



21th Scientific Phycology Meeting Section Phycology in DBG

Göttingen University 9.-12.3.2025

Program & Abstract Book

Webpage

<http://phykologie-sektionstagung2025.de/>

Contact

sektionstagung@uni-goettingen.de

Venue

[Alte Mensa](#)

Conference and event center

Wilhelmsplatz 2

D - 37073 Göttingen

Information

- The conference venue is barrier-free
- All talks take place in the [Adam-von-Trott Saal](#) (1st floor)
- Coffee breaks are in the [foyer](#) (1st floor)
- The Poster sessions take place in different rooms of the venue building
- Lunch, supper and conference dinner are located in the [Hannah-Vogt-Saal](#) and [Emmy-Noether-Saal](#) (ground floor)

Sunday, March 9th

13:00 **Registration open**

15:00 *Welcome reception at Alte Mensa (Coffee & Cake)*

15:30 **Welcome remarks** (Maike Lorenz, Claudia Büchel)

Session 1 (15:45 – 16:45)

Short talk presentations, 12 + 2 min

15:45 – 16:00 Session 1/Talk 1: Max Angstenberger (Frankfurt)
*Efficient nuclear genome editing enables the creation of high light tolerant *Chlamydomonas reinhardtii* strains*

16:00 – 16:15 Session 1/Talk 2: Yuliia Lihanova (Leipzig)
Using the power of cis-regulatory elements to study gene function in green algae

16:15 – 16:30 Session 1/Talk 3: Marie Wünsch (Rostock)
*Heterologous *Lhcx* expression in the diatom *Phaeodactylum tricornutum**

16:30 – 16:45 Session 1/Talk 4: Kohei Takahashi (Tübingen/ JPN)
*Identification and molecular genetic bases of three sex phenotypes in *Pleodorina starrii**

16:45 – 18:00 Poster session 1 (Poster 1-16)

18:00 – 19:00 *Supper*

19:15 – 19:45 SchülerInnen-Preis

20:00 – 21:00 Plenary Lecture: Susana Coelho (Tübingen)
The curious world of brown algal mating rituals

Monday, March 10th

8:30 *Check-in / Info-Desk open*

Session 2 (8:45 – 10:15)

Short talk presentations, 12 + 2 min

- 8:45 – 9:00 Session 2/ Talk 1: Kiara Franke (Rostock)
A fixed photosynthetic quotient neglects seasonal differences in kelp net primary production, especially under warming
- 9:00 – 9:15 Session 2/ Talk 2: Tomáš Grivalský (Třeboň, CZ)
*Characterization of a bidirectional promoter in the diatom *Phaeodactylum tricornutum**
- 9:15 – 9:30 Session 2/ Talk 3: Elisa Merz (Konstanz)
Success is more than photosynthesis – The activity of benthic diatoms in the dark
- 9:30 – 9:45 Session 2/ Talk 4: Chirara Giossi (Konstanz)
Combined effect of temperature and light stress on the photoprotection capacity of a model diatom
- 9:45 – 10:00 Session 2/ Talk 5: Martina Pichrtová (Prague, CZ)
*The role of phenolics in stress tolerance in *Zygnematophyceae**
- 10:00 – 10:15 Session 2/ Talk 6: Anna Busch (Köln)
*Diversity and ecophysiology of the conjugating green algae (*Zygnematophyceae*), with special reference to their photoprotective strategies*
- 10:15 – 10:45 *Vitamin & Coffee break*

Session 3 (10:45 – 12:15)

Short talk presentations, 12 + 2 min

- 10:45 – 11:00 Session 3/ Talk 1: Daniela Glück (Rostock)
Macroalgae Matters: Sustainable Coastal Solutions from Beachwrack for Nutrient Supply and Coastal Management
- 11:00 – 11:15 Session 3/ Talk 2: Helen Feord (Potsdam)
Elucidating the mechanisms underlying streptophyte glacier ice algae adaptation to extreme variations in light availability
- 11:15 – 11:30 Session 3/ Talk 3: Mirjam Paasch (Potsdam)
Effect of nutrient composition on cell growth, color, and photophysiology of cultured glacier ice algae
- 11:30 – 11:45 Session 3/ Talk 4: Hanna Eisenberg (Bremerhaven)
Native proteins from microalgae as a replacement for serum in mammalian cell culture
- 11:45 – 12:00 Session 3/ Talk 5: Heiko Wagner (Leipzig)
Photosynthesis-driven biocatalysis in cyanobacteria: A sustainable approach to chemical precursor production
- 12:00 – 12:15 Session 3/ Talk 6: Alexander Kuß (Köln)
Growth and nutrient uptake of site adapted microalgae-bacteria consortia in multiple undiluted, high strength landfill leachates
- 12:15 – 13:15 *Lunch*

Session 4 (13:15 – 15:00)

Short talk presentations, standard: 12 + 2 min

- 13:15 – 13:45 Session 4/ Talk 1: Jörg Ullmann (Klötze)
Current Status of Industrial Microalgal Biotechnology in Germany as Emerging Sector of the Blue Bioeconomy
- 13:45 – 14:00 Session 4/ Talk 2: Dania Awad (München)
Lab cultivation of coralline red algae: A promising carbon storage agent
- 14:00 – 14:15 Session 4/ Talk 3: Cedric Hering-Peter (Kiel)
Characterization of floc-forming and fast-sedimenting microalgae-bacteria consortia in bioremediation

14:15 – 14:30	<u>Session 4/ Talk 4:</u> Niels Holm (Kiel) <i>Wastewater purification with fast settling microalgae-bacteria consortia</i>
14:30– 14:45	<u>Session 4/ Talk 5:</u> Christian Kleinert (Köthen) <i>Milking of extracellular oils from <i>Botryococcus braunii</i>: A technical-scale study using 28-litre flat-panel airlift reactors</i>
14:45 – 15:00	<u>Session 4/ Talk 6:</u> Juliane Poturnak (Köthen) <i>Analysis of Cobalamin and Pseudocobalamin Composition in Microalgae Cultures</i>
15:00 – 15:30	<i>Vitamin & Coffee break</i>
15:30 – 17:00	Excursions (Guided City Tours), start in front of Alte Mensa
17:00 – 18:30	Poster session 2 (Poster 17-35)
18:30 – 19:30	<i>Supper</i>
19:30 – 21:30	General Assembly/Get together
ca. 20:30	Auction

Tuesday, March 11th

8:30 *Check-in / Info-Desk open*

Session 5 (8:45 – 10:15)

Short talk presentations, 12 + 2 min

8:45 – 9:00	<u>Session 5/ Talk 1:</u> Dennis Nürnberg (Berlin) <i>Far-red light-driven nitrogen fixation in free-living and symbiotic cyanobacteria</i>
9:00 – 9:15	<u>Session 5/ Talk 2:</u> Shujie Wu (Berlin) <i>Far-red light photosynthesis contributes to a saline soil crust ecosystem</i>
9:15 – 9:30	<u>Session 5/ Talk 3:</u> Stefan Barthel (Göttingen) <i>Changes in the biodiversity of soil algae in arable land - a pilot study using multiple DNA-Metabarcoding</i>
9:30 – 9:45	<u>Session 5/ Talk 4:</u> Pengyu Ji (Konstanz) <i>Nutrient availability affects stalk formation by the benthic diatom <i>Achnathidium minutissimum</i></i>

- 9:45 – 10:00 Session 5/ Talk 5: Bertille Burgunter-Delamare (Jena)
A marine Chlamydomonas and its beneficial bacterial partners
- 10:00 – 10:15 Session 5/ Talk 6: Prajwal R. Basavaraju (Leipzig)
From cells to materials: Biopolymer purification, structural and mechanical insights from Chlamydomonas reinhardtii zygospores
- 10:15 – 10:45 *Vitamin & Coffee break*

Session 6 (10:45 – 12:15)

Short talk presentations, 12 + 2 min

- 10:45 – 11:00 Session 6/ Talk 1: Kirthana BijeRaj (Göttingen)
Assessing of freshwater red algae (Rhodophyta) biodiversity: development and application of a DNA metabarcoding approach within the framework of the European Union Water Directive
- 11:00 – 11:15 Session 6/ Talk 2: Mimoza Dani (Duisburg-Essen)
Species delimitation within Achnantheidium minutissimum complex, based on morphological, molecular and ecophysiological approaches
- 11:15 – 11:30 Session 6/ Talk 3: Lenka Caisova (Ceske Budejovice, CZ)
Draparnaldia: insights into alternative mechanisms of multicellularity and terrestrialization in green lineage
- 11:30 – 11:45 Session 6/ Talk 4: Karin Glaser (Freiberg)
Unveiling New Strains of the Deep-Branching Streptophyte Streptofilum: Phylogeny, Unique Traits, and the Description of S. arcticum sp. nov.
- 11:45 – 12:00 Session 6/ Talk 5: Svenja Heesch (Rostock)
Tidying up the Prasiolaceae (Prasiolales, Trebouxiophyceae): new members and new names
- 12:00 – 12:15 Session 6/ Talk 6: Maaïke J. Bierenbroodspot (Göttingen)
Phylogenomics of several streptophyte algae
- 12:15 – 13:15 *Lunch*
- 13:15 – 14:45 **Poster session 3 (Poster 36-50)****

Session 7 (14:45 – 15:45)

Short talk presentations, 12 + 2 min

- 14:45 – 15:00 Session 7/ Talk 1: Thorsten Bauersachs (Aachen)
Heterocyte glycolipids as novel tools to study the phylogeny and evolutionary history of heterocytous cyanobacteria
- 15:00 – 15:15 Session 7/ Talk 2: Thomas Roach (Innsbruck, AT)
Insights into metabolic plasticity under environmental limitations on growth
- 15:15 – 15:30 Session 7/ Talk 3: Martin Lohr (Mainz)
How algae using the photoprotective diadinoxanthin cycle prevent the accumulation of violaxanthin cycle pigments
- 15:30 – 15:45 Session 7/ Talk 4: Tim Rieseberg (Salzburg, AT)
Conserved carotenoid pigmentation in reproductive organs of Charophyceae
- 15:45 – 16:00 Session 7/ Talk 5: Peter Kroth (Konstanz)
Aureochromes – specific photoreceptors in diatoms
- 16:00 – 16:30 *Vitamin & Coffee break*

Session 8 (16:30 – 17:50)

Short talk presentations, (standard: 12 + 2 min)

- 16:30 – 16:50 Session 8/ Talk 1: Andreas Deutsch (Dresden)
Archetypes of Sex: Unmasking Algae's Innocence, the Nathanael Pringsheim Revolution
- 16:50 – 17:05 Session 8/ Talk 2: Olga Matantseva (Duisburg-Essen)
The Central Collection of Algal Cultures (CCAC) pursuing a new role of bioresource centres
- 17:05 – 17:20 Session 8/ Talk 3: Wolf-Henning Kusber (Berlin)
Cultures of microalgae: a taxonomic and nomenclatural perspective
- 17:20 – 17:35 Session 8/ Talk 4: Ladislav Hodac (Illmenau)
Deep learning of phytoplankton morphology from laboratory cultures for automated species classification in environmental samples

17:35 – 17:50 Session 8/ Talk 5: Matthew Dring (Belfast, UK)
The contributions to phycology of Klaus Lüning (1941-2023)

19:00 – 22:00 *Conference Dinner & Prices*

Wednesday, March 12th

9:00 – 12:00 *Optional: SAG offers guided Tours through its facilities (1h each)*
Please sign up [HERE](#)

Departures

Thank you!

This conference is funded by the conference fees of participants.

The meeting is organized by Georg-August-University Göttingen, namely the Dept. of Experimental Phycology and SAG Culture Collection of Algae and the Dept. of Applied Bioinformatics with the aid of the Department of Public Relations, Section Event Management.

The scientific program is realized by local scientific committee supported by the board of Section Phycology in DBG (German Botanical Society). Support by the University of Göttingen, SAG Culture Collection of Algae at Göttingen University and DBG German Botanical Society is gratefully acknowledged.



Session/ No. of Poster	First Author	Title
1/ Poster 1	Andreas Holzinger	Raman Imaging of the rafting kelp <i>Macrocystis pyrifera</i> from California
1/ Poster 2	Michaela Hittorf	The brown alga <i>Ectocarpus siliculosus</i> shows cell wall changes upon infection with <i>Maullinia ectocarpii</i>
1/ Poster 3	Yunyun Pan	Cell Wall Remodeling in the Green Macroalgae <i>Ulva</i> in Response to Environmental Input
1/ Poster 4	Bariş Ballık	Responses of Zygnematophyceae during desiccation and comparing its cell wall polysaccharide secretion patterns to the early land plant <i>Marchantia</i>
1/ Poster 5	Alena-Maria Maidel	Understanding the Lower Macrophyte Limit: A Year-long Experiment and first Results
1/ Poster 6	Johanna Weitzel	From Past to Present, Brackish and Pleasant: The Niche of <i>Chara canescens</i>
1/ Poster 7	Julien Böhm	pam: Fast and Efficient Processing of PAM Data
1/ Poster 8	Sophie Manke	Characterization of microalgae isolated from biological soil crusts on a heavy metal contaminated mining deposit
1/ Poster 9	Yagmur Tarhana Cakir	Changes in the Genetic Biodiversity of Soil Algae and Cyanobacteria under the Influences of Land Use and Vegetation
1/ Poster 10	Viktoriya Petlovana	Diversity of <i>Prorocentrum</i> species revealed by metabarcoding
1/ Poster 11	Viktoria Schinnerl	Seasonal variations in metabolite and transcript profiles in the streptophyte green alga <i>Zygonium ericetorum</i>
1/ Poster 12	Elisa Goldbecker	Comparative transcriptomics of <i>Spirogyra</i> and <i>Mesotaenium</i> reveal conserved molecular programs
1/ Poster 13	Deren Büyüktas	The effect of flavonoids on cyanobacterial motility and their role in symbiotic relationship with land plants
1/ Poster 14	Sadia Khan	Exploring Light-Induced Signaling Pathways in <i>Phaeodactylum tricorutum</i> through Transcriptomic Approaches
1/ Poster 15	Cäcilia Kunz	Investigating the Phenylpropanoid Pathway in Zygnematophyceae
1/ Poster 16	Claudia Ribeiro	<i>Draparnaldia erecta</i> - The alga of the year 2025

Session/ No. of Poster	First Author	Title
2/ Poster 17	Michael Lakatos	Algae biotechnology - an old hat, or hats off to potentials of waste recycling?
2/ Poster 18	Tanja Lakatos	Utilization of Industrial Residual Materials Through Mixotrophic Cultivation of Cyanobacteria for the Production of Valuable Compounds
2/ Poster 19	Ben Schwedhelm	Bring algae home: The first self-sufficient spirulina farm for sustainable & fresh harvests right at home.
2/ Poster 20	Fernanda Miyagi Pita	Assessment of UV-sunscreen mycosporine-like amino acids (MAAs) in two commercially important red algae from Peru
2/ Poster 21	Qian Wang	Effects of marine algal polysaccharides on the human gut microbiome and implications for gut health
2/ Poster 22	Klaus Herburger	Pilot study on scalable seaweed farming in the German Baltic Sea (Alg4Nut joint project)
2/ Poster 23	Md Atiqur Rahaman	Exploring easily harvestable freshwater filamentous algae as a sustainable source of value-added phytochemicals
2/ Poster 24	Ingmar Hofmann	Ecosystem services in eutrophic lakes with fast-settling microalgae-bacteria consortia
2/ Poster 25	Louisa Rau	Isolation of microalgae from agricultural waste water for nutrient removal by sedimenting cultures
2/ Poster 26	Jana Klose	The influence of various microalgae on Zn-dependent metalloenzymes of collagen metabolism
2/ Poster 27	Insa Mannott	Project Algae EPA - production of omega-3 fatty acids from microalgae
2/ Poster 28	Daniel Remias	Plethora of carotenoids: The pigments of Trentepohlia iolithus (Ulvophyceae) revisited with classical and contemporary chromatographic methods
2/ Poster 29	Antonio Gavalás-Olea	Galdieria sulphuraria, an extremophile with promising carbon capture performance through project ALGROW
2/ Poster 30	Lenka Štenclová	Unexpected occurrence of marine secondary metabolites in inland waters of post-mining lakes in north-west of Czechia
2/ Poster 31	Rebekah Brand	From Waste to Bioplastics: Optimizing PHB Synthesis and Recycling in Cyanobacteria
2/ Poster 32	Nadine Sydow	Algae cultivation on aquacultural wastewater as a bioeconomical concept
2/ Poster 33	Michael Sandmann	Establishment of an optical determination method for monitoring the starch content in fast growing algal cultures of Chlamydomonas reinhardtii.
2/ Poster 34	Vanessa K. Grote	Paleoclimate reconstruction by biosignatures of the freshwater microalgae Tetraedron minimum, Botryococcus braunii and Peridinium cinctum
2/ Poster 35	Antonia Schad	Beyond Aquatic Systems: Sustainable Phycocyanin Production In Terrestrial Cyanobacteria

Session/ No. of Poster	First Author	Title
3/ Poster 36	Christina Bock	Dynamic seasonal patterns of microeukaryotic communities across different lake ecosystems
3/ Poster 37	Klaus v. Schwartzenberg	Citizen Science meets Microalgae Collection MZCH - Project DesmidHH monitors biodiversity of Desmids in peat bogs of Hamburg for assessment of biotope quality
3/ Poster 38	Friedrich Altmann	Protein-linked complex carbohydrates as potent species identifiers for microalgae
3/ Poster 39	Konrad Schultz	SoilDiatoms: a new step towards soil bioindication using diatoms
3/ Poster 40	Olena Borysova	Microalgae culture collection IBASU-A: a scientific object of the national heritage of Ukraine
3/ Poster 41	Lenka Procházková	Ecophysiology of several new species of Hydrurus causing golden brown snow in Svalbard, the High Tatras and the European Alps
3/ Poster 42	Lara R. Prella	Ecophysiological responses of islandic diatoms towards abiotic variables
3/ Poster 43	Laura A. Antonaru	The ancient evolution of far-red light photoacclimation in cyanobacteria
3/ Poster 44	Tatiana Mikhailyuk	Two new phylogenetic lineages in filamentous cyanobacteria
3/ Poster 45	Tatyana Darienko	Solotvynia, a New Coccoid Lineage among the Ulvophyceae (Chlorophyta)
3/ Poster 46	Thomas Pröschold	The New Genus Caulinema Revealed New Insights into the Generic Relationship of the Order Ulotrichales (Ulvophyceae, Chlorophyta)
3/ Poster 47	Vivien Hotter	Towards deciphering interactions within the living Skin of the Earth
3/ Poster 48	Viktoriya Petlovana	A new mesophilic isolate of Pleurastrorarcina, a genus previously only reported from arid habitats
3/ Poster 49	Viktoriya Petlovana	Purification of microalgae cultures from fungal and bacterial contaminants
3/ Poster 50	Maryna Zhezhera	Rare Algae Species and Algae from the Red Data Book from the Territory of Left-Bank Polissya (Ukraine)

Efficient nuclear genome editing enables the creation of high light tolerant *Chlamydomonas reinhardtii* strains

Max Angstenberger (1), Claudia Battarra (2), Simone Barera (3), Mehrdad Jaber (2), Edoardo Cutolo (2), Luca dall'Osto (2), Roberto Bassi (4), Claudia Büchel (1)

(1) Goethe University Frankfurt am Main, Germany; (2) University of Verona, Italy; (3) University of Pavia, Italy; (4) Anton Dohrn Experimental Station Naples, Italy

Abstract

Chlamydomonas reinhardtii is the model organism for green unicellular microalgae as well as for plants and in addition has become more and more relevant for sustainable biotechnological applications. Improving the latter is one of the main challenges in order to make such approaches more economically efficient and thereby establish microalgae such as *C. reinhardtii* as suitable platforms for e.g. production of biomass, proteins or lipids. Since Photosynthesis is the fundamental process of biomass accumulation, its investigation and manipulation offers great possibilities in order to optimize bioreactor growth performance. Important photosynthetic genes, like e. g. light-harvesting complex II (LHCII) genes are nuclear encoded and thus make necessary genetic manipulation approaches in this organelle, which unfortunately appear to be quite challenging in *C. reinhardtii* as in most other microalgal species and plants. Here we present the development of highly efficient transgene-based as well as transgene-free nuclear genome editing strategies in *C. reinhardtii*. The latter was used to create transgene-free *C. reinhardtii* strains that exhibit superior autotrophic bioreactor growth performance upon high irradiation and in addition enable new insights into the underlying physiology of the photosynthetic apparatus.

