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

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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.²
(CILIOPHORA: HYPOTRICHIA): MORPHOLOGY, NOTES ON CELL
DIVISION, SSU RRNA GENE SEQUENCE DATA, AND NEOTYPIFICATION

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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, Apogastrostyle nov. gen.¹, because there are, inter alia, important differences in the dorsal infraciliature. Besides the type species, A. rigescens nov. comb.², which seems to be confined to the northern hemisphere, a second marine species, A. szaboi nov. comb.³ (basionym Hemigastrostyle szaboi) can be included. Since no type material of A. rigescens² 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

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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

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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

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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 *10^7 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

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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

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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 flagellates 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

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Abstract

Key words: hyporheisches Interstitial, sandige Sedimente, Sedimentumlagerung, Ciliaten
Biogeographische Barrieren für die Ausbreitung von Ciliaten

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Abstract
The hydrogen-producing mitochondria of *Nyctotherus ovalis*

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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)

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

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**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

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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, Cochliopodidae 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?

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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 Tropical.
SNOW AND ICE AS ARCHIVE
FOR THE GLOBAL DISPERAL OF FLAGELLATES

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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 then 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

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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,
$\text{CO}_2$, and $\text{H}_2$. 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

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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 where 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 RICKETTSIAEAE AS ENDOSYMBIONT OF CILIATES AND ITS IMPLICATIONS FOR EVOLUTIONARY HISTORY, HOST RANGE AND HOST SHIFT MECHANISMS

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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 molecular 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

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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

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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

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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

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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

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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 redoxclines. 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)  

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Abstract  
Some species of the Aeolidoidea are well known to host unicellular symbiotic dinoflagellates of the genus Symbiodinium. The uptake of dinoflagellates as symbionts occurs mostly via cnidar-ian 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 Aeolidoidea. Based on a new Aeolidoidean phylogeny, the occurrence of Symbiodinium within the Aeolidoidea will be discussed.  

Key words: Aeolidoidea, symbiont distribution, Symbiodinium
ÄNDERUNGEN DER BAKTERIELLEN AKTIVITÄT DURCH PROTOZOEANGRAZING IN EINEM CHEMOSTATSYSTEM

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Abstract

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,
AEOLIDIOIDEA) UND SYMBIODINUM

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Abstract

Schlüsselwörter: Cerata, Clade, Nudibranchia, Photosyntheserate, Symbiose, Zooxanthellen
Choosing an Appropriate Short Region of SSU-rDNA for Massively Parallel Environmental Sequencing of Ciliates

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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.

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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
permanenten Wiederbesiedlung erfordert. In der vorliegenden Arbeit wurde nun anhand von
seminatürlichen Protozoengemeinschaften erstmalig der wechselseitige Einfluss von Erwärmung
und Störung getestet. Dazu wurden zu verschiedenen Jahreszeiten Ciliengemeinschaften in
Bypassystemen zum Rhein etabliert und dabei unterschiedlichen Temperatur- und Störungsregimen
ausgesetzt. Es konnte gezeigt werden, dass der Effekt von Erwärmung maßgeblich von dem
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 Störungseignisse auf die Protozoengemeinschaften hing jedoch
maßgeblich von der Jahreszeit ab. Gleich 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

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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 Bryometopida, 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

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Abstract


Key words: Trophische Interaktionen, Mikroorganismen, theoretische Ökologie
EXPERIMENTELLE UNTERSUCHUNGEN ZUM DYNAMISCHEN
VERHALTEN VON EIN-RÄUBER-ZWEI-BEUTE-SYSTEMEN UND EIN-
RÄUBER-DREI-BEUTE-SYSTEMEN

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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
intrinsicer und extrinischer 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

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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

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Abstract
IDENTIFICATION OF THE DOMINANT BACTERIVOROUS PROTISTS IN THE BALTIC SEA

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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

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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

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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