26. Wissenschaftliche Tagung der
DEUTSCHEN GESELLSCHAFT FÜR PROTOZOOLOGIE

21. bis 24. Februar 2007
in Salzburg, Österreich

Präsident der Deutschen Gesellschaft für Protozoologie

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TAGUNGSPROGRAMM

Mittwoch, 21. Februar 2007

Ab 12.00 **ANREISE /REGISTRIERUNG TAGUNGSSTÄTTE ST. VIRGIL**
Ab 17.00 **ANREISE/REGISTRIERUNG JUGENDHERBERGE**

Ab 14.00 **REGISTRIERUNG ZUR TAGUNG IN ST. VIRGIL**

Ab 18.30 **GEMEINSAMES ABENDESSEN**

Donnerstag, 22. Februar 2007

Ab 07.30 **FRÜHSTÜCK**

Ab 08.00 **REGISTRIERUNG ZUR TAGUNG**

09.00-9.30 **Ulrike-G. Berninger**, Salzburg, **Helmut Schmidt**, Kaiserslautern
Begrüßung und Eröffnung der 26. Jahrestagung

Diversität natürlicher Gemeinschaften

Vorsitz**: Steve Wickham,** Salzburg

09.30.-10.15 **JOHN R. DOLAN**, VILLEFRANCHE-SUR-MER, FRANKREICH, MARK R. RITCHIE, SYRACUSE
PLENAR-VORTRAG BIODIVERSITY AND COMMUNITY STRUCTURE OF TINTINNIDS (PLANKTONIC CILIATES) IN THE SE PACIFIC BETWEEN TAHITI AND CHILE: EVIDENCE FOR 'NEUTRALITY'

10.15.-10.30 **Monika Claessens-Kenning**, Steve Wickham (Salzburg), Anton Post (Eilat)
Unexpected high diversity in a natural ciliate community in a resource-poor environment, the Gulf of Aqaba (Red Sea)

10.30-10.45 **Madlen Haentzsch**, Thomas U. Berendonk, Detlef Bernhard, Martin Schlegel (Leipzig)
Ciliate diversity in constructed wetlands

10.45-11.00 **Anke Behnke** (Kaiserslautern), John Bunge, Kathryn Barger (Ithaca, New York), Thorsten Stoeck (Kaiserslautern)
Evaluating spatial and temporal heterogeneity of protistan diversity

11.00-11.30 **KAFFEEPAUSE**

Ökologie I: Klimaeinflüsse und Sukzession

Vorsitz: **Wilhelm Foissner,** Salzburg

11.30-11.45 **Thorsten Stoeck**, Jennifer Kasper (Kaiserslautern), John Bunge (Ithaca, New York), Slava Epstein (Boston)
Protist diversity in light of the paleoclimate data record

11.45-12.00 **Markus Weitere**, Carsten Viergutz, Helge Norf, Marcel Kathol, Johanna Dahlmann, Hartmut Arndt (Köln)
Effekte von Erwärmung auf die Abundanz planktischer und biofilmassoziierter Protozoengemeinschaften**:** die Bedeutung von Resourcenverfügbarkeit und Prädationsdruck

12.00-12.15 **Stefanie Moorthi** (Köln), Astrid Schnetzer, Ivona Cetinic, Rebecca Schaffner, Burt Jones, David Caron (Los Angeles)
Seasonal dynamics of a red tide dinoflagellate (*Lingulodinium polyedrum*) in southern California during 2005

12.15-12.30 **Manfred Wanner**, Willi E.R. Xylander (Görlitz)
Community assembly of terrestrial testate amoebae: how is the very first beginning characterised?

12.30-14.00 **MITTAGSPAUSE**

Ökophysiologie

Vorsitz: **Julian M. V. Schwarz,** Kaiserslautern

14.00-14.15 **Thomas Weisse**, Elke Gächter (Mondsee), Helga Müller (Konstanz), Ulrike Scheffel, Peter Stadler (Mondsee), Michaela Strüder-Kypke (Guelph)
Meseres corlissi: Ökophysiologische Differenzierung innerhalb einer Art

14.15-14.30 **Wilhelm Foissner**, Maria Pichler (Salzburg)
The unusual resting cyst of *Meseres corlissi* (Ciliophora: Oligotrichea): Encystment and genesis of five complex types of wall precursors

14.30-14.45 **Helga Müller** (Konstanz)
Excystierung von *Meseres corlissi* (Ciliophora: Spirotrichea)

14.45-15.00 Christine Klöppel, **Martin Simon**, Helmut Schmidt (Kaiserslautern)
Phosphatidyl-Inositol specific phospholipases in *Paramecium*

15.00-15.15 **Sascha Krenek**, Martin Schlegel, Thomas U. Berendonk (Leipzig)
Paramecium don´t like ice: effect of freezing on *Paramecium caudatum*

15.15-15.45 **KAFFEEPAUSE**

Ökologie II: Morphologie und Ökologie der Ciliaten; Kurzvorstellungen der Poster

Vorsitz: **Helga Müller,** Konstanz

15.45-16.00 Xu Kuidong, **Wilhelm Foissner**, (Salzburg)
Monograph of the Spathidiida (Ciliophora, Haptoria) Volume I: Protospathidiidae, Arcuospathidiidae, Apertospathulidae

16.00-16.15 **Mario Prast** (Salzburg), Ernst Cleven (Weilerswist), Adrian Bischoff (Kiel), Ulrike-G. Berninger (Salzburg)
The impact of ciliates on nitrification in aquatic sediments

16.15-16.30 **Anja Hillmann**, Fabian Westermeier, Arno Tiedtke (Münster), Wolfgang Eichler (Düsseldorf)
A biotechnological approach to reduce antibiotic-resistances in the environment: bacteria, ciliates and sewage treatment plants

16.30-18.00 **POSTERVORSTELLUNGEN**

P1 Martin Kreutz (Konstanz), **Wilhelm Foissner** (Salzburg)
The *Sphagnum* ponds of Simmelried in Germany: a biodiversity hot-spot for microscopic organisms

P2 **Steffen Jost** (Mondsee), Thorsten Stoeck (Kaiserslautern), Jens Boenigk (Mondsee)
Molecular diversity of a protist morphospecies: a comparison between ribosomal and protein-coding genes

P3 **Karin Pfandl**, Jens Boenigk (Mondsee), Antonis Chatzinotas (Leipzig)
Molecular and ecophysiological microdiversity within a flagellate species

P4 Monika Claessens-Kenning, **Mario Prast** (Salzburg)
Concentration of fixed plankton samples via settling: how long is long enough?

P5 **Steffen Kuppardt**, Antonis Chatzinotas, Matthias Kästner (Leipzig)
Elimination of potential pathogens in laboratory systems by protists

P6 **Oliver Gödden**, Ingo Fetzer, Hauke Harms, Antonis Chatzinotas (Leipzig)
Influence of redox changes on microbial eukaryotic communities in contaminated ground water

P7 **Nicolas Derungs**, Therry J. Heger (Lausanne), Enrique Lara (Paris), Edward A.D. Mitchell (Lausanne)
What are the relative effects of litter type, temperature and humidity on testate amoebae community structure?

P8 **Regina Brandstätter**, Ulrike-G. Berninger (Salzburg)
Mixotrophy in flagellates and ciliates - a comparison between two contrasting subalpine ponds

P9 **Gudrun Trinker (**Salzburg), Thorsten Stoeck (Kaiserslautern), Ulrike-G. Berninger (Salzburg)
The impact of a depth-gradient on the microeukaryotes in the Framvaren Fjord (Norway)

P10 Torben Walter, **Ulrike Steinmair**, Steve Wickham (Salzburg)
Changes in the Antarctic ciliate community through time, space, and predation

P11 **Elke Gächter**, Thomas Weisse (Mondsee)
Functional response and selective feeding of the filter feeding freshwater ciliate *Meseres corlissi*

P12 **Anja Scherwaß**, Anke Schulze, Hartmut Arndt (Köln)
Langfristige Entwicklung der Ciliatenfauna im Pelagial des Rheins

P13 **Ute Risse-Buhl**, Kirsten Küsel (Jena)
Colonization dynamics of ciliates in field and flow channels

P14 **Jennifer Wey**, Helge Norf, Anja Scherwaß, Hartmut Arndt, Markus Weitere (Köln)
Frühe Biofilmbesiedlung durch heterotrophe Flagellaten - Regulation und Effekte

P15 **Helge Norf**, Hartmut Arndt, Markus Weitere (Köln)
Experimentelle Untersuchungen zur Bedeutung von Sommer- und Wintererwärmung auf biofilmassoziierte Ciliatengemeinschaften im Rhein

P16 **Alexandra Zuendorf**, Thorsten Stoeck (Kaiserslautern)
Insights into the biogeography of the Uncultured Marine Alveolate Group I (UMA I)

P17 **Helmut Berger** (Salzburg)
Monograph of the Kahliellidae Tuffrau, 1979 (Ciliophora, Hypotricha)

P18 **Hans-Werner Breiner** (Kaiserslautern), Wilhelm Foissner (Salzburg), Thorsten Stoeck (Kaiserslautern)
Colpodidiids finally find their home in the Nassophorea (Ciliata)

P19 **Wilhelm Foissner** (Salzburg), Thorsten Stoeck (Kaiserslautern)
Neokeronopsis nov. spec. (Ciliophora, Spirotrichea), a flagship ciliate from South Africa supports the CEUU hypothesis

P 20 Marion Eppinger, **Julian M.V. Schwarz** (Kaiserslautern), Jens Boenigk (Mondsee), Michael Schweikert (Stuttgart), Wilhelm Foissner (Salzburg), Thorsten Stoeck (Kaiserslautern)
Phylogenetic position of *Aristerostoma marinum* Kahl 1931 and the family Cyrtolophosididae (Ciliophora; Colpodea)

P21 **Julian M. V. Schwarz**, Thorsten Stoeck (Kaiserslautern)
Redescription of *Euplotes trisulcatus* Kahl, 1932 (Ciliophora, Hypotrichida) from the anoxic Framvaren Fjord (South-West Norway)

P22 **Julian M. V. Schwarz**, Rouven Kleist, Thorsten Stoeck (Kaiserslautern)
Homalogastra setosa Kahl 1926: a true cosmopolite?