Keywords

Chlamydomonas reinhardtii, Genome Editing, Biotechnology

Using the power of cis-regulatory elements to study gene function in green algae

Yuliia Lihanova, Raimund Nagel, Torsten Jakob, Severin Sasso

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04103 Leipzig, Germany

Abstract

Technological advances in sequencing techniques resulted in the discovery of thousands of genes. However, a much smaller fraction of sequenced genes have an experimentally validated function. So far, the functions of most genes have been elucidated using a gene knock-out approach, whose limitations still prevent us from exploring essential and redundant genes. To overcome these drawbacks, we established a method based on gene overexpression by activating cis-regulatory elements (CREs) in the genetic background of the algal model species *Chlamydomonas reinhardtii*. Activating CREs are short transcription factor-binding DNA motifs, which activate an endogenous promoter and thus upregulate gene expression. Individual activating CREs can be assembled into cis-regulatory modules (CRMs), also known as enhancers. To identify CREs/CRMs capable of boosting gene expression in *C. reinhardtii*, we quantified the activity of four candidates from the histone genes using flow cytometry. One of the investigated enhancers, called Ehist cons, was found to be highly conserved in the genomes of green algae and upregulated gene expression in *C. reinhardtii* over a distance of at least 1.5 kb. By random integration of Ehist cons in the nuclear genome of *C. reinhardtii*, we generated a mutant library of over 30,000 mutants, of which a few dozen showed interesting phenotypes. This work demonstrates the great potential of activating CREs/CRMs in functional genomics.

Keywords

Chlamydomonas reinhardtii, gene overexpression, enhancer

Heterologous Lhcx expression in the diatom *Phaeodactylum tricornutum*

Marie A. Wünsch (1), Jochen M. Buck (2), Peter G. Kroth (2), Bernard Lepetit (1)

(1) Molecular Stress Physiology, Institute of Biological Sciences, University of Rostock, Rostock, Germany; (2) Plant Ecophysiology, Department of Biology, University of Konstanz, Konstanz, Germany

Abstract

As phytoplankton, diatoms are exposed to intense fluctuations in light quantity requiring them to possess effective photoprotective mechanisms. One of these is the Non-Photochemical Quenching (NPQ), which is the thermal dissipation of excessively absorbed light energy. The fastest sub-type of NPQ is the high-energy-state quenching (qE). qE in diatoms not only requires specific xanthophylls, it compulsory needs the presence of thylakoid membrane-associated Lhcx proteins. These proteins are widespread amongst photosynthetic eukaryotes but their participation in qE on a molecular level is still poorly understood. It was previously demonstrated that one motif within the Lhcx proteins of *P. tricornutum* is critical for its participation in qE. Sequence comparisons show that this motif is highly conserved among Lhcx proteins of other diatoms and is even found with a high degree of homology in haptophytes or green algae. In this work, we complemented a *P. tricornutum* Lhcx1 knockout, lacking qE capacity, with heterologous Lhcx proteins from diatoms, haptophytes and green algae and characterized these mutants' physiology, protein and gene expression levels. We demonstrate that under short light stress some of the heterologous Lhcx proteins, like Lhcx proteins from the centric diatom *Thalassiosira pseudonana*, can restore qE capacity in *P. tricornutum*.

Keywords

Diatoms, Non-Photochemical Quenching, Lhcx proteins

Identification and molecular genetic bases of three sex phenotypes in *Pleodorina starrii*

Kohei Takahashi (1,2), Shigekatsu Suzuki (3), Hiroko Kawai-Toyooka (4), Kayoko Yamamoto (5), Takashi Hamaji (6), Ryo Ootsuki (4,5,7), Haruyo Yamaguchi (3), Masanobu Kawachi (3), Tetsuya Higashiyama (2), Hisayoshi Nozaki (2,3,5,8)

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Abstract

The diversity and evolution of sexual system are well studied in diploid sex-determining species but still little is known in haploid sex-determining species such as algae and fungi. We have recently revealed that *Pleodorina starrii*, one of the volvocine green algae, is the first "trioicous (coexisting of three sexes; male, female, and bisexual strains within one biological species)" species among the haploid sex-determining species. In volvocine green algae, sexes are determined by "sex-determining region (SDR)". Male SDR has MID gene that responsible for sex-determination and male gametogenesis, and female SDR has FUS1 gene known to function as gamete attachment. Based on the sexes of F1 strains obtained from intercrossing, it is assumed that bisexual strain has an identical male SDR as male strain but also has "bisexual factor (BF)" in autosomal region. Through the comparative genomic analyses, we identified the SDRs of *P. starrii* and revealed that bisexual strain retains the same SDR as male strain with duplicated MID as inferred from the intercrossing, and FUS1 has become an autosomal gene. Thus, the presence of both MID and FUS1 in haploid genome may be the genomic basis of trioicy in *P. starrii*. In addition, expression analyses revealed differences in the regulation of expression of these genes in male and bisexual strains, suggesting that may result in phenotypic differences. Currently we continue to work to identify and validate the function of BF.

Keywords

Volvocine green algae, Haploid sex-determination, Life-history evolution

Keynote-Lecture

The curious world of brown algal mating rituals

Susana Coelho,

Max Planck Institute for Biology, Tübingen, Germany

Abstract

Brown algae (seaweeds) evolved complex multicellularity independently from animals and plants, and are therefore a key eukaryotic lineage for investigating developmental processes in a broad evolutionary context. I will give a broad overview of the fascinating biology of these organisms, and discuss recent work from our lab focusing on understanding the molecular and evolutionary mechanisms that regulate mating rituals, sexual life cycles and associated reproductive features in brown algae.

Keywords

A fixed photosynthetic quotient neglects seasonal differences in kelp net primary production, especially under warming

Kiara Franke (1), Frederike Kroth (2), Inka Bartsch (3), Ulf Karsten (1), Concepción Iñiguez (4), Angelika Graiff (1)

(1) Institute of Biological Sciences, Applied Ecology and Phycology, University of Rostock, Rostock, Germany; (2) Department of Earth Observation and Modelling, Institute of Geography, Christian-Albrechts University of Kiel, Kiel, Germany; (3) Alfred Wegener Institute, Helmholtz-Centre for Polar and Marine Research, Bremerhaven, Germany; (4) Department of Ecology, Faculty of Sciences, University of Malaga, Málaga, Spain

Abstract

In the context of climate change, information on coastal carbon cycling is crucial. Kelp forests are important primary producers in coastal ecosystems. Photosynthetic quotients (PQs) are poorly understood, but are fundamental for the conversion of released oxygen into fixed carbon. We studied the kelp *Laminaria hyperborea* in the German Bight (Helgoland) in all four seasons under seasonal ambient (spring: 7°C, summer: 16°C, autumn: 14°C, winter: 6°C) and elevated temperatures ($\Delta +4^\circ\text{C}$) at simulated in situ irradiances. We calculated seasonal PQs from simultaneous measurements of oxygen evolution and carbon fixation in the range 1.7-4.4. Seasonality influenced oxygen production, which correlated with available irradiance, while carbon fixation was stimulated by warming. Net primary production (NPP) modelled with seasonal PQs was 14% higher under warming ($347 \text{ g C m}^{-2} \text{ yr}^{-1}$) than under ambient conditions ($303 \text{ g C m}^{-2} \text{ yr}^{-1}$). Warming exacerbated seasonal differences, resulting in two times higher NPP in spring and three times lower NPP in autumn than under ambient conditions. Comparison with values based on fixed PQs resulted in a 255% overestimation of NPP, neglecting seasonal variations. We therefore recommend modelling NPP rates not with a fixed PQ, but with variable PQs determined under different environmental conditions in order to obtain the full range of NPP in kelps and a reliable assessment of their future role in coastal carbon cycles.

Keywords

photosynthetic quotient, net primary production, kelp

Characterization of a bidirectional promoter in the diatom *Phaeodactylum tricornutum*

Tomáš Grivalský (1), Pavel Hrouzek (1), Petra Divoká (1), Peter G. Kroth (2), Bernard Lepetit (3)

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Abstract

Diatoms play an important role in nature because of their high diversity and abundance. *Phaeodactylum tricornutum* is a model organism for studying diatom biology, due to its easy cultivation and genetic tractability. As *P. tricornutum* produces a wide range of naturally occurring or genetically engineered compounds, it has great potential in biotechnology. Over the past decade, research on *P. tricornutum* with a focus on molecular methods to facilitate metabolic engineering has rapidly advanced. Still, further progress in genetic engineering requires a more comprehensive molecular toolbox with a greater variety of genetic elements, such as promoters, terminators, selection markers, etc. In this study, we describe an endogenous light-inducible promoter from *P. tricornutum* capable of bidirectional transcription. Using the uLoop system, we generated and characterized clones producing two different fluorescent proteins driven by this bidirectional promoter. These clones were tested under various light conditions and growth stages to assess promoter activity. The promoter showed a high bidirectional activity both under low and high light as well as under exponential and stationary growth conditions. In silico analysis revealed regulatory elements potentially responsible for its bidirectional activity. This first study of a bidirectional promoter region in diatoms holds significant potential for metabolic engineering, particularly in applications requiring balanced protein production.

Keywords

Promoter, Diatoms, *Phaeodactylum*

Session 2/ Talk 3

Success is more than photosynthesis – The activity of benthic diatoms in the dark

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Abstract

Primary production is ultimately driven by sunlight, a source of energy that drastically varies over a diurnal cycle. Microphytobenthic communities often dominated by benthic diatoms therefore have to not only metabolically adapt to changing redox conditions, but also to the diel dynamics in their environment. Thus, a better understanding of the niche of oxygenic phototrophs urges for a description of their dark side. Understanding phototroph competitive advantage in the co-evolving redox landscape, requires consideration of their activity over a complete diel cycle, i.e. their metabolic repertoire beyond photosynthesis. Some eukaryotic algae, such as diatoms, are able to switch to respiration of internally stored nitrate via dissimilatory reduction of nitrate to ammonium (DNRA). In the microbial mats of the submerged Middle Island Sinkhole, Lake Huron (USA) the benthic epipellic diatom *Craticula cuspidata* seasonally outcompetes cyanobacteria. To assess, if the competitive advantage of the NO₃⁻-storing diatoms is related to their capability to perform DNRA, we studied the diel activity transitions using stable isotope incubations and in situ microsensor measurements over complete light cycles. We found that this diatom links NO₃⁻ respiration to diel migration into deep (4 cm) sulphidic sediments below the microbial mat. Vertical migration to escape grazers or adjust to changing light conditions is a common behaviour in benthic diatoms, however, *C. cuspidata* spends the majority of the day in dark, anoxic sediments. Thus, diatoms fundamentally impact the biogeochemistry beyond the sunlit realm. The unexpected niche for benthic diatoms revealed in this study emphasises the importance of the dark side of diatoms.

Keywords

microbial mats, diatoms, benthic N-cycle

Combined effect of temperature and light stress on the photoprotection capacity of a model diatom

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Abstract

Diatoms thrive in turbulent waters, complex environments in which light is subject to frequent and extreme light changes. In response, these heterokont microalgae display a fast Non-Photochemical Quenching (NPQ), a form of excess energy dissipation as heat that relies on the xanthophyll cycle, a reversible interconversion of carotenoid pigments. While light is usually regarded as the most important variable influencing photosynthesis, in Nature other environmental drivers (like nutrients, carbon availability, pH or temperature) put these mechanisms to the test. Yet, the combined effects of light and other environmental parameters have not been frequently addressed in photophysiological studies. In this work we applied a broad range of combined temperatures and light intensities on the wild type and different xanthophyll cycle mutants of the pennate diatom *P. tricornutum* and investigated the resulting NPQ dynamics. Both lower and higher temperatures affected these dynamics, however with different effects on the NPQ inducing compared to the NPQ relaxing components. We propose that these are independent from the energy requirements of the cells and rather result from altered xanthophyll cycle activity under different temperatures.

Keywords

Diatoms, Photoprotection, Temperature

The role of phenolics in stress tolerance in Zygnematophyceae

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Abstract

Zygnematophyceae are the closest relatives of land plants (Embryophyta). They are widely used as model organisms for stress tolerance studies in the evolutionary context of plant terrestrialization. Our recent research has focused on the production of phenolics, secondary metabolites typical of higher plants and several algal lineages (e.g. Zygnematophyceae). Due to their chemical structure, phenolics act as natural UV screening compounds. Moreover, their role in other stresses has been proposed. Our experiments with *Spirogyra* showed a significant increase in phenolic content e.g. at low temperature, osmotic stress conditions and increased light intensity. In addition, we performed a screening for phenolic compounds in several strains belonging to different species using HPLC, since the presence of phenolics has only been confirmed in a few zygnematophycean members. The tested strains of *Penium*, *Pleurotaenium*, *Euastrum* and *Staurastrum* contained an identical polar substance with maximum absorption at 285 nm, which is not present e.g. in *Spirogyra*. In contrast, no UV-absorbing substances could be detected in the investigated strains of *Closterium* and *Gonatozygon*. To show an evolutionary pattern in the presence of phenolic substances in Zygnematophyceae, more strains are currently being analyzed. Furthermore, we ask how phenolic content changes both quantitatively and qualitatively with culture age and whether there is a correlation between genome size and phenolic content.

Keywords

phenolics, stress, Zygnematophyceae

Diversity and ecophysiology of the conjugating green algae (Zygnematophyceae), with special reference to their photoprotective strategies.

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Abstract

Despite their rather simple morphology, the Zygnematophyceae are the closest relatives of land plants, sparking significant interest in their evolution. Yet, the taxonomy of these algae does not reflect current phylogenetic insights, resulting in several polyphyletic genera. In particular, the saccoderm desmids from terrestrial and ephemeral habitats are understudied, even though some of them produce interesting secondary pigments with unknown function and chemical identity. In my PhD research, I identified twelve distinct lineages of Mesotaenium-like zygnematophytes and introduced a provisional clade nomenclature. Furthermore, I characterized a new species, *Ancylonema palustre*, which represents a mesophilic relative of common glacier algae. Cultures of this species enabled the study of its reproductive processes and the experimental induction of intracellular secondary pigments. Another key finding was the rediscovery of saccoderm desmids which produce pigmented extracellular mucilage and are now assigned to the genus *Serritaenia*. Research on *S. testaceovaginata* revealed that the pigmented mucilage acts as an effective sunscreen and elucidated potential mechanisms of UVB perception and sunscreen biosynthesis. Overall, the thesis provides new insights into the diversity and cellular adaptations of saccoderm desmids, and emphasizes the value of combining biodiversity research with the functional characterization of non-model organisms.

Keywords

Macroalgae Matters: Sustainable Coastal Solutions from Beachwrack for Nutrient Supply and Coastal Management

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Abstract

Beachwrack, a natural accumulation of macroalgae, seagrass and other organic matter on beaches, is often perceived as waste that disrupts tourism and incurs high disposal costs. However, beachwrack plays a vital role in coastal ecosystems by providing nutrients and stabilizing sediments. This study explores whether beachwrack can be repurposed as a sustainable substrate for coastal vegetation. We conducted a 12-week growth experiment using different substrates—beachwrack, compost, and only sand—to cultivate marram grass (*Ammophila arenaria*), a key dune stabilizing plant. Plant measurements were taken biweekly, and sediment samples were analyzed for moisture and nutrient availability. Preliminary results indicate that marram grass exhibited the fastest growth rates and highest moisture retention when grown in beachwrack substrate. While isotopic analyses to trace nutrient uptake from decaying macroalgae are still ongoing, our findings suggest that beachwrack can enhance nutrient supply for coastal vegetation. However, potential risks from contaminants must be considered, as well as the composition of the beachwrack. Therefore, in a second part of the experiment, the seasonal composition of the beachwrack was investigated at several locations in the Baltic Sea, e.g. in Germany and Sweden. With climate change potentially increasing macroalgal dominance in beachwrack composition, repurposing beachwrack as a substrate could offer a sustainable solution for coastal management.

