



**Abstracts of the 5th Annual Meeting of the
Gesellschaft für Biologische Systematik
(Society for Biological Systematics)**

Roland Melzer & Michael Schrödl (eds)

**Electr. Suppl. 2. - to:
Org. Divers. Evol. 3(1): 72. 2003**

Preface

In the following, 36 short communications are given that were presented as lectures or posters at the 5th Annual Meeting of the GfBS (see www.gfbs-home.de/) held in Munich, 18-20 September 2002. The meeting was organized by the Botanische Staatssammlung München (BSM), Zoologische Staatssammlung München (ZSM), Department Biologie I of Ludwig-Maximilians-Universität München (LMU), and the GeoBio-Center^{LMU}.

The main topics were (i) theory of systematics, mechanisms of evolution, molecular systematics; (ii) biodiversity and collection information systems; and (iii) special issues concerning various taxa, in particular Coniferales, Anthozoa, Brachiopoda, Mollusca, Acanthocephala, Nematoda, Arthropoda and Vertebrata. An invited lecture was given by Bernd Schierwater ("Molecular development and molecule morphology in systematics: back to the future?"), and a public lecture by Ragnar Kinzelbach ("Der Seidenschwanz *Bombycilla garrulus* in Europa vor 1758").

In addition, a curators' meeting – organized by Marion Kotrba (ZSM) – and a meeting of the "Young Systematists" – organized by Sybille Seifried (Oldenburg) – were held in parallel sessions.

The organizers thank all those persons who spent time and energy to make this meeting a successful one, and send a "vivat, crescat, floreat" towards the GfBS.

Roland Melzer, Michael Schrödl (ZSM)

editors of the abstracts

Theory of systematics, mechanisms of evolution, and molecular systematics

Traces of evolution: horizontal gene transfer of a group I intron

Ingo Busse, Angelika Preisfeld

Universität Bielefeld, Fakultät für Biologie, Postfach 100 131, D-33501 Bielefeld; e-mail: ingo.busse@uni-bielefeld.de

Euglenid flagellates represent a morphologically and genetically diverse taxon which is difficult to delimit. Utilisation of SSU rDNA data for phylogeny reconstruction allowed insights into the evolutionary history of this taxon, as well as into the evolution of the ribosomal RNA molecule.

A characteristic feature of euglenid SSU rDNA is its pronounced length polymorphism reaching up to more than 4,500 nucleotides in *Distigma sennii*. This elongation is solely based on extended variable regions which are transcribed and take part in the mature ribosomal RNA.

Ploeotia costata is a phagotrophic euglenid with a complex ingestion apparatus. Analyses of the SSU rDNA sequence revealed the presence of a group I intron in a highly conserved region of the gene. RT-PCR amplification confirms that the intron is actively splicing and thus missing in the mature rRNA. The presented study is the first report on group I introns among euglenozoans. Secondary structure predictions indicate that paired segments P1-P10 are present as well as several conserved elements typical of group I introns and of subclass IC1 in particular. Phylogenetic analyses of SSU rDNA sequences show good support for the placement of *Ploeotia costata* within the Euglenozoa, whereas analyses of intron data sets uncover a close phylogenetic relation of the *Ploeotia* intron to homologous introns from *Acanthamoeba*, *Aureoumbra lagunensis* and red algae of the order Bangiales. Discrepancies between SSU rDNA and intron phylogenies indicate lateral spread of the group I intron. Monophyly of IC1 516 introns from *P. costata*, *A. lagunensis* and rhodophytes is supported by a unique secondary structure element: helix P5b possesses an insertion of 19 nt length with a highly conserved tetraloop which is supposed to take part in tertiary interactions. Neither functional nor degenerated ORFs coding for homing endonucleases can be identified in Pco.S516. Nevertheless, degenerated ORFs with His-Cys box motifs in closely related intron sequences indicate that homing may have occurred during evolution of the investigated intron group.

Phylogenetics of the high mountain geometrid moth genus *Glacies*, based on morphology and mitochondrial DNA sequences

Sven Erlacher^{1,2}, Axel Hille², Michael A. Miller², Gerhard M. Tarmann³

¹ Institut für Spezielle Zoologie und Evolutionsbiologie mit Phyletischem Museum, Friedrich-Schiller-Universität, Erbertstr. 1, D-07743 Jena; e-mail: erlacher@zsm.mwn.de

² AG DNA-Tax, Zoologische Staatssammlung München

³ Tiroler Landesmuseum Ferdinandeum, Innsbruck, Austria

According to the present state of knowledge, the genus *Glacies* Millière, 1874 (Geometridae: Ennominae) consists of 10 species: *G. alticolaria* Mann, *G. alpinata* Scop., *G. baldensis* Wolfsb., *G. belzebuth* Prav., *G. bentelii* Rätz., *G. canaliculata* Hoch., *G. coracina* Esp., *G. noricana* Wgn., *G. spitzi* Rbl., and *G. wehrlii* Vorbr. All of these are restricted to the European high mountains, with the greatest number of species known from the Alps. Some are also to be found in the Pyrenees, Vosges, Sudeten, High Tatra, Carpathians and the Balkans. Only one species, *G. coracina*, has a boreoalpine distribution, but it occurs also in some high mountain regions from Central Asia to Japan.

The genus *Glacies* is characterized by a number of autapomorphies: the basic coloring of the wings is uniformly black to deep brown, the aedeagus shows no cornuti in the inner part, the corpus bursae contains a smooth and longish signum, and finally the lamella postvaginalis in the female genitalia has a strong sclerotization into which the pointed uncus of the male is locked during copulation.

Even though *Glacies* morphology has been studied in detail, e.g. Wehrli (1921, Mitt. Schweiz. Ent. Ges. 13(3/4): 143-206), Povolny & Moucha (1955, Acta Ent. Mus. Nat. Pragae 30: 143-176), no attempt had yet been made to include molecular data in a phylogenetic analysis.

For this reason, we sequenced parts of the mitochondrial genes 12S rDNA and COX1 with an overall length of about 1,800 bp. Molecular data could be evaluated for all species of the genus, as well as for the closely related *Psodos quadrifaria* Sulz. and *Sciadia tenebraria* Esp., except for *G. bentelii* and *G. wehrlii* where no material was available. In addition, 30 morphological characters were used. In this context, the male and female genitalia were of particular interest.

Representatives of the genera *Elophos* Bsd., *Crocota* Hbn. and *Gnophos* Tr. were used as outgroups. All species studied belonged to the tribe Gnophini within the subfamily Ennominae.

The aim of our study was to combine both molecular and morphological data in phylogenetic analyses of the genus in order to determine which partial data sets are most appropriate, and to compare the results of the phylogenetic analyses with the current distribution pattern of the species studied.

Our results show that the well differentiated and more widely distributed species, e.g. *G. alpinata*, *G. coracina* and *G. canaliculata*, diverge basally in the cladogram, whereas the endemic and less differentiated species, e.g. *G. baldensis*, *G. spitzi*, *G. alticolaria* and *G. noricana*, diverge more terminally. These latter species probably evolved during the last ice age. In contrast with earlier authors, e.g. Povolny (1959, XVth Int. Congr. Zool., Sec. II, Paper 17: 1-6), *Psodos*, rather than *Sciadia*, seems to be the sister taxon of the genus *Glacies*.

There are good reasons to take an inventory of all species! But must all of them be described?

Gunnar Gad, Horst Kurt Schminke

AG Zoosystematik und Morphologie, Carl-von-Ossietzky-Universität, D-26111 Oldenburg; e-mail: gunnar.gad@mail.uni-oldenburg.de

One of the main aims of the Systematics Agenda 2000 was to collect and describe within the next 25 years the complete amount of species on the globe before most of them may have disappeared. For this to be achieved there is a great demand for financial support to build up the necessary infrastructure, which includes capacity building, development of computer networks, and improved management of growing collections. At current rates of funding a complete global species inventory would take at least 150 years. Estimates of total species numbers are so high that it appears doubtful that the goals of the Systematics Agenda 2000 could be reached in a reasonably short time. It has therefore been suggested, among others by the Global Taxonomy Initiative, to set priorities for the accomplishment of partial goals.

In view of the assumed high number of unknown species the question arises: Is it really necessary that all newly discovered species are described? The answer is no, because not all species contain the same amount of scientific information and there are obvious differences in the amount of knowledge that can be gained from their discovery. However, for choices to be made and priorities to be set there is one important prerequisite: that material ideally of all species is secured through comprehensive sampling programmes so that it is available for study. It is assumed that species with the highest information content are those which represent a completely new taxon and a new body plan or ground pattern. The other extreme are new species belonging a taxon of which many similar species are already known. As an example for a new taxon let us take the Loricifera.

