

**A FORGOTTEN SYNAPOMORPHY IN TINTINNID CILIATES
(CILIOPHORA, SPIROTRICHA, TINTINNINA):
A LIGHT AND SCANNING ELECTRON MICROSCOPIC STUDY
OF THE CLOSING APPARATUS**

Sabine Agatha

Department of Organismic Biology, University of Salzburg, Hellbrunnerstrasse 34, A-5020
Salzburg, Austria

E-mail: sabine.agatha@sbg.ac.at (Sabine Agatha)

Abstract

A membranous closing apparatus shuts the lorica opening in disturbed tintinnids of six genera belonging to four families. The homology of the closing apparatuses is investigated, using data from the literature and Mediterranean tintinnids studied *in vivo* and in the scanning electron microscope. For the first time, this curious structure is demonstrated in great detail by line drawings and micrographs. The morphological and functional similarities indicate that the foldable closing apparatus is not only a synapomorphy of the genera *Codonella* (Codonellidae) and *Dictyocysta* (Dictyocystidae), as already suggested eighty years ago, but also of *Codonaria* (Codonellidae) and *Codonellopsis* (Codonellopsidae). In *Codonaria*, *Codonella*, and *Dictyocysta*, the apparatuses represent the anterior portions of membranous sacs lining the lorica bowls; the term "lorica sac" is introduced for these probably homologous envelopes. The close relationship of the genera *Codonella*, *Codonellopsis*, and *Dictyocysta* is also inferred from sequence analyses of the SSrRNA gene and the ultrastructure of the capsules. It contradicts the exclusively lorica-based current classification of the tintinnid ciliates. Since the closing apparatuses in *Salpingacantha* and *Salpingella* (Tintinnidae) differ in their morphology from those in the genera mentioned above (diaphragm-like vs. with triangular folds), a homology of the structures seems unlikely. This assumption is corroborated by the different orientation of the adoral zone of membranelles in contracted specimens (oblique vs. perpendicular to the main cell axis) and the position of *Salpingella* in the SSrRNA phylogenies.

The study was supported by the Austrian Science Foundation (FWF; Project P20461-B17).

Key words: classification, lorica sac, morphology, phylogeny, taxonomy, ultrastructure

**APOGASTROSTYLA RIGESCENS (KAHL, 1932) NOV. GEN., NOV. COMB.‡
(CILIOPHORA: HYPOTRICHIA): MORPHOLOGY, NOTES ON CELL
DIVISION, SSU rRNA GENE SEQUENCE DATA, AND NEOTYPIFICATION**

**Helmut Berger^{1,*}, Liqiong Li², Jie Huang²,
Mann Kyoon Shin³, Weibo Song², Khaled A. S. AL-Rhasheid⁴**

¹ Consulting Engineering Office for Ecology, Radetzkystr. 10, 5020 Salzburg, Austria

² Laboratory of Protozoology, Ocean University of China, Qingdao 266003, China

³ Department of Biology, University of Ulsan, Ulsan 680-749, Korea

⁴ Zoology Department, College of Science, King Saud University, Riyadh 11451, Saudi Arabia

* E-mail corresponding author: office@protozoology.com (Helmut Berger)

Abstract

The morphology, the infraciliature, some ontogenetic stages, and the SSU rRNA gene sequence of the little-known marine 18-cirri hypotrich *Tachysoma rigescens* (Kahl, 1932) Borror, 1972 [basionym *Oxytricha (Tachysoma) rigescens*], isolated from mariculture waters near Qingdao, China, were investigated. The species is characterised, inter alia, by narrowly spaced, small, colourless cortical granules and several ring-shaped structures in the cytoplasm. The caudal cirri and the simple dorsal kinety pattern (3 bipolar kineties) obviously taken over from the ground pattern of the Hypotricha, the composition of the adoral zone of the proter from new and parental membranelles, as well as the presence of two 'extra' cirri behind the rear end of the right marginal row strongly suggest a misclassification in *Tachysoma*. The SSU rRNA gene sequence data indicate that *T. rigescens* branches off very early in the Hypotricha tree, which supports the hypothesis that the 18-cirri pattern occurred probably already in the last common ancestor of the Hypotricha. A detailed survey of the early branching 18-cirri hypotrichs and similar taxa reveals that for *T. rigescens* a new genus has to be established, *Apogastrostyla* nov. gen.‡, because there are, inter alia, important differences in the dorsal infraciliature. Besides the type species, *A. rigescens* nov. comb.‡, which seems to be confined to the northern hemisphere, a second marine species, *A. szaboi* nov. comb.‡ (basionym *Hemigastrostyla szaboi*) can be included. Since no type material of *A. rigescens*‡ is available and the type locality is not known the Chinese population is fixed as neotype. Funded by the Austrian Science Fund (FWF; Project P20569-B17; H. Berger), the Natural Science Foundation of China (project numbers: 30870264, 40906065); and the Center of Excellence in Biodiversity, King Saud University (111 Project [No. B08049]). ‡ This name is disclaimed for nomenclatural purposes (ICZN 1999, Article 8.3).

Key words: cell division, infraciliature, ontogenesis, phylogeny, Spirotricha, taxonomy

PROTOZOA IN THE RHIZOSPHERE OF PLANTS

Michael Bonkowski

Universität zu Köln, Zoological Institute, Dept. Terrestrial Ecology,
Otto-Fischer Str. 6, 50674 Köln, Germany

bonkowski@rhizosphere.de

Abstract

Although protozoa are the primary consumers of bacteria in soil, the consequences of protozoan predation for the composition and functioning of bacterial communities are poorly understood. Since protozoan predation on bacteria peaks in the rhizosphere of plants, the frequently observed beneficial effects of protozoa on plant growth are generally accounted for the release of nutrients from consumed bacterial biomass, i.e. the 'microbial loop in soil'.

However, this interplay over three trophic levels in the plant rhizosphere, i.e. between plants via exudates, bacteria and protozoa is much more complex than previously assumed. Strong feeding preferences of protozoa paired with high consumption rates are rapidly shifting diversity, metabolism and function of rhizosphere bacterial communities thereby modifying bacteria-plant interactions. Plant physiology, gene expression, hormonal balances, the architecture of the root system, shoot development and plant biomass are strongly altered. Most remarkably, protozoa and mycorrhizal fungi strongly interact by exerting contrasting effects on root growth and nutrient allocation. Because the regulation of root architecture is a key determinant of nutrient- and water-use efficiency in plants, our data show that microbial grazers significantly shape microbial interactions in the rhizosphere, and can not be ignored if we want to achieve a mechanistic understanding of rhizosphere processes.

Keywords: Acanthamoeba, Arabidopsis, root growth, diversity of bacteria

CERCOZOAN DIVERSITY AND PHYLOGENY: A MORPHOLOGICAL AND MOLECULAR SURVEY OF SOIL EXTRACTED CERCOZOANS

Marian Brabender, Anne Domonell, Frank Nitsche, Hartmut Arndt

University of Cologne, Biowissenschaftliches Zentrum, Zoological Institute, Dept. General Ecology and Limnology, Otto-Fischer-Str. 6, 50674 Cologne, Germany

**E-mail corresponding author:* marian.brabender@uni-koeln.de (Marian Brabender)

Abstract

Cercozoans are among the most common and abundant protozoans in soil and freshwater ecosystems. These biflagellate and bacterivorous protists are of enormous diversity and comprise high numbers of cryptic species among others because of their metabolic body structure. By combining morphological and genetical investigations we contribute to the continuously enlarging but still fragmentary gene bank data base and higher resolution of cercozoan taxonomy. Modified liquid aliquot methods revealed tremendous numbers of cercozoans and highlighted this group to form approximately 60% of the cultivable protozoan community. All our cultures were established from grassland or woodland soils sampled in eastern Germany. We present ITS2 and 18S rDNA based phylogenetic trees and potential new taxa detected by their DNA sequences differing unambiguously from already established data bases or by yet unknown morphological characters. One extraordinary four-flagellated cercozoan will be described in more detail.