Keywords

Coastal vegetation; nutrient cycling; Macroalgae-based substrates

Elucidating the mechanisms underlying streptophyte glacier ice algae adaptation to extreme variations in light availability

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Abstract

Glacier ice algae of the streptophyte genus *Ancylonema* live on glaciers globally, including the Greenland Ice Sheet, and bloom despite low temperatures and very high light intensities. In polar regions, the long polar night also imposes additional abiotic stressors. However, the cellular mechanisms responsible for *Ancylonema*'s resistance and adaptation to high light stress or to prolonged darkness are not known. We addressed this knowledge gap by evaluating the functional responses of a Greenland Ice Sheet *Ancylonema*-dominated microbiome to in-situ light conditions and continual darkness during a 12-day period using amplicon sequencing, metatranscriptomics, and metaproteomics. The microbial community did not substantially change during the 12 days of dark incubation; however, heterotrophs became more transcriptionally active in the dark. Metatranscriptomic and metaproteomic analyses showed that *Ancylonema* cells underwent high oxidative stress in the light. However, after 12 days in darkness, the algal cells retained functional photosynthetic machinery but downregulated their expression of early shikimate pathway enzyme transcripts. Transcriptional reprogramming linked to sugar uptake and phytohormone signalling was also identified in the dark, providing an insight into the first steps towards algal cell survival through the polar night. These results provide essential clues regarding the adaptation of these streptophyte species to a harsh and extremely variable environment.

Keywords

Glacier Ice Algae; Light Stress, Polar night

Effect of nutrient composition on cell growth, color, and photophysiology of cultured glacier ice algae

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Abstract

Glacier ice algae of the genus *Ancylonema* are the main primary producers on glacier ice surfaces, where they thrive under high light and low nutrient availability. *Ancylonema* cultures were only recently established but an in-depth optimization of their laboratory growth conditions and nutrient requirements is still missing. In this study we tested if supplementing a 100-fold diluted 3N BBM medium with different media components (e.g. iron, vitamins) influences glacier ice algae growth, color and photophysiology. Media supplementation with both iron and vitamins contributed to a modest increase in growth rates, while cultivation with increased iron led to a dark brown coloration of the in culture normally light green cells. Preliminary analyses of extracted hydrophilic pigments by UV-VIS indicates that the glacier ice algae formed purpurogallin, which likely caused the dark coloration. Analysis is underway to evaluate if intracellular iron precipitates could also be a cause for the change in cell color. The photophysiology of the algae treated with increased iron and vitamin concentrations was evaluated by Pulse-amplitude modulated fluorometry. Our results reveal that neither vitamins nor iron supplementation had an effect on the maximum photosynthetic potential and light utilization efficiency at normal light conditions, but increased iron had a slightly negative effect after exposure of the cells to high-light stress for 48 hours despite the dark coloration of the cells.

Keywords

Glacier ice algae, cultivation, PAM fluorometry

Native proteins from microalgae as a replacement for serum in mammalian cell culture

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Abstract

The project presented here aims to replace fetal bovine serum (FBS) with an algae-based serum for the cultivation of Chinese Hamster Ovary (CHO) cells. CHO cells are most commonly used as an expression platform for recombinant proteins, such as monoclonal antibodies [1]. In addition, CHO cells have the potential to serve as an alternative for animal testing, e.g., for testing toxin activity in acellular pertussis vaccine [2]. For the in vitro cultivation of mammalian cells, FBS is an important supplement for cell proliferation as it contains proteins, growth factors, hormones, amino acids and vitamins [3]. However, the components of FBS are not yet fully identified and the quality of the serum is not stable between batches [4]. These and many other concerns highlight the need for an effective alternative for FBS in the cultivation of mammalian cells. For this research, we chose the red extremophile microalgae *Galdieria sulphuraria*, which is rich in protein and can be grown on various organic carbon sources, resulting in a higher biomass yield [5]. We extracted native protein fractions in different growth phases and verified their activity using enzyme activity assays. Both, the algae crude extracts and native protein were tested as FBS replacement in CHO cultures. In addition, both fractions were heat-inactivated and also examined with regard to cell vitality, proliferation, as well as toxic effects on CHO cells. The enzyme activity assays revealed a successful extraction of native protein. Furthermore, crude and protein extracts exhibited a stimulating or inhibiting effect on CHO cells, depending on whether they were native or heat-inactivated

Keywords

Galdieria sulphuraria, native protein, Fetal Bovine Serum

Photosynthesis-driven biocatalysis in cyanobacteria: A sustainable approach to chemical precursor production

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Abstract

Photosynthesis-driven whole-cell biocatalysis in cyanobacteria presents a promising approach for the sustainable production of chemical precursors. This method utilizes water as both an electron and oxygen source, CO₂ as a carbon source, and light as an energy source. One such promising biocatalytic project is the biotransformation of cyclohexanol to produce nylon precursors using engineered *Synechocystis* sp. PCC 6803. The presented biotransformation involves a complete enzyme cascade for the conversion of cyclohexanol to ϵ -caprolactone, catalyzed by heterologous expressed enzymes. In order to enhance the sustainability of this approach, cyclohexanol can be derived from lignin depolymerization, to replace the fossil compounds used today for nylon production. Recently, the whole process has been scaled up from small batch reactions to various photo-bioreactor configurations. Future research aims to use these results as a basis for carbon and energy balances to demonstrate feasibility and improve process performance. This research will advance the development of an environmentally friendly, light-driven biocatalytic process and contribute to sustainable chemical production.

Keywords

Cyanobacteria, biotechnology

Growth and nutrient uptake of site adapted microalgae-bacteria consortia in multiple undiluted, high strength landfill leachates

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Abstract

This study presents the assessment of a microalgae-bacteria consortium (MBC) isolated from a landfill in Lindlar, Germany. Growth and major nutrient removal capabilities were examined in four landfill leachates (LL) from three different German landfills, containing $\text{NH}_4^+\text{-N}$ concentrations between 244-934 mg/L and COD between 502-2076 mg/L. Microalgae growth was observed in all leachates with growth rates ranging from 0.4 to 1.2 g dry weight per liter and day. In contrast to previous studies, dilution or pretreatment of leachates was not necessary, indicating an unusually high tolerance for the site adapted microalgae under the given conditions. Highest accumulated biomass concentrations and second highest growth rate during 15 days of culturing was observed in LL with highest NH_4^+ concentrations. After 15 days of culturing, concentrations PO_4^{3-} , COD, NO_2^- and NO_3^- were significantly lower in MBC cultures in comparison to control cultures without inoculation. Inoculation however, had no significant effect on NH_4^+ decrease in most of the leachates tested. Consequently, it is presumed that the present microalgal species used NO_2^- and/or NO_3^- as primary nitrogen source instead of NH_4^+ despite the sufficient presence of NH_4^+ . Steady growth rates of microalgae could be similarly observed under different pH values (6, 7, 8 and 9), suggesting a tolerance to NH_3 as well. High ammonia tolerances of site adapted microalgae might enable an industrial scale integration of microalgae into conventional, bacterial based wastewater treatment systems, offering the possibility to save resources and recover nutrients from waste streams.

Keywords

microalgae-bacteria consortia, Wastewater treatment, Landfill leachate, Site adapted microalgae, Ammonia tolerance, High strength wastewater

Current Status of Industrial Microalgal Biotechnology in Germany as Emerging Sector of the Blue Bioeconomy

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Abstract

Germany has emerged as one of the leading players in the development of industrial algal biotechnology since the 1970s, leveraging its advanced research infrastructure, innovative technologies, and growing market interest. This presentation provides an overview of the current state of microalgal biotechnology in Germany, emphasizing the structure of this emerging sector within the blue bioeconomy, key advancements in cultivation systems, and applications across various industries. Microalgae are increasingly utilized for food, feed, biofuels, pharmaceuticals, and cosmetics, driven by the demand for novel bioactives, resource efficiency, sustainability, landless biomass production, indoor farming, and integration into a circular economy. Notable initiatives include the establishment of mid-scale photobioreactor facilities, collaborations between academia and industry to optimize production efficiency, the development of innovative product concepts and go-to-market strategies and others. Despite these advancements, challenges such as high production costs, regulatory barriers, and scalability constraints persist. This presentation will also discuss recent policy developments, public-private partnerships, and the role of German companies and research institutions in shaping the global microalgal biotechnology landscape. By examining ongoing projects and emerging trends, we aim to inspire discussions on the potential of microalgae as a cornerstone of a bio-based economy, particularly in the context of the current multi-crisis scenario and beyond.

Keywords

microalgae bluebioeconomy biotechnology

Lab cultivation of coralline red algae: A promising carbon storage agent

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Abstract

The red, calciferous macroalgae, *Lithophyllum corallinae* plays a pivotal role in marine ecosystems, particular reef formation in temperate oceans, like the Mediterranean sea. This coralline red alga, widely distributed across global marine habitats, is notable to sequester carbon dioxide (CO₂) and precipitate structure building calcium carbonate (CaCO₃) matrices, enabling photosynthetic cementitious biomass formation without external nutrient inputs. These properties position *L. corallinae* as a potential agent for long-term carbon storage and as a performance enhancer in self-healing concrete structures. Nevertheless, laboratory cultivation of *L. corallinae* is crucial to realizing these applications. Our research focuses on optimizing and scaling its cultivation by simulating the natural conditions of the Adriatic Sea, where the algae was collected at an 18-meter depth. Using inductively coupled plasma mass spectrometry (ICP-MS) to analyze site water samples, we determined an optimal media composition. A controlled aquarium setup with precise temperature, pH, light, wave simulation and filtration was established. Growth conditions were refined by varying temperature (5–25 °C), optimizing pH for carbonate availability, and adjusting light spectra and cycles. This work represents the first successful lab-scale cultivation of *L. corallinae*, providing a foundation for its biotechnological application in sustainable concrete technologies as a value adding carbon storage solution.

Keywords

Lithophyllum corallinae, cultivation, carbon storage.,

Characterization of floc-forming and fast-sedimenting microalgae-bacteria consortia in bioremediation

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Abstract

The microalgae-bacteria consortia here described were created by Dr. Niels C. Holm by isolating freshwater samples and selecting it repeatedly for fast-sedimenting structures. This characteristic sedimentation behavior makes this culture suitable for a vast field of biotechnological applications especially in the field of bioremediation. The aim of this project was to make use of a suitable set of methods to describe these communities and their permanent flocculation and sedimentation behavior. We found that metagenomic sequencing combined with scanning electron microscopy allowed us to compare species composition across various samples. The sinking properties of this culture were determined by recovery rate, sinking velocity and particle size. When looking at the found microalgal and cyanobacterial species, we observed a strong dependence on the wastewater or artificial medium used. The sinking properties varied mostly in particle size and sinking velocity, while the recovery rate stayed similar in all media used. Further, the manipulation of (a)biotic physiological parameters such as pH, temperature, salinity, light and antibiotics treatment indicates that floc-formation can serve as an effective protection layer against harsh environmental conditions. Confocal microscopy revealed the presence of a biofilm layer consisting mainly of proteins and polysaccharides which seems to stick the flocs together. The challenging extraction of extracellular polymeric substances (EPS) did not prevent subsequent reflocculation. However, the floc-formation can be effectively inhibited by either antibiotic or enzymatic treatment. Moreover, the extracted EPS can serve as a flocculant for non-flocculating microalgae *Chlorella vulgaris* which both emphasizes the importance of these substances in the floc-forming and sedimentation process. The presented findings uncover driving factors for particle aggregation in these communities and will help to improve biotechnological setups in the future.

Keywords

bioremediation, microalgae-bacteria consortia, extracellular polymeric substances

Wastewater purification with fast settling microalgae-bacteria consortia

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Abstract

The BMBF-project Femak aims to establish a mobile mass algae cultivation facility (MAK) for research and development. This facility, located at the Plön wastewater treatment plant (WWTP), will serve as a prototype to demonstrate how the production of microalgae-bacteria consortia can be integrated into WWTP processes. Unlike conventional algae cultivation, typically conducted in batch processes, the MAK concept enables continuous water treatment by utilizing fast-settling algae in plug-flow reactors. The MAK consists of a photobioreactor and a sedimentation tank for efficient algae recovery and harvesting. The facility can operate using the water output from the WWTP. The project's main objectives include year-round production of nutrient-depleted, cold, and oxygen-saturated wastewater for water remediation. Additional goals involve optimizing various operating modes of the bioreactor to maximize biomass production efficiency and investigating the potential applications of the produced biomass. By leveraging and advancing algae cultivation technologies, the Femak project aims to develop innovative solutions for wastewater treatment, reduce environmental impacts, and promote sustainable resource use. Several follow-up projects in various adjacent fields will be presented

Keywords

microalgae-bacteria consortia; WWTP; remediation

Milking of extracellular oils from *Botryococcus braunii*: A technical-scale study using 28-litre flat-panel airlift reactors

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Abstract

In situ extraction, also known as "milking", has emerged as a promising approach to reduce downstream costs and to economically produce low-value substances, such as lipids, from microalgae. The green microalga *Botryococcus braunii* possesses the capacity to secrete substantial quantities of long-chain hydrocarbons into an extracellular matrix, rendering it well-suited for this approach by eliminating costly steps such as harvesting, dewatering, and cell disruption [1]. Based on the identification of two *B. braunii* strains (both B race) as potential candidates for the milking process in previous studies [2,3], the objective of current investigations is to demonstrate the practical suitability of the milking process for industrial application by scaling up to higher culture volumes, including process optimization regarding higher hydrocarbon yields. For this, the cultivation was initially transferred from 6 L to 28 L flat-panel-airlift-(FPA)-reactors. The optimal light intensity for algae growth and hydrocarbon formation was determined to be between 500 and 800 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$. A substantial enhancement in biomass and hydrocarbon productivity to 1.0 g L⁻¹ d⁻¹ and 0.50 g L⁻¹ d⁻¹, respectively, was observed in comparison with cultivation at low light intensity. [1] Griehl, C., Kleinert, C., Griehl, C., Bieler, S. (2015) https://doi.org/10.1007/978-94-007-6111-1_10 [2] Kleinert, C., Griehl, C. (2021) https://doi.org/10.1007/978-94-007-6111-1_10 [3] Kleinert, C., Griehl, C. (2022). https://doi.org/10.1007/978-94-007-6111-1_10

Keywords

Botryococcus braunii, hydrocarbons, milking

Analysis of Cobalamin and Pseudocobalamin Composition in Microalgae Cultures

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Abstract

Vitamin B12 (cobalamin) is an essential micronutrient in the human diet. It is required for cell division, blood formation and the function of the nervous system. A deficiency can lead to anemia and neuropsychiatric or neurological disorders. Vegans/vegetarians are particularly affected, as vitamin B12 is mainly found in foods of animal origin and not in plants. The green alga *Chlorella vulgaris*, which absorbs and accumulates vitamin B12 that is synthesized by mutualistic bacteria, can become a suitable vegan source with vitamin B12 levels that are higher than in meat products [van den Oever & Mayer 2022 DOI concentrations vary widely depending on the cultivation conditions. Furthermore, in some cases *Chlorella* products contain, besides biologically active cobalamin derivatives, a significant share of inactive pseudo-cobalamins, which cannot be detected using standard microbiological assays, leading to an overestimation of the vitamin B12 content. To improve the production of vitamin B12-rich *Chlorella*, an UPLC-MS method was developed to quantify the individual derivatives cyanocobalamin, hydroxocobalamin, adenosylcobalamin and methylcobalamin in *Chlorella* after immunoaffinity-based sample preparation. The Q-ToF MS was operated in negative ionization mode, monitoring the characteristic fragment 1328.56 [M – upper ligand]- that is formed by all four investigated cobalamins. Identity was verified by exact mass and MS/MS experiments. The developed method was successfully used to analyze *Chlorella* samples from industrial cultivation process.

Keywords

Chlorella, Vitamin B12, UPLC-MS

Far-red light-driven nitrogen fixation in free-living and symbiotic cyanobacteria

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Abstract

Cyanobacteria played a major role in the oxygenation of early Earth and they continue to be key players in carbon and nitrogen cycles in various habitats. Their photosynthetic capability depends on light quantity and quality. A small, phylogenetically diverse subset of cyanobacteria can perform oxygenic photosynthesis with far-red light through a process called far-red light photoacclimation, or FaRLiP. This phenotype is encoded by a cluster of ~20 genes, and it involves the synthesis of a red-shifted chlorophyll f, together with paralogues of the standard photosynthetic machinery. Here, we test whether far-red light can also drive nitrogen fixation. We use several free-living and symbiotic cyanobacteria from phylogenetically diverse groups and show by biochemical and biophysical methods that these organisms can (i) undergo FaRLiP and (ii) fix nitrogen with pure far-red light. We furthermore discovered a symbiotic cyanobacterium that has undergone significant genome reduction, most likely to fulfil the role as a far-red light-driven nitroplast. The implications of this naturally occurring phenomenon are discussed in terms of its importance in the environment and for biotechnological applications.

Keywords

Cyanobacteria, FaRLiP, Nitrogen fixation

Far-red light photosynthesis contributes to a saline soil crust ecosystem

Shujie Wu, Laura A. Antonaru, Qingfeng Zhang, Janosch Brandhorst, Gian G. Ori, Niels-Ulrik Frigaard, Daniel Canniffe, Michael Köhl, Dennis J. Nürnberg

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Abstract

Photosynthetic organisms in desert environments must contend with extreme conditions, including high temperatures, aridity, and intense radiation. Despite these challenges, microbial communities within soil crusts thrive beneath the surface, making substantial contributions to local primary production under limited light availability. However, the mechanisms enabling these photosynthetic crusts to persist in shaded environments remain only partially understood. This study focuses on the Sabkha Oum Dba salt pan in Morocco, emphasizing the ecological significance of far-red light (700–800 nm) in these environments. Two cyanobacterial strains capable of far-red light photoacclimation (FaRLiP) were isolated and identified as genera of the Nodosilineales, an early-diverging order of filamentous cyanobacteria. To further investigate the functional role of FaRLiP, one of the isolates was employed to develop sand model experiments under laboratory conditions. The resulting cyanobacterial biocrusts closely resembled the natural samples, with red shifted chlorophyll d and f predominantly localized in the lower layers. Light and oxygen microsensor analyses of the biocrusts revealed spectral shifts characteristic of FaRLiP, demonstrating that far-red light drives oxygenic photosynthesis in these deeper layers, thereby underscoring the pivotal role of FaRLiP in supporting microbial photosynthesis and primary production in shaded desert environments.