The discovery of *Nanalaricus mysticus* Kristensen, 1983 (Z. Zool. Syst. Evolut. 21) as the first representative of Loricifera opened up a new chapter in the book of life. *N. mysticus* provided a new basis for the interpretation of the sister group relationships among Loricifera, Kinorhyncha and Priapulida. Its discovery allowed the recognition of a new monophylum, the Scalidophora, containing all three taxa. In addition, a lot of information became available on a new life cycle, on life stages, anatomy, and details of the ultrastructure.

In new taxa like the Loricifera even the second, third, fourth, etc. new species contributes lots of new information. For example, the description of *Pliciloricus enigmaticus* Higgins & Kristensen, 1986 (Smithsonian Contr. Zool. 438) as the first representative of Pliciloricidae revealed the first obvious modification of the body plan of Loricifera, and the life cycle of *Rugiloricus cauliculus* Higgins & Kristensen, 1986 showed the first modified postlarval instar discovered within Loricifera. Species of a new genus from the deep sea led to the discovery of paedogenetic larvae, which are of rare occurrence in the animal kingdom. Another new species from the plateau of the Great Meteor Seamount was found to exhibit many plesiomorphic features and to bridge as a 'missing link' the gap between Nanalaricidae and Pliciloricidae. Each newly discovered species provides new zoogeographical information. For example, with *Pliciloricus hadalis* Kristensen & Shirayama, 1988 (West. Pacif. Zool. Sci. 32) the first loriciferan inhabiting the soft bottom of the deep sea was found. The Loricifera are a good example for the amount of new knowledge that can be gained from the selection of only a few species among one hundred others also available for study.

Species descriptions – not "only descriptive" but a framework of hypotheses

Gerhard Haszprunar

Zoologische Staatssammlung München, Münchhausenstr. 21, D-81247 München; e-mail: haszi@zsm.mwn.de

Systematists are often confronted with the view of non-systematists – but sometimes also of colleagues – that species descriptions are "purely descriptive" or "lack a causal framework" or "are not based on actual working hypotheses" and thus are of minor scientific impact. Contrary to that commonly expressed point of view the present contribution argues that a well-done description of a new species – and I use my own field of research, malacology, as an example – is a causal framework of working hypotheses. Hypothesis (1), *The specimens under investigation represent at least one of several species concepts which is new to science*, is expressed by adding "sp. nov.". (2) *The phylogenetic position of the new species* is indicated by the genus name and any other placing within higher-ranked clades. Unfortunately it is often overlooked or neglected that the erection of higher-ranked taxa (genera, families, etc.) may result in a paraphyletic status of the "remaining" group. (3) *Each descriptive term is in itself an hypothesis* concerning either the homology or the function of the respective structure, or both. Whereas in many cases these hypotheses seem to be trivial, there are numerous examples where this is not the case. The given framework of hypotheses, on which each species description is based, links taxonomy with the history of science and is directly coupled with functional assumption and phylogenetic analysis and thus with evolutionary biology. There can be nothing more wrong than regarding species descriptions as "purely descriptive". The latter attribute is only valid in cases of pure sequencing work such as the "human genome project", where – interestingly enough – a maximum of only 5 letters is sufficient to do so-called 'big science'.

Molecular development and molecule morphology in systematics: back to the future?

Bernd Schierwater

TiHo Hannover, Ecology & Evolution, Bünteweg 17d, D-30559 Hannover; e-mail: bernd.schierwater@ecolevol.de

For more than a century, morphologists and developmental biologists have collected a tremendous amount of comparative organismal data to sort animal complexity in a phylogenetic context. By adding molecular developmental and molecular systematic data we have just begun to explore the real value of some long-known data sets on the organisms themselves. A wide spectrum of molecular characters can be used to unravel the developmental mechanisms and phylogenetic pathways that underlie animal bauplan changes. For example, regulatory genes can be used to study developmental and evolutionary genetics at the same time, and a variety of DNA sequence markers are

available to reconstruct phylogenetic relationships where morphological characters have failed. Hox genes have the potential to add new multilevel data sets and also enlighten researchers about the mechanistic principles involved in producing the phenotypic picture of similarity and innovation. Ribosomal gene sequences have the well proven potential to identify genealogical relationships over a broad range of taxonomic levels and also harbor a new type of character data, the morphology of rRNA molecules. It is unfortunate that the latter value is widely unexplored yet, since molecule morphology might provide phylogenetically highly informative characters that are as useful as many morphological characters. The treatment of developmental data and molecule morphology data as characters to be examined in a larger phylogenetic context with all of the other sources of character state data is advocated as a sensible way to approach modern systematics and phylogenetics.

Chloroplast phylogeny of asplenioid ferns (Aspleniaceae, Polypodiidae)

Harald Schneider¹, Steve J. Russell², Ray Cranfill³, Johannes Vogel²

¹ Albrecht-von-Haller Institut für Pflanzenwissenschaften, Universität Göttingen, D-37073 Göttingen; e-mail: hschneid@duke.edu

² Botany Department, The Natural History Museum, London, UK

³ University Herbarium, University of California, Berkeley, USA

Molecular phylogenies have been generated to investigate relationships among species and putative segregates in *Asplenium*, one of the largest genera in ferns. Of the approx. 700 described taxa 95 have been included in a phylogenetic analysis using four chloroplast genome regions: two coding regions, *rbcL* and *rps4*, and two non-coding regions, *rps4-trnS* spacer and the *trnL-trnF* spacer. Our results support *Hymenoasplenium* as the sister lineage to all other asplenioid ferns, and all other putative satellite genera such as *Ceterach* and *Phyllitis* are nested within this asplenioid clade. Instead of the classical and well-recognised separation into Old and New World clades asplenioid ferns reveal a separation of the deeper branches into tropical and temperate clades. Temperate clades have evolved from tropical, more basal clades, and the phylogeny indicates up to six shifts between temperate and tropical preferences in the evolution of this widespread genus. Implications for speciation processes and biogeographic aspects are discussed, including the re-colonization of temperate regions after the last glacial period, and we present a phylogenetic framework from which the historical biogeography of asplenioid ferns can be inferred for Europe and North America.

Influence of taxon and character sampling on the molecular and morphological systematics of basal Hymenoptera (Insecta: "Symphyta")

Susanne Schulmeister

Division of Invertebrate Zoology, American Museum of Natural History, Central Park West at 79th St., New York, NY 10024, USA; e-mail: schulmei@amnh.org

Many papers have emphasized the importance of large taxon and character samples for molecular systematics (as well as morphological systematics). The importance of these factors is examined for basal Hymenoptera (sawflies, "Symphyta"). The phylogeny of basal Hymenoptera is well supported based on morphological characters. The newest character matrix (Schulmeister 2002) contains 350 morphological characters which support most of the deep branches quite well. Much progress has been made recently on the molecular level. Fragments of four to five genes (12S, 16S, 18S, 28S, COI) have been sequenced for 41 species of basal Hymenoptera (Schulmeister 2002, unpubl. PhD thesis, Univ. Göttingen; Schulmeister et al. 2002, *Cladistics* 18: 455-484). The deep branches of the molecular tree are now largely congruent with those of the morphological cladogram. A strict consensus cladogram is used for comparison, which contains only those clades which are present in the morphological and molecular trees as well as in the simultaneous analysis tree. Smaller data matrices which were created by the removal of taxa or characters from the morphological and molecular data matrices were analyzed and the resulting trees were compared with the consensus cladogram in order to visualize the effect of taxon and character sampling on the phylogenetic systematics of basal Hymenoptera.

Biodiversity and collection information systems

INFOCOMP: Compositae types in German herbaria

Jürke Grau, Philomena Bodensteiner, Alison M. R. Davies, Angela Pillukat

Botanische Staatssammlung München, Menzinger Str. 67, D-80638 München; e-mail: grsystau@botanik.biologie.uni-muenchen.de

The Compositae are the largest family of seed plants with an estimated 25,000 species. They are found in all places colonized by higher plants on all continents and often form significant parts of the most diverse ecosystems. They are not only scientifically interesting but also have economically important representatives. Nomenclatural types are the reference sheets of pressed plants laid down in herbaria. These are directly and permanently connected to their plant names, allow species to be unambiguously identified, and thus underpin even the most modern research techniques (see Hind et al. (eds) 1995, "Advances in Compositae Systematics"). The more traditional and larger a herbarium, the richer it will be in types. For historical reasons, many types originate from developing countries and have attained value through European botanical research. With this project it is now possible to contribute to data repatriation by making this information globally available to scientists.

The INFOCOMP project was established primarily as a pilot scheme for the digital recording of essential components of German herbaria. The project is supported by three graduate scientists and, from time to time, a database/network administrator. The current excellent staff coordination has greatly increased the speed of progress in recent months. With the experience gained, digital imaging in targeted spheres can now be rapidly and successfully completed.

