientiert ist.

Ich schlage vor, als Namen von Gattungen grundsätzlich nur ein zusammengeschriebenes Nomen zu verwenden. (Die Unterscheidung höherer Ränge halte ich nicht für erforderlich.) Die Bezeichnung einer Art sollte i.d.R. zweigliedrig sein und sich aus einem „Artnamen" – möglichst einem Substantiv im Nominativ, bedarfsweise aber auch einem verkürzten Adjektiv – und dem durch Bindestrich verbundenen nachstehenden Gattungsnamen zusammensetzen. Zur Kennzeichnung von Unterarten sollte der Artbezeichnung ein großgeschriebenes Adjektiv in der Normalform, d.h. *nicht* verkürzt und / oder durch einen Bindestrich verbunden, vorangestellt werden. Hierfür bieten sich geographische oder Farbspezifizierungen an. Widmungsnamen wären durch solche Angaben zu ersetzen oder in der Form „Müllersche/r/s XYZ" zu übertragen.

Ordo Zoologiae contra Arbitratum Culturae Formarum – Ein Vorschlag zur wissenschaftlichen Benennung der Haustiere

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Die wissenschaftliche Bezeichnung der Haustiere, und damit verbunden diejenige fast aller ihrer artgleichen Wildverwandten, hat trotz zahlreicher Bemühungen bislang keine allgemein verbindliche Regelung erfahren. Das v.a. in Deutschland – in verschiedenen Varianten – gebräuchliche System der Kieler Schule ist zwar die sinnvollste etablierte Herangehensweise, besitzt aber dennoch erhebliche Schwächen in seiner Begründung und in seiner Ausformung. Tatsächlich bilden Haustiere als durch menschlichen Einfluß entstandene und Hybridformen eine eigenständige taxonomische Kategorie, die weder – wie dies oftmals geschieht – als Spezies noch als Subspezies (und freilich auch nicht als Taxon höheren Ranges) aufgefaßt werden kann. So dies dennoch geschieht, sind die Nomenklaturregeln auf die betreffenden Formen nicht mehr anzuwenden. Sinnvoll ist die nomenklatorische Behandlung der Haustiere als nichtnatürliches Taxon, das keinen Einfluß auf die Benennung der Wildtiere nehmen kann. Eine entsprechende Verbesserung der Nomenklaturregeln wäre leicht durch die Aufnahme eines Satzes wie „Auf Haustieren oder ihren verwilderten Nachfahren beruhende Namen sind (als solche) keine Namen der Artgruppe und damit kein Gegenstand der Nomenklatur.“ zu bewerkstelligen.

Zur Benennung der Haustiere wird folgender Vorschlag unterbreitet:

Der Artname der Haustiere ist derjenige der mit ihnen konspezifischen Wildform und basiert entsprechend den Nomenklaturregeln auf dem ersten verfügbaren Namen für einen Vertreter der Wildform. An diesen wird der Zusatz „*forma domesticata*“ („*f. domesticata*“) angefügt. Der als vollgültiger Namensbestandteil betrachtete Begriff „*f. domesticata*“ bezeichnet den Haustierstatus sprachlich klarer als das von Bohlken für *einige* Haustiergruppen gewählte „forma *domestica*“ (sic), das zudem zu Verwechselungen mit Wildtiernamen führen könnte, und erleichtert durch seine formale Einheitlichkeit bei allen Haustierformen deren Ansprache als Domestikate.

In gleicher Weise wie oben ließen sich verwilderte Haustierpopulationen durch den Zusatz „*forma efferata*“ (= „verwilderte Form“) kennzeichnen.

Ergänzungen dieses Benennungssystems – etwa zur Bezeichnung einzelner Haustierrassen oder zur Herausstellung spezifischer Abstammungsverhältnisse – sind leicht zu konstruieren.

Haratin – Ssandaui – Hottentotten. Die Ethnogenese und Anthroposystematik der Khoiniden

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Ursprung und Geschichte der Khoisanvölker sind seit langem Gegenstand wissenschaftlicher Debatten. Jüngere anthropologische, archäologische und ethnologische Studien zeigen nun, daß die Buschmannvölker bzw. Saniden die Frühbevölkerung Ost- und Südafrikas darstellen, während die anthropologisch und kulturell eigenständigen „Hottentotten“ oder „KhoiKhoi“ bzw. Khoiniden ihren Ursprung in Nordafrika nahmen und sich von dort über weite Teile Afrikas sowie südliche Randgebiete Eurasiens (Iberien, Ligurien, Westarabien) verbreiteten. In Nordafrika finden sich neben khoiniden Anteilen z.B. unter Berbern, Haratin und Dauada eine Vielzahl archäologischer und historischer Spuren von Khoisan, die bis in historische Zeit weite Teile dieses Raumes dominierten. Vermutlich infolge von Klimaveränderungen sind größere Teile dieser „Ur-KhoiKhoi“ von Nordafrika aus in andere Regionen abgewandert. Eine Wanderungswelle führte – unter „Zurücklassung“ von starken biotischen Einschlägen unter äthiopiden Gruppen sowie „Restethnien“ wie den Oropom und Teilen der Ssandaui – über das Östliche ins Südliche Afrika. Hier bildeten sie nicht nur die Grundlage der heutigen KhoiKhoi, sondern nahmen auch einen erheblichen Anteil an der Ethnogenese der Südost-Bantu sowie der „Kap-Farbigen“.