P 23 **Sabine Agatha** (Salzburg)
Redescription of *Stenosemella nivalis* (Ciliophora, Spirotricha, Tintinnina) based on live observation, protargol impregnation, and scanning electron microscopy

P 24 **Barbara Auinger**, Karin Pfandl, Jens Boenigk (Mondsee)
Single cell PCR from Lugol-fixed samples for quantitative molecular screening

P 25 Markus Thamm, Stephanie L. Schmidt, Martin Schlegel, **Detlef Bernhard** (Leipzig)
Insights into macronucleus evolution within the genus *Stentor* (Ciliophora, Heterotrichea) revealed from rDNA sequences

P 26 **Simone Marker**, Martin Simon, Helmut Schmidt (Kaiserslautern)
Qualitative and quantitative analysis of variable surface antigen RNA species in *Paramecium tetraurelia*

P 27 **Júlia Katalin Török** (Budapest)
Investigations on clonal cultures of *Arcella* species

18.00-18.30 **MITGLIEDERVERSAMMLUNG DES FÖRDERVEREINS DER DGP (DGPF)**

Ab 19.00 **ABENDESSEN**

Freitag, 23. Februar 2007

Molekulare Diversität I

Vorsitz: **Stefanie Moorthi** (Köln)

Ab 7.30 **FRÜHSTÜCK**

9.00-9.45 **PLENAR-VORTRAG** **GEORGE B. MCMANUS**, GROTON, CONNECTICUT, USA
A TALE OF TWO CILIATES: WHAT DOES CRYPTIC DIVERSITY TELL US ABOUT THE MICROBIAL NICHE?

9.45-10.00 **Jens Boenigk** (Mondsee)
Monadologie - A reassessment

10.00-10.15 **Julia Walochnik** (Wien), Claudia Wylezich (Köln), Rolf Michel (Koblenz)
Molecular phylogeny of *Sappinia diploidea*

10.15-10.45 **KAFFEEPAUSE**

10.45-11.00 **Klaus Hausmann**, Petra Selchow (Berlin), Frank Scheckenbach, Markus Weitere, Hartmut Arndt (Köln)
Kryptische Arten im Morphospecieskomplex eines heterotrophen Nanoflagellaten: Fallstudie *Caecitellus spp.*

11.00-11.15 **Renate Radek** (Berlin), Annelie Maaß (London)
Revision von Strukturen und Probleme der Artbestimmung bei der Flagellatengattung *Staurojoenina*

11.15-13.00 **POSTERSESSION**

13.00-14.00 **MITTAGSPAUSE**

14.00-18.00 **ZUR FREIEN VERFÜGUNG**

18.00 **MITGLIEDERVERSAMMLUNG DER DGP**

Ab 19.30 **GESELLIGER ABEND**

19.45 **VERLEIHUNG DER POSTERPREISE**

20.00 **ABENDBUFFET**

Samstag, 24. Februar 2007

Molekulare Diversität II

Vorsitz: **Julia Walochnik**, Wien

Ab 7.30 **FRÜHSTÜCK**

09.30-10.15 **PLENAR-VORTRAG**
HELMUT PLATTNER, ROLAND KISSMEHL (KONSTANZ)
LESSONS FROM THE *PARAMECIUM* GENOME PROJECT -AND BEYOND

10.15-10.30 **Ilaria Andreoli**, Sergei I. Fokin, Franco Verni, Giulio Petroni (Pisa)
Monophyly versus paraphyly of genus *Frontonia*: a molecular study

10.30-11.00 **KAFFEEPAUSE**

11.00-11.15 **Stephanie L. Schmidt**, Theresa Treuner, Martin Schlegel, Detlef Bernhard (Leipzig)
Multiplex PCR approach for species detection and differentiation within the genus *Spirostomum* (Ciliophora, Heterotrichea**)**

11.15-11.30 **Dana Barth**, Karolin Tischer (Leipzig), Helmut Berger (Salzburg), Martin Schlegel, Thomas U. Berendonk (Leipzig)
High haplotype diversity in *Coleps* (Ciliophora: Prostomatida) populations

11.30-11.45 **Frank Scheckenbach**, Claudia Wylezich, Markus Weitere (Köln), Klaus Hausmann (Berlin), Hartmut Arndt (Köln)
Genetically homogenous populations of two flagellates from abyssal plains of the south-east Atlantic Ocean

11.45 **Ulrike-G. Berninger**, Salzburg, **Helmut Schmidt**, Kaiserslautern
Verabschiedung

12.00 **MITTAGESSEN, ABREISE**

ABSTRACTS DER VORTRÄGE

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MONOPHYLY VERSUS PARAPHYLY OF GENUS *FRONTONIA*: A MOLECULAR STUDY

The peniculine ciliates *Frontonia* are usual members of the pelagic and benthic fauna in both freshwater and marine environments. The genus comprises about thirty species but the validity of some of them still has to be confirmed. Despite the high number of species, few molecular data are available for this genus. Here we present 18S rRNA molecular data of eight different, morphologically recognizable, *Frontonia* species. We were able to classify five of them, *Frontonia leucas*, *Frontonia salmastra*, *Frontonia minuta*, *Frontonia atra* and *Frontonia fusca*. The remaining three species were difficult to classify because either poorly described in literature or completely new species; their detailed morphological characterization is still ongoing. Phylogenetic analysis showed that genus *Frontonia* is paraphyletic, with the clade represented by genera *Apofrontonia* and *Paramecium* branching from within. Despite the observed molecular differences, all analyzed species present the typical gross-morphological features of genus *Frontonia*. According to these data many distinctive traits of genus *Frontonia* could be plesiomorphic characters of limited systematic value. A taxonomic revision of the genus will be necessary in the next future.

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HIGH HAPLOTYPE DIVERSITY IN *COLEPS* (CILIOPHORA: PROSTOMATIDA) POPULATIONS

To date the awareness of the population structure in eukaryotic microbes is very limited. This is exemplified in the scarce knowledge about the genetic variation of ciliates, which contribute to a great extent to the biological diversity and biomass of freshwater ecosystems. The aim of our study was to find a suitable marker system and to elucidate the genetic variation of the common planktonic ciliate *Coleps* (Prostomatida). We employed sequence analyses of the mitochondrial Apocytochrome *b* gene. The analysis of over 100 *Coleps* isolates from a young lake in Germany revealed an unexpectedly high genetic variation of the two dominant *Coleps* species, highly exceeding previously reported values for other ciliates. Furthermore, these two species were found to exclude each other throughout the season. During spring and early summer the mixotrophic *C. spetai* dominated and a few individuals of a third species were detected, the autumn isolates exclusively consisted of the aposymbiotic, heterotrophic C. *hirtus hirtus*.

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EVALUATING SPATIAL AND TEMPORAL HETEROGENEITY OF PROTISTAN DIVERSITY

In the past few years the number of environmental SSU rDNA inventories dealing with microeukaryote diversity increased tremendously. Besides an improvement of phylogenetic resolution of the tree of life, major objectives of such studies are the discovery of novel sequences and organisms, estimates of species richness, and mapping the biogeographic distribution of specific target organisms. Addressing these issues requires a detailed knowledge about the spatial and temporal dynamics of protistan communities in the ecosystem under study. However, most environmental SSU rDNA surveys are based on a single sampling event and on a single sample only. We monitored and here evaluate the spatial and temporal heterogeneity of microbial eukaryote communities (phylotype composition) in an anoxic marine habitat, the Framvaren Fjord (Norway). The application of different statistical tools for community comparison and richness estimates revealed that each of the nine different samples (SSU rDNA clone libraries) provides a different picture of the protistan community structure and diversity of the fjord's water column. Thus, we conclude, that even though SSU rDNA inventories indeed give insight in protistan community structure, due to distinctive heterogeneity, comparison of different sampling sites (e.g. biogeographic regions, ecosystems) might be a delicate issue.

Boenigk, Jens, ÖAW, Institut für Limnologie, Flagellate Ecology Group, e-mail: jens.boenigk@oeaw.ac.at

MONADOLOGIE – A REASSESSMENT

Protist species, diversity and the basic units to measure diversity are controversially discussed since the first microorganisms have been discovered. Molecular methods now provide a resolution exceeding by far that of morphology in many taxa. Despite the methodological advances during the last 300 years, the basic problems of defining protist species and diversity has not been solved. I will discuss the implications of ecophysiological and molecular microdiversity in protists and further demonstrate that, in contrast to current assumptions of cultivation-independent molecular surveys, these approaches are not superior but equivalent or inferior to cultivation-dependent approaches.