Initial teething problems have now been resolved and image format and quality standardized. On average, five images per type are taken: the original label(s) [necessary when determining provenance and authorship of older sheets], the entire sheet, relevant habit detail, and macro images of taxonomically important features – usually the capitulum(a). Special emphasis is placed upon the correct and accurate citation of the protologue.

Types from all seventeen Compositae tribes have been recorded. In total, 350 genera and 1,533 types have been photographed, forming a database of over 7,600 images. The software "iView MediaPro" has been used for the simple organisation of the image and text data, retaining flexibility for other software options. The database software "Filemaker Pro" (with an integrated web interface) allows direct access to the database using TCP/IP from a browser.

It is anticipated that the work in Munich, including the preparation of the information for Internet access, will be completed during 2002. Any updates on progress may be found on the web pages of the Botanische Staatssammlung München (<http://www.botanik.biologie.uni-muenchen.de/botsamml/home.html>), under "Projects".

This project was also presented in this form at the BIOLOG Conference, Bonn 2001 (Grau et al. 2001 in: German Programme on Biodiversity and Global Change, Status Report).

The BIOLOG project AlgaTerra: a database for research on microalgae diversity and systematics

Regine Jahn¹, Richard M. Crawford², Thomas Friedl³, David Lazarus⁴, Linda Medlin², Werner Reisser⁵, Bank Beszteri², Karl Glück¹, Katrin Hamann², Dominik Hepperle³, Friedel Hinz², Viola Huck¹, Anne Jobst⁴, Juliane Kasten¹, Wolf-Henning Kusber¹, Mario Salisch⁵, Sabine Strieben²

¹ Botanischer Garten und Botanisches Museum Berlin-Dahlem (BGBM), Freie Universität Berlin, Königin-Luise-Str. 6-8, D-14191 Berlin; e-mail: r.jahn@bgbm.org

² Alfred Wegener Institut, Stiftung für Polar- und Meeresforschung (AWI), Bremerhaven

³ Experimentelle Phykologie und Sammlung von Algenkulturen (SAG), Universität Göttingen

⁴ Institut für Paläontologie, Museum für Naturkunde (MfN), Humboldt Universität Berlin

⁵ Institut für Allgemeine und Angewandte Botanik, Universität Leipzig

Microalgae are useful tools in global change research, e.g. for monitoring water quality, for the reconstruction of paleoclimates through sediments, and for the assessment of biodiversity in different ecosystems. The taxonomy and in particular the nomenclature used to record these observations is often ambiguous, leading to incompatibility of data sets published by different researchers, that need to be synthesized for global studies. The ecological information available on these taxa is thus doubtful, and modern molecular information cannot be assessed and tied to a correct name. The problems are frequently due to poorly documented nomenclatural types as well as to divergent secondary interpretations of the taxon concept behind the name.

AlgaTerra, a joint project funded by the German Federal Ministry of Education and Research (BMBF), is building up an information system at the BGBM for terrestrial, benthic und planktonic microalgae, which will integrate nomenclatural, taxonomical, morphological, molecular und ecological data via the taxon concept. This primary data will be compiled, evaluated and worked out by five research groups, and will be made available via Internet (www.algaterra.org) starting summer 2004.

Three of Germany's most important microalgal collections are part of this project: the 19th century Ehrenberg Collection (at MfN), the 20th century Hustedt Diatom Collection (at AWI), and the Culture Collection of Algae (SAG). AlgaTerra will make their data available (e.g. types, illustrations and protologues), thus creating a virtual collection. To enhance applied research on microalgae, factual as well as literature data is gathered. An important feature of the project is the linking of molecular data with evaluated taxonomic concepts for unambiguous identification and classification. The AWI and the SAG are supplying molecular data of ecologically and taxonomically important microalgae stored as vouchers by cryo-preservation at the SAG.

The Global Taxonomy Initiative (GTI) – the response to a problem

Christoph L. Häuser, Stefan Schmidt

Staatliches Museum für Naturkunde Stuttgart, Rosenstein 1, D-70191 Stuttgart; e-mail: chaeuser@gmx.de

The Global Taxonomy Initiative (GTI) is a program under the UN Convention on Biological Diversity (CBD), which has been approved by the Sixth Conference of the Parties (COP6) of the CBD in The Hague in April 2002. The purpose of the GTI is to address the shortage of taxonomic expertise and other related impediments that prevent the successful implementation of the overall goals of the Convention globally. The approved GTI program of work contains 18 proposed actions for the participating countries to implement. These actions include, for instance, providing access to and facilitating the exchange of biosystematic information worldwide, the development of taxonomic resources and capacities in particular in developing countries, but also assessments of taxonomic needs and impediments at national, regional and global level, insofar as these are related to the implementation of the CBD. Since August 2002 the State Museum of Natural History ("Staatliches Museum für Naturkunde"), Stuttgart, has taken on the role of the GTI National Focal Point for Germany and serves as a central point of contact for all issues related to the GTI, including for the exchange of information between the CBD Secretariat in Montreal and national CBD focal points, and all institutions and organisations involved in biodiversity research and conservation in Germany.

As a first activity of the German GTI National Focal Point the compilation of a national register of taxonomists with indications of specific areas of expertise has been initiated. It is intended to make information from this database available online via the internet in cooperation with the Federal Agency for Nature Conservation (Bundesamt für Naturschutz). Besides focussing on the development of cooperative links to increase taxonomic knowledge and capacities at the national and international levels, the National Focal Point will be engaged in identifying GTI pilot projects and supporting taxonomic research initiatives. The National Focal Point is further committed to playing an advisory role on all questions related to the implementation of the GTI within the Convention on Biological Diversity for German authorities and institutions.

Currently the GTI is still in an early stage of development and needs enthusiastic support particularly from all areas of biosystematics to make taxonomy as valuable as it can be for the conservation and sustainable use of biodiversity.

The diatom collection of F.-J. Weinzierl – a database project of the Botanische Staatssammlung München and the Bayerisches Landesamt für Wasserwirtschaft

Dagmar Triebel¹, Rolf Klee², Susanne Eichacker², Wiltrud Spiesberger¹, Markus Weiß²

¹ Botanische Staatssammlung München, Menzinger Str. 67, D-80796 München; e-mail: triebel@botanik.biologie.uni-muenchen.de

² Bayerisches Landesamt für Wasserwirtschaft, Gewässerökologische Forschung, Wielenbach

Franz-Josef Weinzierl (1888-1969) established his collection in 1919, maintaining and expanding it until his death. The collection of about 13,000 microscope slides, 2,200 glass vials with vouchers in alcoholic solution, and 700 dried specimens together with Weinzierl's extensive library is now housed in the Botanische Staatssammlung München. For a more intensive use of the collection data, a database application using MS Access has been designed three years ago. The database allows entries mainly with respect to details of the sample (including geographical, locality, and ecological data) as well as on the identification of the diatoms concerned. At present it contains about 8,000 data sets. Public access to the data is provided via Internet. The Web interfaces are programmed using ColdFusion. Several online search options for taxon name, country, collector and images are available to users from the fields of environmental and biodiversity research. The online database is a useful tool to evaluate the biodiversity data of this important reference collection.

Reconstruction of the trophic reference state of lake Ammersee (Bavaria, Germany) by evaluating natural history collections

Rolf Klee¹, Gabi Hofmann², Dagmar Triebel³

¹ Bayerisches Landesamt für Wasserwirtschaft, Gewässerökologische Forschung, Demollstr. 31, D-82407 Wielenbach; e-mail: rolf.klee@lfw.bayern.de

² Glashütten, Germany

³ Botanische Staatssammlung München, Germany

The benthic diatom flora of Ammersee was studied in order to characterize the lake's trophic state. Trophic-tolerant species, meso-eutraphentic and eutraphentic indicator species are dominating today.

To reconstruct the trophic reference state as understood by the EU water quality directives, samples of Ammersee diatoms from two historic collections were examined: those of F. Hustedt and F.-J. Weinzierl. These samples had been collected in 1925, 1940 and 1956, respectively. Although the evaluation is based on only a few samples, their unambiguous indication of oligotrophy can be taken as the reference state of Ammersee. The increase in species numbers of meso-eutraphentic and eutraphentic species from 1925 to 1956 is remarkable. It agrees with the onset of eutrophication at the beginning of the 1950s.

Recent palaeolimnological studies confirm the formerly oligotrophic state of lakes in this region.

Coniferales

Seven at one stroke – new and old characters (LM, SEM) of pollen from Pinaceae, Podocarpaceae and Phyllocladaceae (Coniferales, Gymnospermae)

Barbara Hermanowski

Abteilung Ultrastrukturelle Forschung und Palynologie, Institut für Botanik der Universität Wien, Rennweg 14, A-1030 Wien; e-mail: aon.963005508@aon.at

Mature pollen grains from several genera of the Pinaceae, Podocarpaceae and Phyllocladaceae (Coniferales, Gymnospermae) were investigated with methods of light microscopy (LM) and scanning electron microscopy (SEM). There are differences between the pollen grains of these taxa which make it possible to rapidly differentiate the several genera.