Key words: Cercozoa, Phylogeny, ITS2, Soil protozoa, cryptic species, 18S rDNA

MICROFAUNA DIVERSITY IN SOIL SYSTEMS, FOCUSED ON DIFFERENCES BETWEEN GRASSLAND AND WOODLAND SITES

Anne Domonell, Marian Brabender, Frank Nitsche, Hartmut Arndt

University of Cologne, Biowissenschaftliches Zentrum, Zoological Institute, Dept. General Ecology and Limnology, Otto-Fischer-Str. 6, 50674 Cologne, Germany

*E-mail corresponding author: anne.domonell@uni-koeln.de (Anne Domonell)

Abstract

Research on soil microbiota is one of the frontiers in biodiversity research. These tiny organisms contribute significantly to mineralization processes and key ecosystem functions. Understanding of their biodiversity and fundamental functions are essential for the understanding of the whole ecosystem processes. There is a lack of adequate data on protozoan numbers and their taxonomical structure. This work was focused on community structures of cultivable heterotrophic nanoflagellates (HNF) comparing different grassland and woodland sites. 14 flagellate and 5 amoebae morphotypes were distinguished by light microscopy. Protozoan abundances were tremendous and ranged between 1.3 and 7.0 *10⁷ individuals per g fresh soil. Grassland sites showed higher abundances than woodland sites with surprisingly similar communities all over the different sites.

Key words: biodiversity, soil, protozoans, community structure, liquid aliquot method, HNF

USING TWO INDEPENDENT MOLECULAR MARKERS TO ASSESS PHYLOGENETIC RELATIONSHIPS OF NEW COLPODEA ISOLATES

**Micah Dunthorn, Julia Klier, Hans-Werner Breiner, Wilhelm Foissner,
Thorsten Stoeck**

University of Kaiserslautern, Department of Ecology, Kaiserslautern, Germany

Abstract

Gene trees not reflecting the actual species tree is a common occurrence in molecular systematics. Because of this potential problem in ciliates, we do not necessarily know if analyses based on just the nuclear SSU-rDNA locus are providing accurate inferences of phylogenetic relationships. Here we sample more taxa within the Colpodea using both the nuclear as well as the mitochondrial SSU-rDNA loci. With the increased taxon sampling we are able to more accurately test this mitochondrial marker's efficacy in resolving more shallow ciliate relationship. Furthermore, we suggest possible scenarios of morphological evolution in light of the molecular data.

ANALYZING FOOD WEB INTERACTIONS WITHIN SEMI-NATURAL BIOFILMS WITH THE HELP OF VIDEO MICROSCOPY

Martina Erken*, Nicole Farrenschon, Sophia Speckmann,
Hartmut Arndt and Markus Weitere

University of Cologne, General Ecology, Otto-Fischer-Straße 6, 50674 Köln, Germany

* Corresponding author: martina.erken@gmail.de

Abstract

Protozoan grazing is considered one of the major mortality factors for bacteria in the natural environment and one of the oldest predator prey interactions. Most data addressing these interactions were gained from experiments with planktonic organisms, whereas food web interactions within surface-associated communities (so called biofilms) are as yet poorly investigated. Here we applied video microscopy to analyze the effects of heterotrophic flagellates on bacteria within biofilms established under semi-natural conditions in river bypass systems. We could quantify grazing rates of heterotrophic flagellate and could demonstrate that benthic flagellates generally ingest surface associates bacteria (single cells) without size preference. However, the flagellates showed a selection against bacteria within microcolonies. These observations provided direct evidence, that bacterial microcolony formation is a protection against protozoan grazing. We could also demonstrate the existence of considerable differences in the grazing strategies between different flagellate species. Furthermore, videomicroscopic analyses of time series showed gardening effects around sessile protists probably due to nutrient recycling. Our new approach to apply videomicroscopy for analyzing interactions within semi-natural biofilms offers new insights into the complex processes within biofilm food webs.

Key words: biofilms, heterotrophic flagellates, grazing, predation, ingestion rates, grazing resistance, flow cells, video microscopy

EFFEKT VON SEDIMENTUMLAGERUNGEN AUF CILIATEN DES HYPORHEISCHEN INTERSTITIALS

Katja Felsmann, Ute Risse-Buhl & Michael Mutz

Lehrstuhl Gewässerschutz, Brandenburgisch Technische Universität Cottbus, Seestraße 45,
D-15526 Bad Saarow, Deutschland

E-mail corresponding author: steinfrau@arcor.de (Katja Felsmann)

Abstract

Übermäßiger Eintrag von Feinsand ist eine der Hauptbelastungen von Fließgewässern weltweit. Bereits geringe Fließgeschwindigkeiten verursachen die Umlagerung dieser sandigen Sedimente. In Transportkörpern wie Sandriffel kommt es zu periodischem Rollen der Sedimentkörner. Wohingegen bei Hochwasserereignissen die Sedimentkörner kontinuierlich in Bewegung gehalten werden. In Mikrokosmen wurde der Einfluss periodischer und kontinuierlicher Sedimentumlagerung auf eine Modellciliatengemeinschaft untersucht. Der vagile *Dexiostoma campylum* vermehrte sich nur in Sedimenten ohne Umlagerungsprozesse. Bei periodischem Rollen der Sedimentkörner war die Abundanz von *D. campylum* nach 1 h bereits um 50 % reduziert. Der dorso-ventral abgeflachte *Chilodonella uncinata* erreichte bei periodisch rollenden Sedimentkörnern die maximale Abundanz und die höchsten Wachstumsraten. Im Gegensatz zu stabilen Sedimenten (Kontrolle) und periodischer Sedimentumlagerung war die Abundanz aller Ciliatenmorphotypen bei kontinuierlicher Sedimentumlagerung am niedrigsten. Nachdem der sessile *Vorticella convallaria* 1 h kontinuierlicher Sedimentumlagerung ausgesetzt war, befanden sich im Vergleich zum Startwert 50 % weniger Individuen im Sediment. Dennoch erzielten im weiteren Verlauf des Experimentes *V. convallaria* und *C. uncinata* positive Wachstumsraten. Unsere Ergebnisse zeigen, dass Sedimentumlagerungen, häufig auch intensiviert durch Versandung der Gewässer, die Struktur der Ciliatengemeinschaft im hyporheischen Interstitial beeinflussen.

Key words: hyporheisches Interstitial, sandige Sedimente, Sedimentumlagerung, Ciliaten

Biogeographische Barrieren für die Ausbreitung von Ciliaten

Dominik Forster, Thorsten Stoeck

Technische Universität Kaiserslautern, Abt. Ökologie, D-67663 Kaiserslautern

Abstract

Die phylogenetische Analyse von 18S rDNA Sequenzen, gewonnen aus Umweltproben, ist ein etabliertes Verfahren zur Erfassung mikrobieller Biodiversität. Die in den vergangenen Jahren gewonnen Sequenzinformationen dienen in unserer Studie dazu, biogeographischen Verbreitungsbarrieren von Ciliaten zu untersuchen. Dabei wurden in Datenbanken verfügbare Ciliaten-Sequenzen verschiedener Standorte an Hand mehrerer Kriterien untersucht. Wir konnten durch den Vergleich von Ciliatengemeinschaften anoxischer und oxischer Habitate das Vorkommen von Sauerstoff als eine biogeographische Barriere identifizieren. Weiterhin erhielten wir Hinweise darauf, dass die prähistorische Trennung der Urkontinente Gondwana und Laurasia ebenfalls zur Strukturierung heutiger Biodiversitätsmuster von Ciliatengemeinschaften beiträgt. Keine Effekte auf biogeographische Barrieren konnten hingegen für klimatische Faktoren oder Habitattypfaktoren (Wasser vs. Sedimente) nachgewiesen werden.

The hydrogen-producing mitochondria of *Nyctotherus ovalis*

J.H.P. Hackstein¹, RM de Graaf¹, G. Ricard², MA Huynen², AGM Tielens^{3,4}

¹IWWR, Radboud University Nijmegen; ²CMBI Radboud University Nijmegen; ³University of Utrecht; ⁴Erasmus University Rotterdam

Abstract

It is generally accepted that hydrogenosomes, double membrane bounded organelles that produce hydrogen and ATP, evolved from a mitochondrial ancestor. However, until recently, only indirect evidence for this hypothesis was available because typical hydrogenosomes do neither possess a genome nor an electron transport chain.