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UNEXPECTED HIGH DIVERSITY IN A NATURAL CILIATE COMMUNITY IN A RESOURCE-POOR ENVIRONMENT, THE GULF OF AQABA (RED SEA)

Ciliate diversity was analyzed in the oligotrophic Gulf of Aqaba, during winter mixing, the onset of stratification in spring and during summer stratification. The phytoplankton community in these periods differed distinctly, being dominated either by eukaryotic algae, *Synechococcus* or *Prochlorococcus*. Despite the oligotrophic status of the Gulf, ciliate biomass and diversity were remarkably high. The ciliate carbon: chl *a* ratio was up to 26, indicating a highly efficient and fast use of the homogenous resources – the phytoplankton was dominated by very few algal types, indicating an enormous niche overlap among the grazers. Up to 98% of the ciliates belonged to the same taxonomic group, thus having very similar food niches. The most plausible explanation for the high diversity despite the low prey heterogeneity is the genetic diversity of the autotrophs, particularly of *Synechococcus*. Thus we assume that the high ciliate diversity was provided by specialization and so a very tight packing of niches and highly efficient use of the available resources.

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BIODIVERSITY AND COMMUNITY STRUCTURE OF TINTINNIDS (PLANKTONIC CILIATES) IN THE SE PACIFIC BETWEEN TAHITI AND CHILE : EVIDENCE FOR 'NEUTRALITY'

Tintinnid concentrations were positively related to their prey, assessed as chlorophyll a. Morphological and taxonomic diversity metrics co-varied but were not significantly related to phytoplankton size-diversity. Taxonomic diversity of tintinnids, (H' or Fishers' alpha), was inversely related to chlorophyll concentration and positively to the depth of the chlorophyll maximum layer. Thus, diversity was highest with the least food spread over the largest volume of water. For each community, species abundance distributions were compared to geometric, log-series and log-normal distributions which incorporate different assumptions of the equivalency and interactions of species . For most communities, the observed distribution most closely matched log-series, coherent with the neutral theory of random colonization from a large pool of more or less equivalent species. Occurrence rates of species were correlated with average abundance rather than specific characteristics of biovolume or lorica oral diameter (mouth) size. Species richness of communities was correlated with both the variety of mouth sizes (lorica oral diameters) as well as numbers of species per mouth size, also consistent with random colonization.

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THE UNUSUAL RESTING CYST OF *MESERES CORLISSI* (CILIOPHORA: OLIGOTRICHEA): ENCYSTMENT AND GENESIS OF FIVE COMPLEX TYPES OF WALL PRECURSORS

Meseres corlissi Petz & Foissner (1992) is a rare, oligotrichine ciliate closely related to the common *Halteria grandinella*. We studied encystment, genesis of the cyst wall precursors, and the structure of the resting cyst, using light- and electron microscopy and cytochemistry. The resting cyst of *M. corlissi* has several outstanding features, viz., the wall contains a layer of chitin, the surface is covered by conspicuous globules (lepidosomes) up to 15 µm across, and there are five types of complex cyst wall precursors, each showing six to nine distinct developmental stages. When encysting, the conical body forms a discoidal "head". Then, the cell rotates rapidly and releases the lepidosomes within 5–20s. Then, the four other types of wall precursors are released almost concomitantly. When the wall precursors have left the cell, a second, slow rotation phase occurs, possibly distributing the wall material. Most or even all cyst wall precursors develop in Golgi vesicles and are released by exocytosis. None of the precursors is similar to those reported from other ciliates, suggesting the oligotrichs as a very distinct group of ciliates. (Supported by the FWF, P 16796-B06)

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CILIATE DIVERSITY IN CONSTRUCTED WETLANDS

The use of constructed wetlands for wastewater treatment increased in the last years in consequence of their high hygienisation efficiency. One important element of the purification process is the occurrence of different protozoa species, especially ciliates, which play a dominant role for the removal of bacteria and pathogenic protozoa. To understand the correlation between the ciliate community and the purification potential, more knowledge about the species assemblage and seasonal succession is necessary. Therefore, we analysed the ciliate diversity of one constructed wetland with light microscopy and molecular methods over 18 months. Additionally, the ratios of coliform bacteria were investigated to allow statements regarding the correlation of ciliate assemblage and the amount of bacteria in the effluent of the wetland.
Using the above described analysis 20 different species were detected. Surprisingly, the abundances of some species showed conspicuous seasonal differences in spite of constant amounts of coliform bacteria in the effluent.

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KRYPTISCHE ARTEN IM MORPHOSPECIESKOMPLEX EINES HETEROTROPHEN NANOFLAGELLATEN: FALLSTUDIE *CAECITELLUS* SPP.

Vermeintliche Stämme des marinen Nanoflagellaten *Caecitellus parvulus* erwiesen sich nach Analysen ihrer Struktur und Ultrastruktur (Flagellenlängen, Cytoskelett, Glykokalyx), ihres Verhaltens (Lokomotion, Nahrungserwerb), ihrer Wachstumskurven, ihrer molekularen Daten sowie ihres Lebensraums (Flachwasser, Tiefsee) als unterschiedliche Arten. Die Unterschiede sind so signifikant, dass die bisherige Art *C. parvulus* in insgesamt drei Arten aufgespalten wird: *C. parvulus*, *C. paraparvulus* und *C. pseudoparvulus*. Diese Studie belegt, dass bei der Artdeterminierung soviel unterschiedliche Aspekte zur Biologie eines Einzellers wie möglich herangezogen werden sollten.

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A BIOTECHNOLOGICAL APPROACH TO REDUCE ANTIBIOTIC-RESISTANCES IN THE ENVIRONMENT: BACTERIA, CILIATES AND SEWAGE TREATMENT PLANTS

Sewage treatment plants, especially the biological purification steps, are hotspots for antibiotic-resistant bacteria, which are released in relatively high numbers into the receiving waters. The further entry of antibiotic resistances into the environment – a major threat to human health –should be prevented. We developed therefore a novel approach to reduce the cell-numbers of suspended bacteria by filter-feeding ciliates, the natural predators of bacteria. The capability of the two ciliates *Tetrahymena pyriformis* wt and *Colpidium campylum* to decrease three representative bacteria species (*Escherichia coli*, *Bacillus subtilis* and *Pseudomonas putida*) was analysed at five different temperatures in a 100 ml-scale under batch conditions over 8 h.
These results stimulated upscaling of the experiments to volumes of 2 l and 25 l. In addition the time period was increased to 100 h under continuous conditions: Both *T. pyriformis* wt and *C. campylum* have the potential to reduce efficiently and economically the number of suspended bacteria released into the receiving waters.

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PHOSPHATIDYL-INOSITOL SPECIFIC PHOSPHOLIPASES IN *PARAMECIUM*

GPI-anchors of proteins are usually cleavable by phosphatidyl-inositol specific phospholipases (PI-PLCs). As surface antigens of several protist species are GPI-anchored, enzymes of the PI-PLC family are strongly assumed to be involved in antigen release in the medium, especially during antigenic switching. We report here the analysis of six different PI-PLCs present in *Paramecium tetraurelia*. Whereas PLC-3 and PLC-4 are paralogs to PLC-5 and PLC-6, PLC-1 and PLC-2 are obviously unique. All genes are transcribed and, interestingly, one of the paralogs is always transcriptionally down-regulated, but not silent. The molecular weight of enzymes ranges from 82 to 96 kDa and additionally to the typical X-, Y- and C2-domains, PLC-3 and PlC-5 exhibit calcium binding motifs. Apart from these differences we have shown that not a single PLC is responsible for GPI-cleavage during salt-alcohol extraction of surface proteins and shedding of antigens during antigenic switching. Moreover, we have strong hints that different PLCs can complement one another in some mode of operations. With this PLC variety *Paramecium* seems to become the organism of choice to study PI-PLC and their influence in GPI-anchored proteins.

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PARAMECIUM DON'T LIKE ICE: EFFECT OF FREEZING ON *PARAMECIUM CAUDATUM*

Cryopreservation of protozoa at temperatures below -130°C is an important tool for the *ex situ* conservation of biological and genetic diversity within these organisms. Furthermore it is a useful method for the long-term maintenance of laboratory cultures without losses or changes in their characteristics. So far, quite a number of protozoa have been successfully preserved in this manner, by using different cryoprotective agents e.g. dimethylsulfoxid (DMSO), glycerol or methanol. However, these studies have primarily focused on parasitic and endosymbiotic protozoa. Here we present results on the free living ciliate *Paramecium caudatum*. Some initial earlier work on members of the genera *Paramecium* have been successfully cryopreserved these ciliates using DMSO as cryoprotectant. However, only a small percentage of the frozen cells were viable after thawing. To increase the survival rate of *Paramecium caudatum* under cryogenic storage and to establish viable post-freeze cultures, we have tested several additives for their cryoprotective activity as well as different freeze-thaw processes. Here we will give a short report on the first results regarding the effect of liquid nitrogen storage on different *Paramecium caudatum* strains.

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MONOGRAPH OF THE SPATHIDIIDA (CILIOPHORA, HAPTORIA) VOLUME I: PROTOSPATHIDIIDAE, ARCUOSPATHIDIIDAE, APERTOSPATHULIDAE

The Spathidiidae belong to the subclass Haptoria, a group of rapacious, "lower" holotrichs. The family comprises about 200 described species, most belonging to the time-honoured genus *Spathidium*. Several colleagues doubted the validity of so many *Spathidium* species. However, our monograph shows not only the validity of most described species, but adds 50 new species discovered in over 500 samples from terrestrial biotopes worldwide. Now, the spathidiids consist of over 250 species distributed in four families and 20 (!) genera, several of which are described in this monograph. About half of the species have been described or redescribed with modern methods, and thus each needs an average of eight printed pages in the revision. Accordingly, we split the revision into two parts which form a harmonic unit, but can be used independently. Further, the split facilitates publication, which was considerably delayed because we had to perform basic investigations on ontogenesis, conjugation and resting cysts as well as to describe nearly 100 populations half of which represented new species.
Volume I is now available by Springer publisher, series Monographiae Biologicae, Volume 81, IX + 485pp.