Keywords

soil crust, cyanobacteria, far-red light photoacclimation

Changes in the biodiversity of soil algae in arable land - a pilot study using multiple DNA-Metabarcoding

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Abstract

The intensification of agriculture is a major threat to global biodiversity. Soil algae are a diverse and ecologically significant part of the soil microbiome in arable land. We assessed changes in the biodiversity of soil algae in organic wheat fields of the Hessian domain Frankenhausen (central Germany) and surrounding conventional arable land with wheat and corn as crops. Multiple DNA barcodes (18S, 23S UPA, ITS2, rbcL) identified the soil algae to species level and addressed their relative abundance within the algae community and co-occurrence with other protists. The Xanthophyceae (Stramenopiles), which has been underestimated in most studies, was particularly important. Xanthophyceae and diatoms dominated in spring, while Cyanobacteria prevailed in summer. The soil algae composition was influenced by organic versus conventional agricultural practice and crop type. Still, more research is required to identify factors determining the soil algae biodiversity on arable land.

Keywords

soil algae, agriculture, metabarcoding

**Nutrient availability affects stalk formation by the benthic diatom
*Achnanthes minutissima***

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Abstract

Achnanthes minutissima is a widely distributed freshwater benthic diatom. The alga is capable of producing both capsules as well as stalks to attach cell bodies to surfaces. Both structures consist of extracellular polymeric substances (EPS) that are mainly carbohydrates, and can be induced by a compound secreted by the bacterium *Dyadobacter* sp. 32. There are different hypotheses as to why some diatoms develop stalks. Here, we have studied stalk formation of *A. minutissima* after induction with bacterial compounds at different nutrient compositions in the culture media. Our experiments focused on the frequency of stalk production as well as stalk length, indicating that they may depend differently on the availability of specific nutrients. We furthermore could show that stalk formation only occurs in the light and that it depends on active photosynthesis.

Keywords

Diatom, stalk, nutrients

A marine *Chlamydomonas* and its beneficial bacterial partners

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Abstract

Microalgae are key contributors to global carbon fixation, but the molecular details of their biotic interactions, e.g. with bacteria, are still barely understood (Burgunter-Delamare et al., *Plants*, 2024). So far, we have used the unicellular soil alga *Chlamydomonas reinhardtii* as a model to study algal-bacterial interactions in terrestrial environments (Carrasco Flores et al., *Proc. Natl. Acad. Sci. USA*, 2024). Here, we have used its marine counterpart, *Chlamydomonas* sp. SAG25.89 (Csp). Its draft genome is present (PRJEB38422), and a transformation protocol has been developed (Carrasco Flores et al., *J. Phycol.*, 2021). Marine *Chlamydomonad* algae have recently been shown to be important members of Antarctic phytoplankton blooms (Saggiomo et al., *J. Phycol.*, 2021). As such, Csp is used to investigate algal-bacterial interactions affecting algal fitness in marine environments. The draft genome of Csp and experimental data reveal that it cannot use NO_3^- as a nitrogen source but needs NH_4^+ . We checked whether a diazotrophic partner could complement the NH_4^+ deficiency, which is the case. Moreover, we found a mutualistic bacterium that enhances algal growth and chlorophyll biosynthesis in algal-bacterial cocultures via a yet unknown heat-resistant compound.

Keywords

Chlamydomonas, Algal-bacterial interactions

From cells to materials: Biopolymer purification, structural and mechanical insights from *Chlamydomonas reinhardtii* zygospores

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Abstract

Chlamydomonas reinhardtii is a single-celled model alga (Chlorophyta) that thrives in temperate soils. While gametogenesis and zygote formation have been studied extensively in *C. reinhardtii*, only a handful of publications have investigated the development of the zygote into a dormant zygospore. We know the indispensability of the PKS1 gene during the formation of the zygotic cell wall, which facilitates the maturation of newly generated zygotes into zygospores (Heimerl et al. (2018), *The Plant Journal*, 95, 268–281). Zygospores represent a quiescent phase of the alga, marked by their resilience against challenging environmental conditions. The objective of this project is the purification and structure elucidation of the resilient biopolymer present in the cell wall of *C. reinhardtii* zygospores. Following a series of organic solvent washes and refluxing with various acids and bases, 1.2 mg of a highly resistant biopolymer was obtained from 12.9 g of initial fresh weight cell material. Diverse analytical techniques, including solid-state ¹³C-nuclear magnetic resonance, and Fourier transform infrared spectroscopy were used to investigate the chemical structure of the purified polymer. Our preliminary analysis elucidated an aliphatic polymer consisting of hydroxylated fatty acids crosslinked via ester and ether bonds to form a resistant polymeric network. Our structure is similar to the polymer model proposed for zygospores of *Chlamydomonas monoica* (Blokker et al. (1999), *Planta*, 207, 539–543). To determine the length distribution and molecular weight of the polymer building blocks, we will degrade and analyze the polymer using pyrolysis-GC/MS. The protocol is being optimized in order to scale up production and purify more polymer. Detailed structure elucidation and examination of its mechanical properties will pave the way for beneficial applications in the future.

Keywords

Zygospores, algaenan, polyketide synthase, biopolymer, structure elucidation, NMR

Assessing of freshwater red algae (Rhodophyta) biodiversity: development and application of a DNA metabarcoding approach within the framework of the European Union Water Directive

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Abstract

The main goals of the project are: 1) the development of a reliable and fast method (metabarcoding) for the precise genotypic identification of species of freshwater red algae, including their microscopic sporophytic stages in submerged biofilms not identifiable to species by microscopy; 2) an assessment of the freshwater red algae diversity in Germany using the Harz mountains as an exemplar region; 3) to test the feasibility of freshwater red algae as bioindicators. We will elucidate the distribution patterns of the genotypically distinguished species with respect to habitat features. DNA metabarcoding using the UPA-23S marker effectively helped identify the different genera and species of red algae. A second marker, almost complete *rbcl* gene sequences, helps to calibrate the red algal metabarcodes. So far, a total of 18 species (Batrachospermales) has been identified with the calibrated barcodes. This includes unique species of *Kumanoa*, *Batrachospermum pozoazulense*, *Lemanea fucina* and five species of *Sheathia*.

Keywords

Fresh water Red Algae, Metabarcoding, UPA-23S marker

Session 6/ Talk 2

Species delimitation within *Achnantheidium minutissimum* complex, based on morphological, molecular and ecophysiological approaches

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Abstract

Achnantheidium is a widespread monoraphid, benthic diatom genus abundant in various freshwater habitats with a wide tolerance range. Delimiting *Achnantheidium* species is challenging due to their small size and morphological features overlapping among most related taxa and often a lack of clear morphological criteria for differentiation. To investigate the congruence between morphological, molecular and ecophysiological variability in the *Achnantheidium minutissimum* complex, I applied an integrative taxonomic approach to thirteen monoclonal strains isolated from Germany, Sweden and Spitsbergen. Besides a characterization of valve morphology using light and scanning electron microscopy, I compared sequences of the *rbcl* marker gene and assessed their growth under the combination of different temperatures and salt concentrations. The results revealed a broad congruence between morphological, molecular, and ecophysiological variability, with some clusters assignable to a narrow morphologically described species of the *A. minutissimum* complex. The combined morphological-molecular-eco-physiological approach provides a clearer and more objective picture of species differentiation and ecological profiles. Therefore, extending an integrated taxonomic approach to more strains of diverse geographic origins and spanning a broader range of environmental conditions will be beneficial to better understand the morphological and niche differentiation among different *Achnantheidium* species.

Keywords

Species delimitation, *rbcl* marker, Ecophysiology

Draparnaldia: insights into alternative mechanisms of multicellularity and terrestrialization in green lineage

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Abstract

Green plants contain two main algal lineages: chlorophytes and streptophytes; the latter diverging into land plants. It remains a mystery why chlorophytes, despite some being morphologically complex, never conquered land. I will introduce to you the alga *Draparnaldia*, that we are establishing as a new Chlorophyte model to study alternative mechanisms of multicellularity and terrestrialization in green plants. *Draparnaldia* is unique being the only morphologically complex chlorophyte that also shows adaptations to the terrestrial habitat. Then, I will guide you through our findings from *Draparnaldia*'s genome and transcriptomes sequencing and profiles of its phytohormone repertoire. Specifically, we identified expanded gene families with respect to unicellular *Chlamydomonas* that are linked to multicellularity and adaptations to abiotic stress. Despite *Draparnaldia*'s independent evolution, there are striking morphological and molecular analogies with the establishment of multicellularity and terrestrialization in streptophytes. Similarly, despite *Draparnaldia* synthesizing most of the phytohormones used by land plants, it is missing many of their canonical signaling components. *Draparnaldia* thus represents a powerful stepping-stone to uncover alternative evolutionary trajectories towards multicellularity and terrestrialization in plants. Finally, I will introduce to you topics that we are addressing in our newly established group at the Institute of Plant Molecular Biology, CZ.

Keywords

Unveiling New Strains of the Deep-Branching Streptophyte *Streptofilum*: Phylogeny, Unique Traits, and the Description of *S. arcticum* sp. nov.

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Abstract

Streptofilum capillatum forms a phylogenetically deep branch within the streptophytes and its unique cell covering composed of piliform scales – thus, it immediately attracted scientific attention after the description in 2018. Its phylogenetic position and taxonomic rank remain topics of ongoing debate. Here, we present additional strains of *Streptofilum*, which were isolated from biocrusts in sand dunes in Germany and Arctic tundra soils. Molecular and morphological analyses, including transmission electron microscopy, confirmed that both new strains belong to the genus *Streptofilum*. The Arctic strain was introduced as a new species, *S. arcticum* sp. nov., based on molecular and morphological distinctions. A detailed analysis of the ecophysiological traits of the two new *Streptofilum* isolates, along with the original strain (SAG 2559), revealed broad temperature tolerance, rapid recovery of photosynthetic efficiency following desiccation, effective photosynthesis under low light, and resilience to high-light conditions. Furthermore, *Streptofilum* demonstrated resistance to enhanced UV radiation, though only *S. capillatum* was able to grow under experimental UV exposure. All *Streptofilum* strains exhibited strong adaptations to water-deprived terrestrial environments, such as biocrusts. These findings suggest that early-diverging streptophytes were already capable of tolerating terrestrial conditions.

Keywords

cell coverage; TEM; ecophysiology;

Tidying up the Prasiolaceae (Prasiolales, Trebouxiophyceae): new members and new names

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Abstract

The Prasiolaceae is a small family of Trebouxiophycean green algae known for their multicellular thalli and their appetite for nutrients: they are typically found at sites frequently fertilised by animals, with their preferred habitats ranging from bird colonies in polar regions to urban sites in temperate latitudes regularly visited by dogs and other mammals. In recent years, the taxonomy of the family has been greatly improved by molecular genetic techniques. Previous studies had, for example, shown the largest genus *Prasiola* to be polyphyletic. To solve this polyphyly, new combinations are proposed for three clades comprising a total of seven species. Moreover, the isolation & cultivation of additional strains have led to the discovery of several new entities. Two new genera with one and two new species, respectively, are currently being described, while the descriptions of several additional new members of the family are in preparation.

Keywords

Prasiolaceae, taxonomy, new taxa

Phylogenomics of several streptophyte algae

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Abstract

The colonization of terrestrial environments by plants represents a landmark event in Earth's biological history, fostering the rise of complex ecosystems. Streptophyte algae, the closest relatives of land plants, were pivotal to this transition, evolving essential adaptations to mitigate abiotic stresses and enable terrestrial life. This study investigates the evolutionary trajectory of streptophyte algae, focusing on their adaptive innovations and strategies for environmental resilience. To address challenges in species tree reconstruction, we developed a robust phylogenomic framework incorporating taxonomic group filtering, which provides refined insights into the evolutionary relationships among the Klebsormidiophyceae, Coleochaetophyceae, and Zygnematophyceae classes of streptophyte algae. Integration of phylogenomic and functional genomic analysis reveals patterns of ancestral trait conservation and adaptive innovation, including the recurrent gain and loss of multicellularity within these lineages.

Keywords

Algae, Phylogenomics, Multicellularity

Heterocyte glycolipids as novel tools to study the phylogeny and evolutionary history of heterocytous cyanobacteria

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Abstract

Heterocytous cyanobacteria are oxygenic photoautotrophs that are common in freshwater environments and terrestrial habitats. Using high performance liquid chromatography coupled to mass spectrometry, we identified a suite of novel glycolipids, so-called heterocyte glycolipids, that are unique to heterocytous cyanobacteria. Extended screening of these lipids, consisting of a sugar functionality bound to long chain alcohols or ketones, resulted in the identification of more than 30 individual HG structures. In cyanobacterial cultures, the distribution of these components largely varies on a family/genus level providing taxonomic information on the cyanobacterial clade complementary to the more established molecular and morphological approaches. Interestingly, we also observed a strong temperature control on the relative abundance of heterocyte glycolipids in cyanobacterial cultures. As we identified heterocyte glycolipids in freshwater and terrestrial environments worldwide as well as in 90-million-year-old sediments, these components allow, for the first time, to trace for the presence of individual cyanobacterial genera and families in the sediment record and reconstruct past lake surface water temperatures. Our study stresses the importance of combining geo- with biological sciences to identify new organic components that (1) allow tracing the evolution of life in Earth history and (2) reconstructing the response of ecosystems to climate and environmental change.

Keywords

Cyanobacteria, lipids, phylogeny

Insights into metabolic plasticity under environmental limitations on growth

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Abstract

Photosynthetic organisms must poise their metabolism to fluctuating environmental factors, which we know little about. Here, physiological, proteomic and metabolomic data will be presented on how *Chlamydomonas reinhardtii* responds to saturating, limiting or fluctuating (FL) light intensity under unrestricted (2 %) or restricted (0.04 %) CO₂ availability. Under all growth conditions, cellular protein content positively correlated with culture growth rates and negatively correlated with cell size, supporting that protein accumulation can accelerate the cell cycle. Under low light, cells invested relatively more in acquiring energy (photosynthetic complexes), and cyclic and chloroplast-to-mitochondria electron flow via organic acids (e.g. malate valve) contributed more to ATP production. Restricting CO₂ enhanced this response since cells needed to power the carbon concentrating mechanism and starch synthesis for its operation. ATP deficiency under restricted CO₂ was also evident by slower repair of photoinhibited PSII. As such, photosynthetic efficiency, as well as respiratory rates, were highly influenced by CO₂ availability, as was the TCA cycle metabolite flux under FL. Chloroplast metabolism responded rapidly (<0.5min) to a change in light intensity under FL, but sugar concentrations were CO₂ independent. Therefore, a major factor in the plasticity of metabolism resides outside the chloroplast.

Keywords

Photosynthesis, Acclimation, Metabolite,

How algae using the photoprotective diadinoxanthin cycle prevent the accumulation of violaxanthin cycle pigments

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Abstract

Plants and many algae possess an inducible photoprotective mechanism known as the violaxanthin (Vx) cycle. In high light, the enzyme Vx de-epoxidase (VDE) catalyzes the conversion of the carotenoid Vx to zeaxanthin that promotes the dissipation of excess excitation energy in the photosynthetic machinery. In low light, zeaxanthin is converted back to Vx by zeaxanthin epoxidase, restoring efficient light harvesting for photosynthesis. Diatoms and haptophytes use a different xanthophyll cycle in which VDE de-epoxidizes diadinoxanthin (Ddx) to diatoxanthin that promotes energy dissipation similar to zeaxanthin. Hypothetically, these algae could also use the Vx cycle for photoprotection because Vx is a precursor of Ddx and always present in small amounts. Under most conditions, however, the Vx cycle pigments do not accumulate in these algae. We identified mechanisms contributing to the preponderance of the Ddx cycle in diatoms and haptophytes. By analyzing the substrate specificity of VDEs from plants and algae, we observed that VDEs from algae with Ddx cycle markedly favor Ddx over Vx, thus minimizing the formation of zeaxanthin from Vx under high light. We also found evidence that – contrary to land plants – diatoms and haptophytes can synthesize Vx by an alternative pathway bypassing zeaxanthin. The evolution of these mechanisms suggests that the Ddx cycle offers a selective advantage over the Vx cycle, e.g. by enabling a faster acclimation to rapidly changing light conditions.

Keywords

xanthophyll cycle, diatoms, haptophytes

Conserved carotenoid pigmentation in reproductive organs of Charophyceae

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Abstract

Charophyceae algae were believed to be the closest relatives of land plants for a long time due to their complex body plans and other land plant-like traits. Although we know nowadays, that Zygnematophyceae are the closest algal relatives of land plants, Charophyceae algae are great models for studying the evolution of several traits that enabled the conquest of land approximately 500 million years ago. Among these traits is the hyperaccumulation of pigments e.g. carotenoids in reproductive organs. Our work even hints at conservation in function of this optically intriguing trait – light protection. With a combination of metabolite profiling and transcriptomics, we could show that the red coloration of Charophyceae antheridia mainly originates from the rare carotenoids gamma- and delta-carotene. Almost depleted LYCOPENE CYCLASES expression levels are a rationale for the accumulation of these intermediates of alpha- and beta-carotene biosynthesis. Additionally, we were the first to detect apocarotenoids – small volatile oxidative break-down products of carotenoids – in Charophyceae. This included extremely high levels of 6-methyl-5-hepten-2-one, a usually rather low abundant apocarotenoid, correlating with its parent carotenoids gamma- and delta-carotene. Overall, our data show the conservation of carotenoid hyperaccumulation and its genetic underpinnings as a protection strategy for reproductive organs in a group diverging more than 600 million years from land plants.

Keywords

Charophyceae, Carotenoids, Reproduction

Aureochromes – specific photoreceptors in diatoms

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Abstract

Aureochromes (AUREOs) are a relatively novel type of blue-light photoreceptors in algae (discovered in 2007), and they so far have only been found in Stramenopiles. They have a very peculiar structure: In addition to a blue-light sensing flavin-binding LOV-domain, they possess a DNA-binding bZIP domain, that is typically found in transcription factors. Therefore, aureochromes can be considered as light-driven transcription factors, allowing very fast responses. The pennate diatom *Phaeodactylum tricornutum* possesses four different aureochromes (PtAUREO1a,1b,1c,2), which are expressed differently throughout the day. We have generated PtAureo knockout cell lines of the diatom *P. tricornutum*. PtAureo1a knockout mutants show a distinctive phenotype of a low capacity for Non Photochemical Quenching (NPQ), a prominent photoprotection mechanism in diatoms. The role of PtAUREO1a has been confirmed by genetic complementation studies in *P. tricornutum*. In transcriptomics experiments, we found that the knockout of PtAureo1a has a drastic impact on global gene expression of the algae, indicating that PtAUREO1a might function as a master switch for blue light induced responses. Furthermore, a knockout of PtAureo1a has an impact on the diel expression of other regulatory factors. Studies on the potential binding sites of Aureochromes via yeast-1-hybrid analyses indicate that PtAureo1a can regulate its own expression.