Here we show that the hydrogenosomes of *Nyctotherus ovalis* possess a mitochondrial genome of a size of more than 48 Kb, of which approximately 42 Kb have been sequenced. This organellar genome is comparable with the mitochondrial genomes of aerobic ciliates, but the number of genes with known functions is reduced. Notably, there is no evidence for genes encoding components of mitochondrial Complex III, IV and V.

The analysis of more than 9.000 gDNA and cDNA sequences, and the gene content of the hydrogenosomal genome allowed a preliminary reconstruction of the organellar metabolism on the basis of 94 "mitochondrial" genes. The data reveal that *N. ovalis* possesses hydrogen producing mitochondria that have a truncated, two step (Complex I and II) respiratory chain, which uses fumarate as electron acceptor. In addition, components of an extensive protein network for the metabolism of amino-acids, defense against oxidative stress, mitochondrial protein synthesis, mitochondrial protein import and processing, and transport of metabolites across the mitochondrial membrane were identified. In addition, we found several genes obtained by horizontal gene transfer that are involved in the metabolism of the hydrogenosome. Thus, the hydrogenosomes of *N. ovalis* are not simply rudimentary organelles but specialized hydrogen producing mitochondria of high complexity.

**“CENTRE OF EXCELLENCE FOR DINOPHYTE TAXONOMY” (CEDIT) AM
DEUTSCHEN ZENTRUM FÜR MARINE BIODIVERSITÄTSFORSCHUNG
(DZMB)**

Mona Hoppenrath

Forschungsinstitut Senckenberg, DZMB, Wilhelmshaven

Abstract

Rezente Dinoflagellaten stehen im Zentrum verschiedener Forschungsbereiche. In marinen Ökosystemen stellen sie einen beachtlichen Anteil der Biodiversität und sie tragen signifikant zur Primärproduktion bei, aber auch zum sekundären Konsum. Viele toxische oder auf andere Weise schädliche Protisten gehören zu den Dinoflagellaten.

Das taxonomische Wissen über lebende Dinoflagellaten ist kärglich und weltweit auf wenige Spezialisten beschränkt. Trotzdem wurden über die letzten Jahrzehnte hinweg viele neue Dinoflagellaten-Taxa beschrieben. Die letzte weltweite Dinoflagellatenartenrevision wurde 1937 publiziert. Seitdem haben sich viele Art- und Gattungs-Charakterisierungen geändert oder wurden emendiert. Jede taxonomische Arbeit fängt mit der Originalbeschreibung der Taxa an, welche oft über verschiedenste europäische Zeitschriften des neunzehnten Jahrhunderts verteilt sind – für viele Wissenschaftler schwer erreichbar oder gar nicht verfügbar.

Das Zentrum wird komplette Listen aller beschriebener rezenter Dinoflagellaten-Gattungen und -Arten mit exakten bibliographischen Daten online zur Verfügung stellen. Zusätzlich sollen alle Originalbeschreibungen als pdf-Dateien bereitgestellt werden. Neben der elektronischen Bereitstellung dieser Hauptdaten wird angestrebt, auch Informationen über Dinoflagellaten von allgemeinem Interesse für die Forschergemeinde verfügbar zu machen, z.B. wichtige „Links“ oder Fotos. In der Zukunft wird eine Hauptaufgabe darin bestehen fixiertes Referenzmaterial (von Massenentwicklungen oder Kulturen) zu archivieren.

Das Zentrum wurde 2005 gegründet und befindet sich im Aufbau. Aktive Beiträge von potentiellen Nutzern durch Diskussionen, konstruktive Kritik, Bereitstellung von Daten und Probenmaterial sind sehr willkommen und sollen durch diesen Vortrag angeregt werden.

**THE GENUS *PARVILUCIFERA* (ALVEOLATA, MYZOOA) -
ULTRASTRUCTURE AND MOLECULAR PHYLOGENY OF TWO RECENTLY
DESCRIBED NEW SPECIES, THAT ARE INTRACELLULAR PARASITES OF
DINOFLLAGELLATES.**

Mona Hoppenrath^{1,3}, Esther Garcés² & Brian S. Leander³

¹ Forschungsinstitut Senckenberg, DZMB, Wilhelmshaven, Germany

² Departament de Biologia Marina i Oceanografia, Institut de Ciències del Mar,
CSIC, Barcelona, Spain

³ Departments of Botany and Zoology, University of British Columbia, Vancouver, Canada

Abstract

The marine parasitic genus *Parvilucifera* was described using morphological and molecular data with the type species *P. infectans* Norén et Moestrup 1999. For all the years it was the only known species of the genus. Most recently, however, two new species were described. The intracellular development and ultrastructure of the parasites that infect marine dinoflagellates will be characterized. One species, *P. sinerae* Figueroa et Garcés 2008, is morphologically very similar to the type species of the genus, and the second species, *P. prorocentri* Leander et Hoppenrath 2008, possesses a combination of features described for perkinsids and syndineans, and also novel characters. Molecular sequence data (SSU rDNA) supported the classification suggested by the morphologies. Comparison of these data with other myzozoans enabled us to build a hypothetical framework for understanding character evolution during the earliest stages of perkinsid and dinoflagellate evolution.

This talk will be given in German.

DIVERSITY OF AMOEBOZOA IN DEEP-SEA SAMPLES FROM THE WESTERN ATLANTIC – A PRELIMINARY REPORT

Alexander Kudryavtsev^{1,2,3}, Jan Pawlowski², Klaus Hausmann¹

¹ Research Group Protozoology, Institute of Biology/Zoology, Free University of Berlin, Königin-Luise-Str. 1-3, D-14195 Berlin, Germany

² Molecular Systematics Group, Department of Zoology and Animal Biology, University of Geneva, 30 quai Ernest Ansermet, CH-1211 Geneva, Switzerland

³ Department of Invertebrate Zoology, Faculty of Biology and Soil Science, St-Petersburg State University, Universitetskaja nab. 7/9 199034 St-Petersburg, Russia

E-mail corresponding author: gocevia@gmail.com (Alexander Kudryavtsev)

Abstract

About 20 strains of marine amoebozoans have been isolated from deep-sea sediment samples (ca. 3800-5200 m deep) collected from the Argentine and Brasil abyssal plains (western Atlantic) during the cruise M79/1 of the German research vessel Meteor in July-August 2009. Out of them, 16 could be brought into a stable prolonged culture allowing an extensive study and identification using morphological and molecular genetic tools. Most of these strains (11) belong to the family Vannellidae and comprise four morphospecies (several morphospecies were represented by multiple strains isolated from different samples). Other species belong to the Dactylopodida, Cochliopodiidae and Variosea. Most of the species found are new. Comparison of the vannellid strains using morphological and molecular genetic markers (nuclear small-subunit ribosomal RNA and mitochondrial cytochrome C oxidase genes) allows further discussion of the problem of polymorphism, genetic structure and distribution patterns of amoebae morphospecies. This study has been supported by the DFG grant HA 818/22-1.

Key words: Amoebozoa, deep-sea sediments, morphology, ultrastructure, molecular phylogeny, species identification

PARASITOLOGY AND TROPICAL MEDICINE- WHY TODAY IN TIMES OF GLOBALIZATION AND GLOBAL WARMING?

Heinz Mehlhorn

Institute of Zoomorphology, Cytology and Parasitology, University of Düsseldorf,
D-40225 Düsseldorf, Germany

E-mail corresponding author: mehlhorn@uni-duesseldorf.de

Abstract

Globalization and global warming are two important phenomena of the presence, although they are often misused by many politicians and also (!) by scientists for fund raising to support dubious projects of various kinds. However, it is fact that the mean yearly temperatures increase since at least 15,000 years, when the last "little ice age" had ended and when walks to England had been possible. On the other hand the increase of temperature was rather slow – even today – so that the animals, plants and also humans had enough time to adapt to the changing environmental conditions. All got and used the chance to leave unpleasant regions and to enter arising better ones. Spreading of the *Homo sapiens* was slow and it took nearly 200,000 years after his exodus out of Africa to settle on all continents. In and all over the human body unpleasant voyagers such as viruses, bacteria and parasites took their chance to spread and to establish separated local populations. However, this globalization was very slow and depended on the walking speed of humans. The increasing use of horses, ships, cars and airplanes ended in a constant speeding up of the globalization, so that today it takes only 24 hours to cross the whole world. Thus the introduction of agents of diseases takes only hours, while it may take weeks or even months to detect them in the crowds of humans and/or animals. The medieval and the early modern times had shown, that epidemics such as plague or cholera pose enormous problems even to the "high developed" European societies, while natural people like the Indians had no chance to survive imported diphtheria or measles etc..