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A TALE OF TWO CILIATES: WHAT DOES CRYPTIC DIVERSITY TELL US ABOUT THE MICROBIAL NICHE?

Strombidium oculatum is a spritotrich ciliate that lives in tide pools at mid-latitudes. It has never been cultivated, but its ecology has been well-studied from field populations. It is phototactic, retains functioning chloroplasts from its food, and has a tidal rhythm of encystment that prevents it from being washed out to the open sea by the incoming tide. DNA sequences from natural populations reveal surprising diversity in this species, suggesting past reproductive isolation. Among the >10 separate clades that can be placed in a monophyletic group is a form recognizable as a separate morphospecies, *S. stylifer*. Unlike *S. oculatum*, the latter is amenable to cultivation and has been isolated from Northern Europe, North America, and Brazil. In vitro observations on its photobehavior, food preferences, and encystment patterns suggest some ideas about niche separation among the clades, but the extent to which the DNA diversity is reflective of niche diversity is not known. In addition to this topic, emerging information on the basin-scale distribution of several of the clades will be discussed in light of the current debate on microbial endemism.

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SEASONAL DYNAMICS OF A RED TIDE DINOFLAGELLATE (*LINGULODINIUM POLYEDRUM*) IN SOUTHERN CALIFORNIA DURING 2005.

Lingulodinium polyedrum is a marine, bioluminescent dinoflagellate that forms massive red tides along the coast of Southern California and is potentially toxic (yessotoxin). However, little is known about its bloom dynamics and impact on the planktonic food web. An 18S rDNA-based quantitative real-time PCR (qPCR) approach was designed for species-specific detection and enumeration of this organism in natural water samples over six orders of magnitude. This qPCR assay was used to follow population dynamics of *L. polyedrum* in the Los Angeles area of the Southern California Bight from March to December 2005. Sampling on a high temporal and spatial resolution (monthly/bimonthly sampling at 20 locations) allowed documenting background abundances in spring and early summer as well as a major bloom in fall 2005. The high sensitivity and the broad dynamic range make the qPCR method a useful new tool for studying population dynamics of this dinoflagellate within mixed assemblages. In conjunction with nutrient analyses and microscopy/flow cytometry counts assessing the overall protistan community structure, this dataset will facilitate the understanding of bloom formation and the ecological role of *L. polyedrum*.

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EXCYSTIERUNG VON *MESERES CORLISSI* (CILIOPHORA: SPIROTRICHEA).

In Laborkulturen des halteriiden Ciliaten *Meseres corlissi* Petz & Foissner 1992 wurde experimentell Excystierung ausgelöst, lichtmikroskopisch beobachtet und fotografisch dokumentiert. Der Vorgang beginnt mit der Ausbildung einer zentralen, nicht pulsierenden Vacuole. Mit zunehmender Größe dieser Vacuole platzt die äußere Cystenhülle. Der Protoplast, der die äußere Hülle durch den so entstandenen Spalt verläßt, ist noch von einer dünnen, flexiblen Cystenmembran umschlossen. Orale Membranellen und eine pulsierende Vacuole werden aktiv und der Ciliat beginnt sich zu drehen. Durch die schneller werdenden Bewegungen wird die flexible Membran ausgeweitet, sie reißt schließlich und entläßt den fertig ausdifferenzierten Ciliaten.
In der Literatur sind sehr ähnliche Abläufe für *Didinium nasutum*, *Nassula ornata, Tillina magna* und viele stichotriche Ciliaten beschrieben.

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LESSONS FROM THE *PARAMECIUM* GENOME PROJECT – AND BEYOND

The laboratories involved in elucidating the genome of *Paramecium tetraurelia* have recently published some essential features of their work (Aury et al. 2006). In a first attempt, manual annotations (e.g. by considering functionally important domains, characteristics of introns, intracellular localization and functional tests/gene silencing) may facilitate automatic annotations in the near feature, while premature automatization is liable to serious errors. Along these lines our lab has contributed by annotating manually about 250 genes, including casein kinase 2, cGMP-activated kinase, phosphatase 2B (calcineurin), pp63/parafusin, SERCA-type Ca^{2+}-ATPase (pump), numerous H^{+}-ATPase subunits, actin superfamily, molecules relevant for membrane interactions (SNAREs, including Synaptobrevin and Syntaxin superfamilies, SNAP-25, and the SNARE-specific chaperone NSF), Ca^{2+}-release channels (notably an Ins-1,4,5-trisphosphate receptor) etc.* All evidence points toward repeated whole genome duplications (WGD, Aury et al. 2006). The last one has generated an amplification effect with generally no diversification (sometimes only on DNA level, but with identical translation products). Genes from previous WGDs have been maintained to a variable degree, some with neofunctionalization, some to account for the considerable structural and functional specialization of these cells. Pseudogenes are rare. No alternative splicing has ever been observed.

Aury, J.-M. 2006 Nature 444:171-178. *Further references: see our group homepage

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THE IMPACT OF CILIATES ON NIRTIFICATION IN AQUATIC SEDIMENTS

The biogeochemical nitrogen cycle is one of the most important element cycles. Many transformations within this cycle are catalyzed by bacteria. Numerous autecological studies on these bacteria have been conducted, but only rarely have they been regarded as part of a food web in which they have to compete for nutrients and substrates and in which they are prey for other organisms such as bacterivorous ciliates. In the recent project, the impact of ciliates on nitrification (the sequential oxidation of ammonium to nitrate via nitrite) was investigated. This process is catalyzed by two groups of bacteria and takes place under oxic conditions in the upper layer of aquatic sediments. Marine and fluvial sediments were transfered into a lab system. The effect of ciliate abundance on nitrification potentials, abundances and composition of nitrifying bacteria and nitrate concentrations was investigated. Results show that increased ciliate abundances lead to higher nitrification potentials and higher abundances of nitrifying bacteria. Food selectivity by the ciliates was ruled out as mechanism. Enhanced nurtient recycling was identified as the main reason for this effect.

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REVISION VON STRUKTUREN UND PROBLEME DER ARTBESTIMMUNG BEI DER FLAGELLATENGATTUNG *STAUROJOENINA*

Symbiontische Flagellaten der Gattung *Staurojoenina* leben in der Gärkammer von Trockenholztermiten (Fam. Kalotermitidae). Bisher wurden fünf Arten namentlich beschrieben, und zwei *Staurojoenina* sp. in der Literatur erwähnt. Der Abgleich eines weiteren Fundes aus *Neotermes cubanus* mit den bekannten Arten ist problematisch, da die Autoren nicht alle heute wichtig erscheinenden Merkmale erwähnen, den gleichen oder ähnlichen Strukturen verschiedene Bezeichnungen verleihen – und dies in englischer, französischer und italienischer Sprache – und erkannte Strukturen abweichend interpretieren. Obgleich wir versucht haben, die Merkmale der Gattung *Staurojoenina* zu revidieren und mit elektronenmikroskopischen Befunden in Einklang zu bringen, ist es nicht möglich, den neuen Fund eindeutig einer bereits beschriebenen oder neuen Art zuordnen. Dies wirft die Frage auf, ob im Zweifel ein Fund besser unbenannt als „spec." belassen, oder um Verwechslungen zu vermeiden, ein eigener Artname verliehen werden sollte.

Maaß, A., Radek, R. (2006): The gut flagellate community of the termite *Neotermes cubanus* with special reference to *Staurojoenina* and *Trichocovina hrdyi* nov. gen. nov. spec. Europ. J. Protistol. 42, 125–141.

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GENETICALLY HOMOGENOUS POPULATIONS OF TWO FLAGELLATES FROM ABYSSAL PLAINS OF THE SOUTH-EAST ATLANTIC OCEAN

The abyssal seafloor at depths of 5000 m is a vast, interconnected environment, covering 60 % of the planets surface. The continuous nature of the habitat and the deep oceans flow regime suggest that extreme endemism amongst microbial eukaryotes might be rare. But to fathom their biogeography in the deep oceans is complicated by inadequate sampling, making it difficult to distinguish rarity from endemism, and the potentially high percentage of cryptic species, undistinguishable by morphology alone.
We have isolated and sequenced the small ribosomal subunit (SSU rDNA) and the first internal transcribed spacer (ITS1) of 25 strains of *Rhynchomonas nasuta* and 33 strains of *Massisteria diva* sp. nov. from three abyssal plains of the South Atlantic Ocean. Strains with identical SSU rDNA and ITS1 isolated from different abyssal plains demonstrate that some lineages occur in the entire deep South Atlantic Ocean. Bottom current activity might thus be strong enough for large scale dispersal of the relevant lineages, repectively species, in timescales shorter than needed for evolutionary diversification detectable at the level of ribosomal markers.

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MULTIPLEX PCR APPROACH FOR SPECIES DETECTION AND DIFFERENTIATION WITHIN THE GENUS *SPIROSTOMUM* (CILIOPHORA, HETEROTRICHEA)

The heterotrichous ciliates *Spirostomum teres*, *Spirostomum minus*, and *Spirostomum ambiguum* are frequent bioindicators for heavily polluted waters and represent important components of microbial communities in such ecosystems. Besides their saprobity, their high sensitivity to numerous toxic substances (heavy metals, pesticides etc.) seems to be a fundamental characteristic making these species to excellent model organisms for ecological, environmental and ecotoxicological studies. However, species identification is still intrinsically tied to traditional morphological methods.
This study presents a rapid, simple, and reliable PCR-based system that allows the unambiguous identification and differentiation between *Spirostomum teres*, *S. minus*, and *S. ambiguum.* Primer specificity was checked thoroughly by multiplex PCR approach not only on *Spirostomum teres*, *S. minus*, and *S. ambiguum* but also on different other ciliates. The sensitivity of this detection system was verified using environmental water samples. Furthermore, the detection of single cells was demonstrated.