Keywords

diatom, photoreceptor, transcription factor

Session 8/ Talk 1

Archetypes of Sex: Unmasking Algae's Innocence, the Nathanael Pringsheim Revolution

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Abstract

Nathanael Pringsheim was botany pioneer, contemporary of Charles Darwin and a distant relative of Ernst Georg Pringsheim, the founder of SAG, the collection of algae cultures at the University of Göttingen. Nathanael Pringsheim observed in an alga how male reproductive cells moved toward and fused with female cells. This was the first recorded instance of fertilization in a living organism, demonstrating that sexuality is a universal principle of life. Drawing on Matthias Schleiden's and Theodor Schwann's cell theory, Pringsheim helped establish a new understanding of the unity of all plants—and even the connection between plants and animals.

Keywords

The Central Collection of Algal Cultures (CCAC) pursuing a new role of bioresource centres

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Abstract

The Central Collection of Algal Cultures (CCAC) of the University of Duisburg-Essen is a unique repository of microalgae with ca. 7500 strains from marine (15%) and freshwater (85%) environments. CCAC is the only repository for > 90% of these strains. This extensive collection includes a significant number of axenic strains and represents a broad phylogenetic diversity, spanning all major algal groups. This makes CCAC an invaluable resource for comprehensive evolutionary and ecological research, multi-omics projects and the development of interdisciplinary collaborations. Furthermore, the collection can provide a virtually inexhaustible resource to assess different physiological styles and molecular mechanisms, offering great potential for developing innovative technologies and environmentally friendly solutions to global challenges such as carbon sequestration and wastewater treatment. Finally, by preserving and providing access to its strains, CCAC not only promotes research, but also conserves algal genetic diversity. In this contribution, we describe how CCAC can promote interaction of experts from different research areas and public sectors to bridge existing gaps and meet the demands of a changing world and science, where both a detailed in-depth understanding of processes and a wide taxonomic coverage are equally important.

Keywords

culture cillection, microalgae

Cultures of microalgae: a taxonomic and nomenclatural perspective

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Abstract

Cultures of microalgae (monoclonal or unialgal strains) used for molecular, physiological, and taxonomical studies must be properly identified with indication of the identification method and the identification reference, complemented by all metadata (collector, date of collection, person who isolated the strain, date of isolation, location, geo reference, permit). If a strain is used to describe a new species, it should ideally be cryopreserved and deposited in a culture collection. Parts of a strain might be fixed and sent to a herbarium and DNA-bank. For diatoms, the latter is the recommended method; for other groups, a combined deposit strategy should be considered for better scientific reuse. According to the current Madrid Code of Nomenclature, living cultures cannot serve as types. Cryopreserved cultures are permitted provided that they are preserved in a metabolically inactive state (e.g. by lyophilization or deep-freezing to remain alive in that inactive state, Art. 8.4.) but the protologue must also include an explicit statement that the culture is preserved in a metabolically inactive state (Art. 40.7). Gathering, diagnosis, illustration, protologue, specimen and nomenclatural type are technical terms of the Code, that are explained to improve phycological workflows from finding new taxa to their publication in a way that is Code-conform. PhycoBank (phycobank.org) is the facility to register algal novelties.

Keywords

integrative taxonomy, nomenclature, types

Deep learning of phytoplankton morphology from laboratory cultures for automated species classification in environmental samples

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Abstract

Manual identification of phytoplankton bioindicators is a skilled and time-consuming process, making it ideal for automation with deep learning to improve consistency across laboratories. However, challenges such as morphological diversity, image acquisition biases, and the lack of taxonomically resolved benchmark image datasets remain. Unlike most previous studies, we trained a convolutional neural network (CNN) to learn species characteristics from well-defined algal strains and applied this knowledge to classify species imaged from environmental samples. Our experiments with freshwater chlorophytes showed that species from the families Hydrodictyaceae, Scenedesmaceae, and Chlorellaceae were particularly promising for automated classification across different imaging setups. We further used the trained CNN to extract deep learning (DL) features from phytoplankton images and investigated whether these features serve as proxies for morphological similarity. The DL features provided accurate clustering of images by species and aligned with morphological similarities described in the literature. Our study highlights the potential of deep learning to support the EU Water Framework Directive by establishing a benchmark image dataset for reproducible phytoplankton monitoring across laboratories. Importantly, a relatively small number of reference strains was sufficient to train an easy-to-use CNN for robust species classification across multiple microscopy and imaging setups.

Keywords

phytoplankton, deep learning, strains

The contributions to phycology of Klaus Lüning (1941-2023)

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Abstract

A summary of the life and work of Klaus Lüning to commemorate his recent death (November 2023). Klaus started with pioneering diving studies of the sublittoral seaweed flora around Helgoland in the 1960s, and combined photobiological experiments on the morphogenetic development of brown and red algae in the lab with the design, construction and maintenance of stations for the continuous long-term monitoring of underwater light quality in the field in the 1970s. Later, he worked in Helgoland and Hamburg on the photosynthesis of different algal groups in the underwater light qualities revealed by his measurements, as well as the sensitivity of red and brown algae to UV-radiation above and below water, and he demonstrated through long-term culture experiments the existence of circannual rhythms in the growth of several kelp species. In response to the demands of funding bodies from the 1990s onwards for studies of applied phycology, he developed tank-systems for growing various seaweeds onshore at Sylt and with colleagues in Denmark, and he continued this after his retirement, concluding with culture experiments on *Ulva* in his cellar, which showed that its growth rate could be maintained for over 2 years without changing the bulk seawater medium. He completed a paper about this shortly before his death, which was published in *Botanica Marina* in December 2023, and the results will be outlined in this presentation.

Keywords

macroalgae, photobiology, aquaculture

Raman Imaging of the rafting kelp *Macrocystis pyrifera* from California

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Abstract

Brown macroalgae of the species *Macrocystis pyrifera* often form large kelp forests along the Pacific shore. While being sessile organisms, thalli also frequently detach from the seafloor and drift ashore sometimes for large distances, reaching intertidal zones and beaches. Live and seemingly healthy kelp was collected in La Jolla, California in July 2023. Punched out discs of the sporophyte blades were chemically fixed, semithin sections illustrate the outer meristoderm and the central medulla region containing acidic polysaccharides. Raman spectroscopy was performed on lyophilized and rehydrated samples (10 μm cross-sections, cryo-microtomy). Raman mapping opened the view on microchemistry, cell walls contain mainly cellulose, but also fucoidan and alginate, which filled the space between the cells in the medulla. In the lumen of the medulla cells, spectrally different compounds were visualized as well as in the apoplast between the cell walls of the meristoderm. Meristoderm cells were filled with photopigments, including the special carotenoid fucoxanthin. The strong carotenoid chain bands (1160 cm^{-1} and 1530 cm^{-1}) were very weak or absent, probably due to photo-bleaching by laser irradiation. Nevertheless, a weak band was found at 1927 cm^{-1} , which can be assigned to the allene group in fucoxanthin. Additionally, the Raman signature included membrane constituting lipids (e.g. 1453 cm^{-1} , CH₂/CH₃ bending) and proteins (e.g. 1237 cm^{-1} , 1672 cm^{-1}). The aromatic contributions (~ 1600 cm^{-1} and high fluorescence background) are likely phlorotannins, produced by polymerization of phloroglucinol and acting as a shelter against environmental stress in brown algae. In summary this study shows that rafting kelp show intact structures and microchemical compositions.

Keywords

fucoidan, alginate, phlorotannin

The brown alga *Ectocarpus siliculosus* shows cell wall changes upon infection with *Maullinia ectocarpii*

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Abstract

Maullinia ectocarpii is an obligate biotrophic parasite infecting brown algae, including *Ectocarpus siliculosus* Ec32. Infection results in hypertrophic infected host cells and likely leads to modifications in the cell wall of the host. Little is known about the cellular processes affected by the infection. Here, we investigate cell wall synthesis related processes and modifications using an RNA-seq dataset of *E. siliculosus* Ec32 infected with *M. ectocarpii*. Cell walls were investigated by immunofluorescence during *M. ectocarpii* infection. Fucans accumulated around the exit holes of *M. ectocarpii* and G-rich alginates were more common than M-rich alginates. Transcriptomic data showed that key enzymes involved in the cell wall synthesis (including alginate and fucan synthesis) were differentially expressed and cell wall modifying enzymes tended to be upregulated during *M. ectocarpii* infection. We therefore conclude, that infection with *M. ectocarpii* leads to cell wall modifications of its host

Keywords

Cell Wall Remodeling in the Green Macroalgae *Ulva* in Response to Environmental Input

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Abstract

Ulva is a globally occurring green macroalga capable of producing large amounts of biomass. The bulk material in this biomass are cell walls, which serve as the only physical barrier between the algal protoplasts and the environment. *Ulva* cell walls are composed of various complex polysaccharides and can alter their composition and structure dramatically in response to changed living conditions (remodeling). As an intertidal alga, *Ulva* is frequently exposed to desiccation stress and sunlight exposure, for example due to tidal and seasonal changes. Exploring the cell remodeling process during desiccation and rehydration will help us understand the survival strategy *Ulva* takes. The experiment is designed to simulate natural desiccation-rehydration cycles in the lab under different light and temperature regimes. Cell wall polysaccharides will be probed with various specific antibodies to identify their distribution patterns. Removal of cell wall polysaccharides via digesting enzymes and evaluating the physiological consequences for cells will allow for identifying functional roles of polysaccharide during stress exposure. Click chemistry and nanoSIMS are used to label monosaccharides and then evaluate cellular polysaccharides re-allocations in situ/in vivo. The composition of the cell wall will be analyzed using advanced microarray profiling techniques, allowing to quantify cell wall remodeling pattern in *Ulva*. This research will provide a systematic workflow for tracking the cell wall formation by using multiple imaging and analytical tools from glycobiology. We anticipate uncovering new mechanisms of cell wall remodeling in intertidal algae.

Keywords

Ulva, cell wall, polysaccharides

Responses of Zygnematophyceae during desiccation and comparing its cell wall polysaccharide secretion patterns to the early land plant Marchantia

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Abstract

Extensive evidence from recent biochemical and genetic studies suggests that land plants inherited their major cell wall components from their algal ancestors, the charophyte green algae (CGA). Zygnematophyceae, a monophyletic late-diverging member of the CGA and sister lineage to all land plants, occurs worldwide in hydro-terrestrial habitats and its cell walls are composed of cellulose, acidic pectic, and branched hemicelluloses such as xyloglucan and mannans. However, the functions of these cell wall components are not well understood and some of them can be secreted beyond the boundaries of the cell wall, suggesting additional non-structural functions in the extracellular space, such as increasing the water holding capacity of the cell. In this study, we start exploring cell wall polysaccharide functions in *Zygnema circumcarinatum* and *Mesotaenium endlicherianum* by exposing them to moderate and long-term (2 weeks and 1 month) desiccation stress in a novel desiccation setup while monitoring their photosynthetic activities, changes in cell wall polysaccharide compositions and secretion patterns. The next part of the project entails comparing the cell wall secretion patterns of Zygnematophyceae with the liverwort *Marchantia* during desiccation, helping to understand the cell polysaccharide footprints and functions of early land plants and their algal ancestors during water-land transition.

Keywords

Molecular evolution, cell wall polysaccharides, desiccation stress

Understanding the Lower Macrophyte Limit: A Year-long Experiment and first Results

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Abstract

Macrophyte vegetation plays a key structural and indicator role in lake ecosystems, contributing to biodiversity and serving as a vital parameter for assessing water quality. The lower macrophyte limit (DIN EN 15460) appears to reflect lake conservation status, yet its primary environmental drivers remain unclear. To address this, a year-long monitoring study (April 2024–April 2025) was conducted at Lake Drewitzer See (Mecklenburg-Western Pomerania, Germany), a meso-oligotrophic, groundwater-fed lake. Monthly assessments included light spectrum composition, nutrient concentrations (water/sediment), chlorophyll content, water transparency, temperature, and water level fluctuations. Underwater drone transects documented macrophyte abundance, and the depth of the lower macrophyte limit was systematically measured. Preliminary results reveal distinct seasonal patterns, including spring phytoplankton blooms, summer stratification, autumnal leaf deposition, and increased winter transparency. Sediment grain size and C:N ratios varied significantly, while sorting grade differences were non-significant. Water content and soil organic matter showed significant differences between depths, with higher values below the lower macrophyte limit (15 m) and at the limit itself (11 m) compared to shallower areas (8 m). Further analyses will investigate how these environmental factors influence macrophyte distribution and the lower macrophyte limit depth.

Keywords

Macrophyte distribution, Sediment compositions, Lake ecosystem dynamics

From Past to Present, Brackish and Pleasant: The Niche of *Chara canescens*

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Abstract

Chara canescens is a characean species occurring exclusively in brackish water, with a distribution range mainly in the northern hemisphere but also in Australia. Unique within its family, it comprises both parthenogenetic, exclusively female populations and populations with a bisexual reproductive strategy. The former are abundant, particularly in Europe, while the latter are rare. Based on this peculiarity, the Biodiversa+ funded ProPartS project aims to use this species to develop strategies for the protection of taxa consisting of interconnected sexual and parthenogenetic reproducing strains. As the basis of this effort, historical and recent distributions of *C. canescens* were assessed. Specimens from four European herbaria, mainly dating back to the 19th century, were analyzed alongside data on current locations. These include brackish areas along coasts and in inland regions where geological features support halophilic species far from today's seas. However, despite the availability of seemingly suitable sites, the species is found in relatively few habitats. To investigate this discrepancy, current studies focus on water chemistry and sediment composition, the microbial and fungal community in the sediment, and the viability of diaspores. Understanding the niche structure of *C. canescens* and potential differences in habitat requirements of sexual and parthenogenetic populations will enable effective conservation measures.

Keywords

Charophytes, niche structure, mapping

pam: Fast and Efficient Processing of PAM Data

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Abstract

PAM devices enable the measurement of light curves that can be used to characterize photosynthesis. For example, they provide information about the maximum electron transport rate. However, these parameters cannot be used directly and must be determined using regression methods. Various models have already been developed for this purpose in recent decades. A solver, such as that available in Excel, is required to utilize the models. However in Excel, especially with larger data sets, the time required and the risk of human error increases and the overall clarity decreases. This is where we came in and developed the R library 'pam'. This offers the possibility of automatically reading and processing raw data. The models of Vollenweider (1965), Platt (1980), Eilers and Peeters (1988) and Walsby (1997) are available for this purpose. Firstly, the fit of the models to the data set can be compared in order to simplify the selection of the model. Furthermore, control plots can be generated, which can be bundled and output as a pdf file, for example, to check the success of the regression and the calculated parameters for each measurement. The processed result can be output as a csv file at the end and used as required, e.g. to generate diagrams. Thus the library 'pam' offers the possibility for fast and efficient processing of PAM Data. The library is available on GitHub (<https://github.com/biotoobox/pam>) and CRAN (<https://cran.r-project.org/web/packages/pam/index.html>).

Keywords

PAM, photosynthesis, R

Characterization of microalgae isolated from biological soil crusts on a heavy metal contaminated mining deposit

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Abstract

One of the largest mining deposits in Freiberg is the Davidschachthalde, which was built from 1944 to 1969 from deposits of flotation residues. These deposited flotation residues consisted primarily of unusable, waste rock with high concentrations of arsenic, lead and cadmium. As a result, heavily contaminated soils with little vegetation developed. These toxic elements leach still today into groundwater and surface water, including the Freiburger Mulde. The tailing was partly covered with other waste material, like construction waste. In those areas, pioneer plants like grasses and birches developed. Nevertheless, some areas are still vegetation-free or accommodate only sparse vegetation and prone to erosion and a potential source for contaminated water and dust even after more than 50 years without mining activities. One possible method to secure the tailing could be the initiation of biological soil crusts (biocrusts). Biocrusts are composed of algae, bacteria, fungi, lichens and mosses and form on the soil surface. They conduct important ecological functions, like soil stabilization, reduction of erosion, increasing the nutrient input and alteration of water retention. Overall, biocrusts can improve the soil conditions for the colonization of higher plants. They can reduce the development of contaminated dust. The emission of contaminated water is also reduced by absorption of rainwater and transpiration through the biomass at the soil surface. The aim of the work is to instigate the possible initiation of biocrusts by applying algae biomass on the surface soil. For this purpose, samples of naturally-developed biocrusts were first taken from the vegetation-free area of the tailing. The algae were isolated and will be ecophysiologicaly characterized with special regard to their heavy metal tolerance. Alga species will be selected as potential candidates to initiate biocrust formation based on their heavy metal tolerance, their growth rate and their ability to secrete mucilage, which 'glues' the soil particles together and thus, stabilize the soil surface.

Keywords

Changes in the Genetic Biodiversity of Soil Algae and Cyanobacteria under the Influences of Land Use and Vegetation

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Abstract

Algae and cyanobacteria are essential components of microbial communities in soil as they provide energy, carbon, and oxygen input to soils. The primary goal of this project is to assess the biodiversity of algae and cyanobacteria in topsoils and associated environments, such as deadwood and tree bark. The study examines how different land use practices, such as canopy opening, deadwood management in forests, fertilization, and soil disturbance in grasslands, affect the diversity of these communities. The project tests several hypotheses: the genetic diversity of soil algae and cyanobacteria is influenced by vegetation type and land use intensity; forest soil algae biodiversity is linked to that of deadwood and tree bark; grasslands harbor higher diversity than forests; and mechanical disturbance and fertilization negatively impact phototrophic diversity. Amplicon-based metabarcoding captures the genetic biodiversity of eukaryotic algae and cyanobacteria. The first results focusing on the Hainich-Dün Biodiversity Exploratorium, utilizing its diverse plots representing different land use forms and intensities, are discussed.