Today the earth harbours nearly 7 000 000 000 (!) humans and the distances have melted to 24 hours at the maximum. Thus the knowledge on the transmission, propagation and treatment of diseases of any kind must be kept alive among scientists and practioners in agriculture, veterinary and human medicine and pharmacy. The today common specialization and the run for excellency must leave enough space (and open positions at universities and governmental institutions) to transfer the knowledge on the diagnosis and treatment of invading agents of diseases to the next generation of scientists. Otherwise the pandemics will be common again and will potentially kill millions: think at the worst case consequences of the sudden occurrence of a virus with the killing potential of HIV or Ebola and its transmission by local mosquitoes! **Therefore: *Ceterum censeo necesse est preservare Parasitologia et Medicina Tropica!***

SNOW AND ICE AS ARCHIVE FOR THE GLOBAL DISPERSAL OF FLAGELLATES

Frank Nitsche, Marian Brabender, Merdan Akbayir and Hartmut Arndt

University of Cologne, Biowissenschaftliches Zentrum, Zoological Institute, Dept. General Ecology and Limnology, Otto-Fischer-Str. 6, 50674 Cologne, Germany

E-mail corresponding author: FNitsche@uni-koeln.de (Frank Nitsche)

Abstract

The global dispersal of flagellates and hence the ubiquitousness of many species is based on the high abundance, the small size and the ability to form cysts. Marine organisms are evenly distributed by the water currents while it is assumed, that fresh water species are dispersed via cysts through wind into the atmosphere. These cysts return to nearly all habitats by simply sedimenting or through precipitation. The mechanisms of cyst formation and the abundances are broadly unknown. For an ubiquitous dispersal enormous amounts of cyst must be distributed as only a fraction arrives at the adequate habitat. Snow and ice allow a quantitative and qualitative study for a defined time and even allow a chronological assignment. For our study we sampled snow and ice in the Alps and on Svalbard. We cultivated the samples and analysed the flagellates morphologically and by sequencing SSU rRNA. The abundance of cultivable flagellates was, against the expectations considerably low. The highest abundance was found in snow samples from the Alps with less than four viable cysts per litre. The dominant species belonged to rhizarians and euglenids. Only fresh water samples resulted in cultures while no cultures could be established in marine media. The low abundances of cultivable protists and the absence of some known ubiquitous species point to the presence and importance of additional ways of dispersal.

Key words: flagellates, biodiversity, dispersal, snow, ice, Arctic, abundance

TRIPARTITE SYMBIOSIS: TERMITES – FLAGELLATES – BACTERIA**Renate Radek**

Division of Protozoology, Institute of Biology/Zoology,
Free University of Berlin, Königin-Luise-Str. 1-3, D-14195 Berlin, Germany

E-mail: rradek@zedat.fu-berlin.de

Abstract

Termites are eusocial insects which decompose lignocellulose efficiently. Lower termites have a dual decomposing system, consisting of the termites' own cellulases and those of their symbiotic gut flagellates. Besides a dense fauna of protists, their dilated hindgut with its strict anoxic center contains numerous bacteria, archaea and yeasts. Generally, neither the protists nor the prokaryotes can be cultured in the lab, rendering investigations concerning, e.g., metabolic functions and life cycles difficult. Each termite species contains a typical set of a few to more than 20 flagellate species. The flagellates belong to two lineages of the super-group Excavata, i.e., oxymonads and parabasalids. The parabasalids possess a so-called 'parabasal apparatus', which is composed of cross-striated fibers originating at the basal bodies attached to dictyosomes. Other common structures are hydrogenosomes which produce ATP via an anaerobic reaction, releasing acetate, CO₂, and H₂. Oxymonads possess neither dictyosomes nor hydrogenosomes. One of their typical features is the pre-axostyle, which connects two pairs of basal bodies. Numerous species of parabasalids and oxymonads are associated with endo- and/or ectobiotic prokaryotes. Specific associations exist; even co-speciations between the two symbiotic partners have been detected. Rarely, motile attached spirochetes or members of the "*Synergistes*" confer motility to the flagellate. The functions of the prokaryotes are generally unclear, but an exchange of metabolites is probable. For example, fixation of dinitrogen and acetogenesis have been proven. Other hypotheses are that ectobionts provide an anoxic environment to their host cell or stabilize its cell form. The hindgut of termites is a veritable treasure chest of new taxa of pro- and eukaryotes and special metabolic capacities.

Key words: cellulose degradation, endo-/ectobacteria, oxymonads, parabasalids, symbiosis, termite flagellates

AQUATIC HETEROTROPHIC PROTISTS ACCELERATE ACTIVITY OF LOTIC BIOFILMS

Ute Risse-Buhl¹, Martina Kasubke^{1,2}, Jeannette Schlieff¹,
Christiane Baschien³, Markus Weitere² & Michael Mutz¹

¹ Department of Freshwater Conservation, Brandenburg University of Technology, Seestraße 45, D-15526 Bad Saarow, Germany

² Department of General Ecology and Limnology, Institute for Zoology, University of Cologne, Otto-Fischer-Str.6, D-50674, Köln, Germany

³ Department of Environmental Microbiology, Technische Universität Berlin, Franklinstrasse 29, D-10587 Berlin, Germany

*E-mail corresponding author: ute.risse-buhl@tu-cottbus.de (Ute Risse-Buhl)

Abstract

Aquatic heterotrophic protists play a major role in structuring the morphology of lotic bacterial biofilms. However, knowledge about the relevance of protists controlling the activity of biofilms associated to particulate inorganic and organic matter is limited. In microcosms we investigated the effect of ciliates on microbial biofilm activity by measuring community respiration of biofilms grown on glass slides and alder leaves. After 7 days exposed to turbulent flow, community respiration of biofilms co-cultivated with the gulper feeder *Chilodonella uncinata* (Phyllopharyngia, Ciliophora) or the filter feeder *Tetrahymena pyriformis* (Hymenostomatia, Ciliophora) grown on glass surfaces was not different from bacterial biofilms, although total microbial biomass was 2.5 to 4.0 times lower in protist-inhabited compared to bacterial biofilms. Hence, biofilms were more active when bacteria were co-cultivated with protists. Community respiration on alder leaves co-cultivated with the fungus *Heliscus lugdunensis* and a multispecies bacterial community was 1.5 times higher in the presence of *Tetrahymena pyriformis* than on leaves without protists. Our results indicate that protists enhance the activity of lotic biofilms. Thus, protists might be of major importance in accelerating microbial processing of particulate organic matter and, hence, the energy flow in lotic environments.

Key words: biofilm activity, respiration, bacteria, fungi, heterotrophic protists

**DESCRIPTION OF A NEW GENUS WITHIN *RICKETTSIACEAE*
AS ENDOSYMBIONT OF CILIATES AND ITS IMPLICATIONS FOR
EVOLUTIONARY HISTORY, HOST RANGE AND HOST SHIFT MECHANISMS**

Martina Schrallhammer^{1,2,*}, Filippo Ferrantini¹, Stefano Galati¹, Claudia Vannini¹, Michael Schweikert², Hans-Dieter Görtz² and Giulio Petroni¹

¹ Department of Biology, University of Pisa, Via A. Volt 4/6, IT-56126 Pisa, Italy

² Biological Institute, University of Stuttgart, Pfaffenwaldring 57, DE-70569 Stuttgart, Germany

*E-mail corresponding author: martina.schrallhammer@bio.uni-stuttgart.de

Abstract

Members of the bacterial family *Rickettsiaceae* are obligate intracellular bacteria, many of the known species cause severe human diseases, e.g. epidemic typhus (*Rickettsia prowazekii*), scrub typhus (*Orientia tsutsugamushi*), and Rocky Mountain spotted fever (*Rickettsia rickettsii*). These bacteria are harbored by hematophagous arthropods such as ticks and lice, with vertebrates as alternate hosts. But not all *Rickettsiaceae* are medically relevant, and little is known about the other species, although there are several good reasons to study these non-pathogenic *Rickettsiaceae*: i) they account for the main contribution to the evolutionary diversity of *Rickettsiaceae*, ii) they display a broad host range including protists, and iii) some of them have been recognized as parasites of their eukaryotic hosts.