Gymnospermous pollen grains can be saccate or nonsaccate. Saccate pollen only occurs in the Pinaceae, Podocarpaceae and Phyllocladaceae, but there is also a small share of nonsaccate pollen grains. The saccate pollen of Podocarpaceae and Phyllocladaceae is distinct from that of the Pinaceae because of its so-called "region of weakness" (Pocknall 1981, New Zealand J. Bot. 19: 259-266). This "region of weakness" is described for the first time for *Podocarpus macrophyllus*, *Dacrycarpus darydioides*, and *Microstrobos niphophilus* (Podocarpaceae). The description of the apertures of *Saxegothaea conspicua* (Podocarpaceae) is also new. The endoreticulate network inside of the sacci and the size of the saccus pores could be used to differentiate the saccate pollen grains at the genus level.

The intine (inner layer of sporoderm) of nonsaccate pollen grains swells during contact with a liquid medium. The consequence of this swelling is the bursting of the exine (outer layer of sporoderm) which results in the separation of intine and exine. Based on these results the various types of gymnospermous pollen grains are compared.

Anthozoa

Coloniality in anthozoans

Verena Häussermann

Zoologische Staatssammlung München, Münchhausenstr. 21, D-81247 München; e-mail: vreni_haeussermann@yahoo.de

Colonies of anthozoans are clonal groups of organisms which are physically connected to one another. Almost all orders of the class Anthozoa have colony-forming members. The best known examples are the reef-building corals.

The validity of the subdivision within the Anthozoa has long been a subject of debate which gained intensity during the last few years (e.g. Berntson et al. 1999, *Mol. Phylog. Evol.* 13: 417-433). Especially the division of orders in the subclass Hexacorallia is discussed very contradictorily. Several recent phylogenetic works confirmed a basal position of the cerianthids outside of the class Hexacorallia (e.g. Daly et al. 2002, *Evolution* 56: 502-510). Thus, sea anemones were the last group within the Hexacorallia which were thought to be exclusively solitary.

An exclusively solitary growth of sea anemones has been accepted as well established (e.g. Shick 1991, "A Functional Biology of Sea Anemones"; Daly et al. 2002). The finding that the skeletons of stony corals have multiple origins (Romano & Palumbi 1996, *Science* 271: 640-642) and might even have been ephemeral left the lack of coloniality in sea anemones as one of the last important morphological characters which justified a separation of these two groups (Daly et al. 2002).

My studies show that the Chilean sagartiid sea anemone *Cereus herpetodes* (McMurrich, 1904) forms flabello-meandroid colonies through intratentacular budding which was hitherto only known from stony corals.

This finding gives new insights into the principles of colony formation in Anthozoa and confirms that the relationships of the anthozoan sub-classes are not clear-cut. It supports the hypothesis of Stanley & Fautin (2001, *Science* 291: 1913-1914) that it may be more phylogenetically accurate to merge the Actiniaria with the orders Scleractinia and Corallimorpharia.

Brachiopoda

Phylogeography of articulate brachiopods (Cancellothyrididae) in the Atlantic and Pacific oceans

Carsten Lüter

Museum für Naturkunde der Humboldt-Universität, Invalidenstr. 4, D-10115 Berlin; e-mail: carsten.lueter@museum.hu-berlin.de

The analysis of 12S rDNA mitochondrial gene sequences of the North Atlantic brachiopod species *Terebratulina retusa* and *T. septentrionalis* showed a sequence-based genetic distance of about 6 % between the two taxa, i.e. divergence between *T. retusa* and *T. septentrionalis* is ten times higher than within each species. This establishes the two taxa as valid species, which is corroborated by morphometrical findings and the occurrence of brooding only in *T. septentrionalis*. The phylogenetic analysis of Atlantic and Pacific species of Cancellothyrididae (concatenated 12S rDNA and 16S rDNA sequences), using terebratellid (long-looped) brachiopod species as outgroup, resulted in paraphyly of the genera *Terebratulina* and *Cancellothyris*, with *C. hedleyi* closest to Atlantic *Terebratulina* spp. Neither species-specific substitution rates nor saturation effects could be detected, thus a molecular clock approach could be employed to date speciation events. The geologically dated divergence between (short-looped) *Liothyrella* spp. from New Zealand and the Antarctic was used to calibrate the rate of 12S divergence at about 0.1 % per million years. Consequently, *T. retusa* and *T. septentrionalis* are inferred to have been diverging for about 60 million years, and radiation of Cancellothyrididae from their last common ancestor to have started about 100 million years ago. This indicates a Mesozoic origin for the present-day distribution of Cancellothyrididae, and the basal position of *T. unguicula* suggests a possible North Pacific centre of origin, and subsequent separate Atlantic and Pacific radiations.

Mollusca

Mitochondrial gene order of the gadilid scaphopod *Siphonodentalium lobatum* (Mollusca) differs greatly from that of other molluscs

Hermann Dreyer, Gerhard Steiner

Universität Wien, Institut für Zoologie, Althanstr. 14, A-1090 Wien; e-mail: Hermann.Dreyer@univie.ac.at

Comparisons of mitochondrial gene arrangements can be informative for reconstructing high-level phylogenetic relationships.

We obtained nearly complete sequences for the mitochondrial genome of *Siphonodentalium lobatum* (Mollusca, Scaphopoda). The size of the genome is about 15 kb, similar to most metazoans. The gene arrangement is markedly different from all seven published complete molluscan mitochondrial genomes. It also shows low similarity to an unpublished gene order of a dentaliid scaphopod. This indicates that rearrangements in gene order are more frequent than in vertebrates or arthropods. Our study contains phylogenetic analyses based on primary sequences and gene order.

A 'protonephridial' stage in kidney development of *Antalis entalis* (Mollusca, Scaphopoda)

Bernhard Ruthensteiner, Gerhard Haszprunar

Zoologische Staatssammlung München, Münchhausenstr. 21, D-81247 München; e-mail: ruthensteiner@zsm.mwn.de

Adult Scaphopoda are exceptional among the Mollusca in lacking a heart, thus ultrafiltration occurs in the pericardial wall adjacent to a perirectal sinus. Our investigations on adult specimens of *Antalis* spp. (Dentaliidae) confirmed the long questioned presence of a renopericardioduct on the left side, whereas no such structure could be found on the right side which is modified for releasing the gametes. Fine-structural studies on the excretory system in juveniles up to the age of 2 weeks post metamorphosis in *Antalis entalis* (Jeffreys, 1869) revealed paired excretory organs consisting of kidneys combined with true, polyciliary terminal cells (cyrtocytes), a 'protonephridial' organisation of the metanephridium that has not yet been reported in any other mollusc. While the histology of the kidney itself corresponds in juveniles and adults, the organization of the ultrafiltration site portion, with terminal cells in juveniles and pericardium with renopericardioduct in adults, differs enti-

rely. In the juvenile stages investigated the large duct-releasing cells of the larval protonephridia are still present but show degeneration.

The present data confirm the hypothesis that the occurrence of proto- versus metanephridial excretory systems among the Metazoa depends on individual development and morphology like body cavities organisation rather than on the systematic placement of the organism. While the excretory duct is formed by outgrowth of the pericardium in Polyplacophora, the adult nephridial system of *Antalis* is formed in the absence of a pericardium by direct mesodermal tube formation. Thus, the proposed non-homology of metanephridial systems of various metazoan phyla because of differing modes of formation becomes doubtful. Also, further evidence is provided for a cytological continuum between protonephridial cyrtocytes and metanephridial podocytes.

Taxonomy and biogeography of Chilean and Magellanic Nudipleura (Gastropoda: Opisthobranchia)

Michael Schrödl

Zoologische Staatssammlung München, Münchhausenstr. 21, D-81247 München; e-mail: schroedl@zi.biologie.uni-muenchen.de

The nudipleuran fauna of South American temperate waters, the Peruvian and Magellanic Provinces, was in extreme taxonomic confusion. Thus a comprehensive revision has been made on the basis of more than 2,000 recently collected specimens which were investigated externally, (micro)anatomically and, when necessary, by histological and ultrastructural (SEM) means. In addition, all relevant type and museum material has been reexamined, revealing an unexpected number of fundamental errors in the original descriptions, e.g. regarding the pleurobranchid genus *Berthella* and the nudibranch genera *Anisodoris*, *Cadlina*, *Tyrinna*, *Geitodoris*, *Gargamella*, *Tritonia*, and *Phidiana*. One striking result is the extreme external and anatomical variability observed in many species. In summary, of 108 Nudipleura species reported for Chile and the Magellanic region, only 65 are still considered to be true species. 28 nominal species (18 Doridoidea, 5 Dendrodoridoidea, 5 Aeolidoidea) will be synonymized as a consequence of this study, 5 nominal species are regarded as nomina dubia, and 1 nominal species is recognized as a nomen nudum.