Keywords

Diversity of *Prorocentrum* species revealed by metabarcoding

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Abstract

Dinoflagellates are a crucial component of marine ecosystems, representing a substantial portion of marine phytoplankton species. Among them, the cosmopolitan genus *Prorocentrum* is one of the most diverse and widespread genera in the ocean, and is often found in both pelagic and benthic environments. *Prorocentrum* species can act as both primary producers and consumers, allowing them to occupy multiple trophic levels in the marine food web. In addition, some species are known to cause toxic blooms. The study focuses on the biogeography of four species (seven strains) morphologically assigned to the genus *Prorocentrum*. The global distribution and abundance of these species was determined by analysis of the V4 and V9 hypervariable regions of their 18S SSU rRNA compared against metabarcoding data from the Tara Oceans expedition. It was found that the V9 sequences from *P. micans* and *P. cordatum* strains have a high relative abundance and global distribution based on Tara Oceans biogeographical data. Within this metabarcoding dataset, *P. micans* ranks first in overall abundance among non-metazoans, and *P. cordatum* is ranked 66. Further data from additional strains, and transcriptome or genome sequences from current strains, are needed to resolve the different species or ecotypes represented by these globally abundant V9 sequences. Acknowledgments

Keywords

Prorocentrum, microbial biogeography, Tara Oceans

Seasonal variations in metabolite and transcript profiles in the streptophyte green alga *Zygonium ericetorum*

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Abstract

In this project we investigate survival strategies of the streptophyte green alga *Zygonium ericetorum* during the growing season in its natural environment. Field samples were collected monthly from Mount Schönwieskopf (2350 m a.s.l.) in Obergurgl, Tyrol, Austria. In-situ algae were exposed to abiotic stress factors such as high light (~2000 $\mu\text{mol photons/m}^2\text{ s}$), UV-A (~5.5 mW/cm^2), UV-B (~23.5 $\mu\text{W/cm}^2$), acidic pH (ranging from 5.5-6.2), as well as elevated water temperatures (up to 27.6°C). The central hypothesis of this study is that significant changes in primary metabolites and corresponding transcriptomic shifts will occur due to the extreme conditions. Metabolite profiling will be conducted using a GC-MS based approach and differentially gene expression analysis will be done using RNASeq. In preliminary transcriptomic analyses 23 million quality filtered reads were assembled de novo into 108,908 transcripts. This large dataset reflects that the natural samples comprise a community which is enriched in *Zygonium*, but contains other organisms such as *Scytonema* sp. We plan to support our transcriptomic data with the study of the proteome. Here, especially the subcellular proteome of lipid droplets is interesting, as their accumulation seems to play an important role in stress adaptations. The results obtained will provide insights into the adaptive mechanisms of *Z. ericetorum*, contributing to our understanding how they cope with environmental changes.

Keywords

Metabolite profiling, Metatranscriptomes, Seasonal variation

Comparative transcriptomics of *Spirogyra* and *Mesotaenium* reveal conserved molecular programs

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Abstract

About 500 million years ago, the ancestor of all living land plants began its conquest of the terrestrial habitat, forever changing the surface of the Earth. By using genomics in a comparative and complementary approach, we can infer which traits enabled plants this conquest of land. To do so, we not only need to look at the genomic content of land plants, but also at those of their closest living relatives. Phylogenomic analyses performed over the last decade have recovered the Zygnematophyceae as the algal sister lineage to land plants. One of the most iconic members of the Zygnematophyceae is *Spirogyra pratensis*, a filamentous alga named for its intricate, spirally arranged chloroplasts. Understanding the molecular biology of this alga has been hampered by a lack of genome data. Here, we present the first assembled genome of *Spirogyra pratensis*. *Spirogyra* has the smallest genome of all streptophyte algae thus far sequenced. Despite its small size, the *Spirogyra* genome contains several characteristic genes that were, until recently, considered to be specific to land plants. To investigate the latter, we exposed *Spirogyra* as well as the single-celled Zygnematophyceae species *Mesotaenium endlicherianum* to a bifactorial gradient of the two important cues, light and temperature, and performed global differential gene expression as well as co-expression network analysis. Using comparative analysis, our data shed light on pathways for intracellular signaling in response to external cues that existed before land was dominated by plants.

Keywords

streptophyte algae, evolution, transcriptomics

The effect of flavonoids on cyanobacterial motility and their role in symbiotic relationship with land plants

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Abstract

Cyanobacteria have symbiotic relationships with diverse land plants, from bryophytes to ferns, gymnosperms, and angiosperms. One specific example is the symbiosis between *Azolla filiculoides* and its cyanobiont *Nostoc azollae*: the cyanobiont is vertically inherited, and both partners co-evolve, which results in full co-dependency. Essential for all cyanobacterial symbioses is the ability to differentiate into motile filaments, hormogonia, upon plant cues. In *Azolla*, hormogonia is required to colonize new tissue and inheritance; however, the molecular cues underlying the symbiotic transfer are only poorly understood. Salicylic acid (SA) is produced by *A. filiculoides* and in land plants as a defense response to different pathogenic microbes in the environment. When SA is exogenously applied to *A. filiculoides*, its cyanobiont's abundance and gene expression are altered. Our preliminary transcriptomic data suggest that SA may control flavonoids, metabolites that in the past have been suggested to influence cyanobacterial motility. We want to test whether SA and flavonoids play a role in cyanobacterial symbiotic relationships. To do that, we investigated the effect of SA and flavonoids produced by *A. filiculoides* on cyanobacterial symbionts. We induced motility in cyanobacteria using far-red light and tested the ability of the phenolic compounds to modulate the transition into hormogonia stages. The results of the treatments were documented using light microscopy and RNA was extracted for further analyses and then sequenced. We set up a machine-learning-based image analysis pipeline and analysed light microscopy images to quantify differentiation into hormogonia and the amount of vegetative cells. We found that SA and the majority of flavonoids tested enhanced hormogonia transition in a symbiotic cyanobacterium. Now, we are analysing the RNA-Seq data obtained from this experiment to connect differential gene expression to the motility phenotype, hereby focusing on genes known to modulate motility, nitrogen-fixation, and those suggested to be related to the communication between cyanobacteria and their hosts.

Keywords

Exploring Light-Induced Signaling Pathways in *Phaeodactylum tricornutum* through Transcriptomic Approaches

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Abstract

In the diatom *Phaeodactylum tricornutum*, plastoquinone pool redox state (PQRS)-mediated retrograde signaling plays a pivotal role in regulating nuclear gene expression in response to light, but the underlying molecular mechanism remains poorly understood. To address this, we performed transcriptomic analyses to examine gene expression dynamics influenced by the PQRS and potential other light triggers. Experimental conditions involved low light (LL) and high light (HL) (30 and 500 $\mu\text{E m}^{-2} \text{s}^{-1}$, respectively), and treatments with DBMIB and DCMU at 0 and 60 minutes. RNA-Seq data revealed distinct gene expression patterns in our experimental conditions. Four major light signaling triggers were identified

Keywords

Retrograde signaling, Light-dependent regulation, Diatoms

Investigating the Phenylpropanoid Pathway in Zygnematophyceae

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Abstract

For successful plant survival, organisms must be able to respond dynamically to rapidly changing environmental conditions. The ability to respond to abiotic challenges was crucial in the process of terrestrialisation that led to the emergence of embryophytes. Based on phylogenetic analyses, their closest streptophyte algal relatives are Zygnematophyceae, on which this contribution focuses. The phenylpropanoid pathway is a key stress response pathway, also producing lignin in vascular plants. Until recently, this pathway was thought to be unique to land plants, however, recent phylogenetic studies have shown that homologs to enzymes involved are also present within streptophyte algae. We treated *Mesotaenium endlicherianum* with different compounds within, before and after the phenylpropanoid pathway. The aim is to investigate whether the addition of phenylpropanoid related compounds induces a feedforward or feedback loop in the transcripts of involved enzymes. (Photo)-physiological measurements were taken to ensure that the cells were not subjected to stress, which could influence the transcriptomic results. To date, no species of streptophyte algae, except for *Closterium* sp. NIES-68, have been transformed. To enable further genomic experiments within the streptophyte algae, we replicated the transformation setup.

Keywords

streptophyte algae, phenylpropanoid, transformation, stress response

Draparnaldia erecta - The alga of the year 2025

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Abstract

Draparnaldia is the morphologically complex green Chlorophyte alga that we are establishing as a new algal model system to study multicellularity and terrestrialization in algae.

Draparnaldia is uniquely suited to study these topics since: (1) It shows morphological similarity with early land plants. It has the Upright System that is branched and it has the intercalary division. It also has the Prostrate System, that function as simple rooting structures and exhibits apical growth. (2) In nature, Draparnaldia lives in both the aquatic and terrestrial habitat, and it shows fascinating morphological adaptations to both habitats. Importantly, these different morphologies can be also induced under laboratory conditions. Moreover, Draparnaldia is easy to culture and grows rapidly, completing its life cycle in just 7-9 days. This alga reproduces via zoospores, that can be induced in large quantities simultaneously, which is important for phenotypic studies. To establish Draparnaldia into a 'full' model system, we generated the following tools and resources for this alga: de novo genome, transcriptomes from different habitats, and profiled its phytohormone repertoire. All of this makes Draparnaldia a powerful model to uncover and study alternative evolutionary trajectories towards multicellularity and terrestrialization in plants.

Keywords

Algae biotechnology - an old hat, or hats off to potentials of waste recycling?

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Abstract

Urgent challenges in the field of algal biotechnology are the optimization of algal production, of process engineering regarding scale-up and a synergistic site implementation of photobioreactors. The utilization of industrial biogenic waste and emitted CO₂ in flue gas by microalgae could help to save production costs and contribute to climate change mitigation. Especially, the shift from previous cultivation technologies mainly under submerged conditions with aquatic microalgae to emerged (air-exposed) biofilm-based processes with terrestrial microalgae, shows several physiological and procedural advantages for more efficient production in emerge photobioreactors (ePBR; Lakatos & Strieth 2017). Reduction of limitations in mass transfer (CO₂ & O₂), thermal stability, photoinhibition, and efficiency of energy (savings: 20 – 40 %) and resource investments (e.g., 90 % less water) were successfully achieved. Furthermore, the ePBR approach opens up the development of new production areas - esp. on façades (Schmidt et al. 2020). A façade-integrated bioreactor technology can be beneficial for both cultivation and building operation. In addition to the CO₂ fixation of enriched exhaust air, there are synergies between the building and the reactor in terms of temperature control. First prototypes are developed and the utilization of waste was tested within the project “Waste to Value”.

Keywords

biogenic waste, flue gas, photobiobioreactor

Utilization of Industrial Residual Materials Through Mixotrophic Cultivation of Cyanobacteria for the Production of Valuable Compounds

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Abstract

Cyanobacteria are typically cultured autotrophically in nutrient-deficient media (e.g., BG11). Four cyanobacterial strains were cultivated mixotrophically on nutrient agar supplemented with various residual materials or sugar derivatives, and their growth rates were determined using chlorophyll fluorescence measurements. Moreover, it was tested whether the addition of different residual materials could stimulate the production of the biodegradable bioplastic polyhydroxybutyrate (PHB) by the cyanobacteria. In these experiments using various nutrient-enriched media, the occurrence of fungi and bacteria was also investigated, as well as the extent to which cyanobacteria could suppress microbial overgrowth through the production of antimicrobial substances. The long-term goal is to establish a circular economy and bioeconomy with the utilization of industrial and agricultural residues by cyanobacteria in order to obtain higher-value substances (pigments, polysaccharides, bioplastics, bioactive substances, fertilizers, etc.) by means of cascade utilization in multi-stage downstream processes. At the same time, these processes fix CO₂, and the remaining cyanobacterial biomass after extraction can still be fully utilized in biogas plants.

Keywords

cyanobacteria, mixotrophic growth, residues utilization

Bring algae home: The first self-sufficient spirulina farm for sustainable & fresh harvests right at home.

Ben Schwedhelm,

MySpirulina GmbH

Abstract

Hailed by NASA and the WHO as the superfood of the future, spirulina—a biological cyanobacterium often referred to as algae—offers unparalleled nutritional benefits, including high levels of protein, essential vitamins, and antioxidants. Despite its immense potential, current spirulina products face challenges with sustainability, transparency, and consumer appeal. MySpirulina is transforming how people interact with algae by bringing spirulina farming directly into their homes. Our self-sufficient, solar-powered windowsill spirulina farm is a complete, all-in-one solution, enabling individuals to sustainably grow and regularly harvest fresh spirulina with ease, incorporating it into their diets. At MySpirulina, our mission is to make algae mainstream by making its cultivation accessible, transparent, and engaging. By empowering people to grow their own spirulina, we aim to demystify algae, emphasize its sustainability, and position it as a vital food source for a healthier planet. Our vision extends beyond health-conscious consumers to communities battling severe malnutrition due to the rapidly changing climate. By making fresh spirulina accessible, we strive to offer a sustainable solution for global food security and create a more resilient future.

Keywords

Spirulina, Biotech, Innovation

Assessment of UV-sunscreen mycosporine-like amino acids (MAAs) in two commercially important red algae from Peru

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Abstract

The increase in ultraviolet radiation due to climate change represent a significant threat to marine ecosystems. MAAs, natural compounds with photoprotective and antioxidant properties, are widely produced by rhodophytes. This study assessed the concentration of MAAs in two commercially important species, *Gracilariopsis lemaneiformis* and *Chondracanthus chamissoi*, cultivated along the central coast of Peru, focusing on seasonal variations. Samples were collected from a marine bottom cultivation system in Ica, Peru, and analyzed using high-performance liquid chromatography and spectrophotometry. Both species exhibited seasonal variations, with the highest total MAA concentrations recorded during summer (*G. lemaneiformis*: 6.46 mg g⁻¹ dry weight; *C. chamissoi*: 13.17 mg g⁻¹ dry weight). The study highlights the complexity of MAA biosynthesis, which is influenced by habitat and environmental factors, affecting each species in distinct ways. The findings underscore the biotechnological potential of Peruvian red macroalgae for developing eco-friendly UV-protective products, attributed to their high MAA concentrations and diversity. Further research is needed to optimize cultivation techniques and enhance MAA production for industrial applications.

Keywords

Mycosporines, Peruvian rhodophytes, marine biotechnology

Effects of marine algal polysaccharides on the human gut microbiome and implications for gut health

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Abstract

Effects of marine algal polysaccharides on the human gut microbiome and implications for gut health Qian Wang, Fred Warren, Klaus Herburger Macroalgae are an abundant source of high-quality marine algal polysaccharides (MAPs) and in recent years, MAPs have attracted great interest as functional foods, pharmaceuticals, and cosmetic applications. MAPs are usually not digested directly in our upper gastrointestinal tract but can be utilized through fermentation by gut microorganisms, which form a complex community in the large intestine. This gut microbiome metabolizes polysaccharides and other food components into numerous functional metabolites, several of which have beneficial effects on the intestinal barrier, gut and cardiovascular health. Meanwhile, a healthy host–microorganism balance must be respected in order to optimally perform metabolic and immune functions and prevent disease development. Therefore, investigating the modulatory effects of MAPs on gut microbiota homeostasis, composition and microbial metabolites is key to understand MAPs' benefits for human (gut) health and their potential nutritional significance. This project studied how four major MAPs – green algal starch, floridean starch, soluble laminarin, hardly soluble laminarin – affect the composition and metabolite production of human gut microbiomes from various donors using in-depth metabolic profiling and metagenomic approaches. Beneficial alterations in microbiome composition will be discussed in light of qualitative and quantitative shifts in MAP fermentation products.

Keywords

Pilot study on scalable seaweed farming in the German Baltic Sea (Alg4Nut joint project)

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Abstract

Seaweed farming is a rapidly growing industry as it can yield large amounts of high-quality biomass and has a relatively low carbon food print, requiring minimal inputs of irrigation and fertilizers. While this sector is well established in (East-)Asia, growing seaweed is not yet widespread in most parts of Europe, even though long coastlines suggest great potential, including in the Baltic Sea. To test the seaweed production potential in Germany, we are setting up scalable onshore seaweed farms in a 2 km long former power plant cooling channel directly connected to the Baltic Sea. The site is located in Lubmin, Northeastern M.-V., where modelling studies suggest an area seaweed productivity of >7 t freshmass/ha/annum. Algal biomass (*Ulva* sp., *Porphyra* sp.) yield and quality will be monitored with a focus on the algal polysaccharide pools. This farming project is part of the Alg4Nut joint research project (2025 – 2028), which aims to investigate the health benefits and methane reduction effects of feeding native Baltic Sea algae to cows, focusing on their impact on animal health, nutrient utilization, and milk quality.

Keywords

Seaweed farming, applied phycology, biomass production

Exploring easily harvestable freshwater filamentous algae as a sustainable source of value-added phytochemicals

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Abstract

Filamentous algae are considered as a cost-effective alternative to unicellular microalgae and a sustainable source of essential fatty acids (EFAs) and other bioactive compounds, including proteins, carbohydrates and pigments. During this study of 91 filamentous algae from the Microalgae and Zygnematophyceae Collection Hamburg (MZCH) 11 strains were selected because of their high growth rate and ease of cultivation. Cell dimension of these algae ranged between of 5.8-117 μm length and 6.4-56 μm width. Algae were cultivated as liquid air lift cultures at 25°C at light intensity of 240 $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$ with a 16:8 h light:dark cycle. After 21 days, dry mass yield varied between 0.11 and 0.70 g L⁻¹. The algae exhibited significant differences in their content of value-added products. *Hyalotheca dissiliens* showed the highest carbohydrate content of 56.4 % of dry weight (dw%), while *Mougeotiopsis calospora* showed the highest protein content of 47.9 dw%. *Klebsormidium nitens* demonstrated a remarkable yield in the essential pigments zeaxanthin, lutein, and neoxanthin reaching 1.15 dw%. Remarkably, *Groenbladia neglecta* had the highest lipid content with 34.4 dw% and an EFAs content of 14.3 dw%. It attained a balanced ω -6/ ω -3 ratio of 3.6, which is ideal for nutritional purposes. Therefore, filamentous algae, being easily harvestable, can serve as a viable alternative to unicellular microalgae for the production of bioactive compounds, particularly nutrient-rich food additives.