Here we present the finding of four strains constituting a new genus within *Rickettsiaceae* as endosymbionts of four different, distantly related ciliate hosts. The intracellular bacteria were molecularly characterized by 16S rRNA gene sequencing followed by *in situ* hybridization with species specific probes. Phylogenetic reconstructions place this new genus basal to *Rickettsia*. Apparently, the here characterized bacteria are still capable to infect different eukaryotic hosts, either permanently or in a transitional way. This finding suggests a new interpretation of the evolutionary history, host range and host shift mechanisms of *Rickettsiaceae*. Accordingly, rickettsial diversification is regarded to rely mainly on the infection of different hosts inhabiting the same natural environment rather than on co-speciation processes originating from an ancient symbiotic relationship.

Key words: emerging pathogen, endosymbiont, Ciliates, *Rickettsia*, *Paramecium*, *Spirostomum*, *Euplotes*, *Diophrys*

KINETOPLASTIDS FROM THE ABYSS: COMPARATIVE ANALYSIS OF PHYLOGENETIC COMMUNITY STRUCTURE AND DIVERSITY

Faezeh Shah Salani^{*}, Hartmut Arndt, Frank Scheckenbach

¹ Faculty of Mathematics and Natural Sciences, Biowissenschaftliches Zentrum
Institute for Zoology, Department of General Ecology and Limnology,
University of Cologne, Otto-Fischer-Str.6, D-50674 Köln, Germany

^{*}E-mail corresponding author: shahcool@web.de (Faezeh Shah Salani)

Abstract

Different clone libraries from deep-sea environments of the Mediterranean and the Atlantic reveal a high amount of novel lineages with no close representatives in genetic databases. High p -distances between all clones and their first BLAST hit (mean values of around 15%) and phylogenetic analyses confirm the preliminary assumption of a specific deep-sea community of kinetoplastids.

Furthermore, the presence of some dominant OTUs in all clone libraries confirms the hypothesis that some marine protists are cosmopolitan despite of geographic barriers and different ecological parameters. Nevertheless, the absence of several kinetoplastid orders - such as Eubodonida, Parabodonida and Trypanosomatida - in the clone libraries, indicate that some groups may not be adapted to the special conditions in the deep-sea. Comparative analyses of community structure between the South Atlantic and the Mediterranean show regional distinctions of the community from the Atlantic, where the characteristic long right-hand tail of low abundant OTUs is absent and the rarefaction curve shows a tendency to reach a plateau.

Key words: kinetoplastid, deep-sea, Biodiversity, community structure, OTU, clone libraries, p -distance, SSU rDNA, phylogenetic relationships, novel lineages

ANTIGENIC VARIATION IN CILIATES CONTROLLED BY RNA INTERFERENCE

Simone Marker¹, Alexandra Müller¹, Eva Schloter¹, Andreas Schäfer¹, Anne
Le Mouél², Eric Meyer² and Martin Simon¹

¹ University of Kaiserslautern; Department of Biology, Gottlieb-Daimler Straße, 67663
Kaiserslautern, Germany

² Ecole Normale Supérieure, Laboratoire de Génétique Moléculaire,
Ecole Normale Supérieure 46, rue d'Ulm, 75005 Paris, France

* E-mail corresponding author: msimon@rhrk.uni-kl.de (M. Simon)

Abstract

Antigenic variation was described to be a general mechanism in parasitic as well as in free-living protists. The expression of variable surface antigen coats is widely used as a masking mechanism but can also be used for detection of special ligands of the cell's environment. The genetic basement of antigenic variation are surface-protein multigene families of genes showing a high degree of similarity. These are expressed in an exclusive manner, meaning that all but one gene is repressed. Consequently, this special mechanism of gene expression is the molecular basis for a proper working antigenic system.

We show here that the exclusive expression of surface antigens is controlled by RNA interference in the ciliate *Paramecium*. This mechanism was shown to use small RNAs to inhibit gene expression in a homology dependent manner. Key enzymes of RNAi are RNA dependent RNA polymerases and we identified an RdRP (*Rdr3*) with a highly divergent catalytic domain. Our data implicates that this enzyme is involved in the synthesis of different classes of short RNAs deriving from truncated transgenes and also from endogenous loci. Moreover, *Rdr3* is involved in silencing of the unexpressed antigen genes. Knock-down of *Rdr3* leads to a breakdown of the antigen system and to a simultaneous expression of all tested surface antigens. Analysis of wild type and *Rdr3* knock-down cells lines by *in vitro* run on transcription reveals that antigen silencing in *Paramecium* occurs on the transcriptional level. As *Rdr3* knock-down also affects histone methylation in the macronucleus, antigenic variation in *Paramecium* turns out to be epigenetically regulated. Even though we now have an idea of the mechanisms involved in exclusive antigen expression and silencing, the most interesting question to clarify will be how one of the genes escapes silencing.

Key words: RNAi, siRNA, transcriptional silencing, RdRP, surface antigen, heterochromatin

EFFECTS OF PROTIST PREDATION, COMPETITION AND A COMBINATION OF BOTH FACTORS ON THE POPULATION SIZE STRUCTURE OF A BACTERIAL STRAIN WITH HIGH PHENOTYPIC PLASTICITY

Christine Willen, Mar Monsonís Nomdedeu, Andre Schieffer, Hartmut Arndt

University of Cologne, Institute of Zoology, General Ecology and Limnology,
Otto-Fischer-Str.6, D-50674 Köln, Germany

*E-mail corresponding author: cwillen@uni-koeln.de (Christine Willen)

Abstract

Morphological changes in a bacterial community are common in most aquatic systems. Selection pressures due to predation or competing nutrient availability may cause a shift in the population size structures. This may lead to stabilized bacterial biomass and reduced trophic transfer efficiency. *Acinetobacter johnsonii* (gamma-proteobacteria) is able to form rod shaped as well as roundish cells, but it also forms colonies, filaments in various size structures. What effects play the most important role for the phenotypic plasticity of this bacterial strain? Three different long-term (several weeks) chemostat experiments were conducted with a different food web complexity and composition in order to discern the role of protist predation by a ciliate (*Tetrahymena pyriformis*) and the role of competition for nutrients with another bacterial strain (*Pedobacter*, CFB-group). Chemostat experiments with single species (*Acinetobacter* alone) and two species (*Acinetobacter* vs. *Pedobacter* or *Tetrahymena* feeding on *Acinetobacter*) as well as three-species systems (coexistence of all three species) were run at constant conditions. Furthermore short term (24 hours) batch experiments were performed with *Acinetobacter* under high grazing pressure by *Tetrahymena pyriformis*.