Of the 65 species regarded as valid, 44 (68 %) were found during collecting for this study. Of these, 13 species (27 %) were undescribed, and 2 species were new for the southern hemisphere. Only two species are added to the Magellanic Province (41 species) which, at least in its southern part, appears well investigated. In contrast, the number of distinct Peruvian Province species increases from 18 to 44, and substantially more new records can be expected from sampling of the virtually unknown northern Chilean and Peruvian coasts.

Many species formerly restricted to a single locality or limited area are shown to have a much wider distributional range. Therefore, and due to extensive taxonomic changes, the degree of endemism of Nudipleura within the Magellanic region decreases drastically from formerly approx. 70 % to 32 %. For the Peruvian Province the degree of nudipleuran endemism is 44 %. The faunal relationships between these and adjacent regions are analyzed and discussed.

New Simrothiellidae (Solenogastres, Mollusca) from the northwestern Indian Ocean

Christiane Todt, Luitfried v. Salvini-Plawen

Institut für Zoologie, Universität Wien, Althanstr. 14, A-1090 Wien; e-mail: a9002654@unet.univie.ac.at

Five new species of Solenogastres sampled in the Mozambique Channel near the Comoro Islands, northwestern Indian Ocean, are presented. The animals were collected in the course of the Campaigne Benthedi (1979) of the Centre National de Tri d'Océanographie Biologique (CENTOB, Brest) in water depths between 520 m and 3,716 m, from soft sediments ranging from clay to muddy sand. They were classified as species of Simrothiellidae, Salvini-Plawen 1978, based on light microscopy analyses of mantle spicule morphology and of the inner organization via serial sections of resin embedded specimens.

The Simrothiellidae are a diverse family of Solenogastres, recently comprising 18 species within 8 genera (*Simrothiella* Pilsbry, 1898; *Cyclomenia* Nierstrasz, 1902; *Kruppomenia* Nierstrasz, 1903; *Biserramenia* Salvini-Plawen, 1968; *Birasoherpia* Salvini-Plawen, 1978; *Helicoradomenia* Scheltema & Kuzirian, 1991; *Plawenia* Scheltema and Schander, 2000; *Spiomenia* Arnofsky, 2000). The family is defined by a radula composed of biserial radula bars with numerous denticles and by paired ventral salivary glands with epithelial gland cells. Integumental spicules are generally hollow needles with simple or differentiated (hooked, capitate) tips, with the exception of the genus *Helicoradomenia* defined exclusively by solid spicules.

One of the new species is placed in the genus *Simrothiella* Pilsbry, 1898, two in *Kruppomenia* Nierstrasz, 1903, and two in *Spiomenia* Arnofsky, 2000.

Acanthocephala

How did the acanthocephalan endoparasitism evolve – a molecular approach in the context of morphological characters

Holger Herlyn

Primatengenetik, Deutsches Primaten-Zentrum, Kellnerweg 4, D-37077 Göttingen; e-mail: hherlyn@gwdg.de

Phylogenetic analysis of the Syndermata (free-living Eurotatoria: Bdelloidea, Monogononta, epizoical genus *Seison*; endoparasitic Acanthocephala: Palaeacanthocephala, Eoacanthocephala, Archiacanthocephala) promises insights into the evolution of acanthocephalan endoparasitism. As a consequence, syndermatan phylogeny attracted considerable attention over the last decades. Based on morphological data three competing hypotheses have been discussed, with *Seison* representing the bdelloidean (Lorenzen 1985, Pp. 210-223 in: "The origins and evolution of lower invertebrates", Clarendon Press), eurotatorian (e.g. Nielsen 1995, Pp. 238-247 in: "Animal evolution", Oxford University Press) or acanthocephalan sistergroup (Ahlrichs 1997, *Zoomorphology* 117: 41-48). So far, 18S rDNA analyses have supported a grouping of Bdelloidea and Acanthocephala (e.g. Garey et al. 1996, *J. Mol. Evol.* 43: 287-292), but without considering data on *Seison*. A recent *hsp82* analysis introduced a fourth possibility with *Seison* at the base of the Syndermata (Welch 2000, *Invertebr. Biol.* 119: 17-26). In the present 18S rDNA approach, maximum likelihood, neighbor-joining and maximum parsimony analyses have been carried out based on 22 species, and for the first time including data on *Seison*. The results strongly support a grouping of *Seison* and Acanthocephala. Moreover, the acanthocephalan phylogeny differs from previous rDNA based studies (e.g. García-Varela et al. 2000, *J. Mol. Evol.* 50: 532-540) in that the Palaeacanthocephala were paraphyletic and the Archiacanthocephala were derived, two assumptions that fit well with a previous analysis based on the presence/absence of special sense organs (Herlyn et al. 2001, *Syst. Parasitol.* 50: 105-16). According to the phylogeny obtained acanthocephalan endoparasitism evolved from a common stem species of *Seison* and Acanthocephala that lived epizoically on a mandibulate. An ancestor of the extant acanthocephalans probably established an endoparasitic lifestyle by invading its mandibulate 'substratum'. Subsequently, vertebrates (or gnathostomes) became part of the acanthocephalan life cycle by feeding on infected mandibulates. Finally, a terrestrial life cycle evolved when the intermediate host conquered land (Herlyn et al. 2002, *Mol. Phylog. Evol.*: in press).

I am indebted to my co-workers Ulrich Ehlers, Oliver Piskurek, Jürgen Schmitz and Hans Zischler for their valuable contributions to this study.

Nematoda

Comparative and functional morphology of corpus, isthmus, and grinder – the initial steps in the origin of the three-part pharynx in nematodes

Alexander Fürst von Lieven

AG Evolutionsbiologie, Institut für Zoologie, Königin-Luise-Str.1-3, D-14195 Berlin; e-mail: lieven@zedat.fu-berlin.de

The distinct morphological regions of the typical tripartite pharynx found in Secernentea reflect several differentiated functions of this organ. Besides the basic functions of sucking and pumping food against the body pressure, the pharynx of rhabditids serves two additional functions restricted to two pharyngeal subunits: (1) The corpus traps bacteria within the closing lumen while excess water is expelled via tube-like extensions that are located behind the stoma at the distal edge of each ray of the triradiate lumen, the pharyngeal tubes; (2) The grinder of the terminal bulb serves for chewing trapped bacteria. The separated sites of trapping and chewing are connected by the isthmus that transports a bolus of bacteria towards the grinder. This complex feeding structure originated step by step from a more simple two-part pharynx consisting only of a corpus and the terminal bulb, as in "Plectidae" that are the closest relatives of the Secernentea within the "Adenophorea". Analysis of video sequences of feeding rhabditids and plectids as well as experiments with paper models of different grinders provided new data to reconstruct this transformation. Within the "Plectidae" the phylogenetic origin of the grinder can be concluded from the ontogenetic recapitulation of longitudinal knobbed rods as are found in adults of closely related leptolaimids like *Chronogaster*. These rods transform to triangular regions of folded and knobbed cuticula in plectids of the *parietinus*-type. These triangular regions can bulge medially when bacteria are chewed, and can also be retracted, drawing some particles into the grinder while the dilated pharynx lumen closes to trap bacteria at the level of the pharyngeal tubes. The more solid chewing plates of the grinder in *Ceratoplectus*, *Plectus parvus*, and *Wilsonema* rotate about a transverse axis and are homologous with those of Secernentea ("Plectidae" is a paraphyletic taxon). Because these plates can not be retracted, an alternative mechanism to transport bacteria towards the grinder must have been the prerequisite for their origin. In *Plectus parvus* and *Wilsonema* the dilated corpus lumen closes while the closed lumen of the region that corresponds to the isthmus of Secernentea dilates. Such a pattern of dilation and closure pushes particles backwards to the grinder. In *Ceratoplectus* dilation of the pharynx lumen goes down to the anterior end of the terminal bulb. Closure of the lumen begins at the level of the nerve ring. Subsequent dilator relaxation pushes excess water in front of the nerve ring forwards while bacteria behind the nerve ring are trapped and enter the grinder. The differentiated patterns of lumen dilation and closure in *Ceratoplectus*, *Plectus parvus*, and *Wilsonema* can be interpreted as the first step in the origin of a separation of trapping bacteria and transporting them towards the grinder, which led to the morphologically discernible units corpus and isthmus found in the Secernentea.