Keywords

Essential fatty acids, Biomass production, Pigments (lutein,zeaxanthin), Nutritional supplements, Sustainability

Ecosystem services in eutrophic lakes with fast-settling microalgae-bacteria consortia

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Abstract

The decline in water quality has led the EU to aim for good ecological status for all major water bodies under the Water Framework Directive. A key challenge for lakes is managing phosphate pollution. Internal phosphate dynamics in lakes depend on oxygen levels. Under anaerobic conditions, phosphate is released into the water. In oxygenated waters, phosphate binds iron to form insoluble complexes that sink to the sediment, removing it from circulation. During stagnation, low oxygen levels in deep zones re-mobilize phosphate, promoting algal growth. The decomposition of algal biomass consumes oxygen or proceeds anaerobically, releasing methane, a potent greenhouse gas. Oxygen depletion spreads from the sediment to higher layers, endangering aquatic life. Mitigation often involves injecting technical oxygen into lakes, a costly and unsustainable solution. The BMBF-project Femak offers an alternative. At the ecosystem Kleine Plöner See, we study phosphate release and oxygenation during stagnation. Despite the Water Framework Directive, phosphate re-mobilization remains critical. The project will expand to include methane measurements, providing insights into phosphate and carbon cycles in eutrophic lakes.

Keywords

microalgae-bacteria consortia, oxygenation strategies, phosphate pollution

Isolation of microalgae from agricultural waste water for nutrient removal by sedimenting cultures

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Abstract

Eutrophication is a global challenge, but simultaneously so is the reclamation of finite resources such as nutrients. Various types of wastewaters offer great potential for nutrient recovery as containing nutrients are often not utilized or discharged directly into bodies of water and thus endanger the ecosystem. The nutrient uptake by microalgae is applied more frequently since it is cost effective and ecofriendly. However, many wastewaters exhibit challenging biotic and abiotic factors for microalgae viability and growth, including high, low or fluctuating nutrient levels, pH, temperature, irradiation and occurrence of different species (Gonçalves et al., 2016). Since microalgae can be highly adapted to these conditions in their habitat (Scott et al., 2010), this work compared microalgae isolated from agricultural waste waters with commonly used laboratory strains. The results revealed that numerous isolates show superior growth compared to laboratory strains in several waste waters. Additionally, Fluorescence-activated cell sorting (FACS) and Streak-plate method (SPM) were compared regarding their ability to create microalgae cultures. FACS resulted in higher cleanness of the culture whereas SPM achieved higher biodiversity for a screening of specific adaptations in the future. An Illumina Amplicon Sequencing revealed co-isolation with bacteria for all cultures leading to possible interactions such as sedimentation for a specific harvesting process with high feasibility.

Keywords

Adaptation, Isolation, Sedimentation

The influence of various microalgae on Zn-dependent metalloenzymes of collagen metabolism

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Abstract

Collagens are the most common proteins found in the skin, connective tissue and tendons and are therefore essential for the human body. The breakdown of collagens is part of the skin ageing process, which can be triggered, among other things, by excessive UV radiation. The overproduction of collagens is a characteristic feature of fibrotic diseases and keloids. Matrix metalloproteases (MMPs) and the astacin proteases Meprin α and β , are Zn-dependent metalloenzymes that may be involved in these processes. Here, we describe the influence of extracts from microalgae on the enzyme activity of these metalloenzymes in vitro. Due to their diversity, microalgae are a good source of potential new active ingredients for pharmaceuticals, cosmetics and food supplements. Extracts of the microalgae *Nannochloropsis oculata*, *Nannochloropsis limnetica*, *Diacronema lutheri* and *Nostoc muscorum* were analysed on their influence on the activity of five MMPs and the meprins. The ethanolic extract of *Nannochloropsis oculata* showed an inhibition of 97.40 \pm 0.46% on Meprin α at a concentration of 0.2 mg/mL.

Keywords

microalgae; metalloenzymes; inhibitors

Project Algae EPA - production of omega-3 fatty acids from microalgae

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Abstract

Eicosapentaenoic acid (EPA), a long-chain omega-3 fatty acid, has significant health benefits, including cardiovascular protection and anti-inflammatory effects. Traditionally produced from fish oil, microalgae are increasingly being used as a sustainable and scalable alternative, avoiding environmental challenges of overfishing and offering customized production through controlled cultivation systems. Despite these advances, challenges such as scalability, extraction costs, and product stability remain barriers to commercial adoption. Here, we present the collaborative project Algen-EPA. The aim of project is the establishment of an EPA production process using microalgae at the production plant of Roval GmbH in Northern Germany. The temperature and light conditions in this area fluctuate seasonally, which makes stable biomass and product yield with a single strain of algae difficult. Part of the project is therefore the search for a suitable winter and summer algae strain. Selected species include *Phaedactylum tricornutum*, *Nannochloropsis oculata*, and *Microchloropsis gaditana*. Lipid production will be investigated under different nutrient and light conditions to make recommendations for the production plant. As starting point the producers bulk chemicals and natural environments are used and adapted if necessary. The selected strains were tested on an industrial scale by project partner Roval GmbH. After selection and optimisation of algae production, a marketable EPA product will be developed.

Keywords

Microalgae, Seasonal production, Eicosapentaenoic acid, EPA

Plethora of carotenoids: The pigments of *Trentepohlia iolithus* (Ulvophyceae) revisited with classical and contemporary chromatographic methods

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Abstract

The genus *Trentepohlia* is known for its representatives living aerophytic on tree bark, rocks or other surfaces, thereby showing a characteristic reddish pigmentation due to high amounts of intracellular carotenoids. In the 70ies, the chemical structures of these compounds were described for the first time, and it seems that each species has individual patterns. However, in the case of *T. iolithus*, which prominently colours the surfaces of exposed silicate rocks in alpine regions in the proximity of rivers, state-of-the-art chromatographic methods were not applied up to now. Consequently, we analysed field samples from the Tyrolean Alps using TLC, HPLC and GC/MS to characterize abundant secondary metabolites, because such compounds are crucial for the survival of microalgae in a non-aquatic habitat. The reddish colour was due to a carotenoid content of 1.5 % per DW, while chlorophylls accounted only for 0.04 %. Alpha- and beta-carotin prevailed in organic extracts, while 6 % of all carotenoids were rare C(2) resp. C(2') hydroxylated derivatives. Most of them were esterified with fatty acids. Aqueous extracts contained sugar alcohols, and meso-erythritol was dominating with about 0.7 % content per DW. In summary, abundant non-plastidal carotenoids can serve as powerful antioxidants and screening compounds against excessive UV and VIS irradiation, while meso-erythritol and related polyols serve as compatible solutes, likely protecting the cytoplasm against desiccation stress.

Keywords

pigmentation, exposure, metabolites

Galdieria sulphuraria, an extremophile with promising carbon capture performance through project ALGROW

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Abstract

The main goal of the project ALGROW is to evaluate if extremophilic microalgae (and more specifically, *Galdieria sulphuraria*) function as biocatalysts to reduce industrial exhaust gas. Acidophilic microalgae are promising to cope with high levels of CO₂, which, in addition to other gases, will drastically reduce the pH of the water. In addition to studying the performance of the gas usage with the selected strain, the residual heat is used to develop a cost-efficient drying protocol for microalgae biomass. The biomass and possible functional ingredients such as phycocyanin, protein content, sugars, and others, are interesting for the local food-producing industry and other non-food applications. Within this project, we pursue three approaches to fulfil the objectives: (1) mimic the gas composition in lab scale experiments with selected microalgae candidates and produce biomass for (2) the establishment of a drying process and extraction cascade, and (3) perform, with the selected microalgae, culturing experiments at the tile factory for prove of principle. In the lab, CO₂ was supplied in different proportions, achieving higher growth between 10% and 30% of CO₂ (up to 10x times higher production than controls). In parallel NO_x was added as sodium nitrite and nitric acid. Here, we will present the results of the growth performance, photosynthetic rates, and metabolite contents of *G. sulphuraria* under different CO₂ and NO_x concentrations.

Keywords

Extremophiles, carbon-capture, flue-gas

Unexpected occurrence of marine secondary metabolites in inland waters of post-mining lakes in north-west of Czechia

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Abstract

Tropical oceans are well-known hotspots of mat-forming filamentous cyanobacteria from the order Oscillatoriales (sensu lato), the producers of a wide range of secondary metabolites. Among them bioactive oligopeptides and depsipeptides are in the special interest. The dolastatins and their derivatives, a group of highly cytotoxic oligopeptides were as well for forty years regarded to be only of marine origin. Recently, dolastatin 10 derivatives aetokthonostatins were discovered to be produced by the invasive cyanobacterium *Aetokthonos hydrillicola* occurring in fresh-water reservoirs of sub-tropical United States. The discovery triggered the question, whether can be other producers of such compounds inhabiting further fresh-water ecosystems. Our metabolomic investigation (HPLC-HRMS/MS with GNPS comparison) of algal mats of inland waters of post-mining lakes in the north-west of Czechia determined production of a rich spectrum of cyanobacterial secondary metabolites. The most prominent group were oligopeptides known to be produced by tropical marine Oscillatoriales, including dolastatin 1, 14 and G derivatives. Their presence was confirmed by the MS/MS spectra (fragmentation analysis). Originally, dolastatins were described from community samples and producers identified as taxa of the genera *Lyngbya* and *Symploca*. However, the genera are highly polyphyletic due to frequent morphological convergence in the oscillatorialean group. By recent metagenomic research the actual producers of dolastatin 10 – *Caldora penicillata* and dolastatin 11 derivatives *lyngbyastatins* – *Okeania* sp. were identified with the phylogenetic position retrieved. Such information for the dolastatin 1, 14 and G and their derivatives is still missing. Complementary analysis of V4-V5 16S rRNA amplicons was conducted here and identified 30 amplicon sequence variants (ASVs) belonging to the order Oscillatoriales. Their phylogenetic analysis found previously undetected lineages e.g. from the marine groups *Sirenicapillariaceae* and *Vermifilaceae*. Present and following research can lead to the determination of the actual producers of less examined dolastatin derivatives and tracing of their impact on the fresh-water environment.

Keywords algal mats, cyanobacteria, cytotoxicity, dolastatins, oligopeptides

From Waste to Bioplastics: Optimizing PHB Synthesis and Recycling in Cyanobacteria

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Abstract

Polyhydroxybutyrate (PHB) is a biodegradable polymer with potential as a sustainable alternative to petroleum-based plastics. This project focuses on optimizing PHB production using *Synechocystis* sp. PCC 6803, a model cyanobacterium, while exploring the feasibility of employing other cyanobacterial strains. Key aspects include the optimization of growth conditions to enhance PHB accumulation alongside the development of environmentally friendly extraction protocols that reduce chemical use and energy consumption. In addition, improvements in staining protocols will be developed to enable precise visualization and quantification of intracellular PHB. A novel component of this study involves investigating the metabolic capability of cyanobacteria to convert PHB breakdown products, such as crotonic acid, back into PHB, thereby exploring the potential for closed-loop recycling within cyanobacterial systems. By integrating these approaches, this research aims to advance our understanding of cyanobacterial PHB metabolism and lay the groundwork for scalable, sustainable bioplastic production technologies.

Keywords

Cyanobacteria, *Synechocystis*, Polyhydroxybutyrate

Algae cultivation on aquacultural wastewater as a bioeconomical concept

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Abstract

A mixed microalgae culture is cultivated on aquacultural wastewater for bioeconomical evaluation. Combined water usage for production of fish and algae/cyanobacteria is a promising system for sustainable nutrient management, whereat access nutrients are transformed into valuable biomass, e.g. for animal feed and fertilizer.

Keywords

Wastewater, algae, aquaculture, nutrients

Establishment of an optical determination method for monitoring the starch content in fast growing algal cultures of *Chlamydomonas reinhardtii*.

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Abstract

Determination of starch in algal cultures is often a combination of cell disruption, extraction, further purification, total hydrolysis of the starch granules and the determination of the released glucose units. These methods are established in different variants, but always have the disadvantage that it is very time-consuming and sometimes also prone to errors. In addition, determination of starch content on a single cellular level is not possible by such extraction-based techniques. This work deals with the development of a method based on optical analysis for rapid single-cell starch monitoring. The established method is based on the analysis of scattered light from individual starch-containing cells in a flow cytometer and can be carried out without complex sample preparation and without the addition of agents. The work is based on a combination of theoretical considerations based on the Lorenz-Mie theory of light scattering and practical investigations combining the application directly in the flow cytometer and the final comparison with "classical" reference analysis. Various cultures of the green algae *Chlamydomonas* were used as model cultures. The theoretical considerations showed that the technique can selectively detect starch in algal cells. Under certain circumstances, however, the results can be influenced by lipid droplets embedded in the algae cells. The comparison between the new method and a reference method showed high correlations in the cultures used.

Keywords

single-cell analysis, flow cytometry, light scattering

Paleoclimate reconstruction by biosignatures of the freshwater microalgae *Tetraedron minimum*, *Botryococcus braunii* and *Peridinium cinctum*

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Abstract

The paleolake Messel was formed around 48 million years ago by a volcanic water vapour explosion. Due to its characteristics (funnel shape, low oxygen exchange), the Messel pit contains an exceptionally high conservation and number of fossil remains of animals, plants, pollen and non-pollen palynomorphs. These include the green algae *Tetraedron minimum* and *Botryococcus braunii*, both still widespread in aquatic ecosystems especially lakes and ponds, as well as freshwater peridinioid dinoflagellate cysts, referred to as *Messelodinium thielepfeifferae*. In order to depict the occurrence of algal blooms and establish a connection to the changing environmental conditions, we aim to identify their specific biosignatures. Along with their known diagenesis products, specific alkanes, triterpenes, lipids and sterols in the lake sediments are compared with those in cultivated algae with GC-MS measurements, similar to the analysis of terrestrial input in geological investigations. Therefore, different strains of *Tetraedron minimum*, *Botryococcus braunii*, *Peridinium cinctum* and spec. are grown under various temperatures and N. The results may also be of interest for existing ecosystems as the period of deposition mainly comprises the Eocene, the latest greenhouse period of the earth is therefore considered as an approximation for global warming.

Keywords

Biosynthesis-products, Paleoclimate, Diagenesis

Beyond Aquatic Systems: Sustainable Phycocyanin Production In Terrestrial Cyanobacteria

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Abstract

Phycocyanin, a natural, vibrant blue pigment with applications in food, cosmetics, and pharmaceuticals, is traditionally derived from aquatic cyanobacteria such as *Spirulina*. However, conventional large-scale production often faces sustainability challenges, including high water usage and energy-intensive harvesting processes. Terrestrial cyanobacteria offer a promising alternative, as they are adaptable to cultivation in less resource-intensive systems. Beyond their environmental advantages, terrestrial strains may produce phycocyanin with unique properties that are highly valued in industrial applications, such as improved thermostability and enhanced tolerance to acidic environments. To explore this potential, we screened a diverse collection of terrestrial cyanobacteria, including newly extracted strains, for their growth characteristics, phycocyanin yield, and pigment stability. By identifying strains with high productivity and optimized pigment properties, we aim to advance the development of a more efficient, adaptable and eco-friendly phycocyanin production system.

Keywords

phycocyanin, terrestrial cyanobacteria, biotechnology

Dynamic seasonal patterns of microeukaryotic communities across different lake ecosystems

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Abstract

Freshwater ecosystems host a huge diversity of eukaryotic protists, with community structures shaped by various factors, including habitat size, lake chemistry, biotic interactions, and seasonal dynamics. In this study, we used Illumina high-throughput sequencing targeting the V9 region of the SSU rRNA to explore the diversity and temporal variability of eukaryotic plankton communities in 12 freshwater lakes located in Austria and Germany. Samples were collected biweekly over one calendar year to provide a comprehensive temporal dataset. Distinct differences in the dominance of taxonomic groups were observed across lakes, highlighting unique ecological dynamics in each system. Nonetheless, major taxonomic groups such as Viridiplantae, Chrysophyceae, and Dinophyceae were consistently present in nearly all lakes. Non-metric multidimensional scaling (NMDS) analysis based on Bray-Curtis distances showed that samples clustered more strongly by geographic location than by season, with Austrian lakes forming a tighter group compared to the more distinct clustering of the four German lakes. In contrast, within individual lakes, NMDS analyses revealed clear seasonal dynamics, where community structures followed a cyclical pattern throughout the year. This seasonal progression was more pronounced in German lakes, whereas Austrian lakes exhibited a subtler temporal trend. The observed seasonal patterns were primarily driven by dominant taxa, while rare species contributed minimally to the overall seasonal arrangement. This study demonstrates the intricate temporal variability of freshwater plankton communities, emphasising the influence of dominant taxa in driving seasonal patterns within diverse lake ecosystems.

Keywords

Citizen Science meets Microalgae Collection MZCH - Project DesmidHH monitors biodiversity of Desmids in peat bogs of Hamburg for assessment of biotope quality

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Abstract

The Hamburg Citizen Science project DesmidHH regularly monitors peat bogs and natural conservation areas in Hamburg and surroundings. The project is supported by the Microalgae and Zygnematophyceae Collection Hamburg (MZCH <https://www.biologie.uni-hamburg.de/en/einrichtungen/wissenschaftliche-sammlungen/algensammlung.html>, UHH) which provides Desmid material for training of species identification. Furthermore DesmidHH is supported by the group Plankton Ecology and Evolution <https://www.biologie.uni-hamburg.de/en/forschung/oekologie-biologische-ressourcen/planktoek.html> (UHH) regarding ecological analyses. It is known that the biodiversity of microalgae from the group of Desmidiaceae (Desmids, conjugating green algae, Zygnematophyceae) is a strong bioindicative parameter for the estimation of the ecological value of peat bogs and other wetland biotopes. The DesmidHH group has established a standardized sampling and data treatment protocol to analyse Desmid biodiversity in peat bogs. After microscopical identification and validation of the taxa the Desmid occurrences are entered into a database using the software DesmidDatabaseV3.09 [http://www.science4all.nl/?Biology\(M.v.Westen,2024\)](http://www.science4all.nl/?Biology(M.v.Westen,2024)). An integrative conservation value according to Coesel (2001, *Biodiv. & Conserv.* 10) Options to monitor the Desmid biodiversity in restored swamps and peat bogs with respect to biotope management and carbon sequestration capacities will be discussed.