Key words: protist predation, competition, phenotypic plasticity, chemostat experiments, batch experiments

Protist diversity in the Black Sea redoxcline and comparable systems

Claudia Wylezich^{1,*} & Klaus Jürgens¹

¹Leibniz Institute for Baltic Sea Research Warnemuende, Biological Oceanography, Molecular and Microbial Ecology, Seestr. 15, 18119 Rostock, Germany

*E-mail corresponding author: claudia.wylezich@io-warnemuende.de

Abstract

The Black Sea is the World's largest permanently stratified basin. A stable halocline separates the water column into the upper oxygenated layer and the underlying oxygen deficient and anoxic/sulphidic layer. Such pelagic redoxclines, which occur in a very similar way also in other stratified marginal seas (Baltic Sea, Cariaco Basin) or coastal marine environments (some fjords), are relevant sites for diverse microbially-mediated biogeochemical transformations within the nitrogen, sulphur and carbon cycles. Molecular studies of the prokaryotic diversity revealed strong compositional shifts along the redox gradients and identified key taxa for important processes (chemoautotrophy, nitrification, denitrification, sulphur oxidation etc.). Much less studies have been performed for microbial eukaryotes. We present here the first quantitative species composition of protists in the Black Sea redoxcline, investigated by a combination of molecular techniques (RNA-derived fingerprint analysis and clone libraries of the SSU rRNA) and classical microscopical methods. In accordance with former studies on the protist composition of the Baltic Sea redoxcline, we reveal a complex protistan community structure with distinct shifts within the redox gradient. We found mainly *Pleuronema* and *Strombidium* species in the redoxcline of the Black Sea, whereas *Metacystis* species dominate the ciliate assemblage of the Baltic Sea. Concerning flagellates, jakobids seem to dominate sulphidic waters of the Baltic Sea, whereas the flagellate community of the Black Sea mainly constitute stramenopiles and ancyromonads. Compared to diversity, much less is known about functions of protists at oxic-anoxic interfaces, partly due to methodological limitations. Further studies have to focus on quantifying bacterivory and on experimentally evaluating the impact of protists on prokaryotic community dynamics and activity.

Key words: pelagic redoxcline, oxic/anoxic, sulphidic, Black Sea, Baltic Sea, heterotrophic nanoflagellates, ciliates, prokaryotic community

PROTIST BACTERIVORY IN TWO BALTIC SEA REDOXCLINES: A FIRST VIEW OF A COMPLEX SYSTEM

Ruth Anderson^{1,*}, Felix Weber^{1,*}, Klaus Jürgens¹

¹ IOW - Leibniz Institute for Baltic Sea Research Warnemünde, 18119 Rostock, Germany

*E-mail corresponding author: ruth.anderson@io-warnemuende.de (Ruth Anderson)

Abstract

Landsort and Gotland Deep in the central Baltic Sea are characterized by a vertical transition from oxic- to suboxic and sulphidic waters, termed pelagic redoxcline. This environment presents steep physico-chemical gradients which have been shown to host a diverse and highly active bacterial community of great relevance for carbon- and nitrogen cycling in the Baltic. However, relatively little information has been unveiled for the protist communities which feed on these bacteria. In this study we compare grazing in 3 depths situated in the suboxic, interface and anoxic/sulphidic zones of Gotland and Landsort Deep, by assessing the disappearance of FLBs (fluorescently labeled bacteria) after a period of 24h, and present an overview of the community structure employing classical microscopy techniques. Our results show changes in the grazing impact and community structure throughout the oxygen gradient, and, interestingly, between zones of similar physico-chemical characteristics in both study sites. Additionally, all indications point towards ciliates being the major bacterivores in pelagic redoxclines.

Key words: bacterivory / redoxcline / protists / Baltic Sea / FLB / community structure

**SYMBIONT DISTRIBUTION IN DIFFERENT AEOLIDOIDEAN SPECIES
(MOLLUSCA, NUDIBRANCHIA)**

Sabrina Bleidissel, Angelika Preisfeld

1 Institute of Biology - Zoology and Didactics of Biology,
Bergische University Wuppertal, Gausstr. 20, D-42119 Wuppertal, Germany

* E-mail corresponding author: bleidiss@uni-wuppertal.de (Sabrina Bleidissel)

Abstract

Some species of the Aeolidioidea are well known to host unicellular symbiotic dinoflagellates of the genus *Symbiodinium*. The uptake of dinoflagellates as symbionts occurs mostly via cnidarian food organisms. The symbionts are mainly incorporated in the cerata tissue. With help of this symbiosis, the adult slugs are able to overcome a period of food shortage by getting photosynthetic products from their symbiotic partners. *Symbiodinium* is based on molecular data divided into eight distinct clades, which are labelled from A to H. In this study, we investigate the distribution of three *Symbiodinium* clades within the Aeolidioidea. Based on a new Aeolidioidean phylogeny, the occurrence of *Symbiodinium* within the Aeolidioidea will be discussed.

Key words: *Aeolidioidea, symbiont distribution, Symbiodinium*

ÄNDERUNGEN DER BAKTERIELLEN AKTIVITÄT DURCH PROTOZOEN- GRAZING IN EINEM CHEMOSTATSYSTEM

J. Cesarz, A. Scherwass, C. Willen, H. Arndt

Universität zu Köln, Allgemeine Ökologie,
Biowissenschaftliches Zentrum, Otto-Fischer-Str. 6, 50674 Köln

jcesarz@smail.uni-koeln.de

Abstract

Die Mikrobiologie kennt verschiedene Methoden, um Aktivität von Bakterien nachzuweisen. Eine mögliche Methode ist die Verwendung des Substratanalogons CTC (=5-Cyano-2,3-Ditolyltetrazoliumchlorid), zum Nachweis der respiratorische Aktivität. Dabei wird CTC während der Atmungskette zu CTC-Formazan umgesetzt. Daneben kann man mittels Fluoreszenz-in-situ-Hybridisierung (FISH) einen Nachweis für Wachstumsaktivität von Bakterien finden, wenn man rRNA-Sequenzen als Sonden benutzt, da die Proteinbiosynthese die Anwesenheit von Ribosomen voraussetzt.

In der vorliegenden Studie wurden diese beiden Methoden verwendet, um Unterschiede in der Aktivität von Bakterien (*Acinetobacter johnsonii*) unter Einfluss von Fraßdruck durch einen Ciliaten (*Tetrahymena pyriformis*) in Chemostatsystemen zu untersuchen. Dabei sollte vor allem eine mögliche Veränderung der bakteriellen Aktivität unter chaotischen bzw. statischen Abundanzveränderungen der Bakterien betrachtet werden.

Erste Ergebnisse zeigten deutliche Unterschiede in der bakteriellen Aktivität, die auf dem Poster diskutiert werden.

**PHOTOSYNTHETISCHE UND MOLEKULARBIOLOGISCHE ERGEBNISSE
ZUR SYMBIOSE ZWISCHEN *PHYLLODESMIUM BRIAREUM* (MOLLUSCA,
AEOLIDOIDEA) UND *SYMBIODINIUM***

Antonia Kemper, Angelika Preisfeld

*Zoologie und Biologiedidaktik,
Bergische Universität Wuppertal, Gaußstraße20, 42119 Wuppertal, Deutschland*

**E-Mail an den Autor: antoniakemper@web.de*

Abstract

Die marine Nacktschnecke *Phyllodesmium briareum* (Mollusca, Aeolidioidea) besitzt eine weit verzweigte Mitteldarmdrüse. Diese durchzieht den gesamten Schneckenkörper, sowohl den Fuß als auch die charakteristischen Körperanhänge (Cerata). Durch die Mitteldarmdrüse kann sie photosynthetisch aktive Symbionten der Gattung *Symbiodinium* einlagern, welche sie mit ihrer Nahrung aufnimmt und nicht verdaut. Mithilfe der Photosyntheseprodukte ihrer Symbionten kann die Schnecke eine längere Zeit ohne zusätzliche Nahrungsmittel überleben. Der Dinoflagellat *Symbiodinium* wird aufgrund molekularsystematischer Analysen in acht verschiedene Clades eingeteilt. Im Langzeithungerversuch mit lebenden Schnecken konnte gezeigt werden, dass sich die Cladezusammensetzung in der Schnecke, bezogen auf drei *Symbiodinium* Clades, innerhalb dieser Zeit ändert. Die Methoden und die Ergebnisse werden hier diskutiert.