Arthropoda

A new 'great appendage' arthropod and implications for the early evolution of Arthropoda

Andreas Maas¹, Dieter Waloßek¹, Chen Junyuan²

¹ Sektion für Biosystematische Dokumentation, Universität Ulm, Helmholtzstr. 20, D-89081 Ulm; e-mail: andreas.maas@biologie.uni-ulm.de

² Early Life Research Center, Chengjiang, Yunnan, China

A new arthropod from the Lower Cambrian Chengjiang fauna of south-west China is introduced. The first pair of appendages are conspicuous, anteriorly directed and spine-bearing predatory limbs, as are characteristic for a number of Lower to Middle Cambrian arthropods, the so-called 'great appendage' arthropods from the Chengjiang and Burgess Shale biota. The new species is known from only three specimens, but can be clearly distinguished from similar species by its tagmosis and the morphology of its 'great appendage'. Especially the differences in morphology of the predatory limbs and the segmental composition of the head in the 'great appendage' arthropods imply that this group is not monophyletic. Rather, those species, including the new form, which have relatively short raptorial legs, i.e. limbs consisting of three to five portions distally drawn out into spines, may form a monophyletic unit. On the other hand, the species with long 'great appendages' consisting of at least seven portions, e.g. the anomalocarids, most likely belong to another phylogenetic lineage. Similarities in morphology and use of the short 'great appendages' to the chelicera of the Chelicerata lead us to the assumption that this type of predatory limbs could be the precursor structure to the chelicera. Consequently, the species with short 'great appendages' would represent derivatives of the early stem lineage toward the crown group of Chelicerata. The stem species of Chelicerata *sensu stricto* would then have acquired a prosoma as a fusion product of the anterior body segments. This forms our working hypothesis for future investigations on such arthropods.

Evolution of arthropod eye development: pattern formation in lateral ocelli of *Parabuthus transvaalicus* Purcell, 1899

Roland R. Melzer, Andrea Spreitzer

Zoologische Staatssammlung München, Münchhausenstr. 21, D-81247 München; e-mail: melzer@zi.biologie.uni-muenchen.de

Studies on the cellular architecture and structure of the array of ommatidia as well as on their morphogenesis have provided a set of characters suggesting that the compound eyes of Crustacea and Hexapoda are homologous (Paulus 2000, J. Zool. Syst. Evol. Research 38: 189-208; Melzer et al. 2000, Naturwiss. 87: 308-311). Do these features represent autapomorphic conditions of the Crustacea and Hexapoda (Pancrustacea), a taxon recently favoured instead of Tracheata? To understand this better, outgroup comparisons have to be made with other arthropod lineages. Here we study eye development and patterning in scorpions, Chelicerata with ancestral features. In these, lateral ocelli are found made of sensory units thought to be reminiscent of an ancestral compound eye organization.

Initially each ocellus is composed of an array of equally distributed retinula or R-cell precursors surrounded by accessory cells. Secondly, rhabdomic microvilli are formed at initiation sites where several precursor cells meet. Here, R-cell precursors are clustered around the rhabdom portions. Although these clusters do not have a fixed number of cells, a plane of bilateral symmetry is seen in them, and some are characterized by a fan-like arrangement of R-cell precursors. At this stage, arhabdomic and pigment cell protrusions grow and project into the R-cell clusters or form layers between them. Finally the latticed rhabdom is developed.

Contrary to this, in Arthropoda with compound eyes precursor cell clusters exhibiting distinct patterns are found, having fixed cell numbers and following each other in a defined sequence, and they are formed prior to the rhabdom. These differences could be seen as supporting the interpretation of crustacean and hexapod compound eye features as apomorphic. However, there are remarkable similarities between *Parabuthus* clusters and early 'arc-like' preclusters found at the onset of ommatidial development. Thus, early steps of the pattern formation might be highly ancestral and point to what might be the arthropod groundplan condition.

Tisbidae (Crustacea, Harpacticoida) as a monophyletic taxon

Sybille Seifried

AG Zoosystematik & Morphologie, FB 7 - Biologie, Geo- & Umweltwissenschaften, Universität Oldenburg, D-26111 Oldenburg; e-mail: sybille.seifried@mail.uni-oldenburg.de

The Tisbidae sensu Lang (1948, "Monographie der Harpacticiden") contain three marine subfamilies. Species of Cholydiinae are parasites or commensals of cephalopods or fishes. Mainly littoral and phytal species, such as the numerous *Tisbe* species, belong to Tisbinae. The taxon Idyanthinae contains mostly deep-sea taxa. *Idyanthe*, *Marsteinia* and *Zosime* are omnipresent at depths between 200 and 6,000 m.

After a complete revision of the system of Harpacticoida it emerged that the species of Tisbidae sensu Lang (1948) belong to three different, not closely related taxa. All species of Tisbinae and Cholydiinae can be united in one monophyletic taxon. The species of Idyanthinae represent two completely different evolutionary lines within Harpacticoida, to one of which the aberrant *Styracothorax gladiator*, formerly the only species of Styracothoracidae, can be assigned.

The larval stages of *Eudiptomus gracilis* (G. O. Sars, 1863) (Copepoda, Crustacea)

Michael Mayer, Dieter Waloßek

Universität Ulm, Sektion Biosystematische Dokumentation, Helmholtzstr. 20, D-89081 Ulm; e-mail: rotmilan_2000@yahoo.de

The larvae and the adult of the calanoid freshwater copepod *Eudiptomus gracilis* (Sars, 1863) were examined by electron microscopy, whereby in particular the naupliar stages were characterized and documented. The results were compared with the drawings in the textbooks of Kiefer & Fryer (1978, Binnengewässer 26, pt 2) and Einsle (1993, Süßwasserfauna v. Mitteleuropa 8(4-1)), and a number of discrepancies were noted. In particular, the segment boundaries of the limbs have often been missed or omitted, the basal diaphragms and whole sections of the limbs have not been drawn, and development stages were omitted or even replaced by non-existing constructs. Comparison of the ontogeny of *Eudiptomus gracilis* with that of other representatives of the Copepoda made clear that, after alignment, the larval patterns in each taxon of the considered copepod taxa – Harpacticoida, Calanoida and Cyclopoida – are quite uniform. They differ from each other only by suppression of segments and limbs in individual stages. Ontogeny patterns are therefore considered as useful characters for phylogenetic analyses within the Crustacea. Besides this, the study provides an improved basis for the determination of larval stages in the field, needed equally by systematists, comparative morphologists, limnologists and ecologists.

Phylogeny of calanoid copepods from the Antarctic

Sabine Grabbert, Hans-Uwe Dahms

Universität Oldenburg, FB 7 - AG Zoosystematik und Morphologie, D-26111 Oldenburg

Comparatively little is known about phylogenetic relationships among calanoid copepods, although their ecological importance in marine systems is evident and well studied. Existing hypotheses about phylogenetic relationships are mainly based on morphological structures. Their changes are assumed to be mainly influenced by 'natural selection'. A different approach are investigations of genes on the molecular level, assuming that mutation ratios depend largely on time and using a molecular clock for the reconstruction of the pathways of copepod evolution.

Copepods investigated in this study were collected in the Atlantic sector of the Antarctic during the Antarctic cruise ANT XVII-3 of RV Polarstern from Kap Norvegia to the Antarctic Peninsula. DNA sequences of a 650 base pair portion of the nuclear 18S rRNA gene and of a 633 base pair region of the mitochondrial cytochrome oxidase I (COI) gene were determined for 15 species of the genera *Calanus*, *Calanoides*, *Metridia*, *Ctenocalanus*, *Paraeuchaeta*, *Spinocalanus*, *Rhincalanus*, *Gaetanus*, *Stephos*, *Eucalanus*, *Heterorhabdus* and *Microcalanus*. The 18S sequences were analysed to construct the main branches of the tree between families and genera, while sequences of the faster evolving mtCOI gene built the terminal ends for closely related copepod taxa.

A comparison of the first molecular phylogenetic tree for calanoid copepods from the Antarctic with a morphology-based tree shows a high similarity in the main pattern. This confirms the suitability of the chosen genes for the fact that both molecular and morphological structures deal with the same evolutionary background and compare homologous traits. Combining these relatively independent methods will provide a more reasonable hypothesis of phylogenetic relationships among calanoid copepods.