Haratin – Sandawe – Hottentotts. The Ethnical History and Biosystematics of the Khoinids

The origin and the history of the Khoisan peoples has been the subject of scientific debate for a long period of time. Recent bioanthropological, archaeological and ethnological research could show that the Bushmen or Sanids originated from Eastern and Southern Africa, whereas the culturally highly-separated “Hottentotts” or “KhoiKhoi” form a bio-taxon of its own right, the Khoinids, who had their origin in Northern Africa. This area still hosts archaeological remains of Khoinid peoples, is mentioned in historical texts describing indigenous Khoisans, and supports remnant groups of these, especially among the Berbers, Haratin and Dawada. Larger parts of the early Khoinids migrated from the present-day Sahara into other regions – probably driven by climatic change. Important Khoinid population elements thus can be found among Southern African KhoiKhoi, Bantu and “Coloureds” as well as in Eastern Africans, Southern Europeans and Western Arabs.

Identifying sequence heterochronies in Lissamphibia

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The larvae of anuran amphibians have undergone major adaptive changes (e.g. in feeding mode) in relation to many aspects of their life history. As part of an on-going study, the timing of cranial muscle development in larval lissamphibians was analysed from a comparative, phylogenetic perspective to investigate its potential role in the evolution of this group. In particular, the development and differentiation in the cranial muscles in five frog species was determined using classical histology. The developmental timing data were analyzed quantitatively using the event-pair based Parsimov technique. Parsimov is a new parsimony-based method that can be used to interpret developmental timing data in a phylogenetic framework and establish the minimum number of heterochronic events that must have taken place to explain the data. We could distinguish between those traits showing strong phylogenetic signal and those that were more plastic and apparently evolved in response to the demands of the larval feeding mode. Our results corroborated previous observations that the cranial muscle tend to develop from anterior to posterior, with the mandibular arch muscles differentiation first, followed by the hyoid and branchial arch muscles. However, the results also support the novel observation that the development of eye muscles is characterized by an unexpectedly high degree of heterochrony.

Staubhafte Enthüllungen
REM-Untersuchung an zwei Spezies der Familie Coniopterygidae (Neuroptera)

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Mit einer Vorderflügellänge von maximal 5mm sind Coniopterygidae die Winzlinge unter den Netzflüglern. Den Namen „Staubhaft“ verdanken sie dem aus hypodermalen Drüsen ausgeschiedenen Wachs. Von der Erforschung ihrer Ultrastrukturen ist funktionsmorphologisch und phylogenetisch Aufschlussreiches zu erwarten. Die Arten *Aleuropteryx juniperi* OHM, 1968 und *Semidalis aleyrodiformis* (STEPHENS, 1836) wurden als Vertreter der Unterfamilien Coniopteryginae und Aleuropteryginae gewählt. Aus den vielfältigen Ergebnissen einige Auszüge: Die bei Coniopterygiden verbreiterte Innenseite der Labialpalpen-Endglieder weist eine spezifische Oberfläche auf: Noppen bilden durch stellenweise Verdichtungen ein netzartiges Muster. Bei *A. juniperi* ist die entsprechende Oberfläche im Vergleich zu *S. aleyrodiformis* halb so groß; weiters ist die Lacinia von *A. juniperi* mit halb so vielen, doppelt so dicken Borsten bespickt. Diese Merkmale und die unterschiedlichen Ernährungsweisen dieser beiden Arten nähren die folgende Hypothese: Bei *A. juniperi* ermöglicht die Festigkeit der Borsten, Schildläuse, die bevorzugte Beute dieser Art, vom Blatt abzulösen. Die Lacinia von *S. aleyrodiformis* hingegen dient dieser weniger räuberischen Art als Bürste, um Pollen aus Pflanzen zu sammeln. Spielraum für Interpretationen bieten auch Aufbau und Struktur der Ventralsäckchen von *A. juniperi*. Ursprung und Funktion dieser die Aleuropteryginae auszeichnenden Organe sind bisher nicht geklärt. Die Hypothese einer Reexpression abdominaler Extremitäten wird diskutiert. Die vorliegende Studie gibt einen Einblick in das unausgeschöpfte Potential der Ultrastrukturforschung bei Neuroptera. Ihre Ergebnisse sollen eine Grundlage für zukünftige vergleichende Analysen der Neuropterida darstellen.

NOTIZEN