Schlüsselwörter: Cerata, Clade, Nudibranchia, Photosyntheserate, Symbiose, Zooxanthellen

Choosing an Appropriate Short Region of SSU-rDNA for Massively Parallel Environmental Sequencing of Ciliates

Julia Klier, Micah Dunthorn, and Thorsten Stoeck

University of Kaiserslautern, Department of Ecology, Kaiserslautern, Germany

Abstract

Massively parallel tag sequencing technologies can only read short nucleic segments, such as the hypervariable V4 and V9 regions of the small subunit rDNA (SSU-rDNA). As more studies are being designed and implemented using tag sequencing approaches for environmental diversity of ciliates, the question of how sequence similarities of these short regions translate into the full-length SSU-rDNA similarities found in previous studies. Partitioning sequences from a broad sample of ciliates into the full SSU-rDNA, just the V4, and just the V9 regions, shows that the distances from V4 are more similar to the full SSU-rDNA than is V9 both within species and among species. Furthermore, V4 and the full SSU-rDNA have more similar distances independent of taxonomic units. We conclude that environmental diversity studies implementing parallel tag sequencing approaches should target the V4 region so that the new estimates can be more clearly compared to previous analyses.

ÖKOLOGISCHE PRINZIPIEN MITTELS PROTOZOENGEMEINSCHAFTEN ENTSCHLÜSSELN: WECHSELWIRKUNGEN VON ERWÄRMUNG UND STÖRUNG AUF BIOFILMASSOZIIERTE CILIATENGEMEINSCHAFTEN.

Hanna Marcus^{1*}, Jennifer Wey¹, Helge Norf^{1,2}, Markus Weitere¹

¹ Institute for Zoology, Department of General Ecology and Limnology, University of Cologne, Biowissenschaftliches Zentrum, Otto-Fischer-Str.6, D-50674 Köln, Germany

² Bundesanstalt für Gewässerkunde, Referat U2, Am Mainzer Tor 1, 56068 Koblenz, Germany

*E-mail corresponding author: hannamarcus@gmx.de (Hanna Marcus)

Abstract

Aufgrund ihrer hohen Reproduktionsraten eignen sich Protozoengemeinschaften sehr gut zum Testen ökologischer Prinzipien. In der aktuellen Debatte über die Folgen der Klimaerwärmung stehen Fragen zur Reaktion von Lebensgemeinschaften auf Erwärmung im Fokus der Forschung. Bisher konnte dabei gezeigt werden, dass sich Erwärmung positiv auf die Besiedlungsgeschwindigkeit, aber negativ auf die Kapazität von Lebensgemeinschaften auswirken kann. Unter natürlichen Bedingungen stehen die Gemeinschaften jedoch oft unter dem Einfluss von Störung, was eine permanente Wiederbesiedlung erfordert. In der vorliegenden Arbeit wurde nun anhand von seminaturalen Protozoengemeinschaften erstmalig der wechselseitige Einfluss von Erwärmung und Störung getestet. Dazu wurden zu verschiedenen Jahreszeiten Ciliatengemeinschaften in Bypassystemen zum Rhein etabliert und dabei unterschiedlichen Temperatur- und Störungsregimen ausgesetzt. Es konnte gezeigt werden, dass der Effekt von Erwärmung maßgeblich von der Stärke der Störung abhängt. Während in ungestörten Systemen eine Temperaturerhöhung einen negativen Effekt auf die Ciliatendichte hatte, verhielt es sich in gestörten Systemen umgekehrt. Die Wirkung der Störungsereignisse auf die Protozoengemeinschaften hing jedoch maßgeblich von der Jahreszeit ab. Gleiche Störungsintensitäten hatten im Winter starke Effekte, während sie im Sommer keine Effekte hatten. Die Untersuchungen zeigen, dass sowohl die gegebenen Störungszustände als auch die Jahreszeit bei der Bewertung von Klimafolgen auf Lebensgemeinschaften berücksichtigt werden müssen.

Key words: Ökologische Prinzipien, Klimaänderung, Temperatur, Störung, Mikrobielle Ökologie, Biofilm, Ciliaten

**PHYLOGENETIC POSITION OF THE SMALL CILIATE
MICRODIAPHANOSOMA ARCUATUM**

Pablo Quintela-Alonso*, Frank Nitsche, Hartmut Arndt

Institute for Zoology, Biowissenschaftliches Zentrum - AG Arndt, Department of General Ecology and Limnology, University of Cologne, Otto-Fischer Strasse 6, D-50674 Cologne, Germany

*E-mail corresponding author: pquintel@uni-koeln.de (Pablo Quintela-Alonso)

Abstract

Microdiaphanosoma arcuatum Wenzel, 1953, is a world-wide distributed ciliate, recorded mainly in soil samples, that we have also identified in ground water samples from South Africa. This ciliate has been frequently overlooked or not determined due to its extremely small size (length about only 12 µm in our samples). The genus *Microdiaphanosoma* is nowadays included in the class Colpodea, subclass Bryometopia, order Bryometopida, family Kreyellidae. We have determined the first complete small subunit rRNA (SSrRNA) gene sequence of this Kreyellidae and show the phylogenetic tree giving more information about the systematic position of this species.

Key words: Ciliophora, Colpodea, phylogeny, small subunit rRNA.

**EXPERIMENTELLE UNTERSUCHUNGEN ZUM DYNAMISCHEN
VERHALTEN VON EIN-RÄUBER-ZWEI-BEUTE-SYSTEMEN UND EIN-
RÄUBER-DREI-BEUTE-SYSTEMEN**

**Schieffer, Andre* ; Willen, Christine; Monsonís Nomdedeu, Mar;
Arndt, Hartmut**

Allgemeine Ökologie und Limnologie, Institut für Zoologie,
Universität zu Köln, Otto-Fischer-Str. 6, 50674 Köln

*E-mail corresponding author: Andre.Schieffer@uni-koeln.de (Andre Schieffer)

Abstract

Räuber-Beute-Systeme bieten ein fundiertes Werkzeug zur Untersuchung und zum Verständnis populationsdynamischer Phänomene. Vorangegangene Untersuchungen an Ein-Räuber-zwei-Beute-Systemen mit dem Ciliaten *Tetrahymena pyriformis* als Räuber und zwei verschiedenen Bakterienarten als Beuten konnten zeigen, dass durch eine Variation experimenteller Parameter verschiedene Dynamiken im Verhalten der untersuchten Systeme erzielt werden konnten. Dies konnte durch ergänzende modelltheoretische Untersuchungen weitestgehend gestützt werden. Untersuchungen an eigenen definierten Laborsystemen wie Ein-Räuber-zwei-Beute-Systemen, sowie Ein-Räuber-drei-Beute-Systemen werden vorgestellt und diskutiert. Durch computergestützte Modellierung wird versucht, das dynamische Verhalten durch Modifikation intrinsischer und extrinsischer Faktoren darzustellen und einen Vergleich mit experimentellen Daten zu ermöglichen.

Key words: Trophische Interaktionen, Mikroorganismen, theoretische Ökologie

**EXPERIMENTELLE UNTERSUCHUNGEN ZUM DYNAMISCHEN
VERHALTEN VON EIN-RÄUBER-ZWEI-BEUTE-SYSTEMEN UND EIN-
RÄUBER-DREI-BEUTE-SYSTEMEN**

**Schieffer, Andre* ; Willen, Christine; Monsonís Nomdedeu, Mar;
Arndt, Hartmut**

Allgemeine Ökologie und Limnologie, Institut für Zoologie,
Universität zu Köln, Otto-Fischer-Str. 6, 50674 Köln

*E-mail corresponding author: Andre.Schieffer@uni-koeln.de (Andre Schieffer)

Abstract

Räuber-Beute-Systeme bieten ein fundiertes Werkzeug zur Untersuchung und zum Verständnis populationsdynamischer Phänomene. Vorangegangene Untersuchungen an Ein-Räuber-zwei-Beute-Systemen mit dem Ciliaten *Tetrahymena pyriformis* als Räuber und zwei verschiedenen Bakterienarten als Beuten konnten zeigen, dass durch eine Variation experimenteller Parameter verschiedene Dynamiken im Verhalten der untersuchten Systeme erzielt werden konnten. Dies konnte durch ergänzende modelltheoretische Untersuchungen weitestgehend gestützt werden. Untersuchungen an eigenen definierten Laborsystemen wie Ein-Räuber-zwei-Beute-Systemen, sowie Ein-Räuber-drei-Beute-Systemen werden vorgestellt und diskutiert. Durch computergestützte Modellierung wird versucht, das dynamische Verhalten durch Modifikation intrinsischer und extrinsischer Faktoren darzustellen und einen Vergleich mit experimentellen Daten zu ermöglichen.