Biodiversity of Crustacea Peracarida obtained in the Antarctic deep sea during the expedition ANDEEP I (ANT XIX-3): preliminary results

Angelika Brandt¹, Wiebke Brökeland¹, Ute Mühlenhardt-Siegel¹, Michael Raupach², Gabriela Strieso², Gisela Wegener¹

¹ Zoologisches Institut und Zoologisches Museum, Universität Hamburg, Martin-Luther-King-Platz 3, D-20146 Hamburg; e-mail: ABrandt@zoologie.uni-hamburg.de

² Ruhr-Universität Bochum, Germany

Knowledge on the composition of the Antarctic deep-sea fauna is generally scarce. During the expedition ANDEEP I (ANTarctic benthic DEEP-sea biodiversity: colonisation history and recent community patterns), ANT XIX-3, with RV Polarstern in January/February 2002, samples were taken in the Antarctic deep sea between 1,000 and about 4,000 m in the Drake Passage and the area of the South Shetland Islands. Until now only peracarids from epibenthic sledge samples (with the supranet starting 1 m above the ground and the epinet starting 27 cm above the ground) have been sorted and counted. Amphipoda, Isopoda and Cumacea were the most abundant peracarids. Interestingly, besides Isopoda, Amphipoda also showed a high abundance at some deep-sea stations. Mysidacea and Tanaidacea were much less abundant. Within the Amphipoda the Lysianassoidea dominated. Munnopsidae were the most dominant family of the Isopoda, followed by the Haploneiscidae at some stations. Within the Cumacea, Diastylidae, Leuconidae and Nannastacidae occurred most frequently in the samples.

A phylogenetic approach to Antarctic *Epimerias* (Epimeriidae, Amphipoda, Crustacea)

Anne-Nina Lörz, Angelika Brandt

Zoologisches Institut und Zoologisches Museum, Universität Hamburg, Martin-Luther-King-Platz 3, D-20146 Hamburg

Epimeriidae are dominant members of the Antarctic benthos with a circumantarctic distribution. Of six known genera of Epimeriidae in the Southern Ocean, *Epimeria* is by far the most speciose, containing 18 of the 26 species. Phylogenetic studies based on molecular and morphological characters show that Epimeriidae and Iphimediidae may not be sister taxa. The monophyly of Antarctic *Epimeria* species is questioned. The high intraspecific variability of single morphological characters supports the assumption of a rapid speciation of the genus *Epimeria* nowadays occurring in the Southern Ocean.

Diversity of the Desmosomatidae of the Angola Basin from DIVA 1 (2000)

Saskia Brix

Zoologisches Institut und Museum, Universität Hamburg, Martin-Luther-King-Platz 3, D-20146 Hamburg; e-mail: sbrix@zimserv.zoologie.uni-hamburg.de

The Desmosomatidae are the most abundant family in the material sampled during the DIVA 1-Expedition with the "RV Meteor" (M48-1) in July 2000. Samples were collected in the Angola Basin using an epibenthic sledge. Twelve stations were sampled between 16°14.3'S 05°26.7'E and 22°20.2'S 03°18.3'E, at 5,125-5,450 m depth. Preliminary studies have been conducted for seven of the twelve stations.

Formalizing wing venation for databasing and identification

Fabian Haas

Sektion Biosystematische Dokumentation, Helmholtzstr. 20, D-89081 Ulm; e-mail: fabian.haas@biologie.uni-ulm.de

The Pterygota are by far the largest taxon and thus identification of single taxa within this group can be difficult. A system allowing a computer database approach to this problem would be helpful in order to efficiently identify insect wings or parts of insect wings (extant and fossil). In order to design such a system, computers have to be taught wing venation, which is done by formalizing the venation pattern. The formalization must be robust, i.e. systems based on homology are not useable. Specialists for different taxa often have different opinions on homology of specific veins, if the homology is clear at all. A change in presumed homology would then corrupt the datasets or would require time-consuming 'translations' to adopt the new system. The formalization must be capable of dealing with a large number of structures, and must be expandable to accommodate new structures without making the previous formalization obsolete. It must be simple enough to deal with very many datasets. It should be easy to learn and make operational decisions for specific structures. Automatic processing of wing venation patterns, by image recognition systems, is highly desirable to process large numbers of venation patterns. The formalization must be powerful enough to produce small groups of taxa, but need not discriminate single species. In spite of the seemingly complicated task, similar formalization schemes have been successfully developed in forensic science in order to make people identifiable with certainty. Alphonse Bertillon was the first to devise such a system (in use since 1882), using body measures and shapes from tip to toe of the delinquent. Subsequently, Francis Galton (after 1872) found finger prints to be useful for identification. In both cases following the formalization scheme singled out a small group of people, about ten, sharing similar features in body measures or finger prints. This low number allows a quick selection. Finger prints became the dominant method and are electronically processed in order to cope with the huge number of prints. A similar system appears useful and feasible for insect wings.

Evolution of prothoracic structures in Mantodea (Insecta: Polyneoptera: Dictyoptera) and their significance for mantodean phylogeny

Frank Wieland

Institut für Zoologie und Anthropologie, Berliner Str. 28, D-37073 Göttingen; e-mail: fwielan@gwdg.de

Research on mantodean systematics has previously been restricted to typological classification. At present, the classification introduced by Beier (1968, *Handb. Zool.* IV/2, 2: 1-47) is still in use. In dictyopteran studies based on phylogenetic systematics (Klass 1995, "Die Phylogenie der Dictyoptera"; Thorne & Carpenter 1992, *Syst. Ent.* 17: 253-268) the relationships within the Mantodea remained almost unconsidered.

Evolution of the front legs to raptorial organs led to various structural changes in the mantodean prothorax. Some of its characters can be used to analyze the phylogenetic relationships among the mantodean taxa.

According to Beier (1968), the ventral part of the anterior prothorax in Mantodea consists of a single, elongate plate which is named "basisternal plate" by the present author. However, this condition is to be interpreted as derived within the Mantodea. In the ground pattern of the group a slender clasp (named "basisternal clasp" by the author) is bordering the cervix caudally. This condition is found in the supposed basal branches of the Mantodea (*Mantoida*, *Chaeteessa*, *Metallyticus* and some "Amorphoscelidae"), which leads to the conclusion that it is plesiomorphic. The taxa also possess a short, almost square prothorax which is also considered to be plesiomorphic. The origin of the basisternal clasp is obscure. It either consists of the fused preepisternites or of the preepisternites including the basisternite.

Within the Mantodea the basisternal clasp has elongated and thus forms the basisternal plate. Some species of the "Amorphoscelidae" and the Eremiaphilidae have a very short basisternal plate. In the Hymenopodidae it is longer. Within the Mantidae the plate may become rather long, in many species even longer than the plate's width. The transformation of the basisternal clasp into the basisternal plate is interpreted as a synapomorphic character for parts of the "Amorphoscelidae", for the Eremiaphilidae, Hymenopodidae, Mantidae and Empusidae. The "Amorphoscelidae" as currently delimited are obviously paraphyletic.

Syntopic and synchronic occurrence of closely related species of the genus *Scarites* Fabricius in Amazonian Brazil (Insecta, Coleoptera, Carabidae, Scaritinae)

Martin Baehr

Zoologische Staatssammlung München, Münchhausenstr. 21, D-81247 München; e-mail: Martin.Baehr@zsm.mwn.de

A sample of ground beetles of the genus *Scarites* from Várzea areas in the vicinity of Manaus, Amazonian Brazil, was examined. During an ecological survey four closely related species of the subgenus *Scarites* s. str. and two species of the subgenus *Lophogenius* Motschulsky were collected at the same locality. Apart from *Scarites* (s. str.) *cayennensis* Dejean, *S.* (s. str.) *illustris* Chaudoir, *S.* (*Lophogenius*) *trivialis* Chaudoir, and *S.* (*Lophogenius*) *smithi* Linell, three species were new: *Scarites* (s. str.) *angustsulcatus* Baehr, *S.* (s. str.) *nitidiceps* Baehr, and *S.* (s. str.) *strigifrons* Baehr (see Baehr 2002, Spixiana 25(3): 225-237).

There are problems raised by the evolution and ecological balance of syntopic and apparently even synchronic occurrence of four species of extremely close relationships and similar size and structure. In spite of slightly different sizes and shapes of the mandibles in the four species of *Scarites* s. str., no evidence is available so far that different feeding strategies could be responsible for the balance of their syntopic occurrence. For further discussion see Baehr (2002).

Many small or a few large eggs – morphology and reproduction strategies in aculeate Hymenoptera

Michael Ohl, Daniela Linde

Museum für Naturkunde, Institut für Systematische Zoologie, Invalidenstr. 43, D-10099 Berlin; e-mail: michael.ohl@rz.hu-berlin.de

The number of ovarioles and the number and size of mature oocytes in aculeate Hymenoptera has taxonomic, phylogenetic, and adaptive significance. The female internal reproductive systems of almost 70 species of apoid wasps, representing close to 40 genera, were examined, and the morphological data compared with the respective female reproductive strategies.

Non-parasitic apoid wasps have six ovarioles (three per ovary), which is probably the plesiomorphic condition in Apoidea (sphecid [now apoid] wasps + bees). Cleptoparasitic species have an increased number of eight ovarioles, and both cleptoparasitoids and pseudoparasitoids (e.g. *Chlorion*: no nest construction, temporary paralysis, prey recovers after oviposition) have also signifi-

cantly more mature oocytes than non-parasitic species. Pseudoparasitoids exhibit the plesiomorphic pattern of six ovarioles, but have by far the highest number of mature oocytes (up to 21). Additionally, mature oocytes of parasitic wasps and bees are significantly smaller than those in non-parasitic species.