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PROTIST DIVERSITY IN LIGHT OF THE PALEOCLIMATE DATA RECORD

Climate changes over geological time have influenced the evolution of biodiversity, ultimately leading to its present pattern. We consider the current paleoclimate data record, inferring that present-day hot and cold environments should contain, respectively, the largest and the smallest diversity of ancestral lineages of microbial eukaryotes. We investigate this hypothesis by analyzing an original dataset of 18S rRNA gene sequences from the High Arctic, and data from the existing literature on 18S rRNA gene diversity in hydrothermal vent, temperate sediment, and anoxic water column communities. Against all expectations, the community from the extreme cold environment emerged as the richest observed to date in protistan phylotypes, and most diverse in ancestral lineages. This pattern can best be explained by the natural selection sweeps on microbial eukaryotes repeatedly caused by low temperatures and global anoxia of Snowball Earth conditions. It implies that cold refuges persisted through the periods of greenhouse conditions, which agrees with some, although not all, current views on the extent of the past global cooling and warming events. We therefore identify extreme cold environments as promising targets for microbial discovery.
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MOLECULAR PHYLOGENY OF *SAPPINIA DIPLOIDEA*

The genus *Sappinia* was established in 1896 by DANGEARD for a free-living amoeba with a dense glykocalyx and pedicellate "cysts". In 1912 ALEXEIEFF transferred an amoeba that had been named *Amoeba diploidea* because of its double nucleus by HARTMANN & NÄGLER in 1908 to this genus and called it *Sappinia diploidea*.
The aim of the current study was to investigate the phylogenetic relationships within the genus *Sappinia*. The 18S rDNA of eight different strains of *Sappinia* was sequenced and compared to one another, to the neotype of *S. diploidea* and to other representatives of the Amoebozoa by multiple sequence alignment and cluster analysis.
Altogether, the phylogenetic position of the genus *Sappinia* within the Thecamoebidae was corroborated, however, it was shown that there are high sequence dissimilarities between the different *Sappinia* strains and that the establishment of new species within this genus will be inevitable. The clarification of the relationships within the genus *Sappinia* is essential, last but not least because *S. diploidea* has been identified as the causative agent of encephalitis in an otherwise healthy young man in 2001.

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COMMUNITY ASSEMBLY OF TERRESTRIAL TESTATE AMOEBAE: HOW IS THE VERY FIRST BEGINNING CHARACTERISED?

We used litterbags buried into four sandy soils to study the early colonisation of testate amoebae. In the course of "succession", no replacement of species was observed. The litterbag cellulose exposed at the youngest, nutrient-poor mining site had been colonised firstly in high abundances, while the older sites with undisturbed soil revealed only a low amoebal colonisation. Besides the (expected) small-sized *r*-strategists, large-sized *K*-strategists occurred in high densities. Some species which colonised in high abundances the target (litterbag) substrate were not found in the adjacent source substrate and vice versa, stressing the importance of the substrate quality. In the course of the experiment, the influencing environmental factors became more complex, as shown by redundancy analysis. Concerning the amoebal community, there was a change from variability to stability, as visualised by cluster analysis.These observations point to a stochastic beginning of immigration and community assembly, changing to a more deterministic course. Our findings are discussed in the light of a neutral community model.

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MESERES CORLISSI: ÖKOPHYSIOLOGISCHE DIFFERENZIERUNG INNERHALB EINER ART

Dieser Vortrag fasst die ökophysiologischen Untersuchungen an dem oligotrichen Süßwasser-Ciliaten *Meseres corlissi* der letzten 3 Jahre zusammen. Dabei wurden klonale Kulturen von 4 verschiedenen Kontinenten im Labor untersucht. Die Artidentität aller Isolate wurde durch Sequenzierung der kleinen ribosomalen RNA-Untereinheit (ssu RNA) bestätigt. Die Ergebnisse zeigten erhebliche intraspezifische Unterschiede, die mit zunehmender geografischer Distanz der Herkunftsorte der Isolate anstiegen. Signifikante Unterschiede wurden ermittelt bezüglich der Ingestions-, Wachstums- und Produktionsraten, des Zellvolumens, der Sensitivität der Klone gegenüber Temperatur- und pH-Änderungen sowie der Faktoren, die die En- und Exzystierung auslösen. Die erzielten Ergebnisse werden im Hinblick auf die Fragen der Artbildung und des für die Ciliaten geeigneten Artkonzeptes diskutiert.

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EFFEKTE VON ERWÄRMUNG AUF DIE ABUNDANZ PLANKTISCHER UND BIOFILMASSOZIIERTER PROTOZOENGEMEINSCHAFTEN: DIE BEDEUTUNG VON RESOURCENVERFÜGBARKEIT UND PRÄDATIONSDRUCK

Klimamodelle sagen eine deutliche Erwärmung der Erdatmosphäre in den nächsten Jahrzehnten voraus. Es ist Aufgabe von Ökologen, Mechanismen aufzudecken, wie Temperaturänderungen zu Änderungen in der Struktur und Funktion von Lebensgemeinschaften führen können. Im Rahmen des Schwerpunktprogramms „Impact of climate variability on aquatic ecosystems (AQUASHIFT)“ haben wir sowohl planktische, als auch biofilmassoziierte Protozoengemeinschaften aus dem Rhein auf Änderungen durch experimentelle Erwärmung untersucht. Dabei wurde gezeigt, dass sich die Gesamtabundanz natürlicher isolierter Biofilm- und Planktongemeinschaften kaum mit Erwärmung ändert (vgl. auch Beitrag von Norf et al.). Unter Zugabe von Ressourcen kam es jedoch zu einer deutlichen Stimulation durch Temperaturerhöhung, was zeigt, dass die natürlichen Gemeinschaften eher nährstoff- als temperaturlimitiert sind. Ebenso führt die Präsenz von Makrograzern (hier: Muscheln als Grazer planktischer Flagellatengemeinschaften) zu einer verstärkten Anfälligkeit der Protozoengemeinschaften gegenüber Temperaturänderungen. Dies lässt sich durch eine divergente Entwicklung der Fressraten der Makrofauna und der Wachstumsraten der Protozoengemeinschaft erklären. Die Ergebnisse zeigen, dass sich die Kontrollmechanismen (sowohl „bottom-up“ als auch „top-down“) entscheidend auf die Sensitivität von Protozoengemeinschaften gegenüber Erwärmung auswirken.

ABSTRACTS DER POSTER

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REDESCRIPTION OF *STENOSEMELLA NIVALIS* (CILIOPHORA, SPIROTRICHA, TINTINNINA) BASED ON LIVE OBSERVATION, PROTARGOL IMPREGNATION, AND SCANNING ELECTRON MICROSCOPY

Stenosemella nivalis (Meunier, 1910) Kofoid & Campbell, 1929 is widely distributed in coastal waters. The samples were collected in the pelagial of the Irish Sea near the Isle of Man during spring. The specimens were studied in vivo, after protargol impregnation, and in the scanning electron microscope. Lorica ~ 53 × 40 µm in size, amphoriform, incrustrated by quartz particles, except for hyaline collar with ~ 7 ellipsoidal windows. Cell in extended state ~ 55 × 18 µm, attached to bottom of lorica by ~ 7 µm long stalk; in protargol preparations, specimens usually contracted and only 34 × 21 µm in size. Nuclear apparatus composed of two ellipsoidal macronuclear nodules and usually two globular micronuclei. Somatic ciliary pattern of most complex type, viz., comprises a right, left, and lateral ciliary field as well as a monokinetidal ventral kinety, a dikinetidal dorsal kinety, and a dikinetidal posterior kinety. Oral apparatus transversely orientated at apical cell end. Adoral zone of membranelles closed, composed of ~ 18 collar membranelles and one buccal membranelle. Endoral membrane probably monostichomonad. Collar membranelles bear some striae. Tentaculoids insert at intermembranellar ridges. Oral primordium originates in subsurface pouch posterior to lateral ciliary field.
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SINGLE CELL PCR FROM LUGOL-FIXED SAMPLES FOR QUANTITATIVE MOLECULAR SCREENING

Molecular and morphological surveys on protist diversity usually yield largely different estimates and most environmental sequences can currently not be linked to known taxa. One main issue to overcome these problems is to combine quantitative molecular and morphological single-cell analysis of fixed plankton samples. So far, attempts to analyse the DNA sequence from preserved microplankton samples focussed mainly on alveolate taxa, i.e. organisms with a presumably high copy number of the 18S rRNA gene. Further, despite the presumably high copy number of the 18S rRNA gene in the (so far) investigated alveolates, the success in field samples is usually low and mostly allows for sequencing of short fragments only. Here we propose an optimised protocol combining a microscopical screening with direct single-cell PCR of protist and microalgal cells using field samples preserved with Lugol's iodine solution. In contrast to other approaches, this method allows for a direct comparison of molecular and morphological surveys: our molecular investigations are based on single cells, not on gene copy numbers as, for instance, in clone libraries.