Keywords

Desmidiaceae, bioindication, Zygnematophyceae, Conjugating green algae, biodiversity monitoring

Protein-linked complex carbohydrates as potent species identifiers for microalgae

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Abstract

Many eukaryotic proteins are decorated with oligosaccharides, of which the asparagine-linked N-glycans are the most complex and evolutionary oldest type. Recent rather incidental and surprising findings revealed for algal N-glycans a structural diversity that was totally unknown from embryophytes (land plants) or even vertebrates. Commercial *Chlorella* products exhibited a dozen or more clearly different N-glycan patterns, which did not the least correlate with the chosen designations as *C. vulgaris* or *C. pyrenoidosa*. A few lessons could already be learned. a) N-glycan patterns correlate with genetic markers, e.g., with (18S)-ITS1-5.8S-ITS2-(23S) barcodes. This argues for a chromosomal root of the glyco-diversity b) Mass spectrometric patterns are based on profound structural differences c) Similar barcodes, however, can occur in strains with fundamentally different N-glycans. So, DNA homologies even in the 98-99% range can be misleading d) Different N-glycan patterns were also observed with *Scenedesmaceae* strains. That is, the glyco-diversity is not confined to *Chlorella*-clade algae. The question arises as to the biological role of the apparently limitless structural diversity of algal N-glycans. In a more practical sense, one can think about the value and applicability of N-glycan analysis for strain characterization and identification as well as product authenticity.

Keywords

N-glycans, strain characterization, glycoproteins

SoilDiatoms: a new step towards soil bioindication using diatoms

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Abstract

Diatoms are an ecologically significant and highly diverse group of microalgae. They are abundant components of the Phytoplanktonic and -benthic communities of almost all marine and freshwater habitats, but are also ubiquitous in terrestrial habitats such as soil, anthropogenic structures, mosses, bark or rock. However, in contrast to their aquatic counterparts, terrestrial diatoms are far from being as well studied and understood. Diatoms are also well established bioindicators for water quality assessments (e.g. European Water Framework Directive) and paleoecological reconstructions and their sensitivity to multiple abiotic factors, for example, eutrophication, pH and salinity, is well documented. As well as water quality, soil quality is highly important. Soils have a high value for biodiversity, agriculture, recreation and are also tightly connected to water quality. They play an important role in nutrient cycling and the key nutrient that dictates the global biological productivity is soil phosphorus. Terrestrial diatoms are important primary producers in soils and can significantly influence nutrient cycling, soil stabilization, including mesic agricultural soils. Within the new project "SoilDiatoms" we will study the biodiversity and ecology of terrestrial diatoms with the aim to eventually create a proof-of-concept for a Soil Diatom index for soil quality monitoring. Within this framework we will especially focus on phosphorus as a key factor in soil ecosystems.

Keywords

diatoms, soil, bioindication

Microalgae culture collection IBASU-A: a scientific object of the national heritage of Ukraine

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Abstract

The Microalgae Culture Collection of M.G. Kholodny Institute of Botany, NAS of Ukraine (IBASU-A) was established in the 1960s. Today it is one of the largest collections in Ukraine which comprises about 500 strains of algae, representatives of Cyanobacteria, Chlorophyta, Charophyta, Euglenophyta, Heterokontophyta, as well as 270 strains of bacterial consortia isolated from algal cultures. The main part of the collection consists of green algae, the leading taxonomic group of the Ukrainian algal flora. Most of the strains (300) were isolated from freshwater and terrestrial habitats of different regions of Ukraine. IBASU-A has been ranked as a part of the Ukrainian national heritage since 2013. It consists of several separate collections, including sets of authentic strains, mutants, cultures of rare species, and strains for biotechnological purposes. The main object of the IBASU-A is to isolate, keep and supply algal strains for use in research and biotechnology. For example, the IBASU-A strains of species belonging to Chlorellaceae, Scenedesmaceae and Selenastraceae were used in different applied projects as test-objects for assessment of toxicity and carcinogenicity of synthetic organic substances or biological agents in the treatment of different types of industrial waste. The same strains were successfully used in another project as active producers of biomass for biofuel production. The study has received funding through the EURIZON project, grant agreement No.871072.

Keywords

IBASU-A, culture collection, strain, algae, Ukraine

Ecophysiology of several new species of *Hydrurus* causing golden brown snow in Svalbard, the High Tatras and the European Alps

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Abstract

Most chrysophytes are part of plankton in lakes. Some are attached to stones in cold brooks, while others occur as neuston. During snow melt, golden-brown blooms of chrysophycean algae occur in polar and alpine regions. In this study, we sampled microalgae responsible for this phenomenon, isolating laboratory strains from waterlogged snow near basal ice, transient streams on glacier surfaces, and snow in depressions. The blooms reached population densities of 106 cells per ml meltwater. Surprisingly, the 18S rRNA gene phylogeny placed all eight new strains in the Hydrurales. Some of them were closely related in 18S rRNA to the macroscopic species *Hydrurus foetidus*, but they differed in ITS2 and their dominant life cycle stage was as unicellular flagellate. Tetrahedral zoospores were observed. We believe that flagellates are beneficial for active migration in the waterlogged snowpack in accordance to light preferences. Fluorimetry indicated that Arctic populations have photosystem II adapted to high light levels. Polyunsaturated fatty acids support cells to thrive at temperatures around 0°C but their proportion differed between species. The cells contained compatible solutes as an antifreeze agent. The main pigment (after chlorophyll-a) was fucoxanthin, causing the overall golden-brown colour. results indicate that limnetic and cryosestic chrysophytes are closely related both taxonomically and ecologically.

Keywords

phylogeny, cell ultrastructure, snow, fluorimetry, pigments, cryoflora

Ecophysiological responses of islandic diatoms towards abiotic variables

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Abstract

Along the rocky shore of Iceland, seasonal changes result in strong fluctuations of abiotic variables such as temperature, light availability and salinity. Many of those rocks are covered by macroalgae, however, also benthic microalgae can be found here. Despite the diatoms significant contribution to their ecosystem, their response to these abiotic changes has not yet been investigated. Photosynthetic as well as growth responses towards varying light availability, temperature and salinity of nine islandic benthic diatom isolates were determined. All nine isolates displayed a high photo-physiological plasticity with no photoinhibition at up to 1400 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$. The overall maximum photosynthesis was found at 130 $\mu\text{mol O}_2 \text{mg}^{-1} \text{Chl a h}^{-1}$, and all isolates were light saturated between 12 and 105 $\mu\text{mol photons m}^{-2} \text{s}^{-1}$. Furthermore, all isolates displayed a broad photosynthetic and respirational performance over the 5 – 40 °C temperature range. Photosynthetic optimum temperature was found between 5 – 25 °C, however respirational optimum was always higher than those found for photosynthesis. Similarly, optimum growth temperature, tested between 1.5 – 25 °C, was also found between 5 – 25 °C, while most isolates preferred 15 °C or higher. Concerning salinity, isolates displayed growth between 1 SA and 65 SA with optimum salinities found between (5) 25 SA and 33 SA. No growth was found at salinities above 65 SA.

Keywords

Diatom, ecophysiology, iceland

The ancient evolution of far-red light photoacclimation in cyanobacteria

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Abstract

Cyanobacteria oxygenated the atmosphere of early Earth and continue to be key players in global carbon and nitrogen cycles. A phylogenetically diverse subset of extant cyanobacteria can perform photosynthesis with far-red light through a process called far-red light photoacclimation, or FaRLiP. This phenotype is enabled by a cluster of ~20 genes, and involves the synthesis of red-shifted chlorophylls f and d, together with paralogues of the ubiquitous photosynthetic machinery used in visible light. The FaRLiP gene cluster is present in diverse, environmentally important cyanobacterial groups but its origin and evolutionary history have remained unclear. This study takes advantage of the recent increase in (meta)genomic data to clarify this issue; sequence data mining, metagenomic assembly, and phylogenetic tree networks were used to recover more than 600 new FaRLiP gene sequences. These data enable high-resolution phylogenetics and - by relying on multiple gene trees, together with synteny - support FaRLiP appearing early in cyanobacterial evolution. Sampling information shows that considerable FaRLiP diversity can be observed in microbialites to the present day, and the process may have been associated with microbial mats and stromatolite formation in the early Paleoproterozoic. The ancestral FaRLiP cluster was reconstructed, and results consistently indicate that oxygenic photosynthesis using far-red light may have played a significant role in Earth's early history.

Keywords

photoacclimation, evolution, metagenomics

Two new phylogenetic lineages in filamentous cyanobacteria

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Abstract

During revision of the algae culture collection of the Institute of Botany (IBASU-A), interesting strains of cyanoprokaryotes were discovered, which appeared new phylogenetic lineages of the genus rank. The first strain was morphologically close to *Microcoleus*. Trichomes straight, cylindrical, narrowed and curved at the ends, sheath firm, homogeneous, hyaline or yellowish. Trichomes slightly constricted at the cross walls, cell shorter than wide. End cells elongated, conical-rounded and bent. The cyanobacterium was isolated from biocrusts of chalk outcrops of the Kharkiv Region (Ukraine). The strain was phylogenetically close to several cyanobacteria identified as *Microcoleus* from biocrusts of Algeria and China deserts. These strains form a separate lineage between Microcoleaceae and Coleofasciculales. The second strain was isolated from biocrusts of the Baltic Sea sand dunes (Warnemünde, Germany). The cyanobacterium has a *Leptolyngbya*-like morphology. The study has received funding through the EURIZON project, grant agreement No.871072.

Keywords

cyanobacteria, new lineages, IBASU-A

Solotvynia, a New Coccoid Lineage among the Ulvophyceae (Chlorophyta)

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Abstract

Coccoid Ulvophyceae are often overlooked despite their wide distribution. They occur as epiphytes on marine seaweeds or grow on stones or on shells of mussels and corals. Most of the species are not easy to identify based solely on morphology. However, they form two groups based on the flagellated cells during asexual reproduction. The biflagellated coccoids are monophyletic and represent the genus *Sykidion* (Sykidiales). In contrast, the quadriflagellated taxa are polyphyletic and belong to different genera and orders. The newly investigated strains NIES-1838 and NIES-1839, originally identified as *Halochlorococcum*, belong to the genus *Chlorocystis* (*C. john-westii*) among the order Chlorocystidales. The unidentified strain CCMP 1293 had almost an identical SSU and ITS-2 sequence to *Symbiochlorum hainanense* (Ignatiales) but showed morphological differences (single chloroplast, quadriflagellated zoospores) compared with the original description of this species (multiple chloroplasts, aplanospores). Surprisingly, the strain SAG 2662 (= ULVO-129), together with the published sequence of MBIC 10461, formed a new monophyletic lineage among the Ulvophyceae, which is highly supported in all of the bootstrap and Bayesian analyses and approximately unbiased tests of user-defined trees. This strain is characterized by a spherical morphology and also form quadriflagellated zoospores, have a unique ITS-2 barcode, and can tolerate a high variation of salinities. Considering our results, we emend the diagnosis of *Symbiochlorum* and propose the new genus *Solotvynia* among the new order Solotvyniales.

Keywords

ITS-2 secondary structure; marine coccoids; SSU/ITS phylogeny

The New Genus *Caulinema* Revealed New Insights into the Generic Relationship of the Order Ulotrichales (Ulvophyceae, Chlorophyta)

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Abstract

Traditionally, the order Ulotrichales comprised green algae of an unbranched, uniseriate, filamentous morphology. However, since the establishment of ultrastructural features, the circumscription of this order has dramatically changed. Some genera and species have been excluded from this order and others with different morphologies (sarcinoid, branched filaments or even parenchymatous taxa) have been included. Phylogenetic analyses have confirmed the monophyly of this order, but its differentiation from the Ulvales and Acrosiphoniales remains difficult because of the lack of synapomorphies at every level (morphology, molecular signatures). To demonstrate the difficulties of placement into genera and orders, we investigated two sarcinoid taxa with the absence of zoospore formation. SSU and ITS rDNA tree topology and the ITS-2/CBC approach revealed that both strains SAG 2661 and CCAP 312/1 belong to *Ulosarcina terrestrica* and the newly erected genus *Caulinema*, respectively. The species conception using this approach was evaluated by sequencing the plastid-coding gene *tufA*, a commonly used barcode marker for green algae. All three molecular markers resulted in similar topologies at the generic and species levels, which is consistent with the ITS-2/CBC approach and *tufA* for barcoding. The reevaluation of the ultrastructural features revealed that the presence of organic scales on the surfaces of motile cells is characteristic for the order Ulotrichales and can be used for separation from the closely related orders. As a consequence of our study, we propose the new genus *Caulinema* for strain CCAP 312/1.

Keywords

ITS-2 secondary structure; SSU/ITS phylogeny; *tufA* phylogeny

Towards deciphering interactions within the living Skin of the Earth

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Abstract

Biocrusts (BC) are intriguing communities composed of heterotrophic bacteria and fungi as well as photoautotrophic cyanobacteria, algae, mosses and lichens. Often referred to as the Skin of the Earth, latest estimates state that they cover about 12% of all terrestrial surface. BC are found globally where light is available but otherwise harsh conditions make the prevailing growth of higher plants impossible. They dominate arid regions such as the poles, deserts, and high alpine environments, where they are pivotal ecosystem engineers that offer a wide array of ecosystem services stabilising the soil surface, preventing erosion, fixing carbon and nitrogen, and building up organic soil biomass that enables later plant settlement. Moreover, BC immobilise heavy metals in contaminated soils, making them promising communities for bioremediation applications. Despite their long-known ecological importance, many aspects of BC are still poorly understood. Biochemical and molecular processes underlying their ecological functions, interactions between the many different microorganisms that build a BC, and the role of secondary metabolites in these interactions are, with very few exceptions, still unknown. To develop a model system to investigate molecular mechanisms in BC from Europe, we isolated bacteria from an Arctic BC and started co-cultivation with *Chlorella vulgaris*. Here, we present the first results of our work towards deciphering interactions within the living Skin of the Earth.

Keywords

Biocrust, Interactions, Soil

A new mesophilic isolate of *Pleuraestrosarcina*, a genus previously only reported from arid habitats

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Abstract

The genus *Pleuraestrosarcina* with its two species *P. brevispinosa* and *P. terriformae* was exclusively found in arid soils. Despite the huge efforts using metabarcoding approaches, *Pleuraestrosarcina* has not been reported and only a few cultures are available in public culture collections. This genus is very difficult to identify solely by morphology especially if the typical akinetes are absent. During the evaluation of the holdings of the Algal Culture collection of the Kyiv University (ACKU), we studied a strain showing morphological similarities to both *Pleuraestrosarcina* species because of the presence of akinetes. In contrast to the other strains which all originated from desert or dry soil habitats, the strain ACKU 382 was isolated from a mesophilic habitat (Kaniv Nature Reserve, Ukraine). The phylogenetic analyses using a multiple gene approach (SSU, ITS, *tufA*, *rbcl*) confirmed that this strain belongs to *Pleuraestrosarcina*. The ITS-2/CBC approach revealed that ACKU 382 represents a new isolate of *P. brevispinosa*. Both known species are characterized by unique compensatory base changes in the secondary structure of ITS-2. To find additional support for these species, we searched for molecular signatures among the two plastid-coding genes at the amino acid level. The comparison of both markers showed different resolution power. Whereas *tufA* confirmed the split into two species without recognition of the varieties, *rbcl* distinguished the varieties by unique synapomorphies similar to the concatenated dataset of SSU and ITS. The strain ACKU 382 has new variants of ITS-1 and ITS-2 and has three unique amino acids in *rbcl*. As a consequence, we proposed a new variety for this strain.

Keywords

DNA barcoding; intrageneric variation; species concept

Purification of microalgae cultures from fungal and bacterial contaminants

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Abstract

The work is focused on the selection of optimal methods for the purification of microalgae strains from the collections of ACKU and IBASU-A from contamination with bacteria and microscopic fungi. The both collections were screened and some strains were found to be contaminated with fungi (*Cladosporium*, *Aspergillus*, *Acremonium*, yeast, *Mycelia sterilia*) and bacteria. The ACKU strains selected for the experiment were 65-02 (*Bracteacoccus* sp.), 104-02 (*Chlamydomonas* sp.), 192-03 (*Chlamydomonas moewusii*), 221-03 (*Chlamydomonas* sp.), 222-03 (*Chlorochytrium hypanicus*), 277-03 (*Scenedesmus obtusus*), 395-05 (*Dilabifillum* sp.), 435-06 (*Desmodesmus abundans*), 538-06 (*Chlorococcum echinozygotum*), 919-010 (*Parietochloris* sp.), 1174-12 (*Scotiellopsis* sp.) and IBASU Prim 14-13 (*Myrmecia biatorellae*). The effect of Carbendazim, Antibiotic Antimycotic Solution (AAS) and Nuosept BMC-422 (BMc) on fungal and bacterial contamination of green algae cultures with different morphological structure types was studied. It was found that AAS and BMc inhibit or completely stop the growth of algae at the declared concentrations, so they cannot be used to purify strains from fungal and bacterial contamination. Carbendazim was found to be effective in purifying some strains of algae from contamination with *Aspergillus* fungi. As a result, axenic cultures were obtained for strains 65-02, 192-03, 221-03 and 277-03. The study has received funding through the EURIZON project, grant agreement No.871072.

Keywords

ACKU, IBASU-A, fungal contaminants

Rare Algae Species and Algae from the Red Data Book from the Territory of Left-Bank Polissya (Ukraine)

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Abstract

Important results of studies on rare algae species, the compilation of red lists, and red books include the inclusion of 61 algae species in the 4th edition of the Red Book of Ukraine (2021) and works dedicated to algosozology, particularly "Fundamentals of algosozology" (2008). Rare species are those for which no more than five locations are known within Ukraine. Left-Bank Polissya (LBP) is a natural-geographical region in Ukraine located on the left bank of the Dnipro River and includes the northeastern areas of the country (Chernihiv and Novhorod-Siversky Polissya). According to literature and original data, the algal flora of LBP water bodies includes 1854 species (2232 intraspecific taxa). Rare species for Ukraine's flora amount to 194 species and intraspecific taxa (8.7% of the total diversity of LBP algal flora). These include representatives of Charophyta (34 species), Chrysophyceae (32), Euglenophyta (31), Bacillariophyceae and Xanthophyceae (27 each), Chlorophyta (20), Cyanophyceae (19), Cryptophyceae (3), and Dinophyceae — 1 species. The largest number of rare species was found in swamps (93 species) and rivers (77), followed by floodplain water bodies (48), ponds (26), and ephemeral water bodies (7 algae species). Four algae species listed in the Red Book of Ukraine are known from the region: *Euastropsis richteri* (Schmidle) Lagerheim (swamps, 2 records); *Oedogonium plagiostomum* var. *tanaiticum* Y.V.Roll (Desna River, floodplain lakes, pond, 4 records); *Bambusina borreri* (Ralfs) Cleve (swamps, floodplain lakes, 3 records); *Spirogyra reinhardii* Khmelevesky (swamp, 1 record).

Keywords

rare algae species, Left-Bank Polissya, swamps