Key words: Trophische Interaktionen, Mikroorganismen, theoretische Ökologie

KINETOPLASTIDS FROM THE ABYSS: COMPARATIVE ANALYSIS OF PHYLOGENETIC COMMUNITY STRUCTURE AND DIVERSITY

Faezeh Shah Salani*, Frank Scheckenbach, Hartmut Arndt

¹ Faculty of Mathematics and Natural Sciences, Biowissenschaftliches Zentrum
Institute for Zoology, Department of General Ecology and Limnology, University of Cologne,
Otto-Fischer-Str.6, D-50674 Köln, Germany

*E-mail corresponding author: shahcool@web.de (Faezeh Shah Salani)

Abstract

Different clone libraries from deep-sea environments of the Mediterranean and the Atlantic reveal a high amount of novel lineages with no close representatives in genetic databases. High p -distances between all clones and their first BLAST hit (mean values of around 15%) and phylogenetic analyses confirm the preliminary assumption of a specific deep-sea community of kinetoplastids.

Furthermore, the presence of some dominant OTUs in all clone libraries confirms the hypothesis that some marine protists are cosmopolitan despite of geographic barriers and different ecological parameters. Nevertheless, the absence of several kinetoplastid orders - such as Eubodonida, Parabodonida and Trypanosomatida - in the clone libraries, indicate that some groups may not be adapted to the special conditions in the deep-sea. Comparative analyses of community structure between the South Atlantic and the Mediterranean show regional distinctions of the community from the Atlantic, where the characteristic long right-hand tail of low abundant OTUs is absent and the rarefaction curve shows a tendency to reach a plateau.

Key words: kinetoplastid, deep-sea, Biodiversity, community structure, OTU, clone libraries, p -distance, SSU rDNA, phylogenetic relationships, novel lineages

MOBILE GENETISCHE ELEMENTE, INTRONS GRUPPE II UND III, ALS PHYLOGENETISCHER MARKER

S. Stratmann¹, Ingo Busse, Angelika Preisfeld¹

Institut für Zoologie und Biodidaktik,
Bergische Universität Wuppertal, Gaußstr. 20, 42119 Wuppertal, Germany

Abstract

Die Euglenida (Euglenozoa) sind eine morphologisch sehr heterogene Gruppe von Flagellaten, die sowohl heterotrophe als auch phototrophe Organismen umfasst. Die Entstehung der phototrophen Euglenida durch sekundäre Endocytobiose ist ein beeindruckendes Beispiel für einen evolutionären Quantensprung. Eine Besonderheit der bereits vollständig sequenzierten plastidären Genome von *Euglena gracilis* und *Euglena longa* ist der hohe Anteil an Gruppe II und III Introns. Sowohl Introntranslokation als auch der Verlust von Introns gelten als seltene evolutive Ereignisse und eignen sich daher als Marker, um die Phylogenese der Plastiden zu rekonstruieren. In diesem Zusammenhang wurde das Auftreten von Introns der Gruppe II und III sowie deren Verteilung im plastidären Gen *TufA* (plastidärer Elongationsfaktor) bei verschiedenen phototrophen Euglenida untersucht. Die Intronverteilung wird einer phylogenetischen Rekonstruktion, basierend auf kernkodierten SSU rDNA-Daten (Marin et al. 2003), gegenübergestellt und diskutiert.

IDENTIFICATION OF THE DOMINANT BACTERIVOROUS PROTISTS IN THE BALTIC SEA

Felix Weber^{1,*}, Claudia Wylezich¹, Alexander P. Mylnikov², Ramon Massana³, Klaus Jürgens¹

¹ Leibniz Institute for Baltic Sea Research Warnemuende, Biological Oceanography, Molecular and Microbial Ecology, Seestr. 15, 18119 Rostock, Germany

² Institute for Biology of Inland Waters, Russian Academy of Sciences, Borok, Yaroslavskaia obl. 152 742, Russia

³ Institut de Ciències del Mar, CMIMA (CSIC), Passeig Marítim de la Barceloneta 37-49, 08003 Barcelona, Catalonia, Spain

*E-mail corresponding author: felix.weber@io-warnemuende.de

Abstract

Currently, neither the key players nor the quantitative contribution of certain bacterivorous protist groups are known for Baltic Sea surface waters. In order to close this knowledge gap, we chose the approach of oligotrophic enrichments and subsequent molecular identification of bacterivorous nanoflagellates as well as probe design for in situ quantification. Here we present results from incubations with water samples from a coastal, brackish site in the South Western Baltic Sea (salinity 15-17 PSU). Unamended incubations of whole and prefiltered water served to promote the growth of heterotrophic protists. Epifluorescence microscopy revealed that phototrophic organisms decreased while the number of heterotrophic flagellates (HF) increased towards a peak after 5 to 7 days of incubation. The population maximum in HF was used for the analysis of protist composition by 18S rRNA clone libraries. Clone libraries were dominated by a large number of sequences related to uncultured chrysophytes and *Paraphysomonas* species. Moreover, filter-feeding choanoflagellates and assumingly mixotrophic *Bolidomonas*-like flagellates seem to constitute a significant amount of bacterivores in our incubations. It remains to be tested, whether the taxa dominating in clone libraries are also relevant in situ by using already established and, based on the 18S rRNA sequences from the clone libraries, newly designed oligonucleotide probes for fluorescent in situ hybridisation.

Key words: Baltic Sea, bacterivorous protists, oligotrophic enrichment, 18S rRNA, uncultured chrysophytes, oligonucleotide probes

THE ALVEOLATA PELLICLE: UNIQUE, CHARGED AND REPEATED

Sven B. Gould*, Christopher D. Goodman, Lesleigh G. K. Kraft,
Giel van Dooren, Kristina Ford, Andrew Cassin, Tony Bacic,
Geoffrey I. McFadden, Ross F. Waller

School of Botany, University of Melbourne, VIC-3010 Parkville, Melbourne, Australia
*current affiliation: HH-Universität Düsseldorf, Botanik III, 40225 Düsseldorf, Germany

Abstract

The pellicles of Alveolata share a common organisation, yet perform very divergent functions. We recently showed that a family of proteins are common and unique to this subpellicular network. For the purpose of identifying further proteins that contribute to this structure, the proteome of the pellicle was defined for *Tetrahymena thermophila* using electrospray ionisation on a QSTAR Elite hybrid quadrupole time-of-flight mass spectrometer. We found 1173 proteins associated with this structure and about two-thirds of them seem common to other Alveolata. Amongst the proteins for which we confirmed the localisation in different Alveolata, were novel proteins of the *Tetrahymena* oral apparatus and potential invasion-related proteins of *Toxoplasma* and *Plasmodium*. Furthermore, of the common proteins was a high fraction with charged repetitive motifs. A bioinformatic screen shows such charged repetitive motif proteins, or CRMPs, are highly enriched in Ciliophora and Apicomplexa. Some CRMPs represent large novel classes, are hard to identify by classical blast-searches, and represents a whole new array of so far unrecognised major cytoskeletal players in Alveolata.

PROTISTAN PARASITES OF ALGAE

Sebastian Hess^{1,2}

¹Botanisches Institut, Zentrum für Biowissenschaften,
Universität zu Köln, Zùlpicher Straße 47b, 50674 Köln, Deutschland

²Student der Rheinischen Friedrich-Wilhelms-Universität Bonn, Deutschland

E-mail: s-hess@web.de

Abstract

With modern techniques of isolation and culturing some cultures of parasitic protists attacking freshwater algae (mainly Zygnematophyceae) have been established. Besides several members of the Vampyrellidae Zopf belonging to the genera Vampyrella, Hyalodiscus and Leptophrys two strains of an unknown parasitic flagellate with cercozoan affiliation (PC01 and PC02) have been isolated. Preliminary observations about morphology, infection cycle, host preference and the genetic position in the tree of life are presented. Furthermore the poster shows some techniques to enrich, isolate and culture parasitic protists from natural samples and lists the main questions that will be addressed in future.

Key words: algae, parasites, Vampyrellidae, Cercozoa