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MONOGRAPH OF THE KAHLIELLIDAE TUFFRAU, 1979 (CILIOPHORA, HYPOTRICHA)

The Kahliellidae Tuffrau, 1979 (Trans. Am. microsc. Soc., 98, 521-528) are a moderately large group of hypotrichs (= stichotrichs). Most of the genera (*Kahliella* Corliss, *Deviata* Eigner, *Neogeneia* Eigner, *Parakahliella* Berger, Foissner & Adam, *Pseudokahliella* Berger, Foissner & Adam, *Trachelochaeta* Srámek-Husek, *Wallackia* Foissner) possibly belonging to this group have been established within the last three decades. The supposed apomorphy of the kahliellids is the preservation of parental cirri after cell division which is, unfortunately, not a very strong feature. Several kahliellids have a *Gonostomum*-like oral apparatus, indicating a close relationship of *Gonostomum* Sterki and the kahliellids. Besides the taxa mentioned above, some genera of uncertain position, for example, the recently established genus *Saudithrix* Foissner, AL-Rasheid & Berger are treated in the present monograph. The revision of the kahliellids will be the fourth part of the monograph of hypotrichs published in the series Monographiae biologicae (Springer).
The financial support of the project by the Austrian Academy of Sciences (APART, Austrian Programme for Advanced Research and Technology; Project 10940) is greatly acknowledged.

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MIXOTROPHY IN FLAGELLATES AND CILIATES – A COMPARISON BETWEEN TWO CONTRASTING SUBALPINE PONDS

Mixotrophy commonly refers to the combination of photoautotrophic and heterotrophic (phagotrophic) nutrition in a single individual and is quite common among planktonic flagellates, ciliates and other protists. The types of mixotrophy reported range from nearly pure phototrophy to nearly pure heterotrophy. Despite much existing work, little is known about the factors controlling the different nutritional modes in natural protistan communities. The aim of our study is to investigate two abiotically and biotically differing subalpine ponds near Salzburg. Abiotic parameters (temperature, conductivity, pH, saturation with oxygen, light intensity, ammonium, nitrite, nitrate, orthophosphate) as well as biotic parameters (abundance and taxonomic composition of metazooplankton, abundance of mixotrophic, heterotrophic and autotrophic flagellates, abundance and taxonomic composition of ciliates and abundance of bacteria) between both ponds are compared. In order to quantify mixotrophy, food tracer experiments employing fluorescently labelled bacteria (FLB) and natural communities from the sampling sites are conducted. We hypothesize that differences in the abiotic and biotic factors affect mixotrophic nutrition among flagellates and ciliates and can help explaining the control mechanisms for mixotrophy in natural communities.

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COLPODIDIIDS FINALLY FIND THEIR HOME IN THE NASSOPHOREA (CILIATA)

Even twenty-five years after the discovery in a grassland soil of Afghanistan, the taxonomic assignment of the ciliate genus *Colpodidium* Wilbert, 1982 is vague. Originally, based on morphology, this genus was placed in the class Colpodea. Foissner's detailed revision of the genus in 1995 found some conspicuous morphological characters that first led to the establishment of a family (Colpodidiidae Foissner 1995) and eventually to a new order (Colpodidiida Foissner et al. 2002), and the suggested assignment of *Colpodidium* (and the order Colpodidiida) to the class Nassophorea. Despite a remarkable increase in the number of species, no sequence data were available to confirm or reject either assignment. We here present 18S rDNA sequence-based phylogenetic analysis of the type species, *Colpodidium caudatum* (in vivo size 55-70x25-35 µm, with a short, slightly curved paroral membrane, 1 large adoral organelle and two posterior kineties with dikinetids anteriorly), isolated from a soil sample from Namibia, South-West Africa. Bayesian inference methods as well as evolutionary distance analyses undoubtedly confirm the assignment of *C. caudatum* to the class Nassophorea. We will analyze additional taxa to resolve the phylogeny of colpodidiids below the class-level.
Supported by grants of the DFG and FWF.

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CONCENTRATION OF FIXED PLANKTON SAMPLES VIA SETTLING: HOW LONG IS LONG ENOUGH?

Enumerating plankton cells, especially ciliates, usually requires settling samples in order to concentrate the cells. The time sufficient to settle all ciliates has, however, never been established. Therefore an improvement of this method was an important part of this work. Ciliate density was used to calculate the theoretical settling time of fixed ciliates with the Stokes equation. To determine ciliate density (g ml^{-1}) we established a density gradient centrifugation method. We found that ciliate density was in the range 1.02-1.08 g ml^{-1}. Empirical sinking rates were gathered semi-automatically with a digital camera system. The theoretical and empirical settling times were in the same range, but we recommend working with the empirical data that were more reliable: 1.7 mm min^{-1} for fixed marine (41‰) ciliate samples and 2.4 mm min^{-1} for fixed freshwater samples. With these rates settling times can be reduced up to 95% compared to old, experience derived times. Though ciliate density was significantly correlated with settling rates, there was no correlation with particle size and shape.

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WHAT ARE THE RELATIVE EFFECTS OF LITTER TYPE, TEMPERATURE AND HUMIDITY ON TESTATE AMOEBAE COMMUNITY STRUCTURE?

Testate amoeba (TA) abundance and community structure vary according to vegetation, soil, humus type, soil moisture content and temperature. However, as the causalities of these correlations are still not well understood, we initiated two complementary studies: 1) A descriptive study along an altitudinal transect from lake Geneva (370m) to the Jura Mountains (1450m). 2) A mesocosm experiment. Litterbags respectively filled with sterilized oak, beech or spruce litter were placed in containers filled with a homogenized pooled humus from the different forest types. The containers are exposed to 4 combinations of temperature and moisture treatments by simulating summer average temperatures and precipitations of the two extremes of the transect. These two studies will allow us to test the following hypotheses: 1) the density, proportion of active individuals, and diversity of TA are positively correlated with moisture, and with temperature if moisture is sufficient; 2) small TA species are faster colonizers than larger ones and dominate the community under hydric stress; 3) litter type affects TA density, diversity and community structure.

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PHYLOGENETIC POSITION OF *ARISTEROSTOMA MARINUM* KAHL 1931 AND THE FAMILY CYRTOLOPHOSIDIDAE (CILIOPHORA; COLPODEA)

We isolated a very small and fragile ciliate from the Famvaren Fjord, Norway, which we morphologically and ultrastructurally identified as *Aristerostoma marinum* Kahl, 1931 (order Cyrtolophosidida Foissner, 1978, class Colpodea). The organism is obligate marine and cannot survive salinities below 17‰. To date, only a single SSU rDNA sequence of the order Cyrtolophosidida is available from GenBank (*Platyophrya vorax*). Therefore, we sequenced *Aristerostoma marinum* and performed a detailed phylogenetic analysis including all available sequences of the class Colpodea as well as representative sequences of all other ciliate (ribo)classes. The phylogenetic analyses confirm the assignment of *Aristerostoma marinum* and, thus, of the family Cyrtholophosididae, to the class Colpodea. However, in contrast to other orders within the Colpodea, the order Cyrtolophosidida seems to be polyphyletic. The SSU rDNA sequence of *Aristerostoma marinum* identified five previously unassigned environmental SSU rDNA ciliate sequences as members of the order Cyrtolophosidida.

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NEOKERONOPSIS NOV. SPEC. (CILIOPHORA, SPIROTRICHEA), A FLAGSHIP CILIATE FROM SOUTH AFRICA SUPPORTS THE CEUU HYPOTHESIS

Neokeronopsis is a monotypic genus established by Warren, Fyda & Song (2002) for *Holosticha* (*Keronopsis*) *spectabilis* Kahl, 1932, a rare limnetic stichotrichine spirotrich. The flexible body and the cirral pattern, especially the zigzagging row of midventral cirri classify *H. spectabilis* into the family Urostylidae. However, the ontogenesis of the dorsal bristle rows is as in typical oxytrichids, that is, they originate from two anlagen formed within parental rows and de novo. Thus, Warren et al. (2002) could not classify the phylogenetic position of *Neokeronopsis*, but suggested that it might be a highly derived Urostylidae. We discovered a similar, but distinct species in floodplain soil from South Africa. The 18 rDNA classifies the African species within the Oxytrichidae family, viz., near to the genus *Cyrtohymena*. The contrasting morphological and molecular classifications are reconciled by the CEUU hypothesis (Foissner et al. 2004) which suggests convergent evolution of an urostylid cirral pattern in oxytrichs. Both species are about 300 µm long and coloured by cortical granules. Thus, they are biogeographic flagships showing the restricted distribution of certain ciliate species. (Supported by the FWF and DFG)

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FUNCTIONAL RESPONSE AND SELECTIVE FEEDING OF THE FILTER FEEDING FRESHWATER CILIATE *MESERES CORLISSI*

For selective feeding in ciliates, not only geometric parameters, like food size or shape, but also qualitative parameters, such as motility, chemical and physical surface properties of the particles can play an important role.We used a clonal culture of the cosmopolitan, but rare planktonic filter-feeding oligotrich ciliate *Meseres corlissi* as test organism, to perform numerical and functional response experiments with two differently sized *Cryptomonas* sp., and one *Ochromonas* sp. strain. Each prey species was offered as single food in variable food concentrations, or two prey items in combination. Results showed that *M. corlissi* ingested both *Cryptomonas* strains well, the maximum ingestion rate, as well as the maximum growth rate was reached at a lower biomass of the bigger strain. Cell volumes and hence cellular production rates, increased with increasing food concentrations of the smaller *Cryptomonas* strain, while these parameters remained constant over a wide range of food levels with the bigger one. When *Cryptomonas* sp. and *Ochromonas* sp. were offered to the ciliate together, there was a clear positive selection for *Cryptomonas* at all food concentrations. When *Cryptomonas* was available at satiating levels, discrimination against *Ochromonas* was complete. Growth rates and production rates decreased in the presence of *Ochromonas*, in direct proportion to the concentration of *Ochromonas*.
When we offered *Ochromonas* sp. as single food, no feeding avoidance occurred, but cell volumes of the ciliates decreased rapidly, and growth of *M. corlissi* was negative.
Results of our study are in accordance with the optimal foraging theory; the ciliate is able to select the food item, which sustains its optimal growth and to discriminate against less efficient food, and the selectivity depends on the overall food supply.
Meseres corlissi is likely to possess chemosensory abilities.