Cleptoparasitic species have the lowest level of parental investment, whereas all the nest-building species with the high diversity of different reproduction strategies have a significantly higher mean investment. The general prediction of a decrease of lifetime fecundity, with an increasing investment per offspring, implies analogous predictions for the morphology: females with a low level of parental investment should have a higher number of smaller eggs than those with a higher investment. The present data corroborate this prediction. Apoid wasp species with the lowest level of parental investment (pseudoparasitoids and cleptoparasitoids) have the highest number of mature oocytes, which are significantly smaller. There are two different strategies to increase the oocytes number: cleptoparasitoids have an increased number of ovarioles, whereas pseudoparasitoids have the usual lower number of ovarioles with an absolutely higher number of mature eggs at a given time.

Distribution patterns of species of the pollen wasp genus *Ceramius* (Hymenoptera, Vespidae, Masarinae) in the Mediterranean region

Volker Mauss¹, Christiane Botta², Melanie Brüning²

¹ Staatliches Museum für Naturkunde, Abt. Entomologie, Rosenstein 1, D-70191 Stuttgart; e-mail: volker.mauss@stechimmenschutz.de

² Institut für Landwirtschaftliche Zoologie und Bienenkunde, Universität Bonn, Germany

Fifteen species of the genus *Ceramius* occur in the Mediterranean region. They belong to two distinct monophyletic taxa, the species-groups 1 and 7 sensu Richards (1962, "A revisional study of the masarid wasps"). The distribution of these taxa was investigated based on material from 74 public and some private collections (n = 2115 specimens).

Both species-groups show similar, disjunct distribution patterns with some taxa restricted to the West- and others to the East-Mediterranean region. The species can be assigned to the secondary Mediterranean refuges sensu Lattin (1967, "Grundriß der Zoogeographie") as follows: in species-group 1, *C. fonscolombei* Latreille is of Atlantomediterranean, and *C. bureschi* Atanassov of Pontomediterranean origin. The interpretation of the recent distribution of *C. caucasicus* André is more difficult, probably the species is of Syrian origin and extended its range up to the Caucasus region during the Holocene. In species-group 7, *C. hispanicus* Dusmet (Mauss & Castro 2000, Graellsia 56: 87-95) and the taxa of the *C. lusitanicus*-complex are of Iberian origin. Only one of these species (*C. tuberculifer* Saussure) has crossed the Pyrenees during the Holocene and occurs recently also in southern France. Mauretania taxa are the members of the *C. auctus*-complex (Mauss 1998, Ann. Soc. Ent. Fr. (N.S.) 34: 163-183) and of the *C. maroccanus*-complex, the latter being highly

endemic to the Atlas and Anti-Atlas regions (Mauss 1999, Ent. scand. 30: 323-348). *Ceramius palaestinensis* (Giordani Soika) is of Syrian origin.

From the recent distribution of the taxa of species-group 7 it can be deduced that during the Weichselian glaciation at least three isolated refuges for *Ceramius* existed on the Iberian Peninsula. This hypothesis is supported by the results of an analysis of the colour patterns in populations of *C. fonscolombei* from different regions of south-west Europe. There are distinct differences between the two species-groups concerning the number of species (or morphologically distinguishable taxa) and the sizes of the distribution ranges. Taxa of species-group 7 have smaller ranges than taxa of group 1, whereas the number of morphologically distinct taxa is 3 times higher in group 7. The causes for these differences are not clear: The size of the range neither correlates with body size nor with the ecological potency with regard to the inhabited vegetation series (based on maps of vegetation series and the phytoclimate of Spain). The size of the distribution range might be influenced by nest-building behaviour (with highly endemic species constructing mud cells) and by the grade of specialisation with regard to the pollen source.

Vertebrata

Invasions of the Bohemian Waxwing, *Bombycilla garrulus* (Linnaeus, 1758), in central and southern Europe before the year 1758

Ragnar Kinzelbach

Allgemeine und Spezielle Zoologie, Universität Rostock, Universitätsplatz 2-5, D-18055 Rostock; e-mail: ragnar.kinzelbach@biologie.uni-rostock.de

Historical invasions by the Bohemian Waxwing (*Bombycilla garrulus*) to areas outside of its regular breeding and wintering area within Europe (south-west of 55° N and 15° E) were documented by using all dated material available from before the beginning of modern zoology, i.e. 1758 (Linnaeus, Systema naturae, Xth ed.). The chronology of invasions was verified by critical discussion of the sources and by examining the inner consistency of the series, and of correspondence with contemporaneous climatological dates. Detailed results have been achieved (see Kinzelbach 1995, Kaupia, Darmstädter Beitr. Naturgesch. 5: 1-62) as follows:

- (1) The more prominent invasions of the Bohemian Waxwing are statistically not significantly correlated with climatologically relevant dates from the chronicle literature such as extreme winters, frosts, floods or crop failures, nor with years of poor growth of oak trees in southern Germany.
- (2) The frequency of the especially numerous and far-reaching invasions (grade of intensity 1) is approximately constant during the period investigated. The so-called Little Ice Age (a period of prolonged cold winters from the mid 16th to 18th century) had an influence of little significance on invasions by the Bohemian Waxwing.

(3) The oldest documented names of *Bombycilla garrulus* in Europe refer to the unique occurrence of red horn platelets in its plumage, which were then interpreted as flames. Consequently, the bird was named "spintharis", "spinturnix" (Greek), "avis incendiaria" (Latin), "Zünder" (Middle High German, probably already Germanic). From the great plague outbreak around 1350 onward, the name "Pestvogel" (plague bird) came into use, at the beginning of the Thirty Years War the name "Kriegsvogel" (warbird). The name "Seidenschwanz" (sidentsvanz = silk tail) first appeared in 1552 as a denomination of the bird, but it is much older as a name of a peculiar medieval dress; in Saxony it goes back at least to the 12th century. "Bemlin" (little Bohemian), with some variations by dialects, is also a Middle High German term the Bohemian Waxwing shared for a long time with several other irregular winter visitors from the northeast. It refers to migrating people irregularly seeping into central Europe from the east by way of Bohemia, from approximately 1240 on, triggered by the Mongolian invasion of eastern Europe.

The emergence or at least the spreading of these and some six other German and Italian names can be correlated with single, dated invasions and their contemporaneous interpretation. Some of these names were later adopted by other languages in whose areas the species was less known.

(4) The general superstitious belief that the presence of this bird is a sign or omen of or even the cause for fire or the plague is reflected in the earliest known medieval pictures. Later on, pieces of Renaissance art and early scientific drawings or prints depict the species in much detail, partly due to an aesthetic understanding of nature, partly with the aim of a correct and critical description. From the 17th century onwards other, different concepts are found in pictures and the literature, reflecting first the wartime beginning in 1618, then in the 18th century the contrasting tendencies of piety and early enlightenment.

(5) The synoptical examination of historical climatology, zoology, linguistics, cultural history, and the history of the arts plainly shows that all these areas are interwoven. Many isolated, curious events and anecdotes can thus be related to precise scientific statements and causal analysis. This study is a contribution to the field of cultural zoology: the man-animal relationships, here exemplified by the common history of man and waxwing.

Meeting of Young Systematists in the GfBS

The present situation of the "Young Systematists" of the GfBS

Sybille Seifried

AG Zoosystematik & Morphologie, FB 7- Biologie, Geo- & Umweltwissenschaften, Universität Oldenburg, D-26111 Oldenburg; e-mail: sybille.seifried@mail.uni-oldenburg.de

The working group "Young Systematists" of the GfBS (Gesellschaft für Biologische Systematik) is a group of undergraduate, graduate and PhD students and postdocs in biology and palaeontology, who are working in biological systematics. The activities of this self-organized group of young systematists have three main emphases: networking, professional training and perspectives. To find out more about the level of training, the current professional status and future prospects, a questionnaire had been developed and distributed. 73 out of 124 registered "Young Systematists" (59 %) have returned the questionnaire. In addition, 8 young systematists not yet official members of the group have also filled in the questionnaire. The results of the analysis were presented.

Some examples: young systematists have the following professional specializations: (multiple entries were possible; selection): 64 % phylogenetic systematics; 61 % species descriptions, taxonomy; 51 % morphology; 47 % biodiversity; 44 % biogeography; 37 % molecular systematics; 36 % ecology; 23 % anatomy; 12 % palaeontology. Only two "Young Systematists" are employed on a permanent basis.

Systematics in Germany does not receive enough recruits. The mostly well-trained young systematists are predominantly willing to go abroad to continue work in the field of systematics.