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INFLUENCE OF REDOX CHANGES ON MICROBIAL EUKARYOTIC COMMUNITIES IN CONTAMINATED GROUND WATER

This study was performed in a test plant at a reference site in Leuna, Germany, designed for the treatment of anoxic groundwater contaminated with MTBE (methyl tert-butyl ether). The plant mainly functions as a passive container that allows the addition of different electron acceptors. After passing the plant the water is reinfiltrated into the aquifer. The composition of the microbial eukaryotic community was studied in three different treatment containers of this plant (untreated control, addition of H_2O_2, addition of NO_3^-). Additional samples were taken from the down-stream aquifer to assess the influence of the treatment on the eukaryotic community in the aquifer. Its molecular diversity was studied by clone libraries and T-RFLP of the 18S rRNA-genes. Clone libraries from the contaminated groundwater upstream of the reactors are dominated by anaerobic ciliates, whereas fungi and aerobic flagellates play an important role in the reactors. For the H_2O_2 and NO_3^- treatments with their high redox potentials this is not surprising. In the untreated anoxic control, however, the high number of fungal clones was unexpected. After reinfiltration into the aquifer ciliate clones become more abundant again. This finding is supported by the results of the T-RFLP analysis.

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MOLECULAR DIVERSITY OF A PROTIST MORPHOSPECIES: A COMPARISON BETWEEN RIBOSOMAL AND PROTEIN–CODING GENES

We investigated the molecular variation within a protist morphospecies in ribosomal genes (SSU rRNA gene and ITS) and in protein-coding genes (alpha-tubulin, beta-tubulin, actin). Despite strong differences regarding the absolute variation, the different genes yielded in largely similar estimates of the phylogenetic relation between the tested strains. However, distinct strains may cluster differently depending on the gene under study. A multi-gene phylogeny was more robust as compared to single-gene phylogenies.

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THE SPHAGNUM PONDS OF SIMMELRIED IN GERMANY: A BIODIVERSITY HOT-SPOT FOR MICROSCOPIC ORGANISMS

We describe 656 species of bacteria, protists, and micrometazoa occurring in the Simmelried, a three hectare-sized moorland in southern Germany. Each species is shown by an average of two colour micrographs. Further, the surface organization of most main groups is demonstrated by scanning electron micrographs. The Simmelried formed after the last ice-age, that is, about 15,000 years ago. The investigations indicate that the 656 species documented represent only two thirds of the taxa actually present. Thus, a considerable diversity accumulated over 15,000 years, emphasizing the great distribution capacity of micro-organisms. On the other hand, some common species are lacking (e.g., the ciliate *Colpidium colpoda*, the euglenid *Phacus pleuronectes*, and rotifers of the genera *Proales* and *Floscularia*) and many undescribed species were discovered. While a mass of undescribed species is comprehensible in the poorly researched amoebas, flagellates and ciliates, this is surprising in well-known groups, such as euglenids and chrysophytes. Thus, some of the undescribed species might be regional or local endemics.
The book is already out of print, but a cheap (3€) electronic version is available:
http://www.shaker.de/Online-Gesamtkatalog/Details.asp?ID=0&ISBN=3-8322-2544-7&Reihe=0

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ELIMINATION OF POTENTIAL PATHOGENS IN LABORATORY SYSTEMS BY PROTISTS

Protists are important bacterial predators and affect abundances of bacteria in many ecosystems. They are considered to play a key role in the elimination of pathogenic bacteria in constructed wetlands. However, the role of protists in the hygenisation process of waste water is not understood yet. In addition, the process depends on various physical and biological processes such as adsorption, natural die off and lysis by viruses. In the present study, the carbon cycling and the removal of ^{13}C-labelled bacteria by protists was evaluated using stable isotope probing (SIP) of ribosomal RNA. ^{13}C labelled *Escherichia coli* was applied as a model organism and added to microcosms together with isolated protists from a pilot scale constructed wetland. Experiments were performed in order to evaluate the carbon flow and the removal of pathogenic bacteria. The formation of $^{13}CO_2$ from *E. coli* cells and the incorporation of ^{13}C in protisten rRNA were analysed. ^{13}C labelled 18S rRNA was separated by density gradient centrifugation and PCR-amplified with eukaryotic primers followed by T-RFLP analysis. The results show that ^{13}C-labelled *E. coli* cells can be used to label protists from the constructed wetland and to detect a time dependence of ^{13}C incorporation in 18S rRNA.

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QUALITATIVE AND QUANTITATIVE ANALYSIS OF VARIABLE SURFACE ANTIGEN RNA SPECIES IN *PARAMECIUM TETRAURELIA*

Variable surface antigens (SAgs) of *Paramecium* are expressed in a mutually exclusive way leading to only one protein type on the surface. Regulation of the expression status within this multigene family is determined by multiple factors including transcriptional and posttranscriptional mechanisms. A putative regulatory candidate for this serotype determination is RNA. For example, the emergence of protein during a serotype shift is determined posttranscriptionally by mRNA. Moreover, different RNA species, such as anti-sense transcripts, can hold regulatory functions. We present preliminary results on the analysis of SAg RNA using highly sensitive PCR methods. A quantitative real-time RT-PCR study on steady-state mRNA level of different serotypes delivered insight in the serotype-specific mRNA abundances. This revealed the existence of significant amounts of non-serotype SAg transcripts. Furthermore, we established strand-specific transcript detection in *Paramecium* using RT-PCR. We confirmed that reverse transcription of RNA is falsified by unspecific, primer-independent cDNA synthesis on standard RT conditions. Modification of RT conditions resulted in a clear reduction of this effect, enabling specific analysis of RNA for low abundant anti-sense transcripts.

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EXPERIMENTELLE UNTERSUCHUNGEN ZUR BEDEUTUNG VON SOMMER- UND WINTERERWÄRMUNG AUF BIOFILMASSOZIIERTE CILIATENGEMEINSCHAFTEN IM RHEIN.

Jüngste Klimamodelle bestätigen, dass die stärksten Auswirkungen globaler Erwärmung für die jeweils kältesten und wärmsten Monate eines Jahres zu erwarten sind. Mit dem Fokus auf diese Perioden untersuchten wir die Bedeutung lokaler Temperaturerhöhungen für die Entwicklung früher sowie später biofilmassoziierter Ciliatengemeinschaften im Rhein. In Fließzellenexperimenten (frühe Sukzession) wurden neben einer Kontrolle (mittlere Rheintemperatur) im Januar und August 2006 jeweils drei weitere Temperaturmanipulationen bis maximal +6°C bzw. +9°C über Rheintemperatur durchgeführt. Der dritte vorgestellte Versuch beschäftigte sich mit der Bedeutung experimenteller Erwärmung (Kontrolle, +3°C) für ältere Ciliatengemeinschaften, die über mehrere Monate in Rheinwasser gespeisten Fließrinnen kultiviert wurden. Es ließ sich eine geringfügige Zunahme der Sukzessionsgeschwindigkeit zeigen, während die Kapazität der Biofilme für Ciliaten häufig geringfügig abnahm. Des Weiteren zeigten sich einige tendenzielle Unterschiede in der taxonomischen Struktur der untersuchten Gemeinschaften. Insgesamt deuten unsere Ergebnisse eine erstaunliche Unempfindlichkeit der seminatürlichen Ciliatengemeinschaften gegenüber Erwärmung an.

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MOLECULAR AND ECOPHYSIOLOGICAL MICRODIVERSITY WITHIN A FLAGELLATE SPECIES

The molecular diversity of protists and its ecophysiological significance is largely unknown. To assess the ecophysiological microdiversity, tolerance of 54 (globally distributed) and 27 (locally isolated) monoclonal strains of the *Spumella* morphotype (Chrysomonadida) to salinity, pH and temperature was measured and subsequently correlated to genetic distances. Our results suggest that the morphospecies concept is inappropriate to reflect ecological differentiation in protists. Overall genotypic variation is neutral with respect to pH but highly meaningful with respect to temperature and salinity. We conclude that the phylogenetic resolution of the rRNA gene is suitable to detect differences in variation of some ecophysiological parameters, but for some parameters additional marker genes with higher resolution power should generally be included in future studies.

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COLONIZATION DYNAMICS OF CILIATES IN FIELD AND FLOW CHANNELS

In hydrodynamically fluctuating ecosystems biofilm associated ciliates are protected against the drift. Two hypotheses were tested: I) At slow flow conditions the colonization of exposed surfaces by ciliates gets faster, and the abundance, and species number is higher. II) The morphological features of ciliates such as stalks (Peritrichia) and cell flattening (Phyllopharyngia) are adaptations to fast flow conditions. For biofilm development glass slides (field) and clay tiles (flow channels) were exposed for 1 to 336 h at flow velocities of 0.05 to 0.8 m s^{-1}. Initial biofilms are more rapidly colonized at slow flow condi-tions with 2 to 740 times higher abundances. Phyllopharyngia (thigmotactic) dominated the community at the fast flowing stream site and at 0.4 m s^{-1} in flow channels. Peritrichia, which can stand high velocities, were more important in the 0.05 m s^{-1} treatment. A small Hymenostomatia, *Uronema nigricans* (round body shape), was significantly lower abundant at the fast flowing stream site but made up to 48 % of the flow channel community at fast flow conditions. The results show that higher flow velocities cause a delay in ciliate colonization dynamics and a shift in the taxonomic composition.

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LANGFRISTIGE ENTWICKLUNG DER CILIATENFAUNA IM PELAGIAL DES RHEINS

In der vorliegenden Studie wurde die Ciliatenfauna im Plankton des Rheins in einer langfristigen Untersuchung (2000 bis 2005) betrachtet. Dabei lag der Fokus v.a. auf Faktoren, die sich in einer früheren Studie als wichtige Steuerungsmechanismen der Ciliatenabundanz herausgestellt hatten. Dies war zum Einen der Fraß benthischer Prädatoren, der v.a. während Niedrigwasserphasen durch geringe Ciliatenabundanzen erkennbar wurde, und zum Anderen die Verdriftung benthischer Ciliaten zu Beginn von Hochwasserereignissen, die sich in einem Peak benthischer Ciliaten zu Beginn der Hochwässer widerspiegelte.
Es zeigte sich eine deutliche, langfristige Veränderung der Zusammensetzung der Ciliatenfauna im Pelagial des Rheins, die auf die Notwendigkeit langjähriger Untersuchungen hinweist, um mögliche Steuerungsmechanismen des Potamoplanktons zu analysieren.

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REDESCRIPTION OF *EUPLOTES TRISULCATUS* KAHL, 1932 (CILIOPHORA, HYPOTRICHIDA) FROM THE ANOXIC FRAMVAREN FJORD (SOUTH-WEST NORWAY)

A *Euplotes* species has been isolated from below the oxic-anoxic interface of the Norwegian Framvaren Fjord. Based on its morphology it has been identified as *Euplotes trisulcatus* Kahl, 1932. Here we give a short redescription of its morphology based on standard methods, scanning electron microscopy, and a review of the literature. Additionally we were able to show that the population from Framvaren Fjord possesses as yet unidentified bacterial endocytobionts. This particular finding shows that in genus *Euplotes* endosymbionts are still far more distributed than expected. *Euplotes trisulcatus* is a small to medium sized, obligate marine form. Its most characteristic morphological features are the three deep dorsal furrows and four wide dorsal ridges that are best seen in vivo and mostly become inconspicuous if fixed. The species feeds on bacteria and small flagellates.

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HOMALOGASTRA SETOSA KAHL, 1926: A TRUE COSMOPOLITE?

The scuticociliate *Homalogastra setosa* Kahl 1926 (Ciliophora, Oligohymenphora) is one of the most frequently found soil ciliates. Originally isolated and described as part of the moss fauna, it was later reported from many different types of soil - from the tropics to the high Arctic. However, thus far, no marine representative has been reported. Recently, we succeeded to isolate a scuticociliate from anoxic sediments of the Gotland Deep in the Baltic Sea. Based on morphology and ultrastructure we identified the species as *Homalogastra setosa* Kahl 1926. In ecophysiological experiments we evaluated the fundamental ecological niche of the *H. setosa* Gotland population. Its habitat preferences reflect the ambient environmental conditions in the bottom water of the Gotland deep. Based on these results we argue that *H. setosa* may not only be a true cosmopolite, but also one of the few ciliate species that conquered both terrestrial and aquatic ecosystems. Interestingly, phylogenetic analyses do not assign *Homalogastra* to the uronemtids, but rather display the species as an independent lineage in the scuticiliatia.

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INSIGHTS INTO MACRONUCLEUS EVOLUTION WITHIN THE GENUS *STENTOR* (CILIOPHORA, HETEROTRICHEA) REVEALED FROM RDNA SEQUENCES

One of the main characteristics of ciliates is the nuclear dimorphism. For species determination, number and shape of the nuclei (macro- and micronucleus) are of particular importance.
For the genus *Stentor* four different types of macronuclei are described: single beaded, vermiform, nodular, and moniliform. To test our hypothesis that the macronucleus evolution proceeded from the single beaded state to the moniliform state, we analysed ribosomal DNA sequences from eight species of this genus, which represent three different macronuclei types. The phylogenetic analyses indicate that a single beaded macronucleus might represent the ancestral state within the genus *Stentor*, because all species with an elongated macronucleus (vermiform as well as moniliform) group constantly together. Furthermore, our analyses suggest the occurrence of unidentified species complexes within the genus *Stentor*.

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INVESTIGATIONS ON CLONAL CULTURES OF ARCELLA SPECIES

There has been a flurry of investigations in the past 10 years that specifically address the evolutionary placement of different rhizopod lineages. In order to place *Arcella*, one of the key testate amoeba genera, on the phylogenetic tree and study both inter- and intraspecific polymorphism, I established clonal cultures of a variety of *Arcella* species. Clones have been kept in one certain mineral water (without addition of any external compounds) and grown on added bacteria. After one year of work, I am now fortunate to have eight different pure cultures and also axenic (regarding eukaryotes) cultures for applying molecular techniques. In the present study I show the morphological and biometric characterisation of the cultured species and introduce the preliminary results on their SSU rDNA sequence studies.

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THE IMPACT OF A DEPTH GRADIENT ON THE MICROEUKARYOTES IN THE FRAMVAREN FJORD (NORWAY)

The diversity of microeukaryotes from extreme marine environments, such as the Framvaren Fjord in Southern Norway (with sulfide levels in the bottom water 25 times greater than in the Black Sea), is largely unknown. The aim of this study was to investigate the natural abundance of bacteria and flagellates and the grazing impact of the flagellates on bacteria over a depth gradient with changing abiotic conditions. To this end, *in-situ* grazing experiments in the oxic layer (9 metres), the anoxic zone (22 m) and at the oxic/anoxic interface (20 m) were conducted. In addition, bacteria and flagellates were enumerated and differences in their vertical distribution, possibly related to the chemical environment, were recorded. Using FISH we aimed to find out whether the flagellate *Actuariola framvarensis* (isolated from Framvaren Fjord, Stoeck et al. 2005) plays a major role as bacterivore in the microbial food web in the Framvaren Fjord.

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CHANGES IN THE ANTARCTIC CILIATE COMMUNITY THROUGH TIME, SPACE, AND PREDATION

Ciliate communities are affected by biotic and abiotic factors, which have the potential to strongly alter the community composition. To evaluate the impact of environmental factors on ciliates, profile samples (surface - 500 m) were taken in the Bellingshausen and Amundsen Sea along two transects during the ANT XXIII-4 cruise of the German RV "Polarstern". The cruise was from February to April 2006. This period was characterized by declining rates of primary production. Transects lead from the coastal shelf to the open deep sea. Additionally, experiments were conducted manipulating grazing pressure with three different types of predators which might change the community structure and abundance (either the furcilia larva of *Euphausia superba, Oithona similis* or a calanoid copepod).

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FRÜHE BIOFILMBESIEDLUNG DURCH HETEROTROPHE FLAGELLATEN - REGULATION UND EFFEKTE

Parallel zur Bildung eines bakteriellen Biofilms gehören heterotrophe Flagellaten (HF) zu dessen ersten eukaryotischen Besiedlern. HF bilden in der weiteren Sukzession des Biofilms einen trophischen Link zu den Ciliaten und Metazoen. Hier wurde in einem gewässerangebundenen Fließzellensystem auf der Ökologischen Rheinstation der Universität zu Köln die Kontrolle von HF in der frühen Biofilmbesiedlung sowie deren Effekte auf Biofilmbakterien untersucht. Dazu wurden die Zuläufe des Rheinwassers größenfraktioniert, um so selektiv HF (1,2 µm Porendurchmesser), Ciliaten (5 µm) und Metazoen (20 µm) auszuschließen. Erste Ergebnisse zeigen, dass Bakterien in Anwesenheit von HF zu Substratbesiedlung und Mikrokoloniebildung stimuliert werden. Die Regulation der HF selber über ressourcenabhängige Besiedlungsprozesse und Anwesenheit von Ciliaten wird ebenfalls auf dem Poster dargestellt.

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INSIGHTS INTO THE BIOGEOGRAPHY OF THE UNCULTURED MARINE ALVEOLATE GROUP I (UMA I)

Sequencing of 18S rRNA genes amplified from environmental genomic DNA discovered a tremendous diversity of novel eukaryote lineages, most of which belong to the stramenopiles and the alveolates. One major clade without cellular identity within the latter is the enigmatic 'Uncultured Marine Alveolate Group I' (UMA I). Since its first discovery in 2001 in the depths of the Antarctic Ocean sequences of UMA I have been retrieved from several different biogeographic regions, suggesting a ubiquitous dispersal throughout our oceans. On the other hand, a lack of UMA I sequences in many environmental 18S rDNA surveys suggests a restriction to specific geographic regions and/or environments. The goals of our study were twofold: First, we specifically targeted UMA I sequences in circa 20 environmental samples using a newly designed UMA I PCR-primer set to evaluate the occurrence of UMA I in a variety of different geographic regions and/or environments. Second, we performed phylogenetic analyses with our data together with UMA I sequences deposited in GeneBank to identify biogeographic and/or habitat-specific sequence clades within UMA I. We here discuss our current knowledge of the biogeography and the phylogenetic diversity of the UMA I clade.

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