ICS 2026
SUWON, KOREA

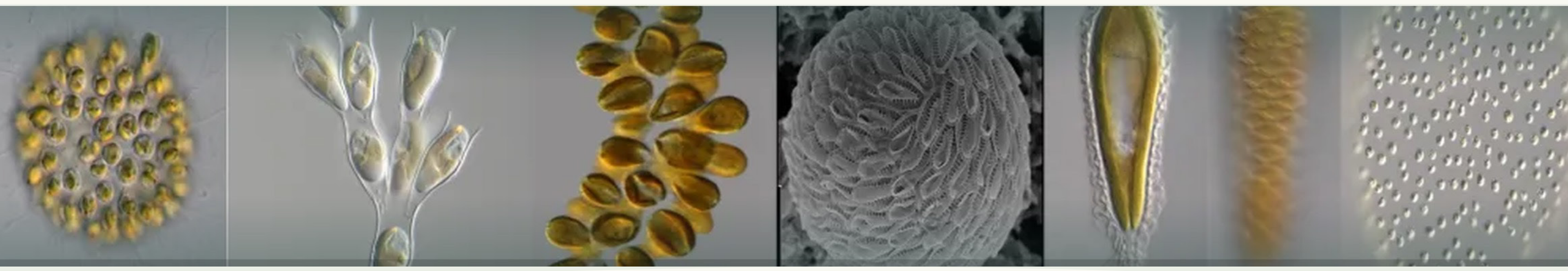
ics2026.org

INTERNATIONAL CHRYSOPHYTE SYMPOSIUM

11th International Chrysophyte Symposium

Jointly held with the Annual Meeting of the Korean Society of Protistologists

June 23-27, 2026
Sungkyunkwan University
Suwon, Korea



Organizers and supporting institutions

THE KOREAN SOCIETY OF PROTISTOLOGISTS · KSOP 한국원생생물학회

사단법인 한국조류학회 THE KOREAN SOCIETY OF PHYCOLOGY

SUNGKYUNKWAN UNIVERSITY 1398 성균관대학교

성균관대학교 SUNGKYUNKWAN UNIVERSITY

BrainKorea21 FOUR 글로벌바이오엑스퍼트 교육연구단

Welcome to the 11th International Chrysophyte Symposium

We are delighted to welcome you to the 11th International Chrysophyte Symposium, held at the Sungkyunkwan University, Suwon, Korea, from June 22–26, 2026. This year's symposium is particularly special as it is a joint meeting with the annual meeting of the Korean Society of Protistologists, fostering even greater collaboration across the field of protistology.

Following our successful gathering in Essen, Germany, in 2022, we continue our tradition of providing a premier global forum for the latest research on all aspects of chrysophyte investigations. Our program will highlight diverse themes, including biodiversity, evolution, ecology, systematics, and experimental morphology. While chrysophytes remain our primary focus, we warmly welcome investigations into allied algal taxa and other protists.

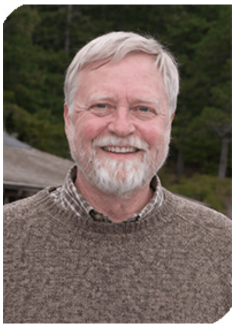
We look forward to an inspiring exchange of ideas in Korea as we advance our collective understanding of these fascinating organisms.

Sincerely,
Hwan Su Yoon and Woongghi Shin

Organizing Committee

Hwan Su Yoon	Sungkyunkwan University
Woogghi Shin	Chungnam National University
Jongsoo Park	Kyungpook National University
Jong Im Kim	Sungkyunkwan University
Robert A. Andersen	University of Washington
Peter A. Siver	Connecticut College
Pavel Škaloud	Charles University in Prague

Invited Lectures



Robert A. Andersen

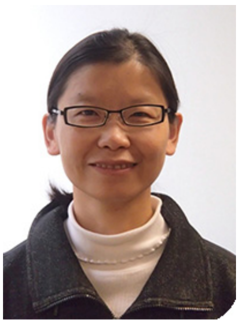
Retired (Director Emeritus CCMP/NCMA, Bigelow Laboratory; Senior Research Scientist, Friday Harbor Laboratories, University of Washington)

Lecture Title

History of chrysophyte symposia, with comments on remaining chrysophyte research problems

Biography

Bob organized the First International Chrysophyte Symposium in 1983, an initiative that has continued through the 11th International Chrysophyte Symposium. He has made outstanding contributions to the systematics of Chrysophyceae and other heterokont algae, including the description of five algal classes and numerous taxonomic orders, families, genera, and species.
His research has been driven by a fundamental question: which algae truly belong to the Chrysophyceae, and how should those now excluded be reclassified. Bob has published 170 peer-reviewed articles, book chapters, and books. His achievements have been recognized with several major honors, including the Tyge Christensen Prize (2000), the Japanese Phycological Society Prize (2002), the Phycological Society of America's Award of Excellence (2015), and the Algal Biomass Organization's Champion of Algae Award (2022).



Ke Hu

Professor, Biodesign Center for Mechanisms of Evolution/School of Life Sciences
Arizona State University

Lecture Title

The initiation, development, and evolution of apical-basal polarity of *Toxoplasma gondii*

Biography

Ke Hu is a professor at the Biodesign Center for Mechanisms of Evolution and School of Life sciences at Arizona State University. The Hu Lab focuses on the structure and function of the cytoskeleton and how the cytoskeleton evolved to support the parasitic life-style of the apicomplexans. Of particular interests are: how a defined cytoskeletal array is constructed, and how the cytoskeleton contributes to movement and force generation. Their strategy is to combine imaging, molecular genetics and evolution-based approaches to determine how key molecules and structures drive these processes, and how the evolution of distinct molecular and structural features contribute to the evolution of intracellular parasitism. Her lab uses an obligate intracellular human parasite, *Toxoplasma gondii*, and its free-living relatives as model organisms, because of their many features that are advantageous for exploring these questions and also because in combination they provide a powerful means of addressing the evolution of parasitism in the phylum Apicomplexa. Equally important, insights into their basic biology will expose vulnerabilities in *Toxoplasma* and other apicomplexan parasites, which can be exploited to design better therapies.

Marek Eliáš

Faculty of Science, University of Ostrava

Lecture Title

The complex evolutionary landscape of the organellar genomes in ochrophytes

Biography

Marek's research focuses on understanding the diversity of life at the molecular, genomic, and cellular levels, with a particular emphasis on protists—one of the most diverse yet understudied groups of eukaryotes. In 2010, he founded the Laboratory of Protist Genomics and Evolution at the University of Ostrava, where he works with students, postdoctoral researchers, and international collaborators. His work primarily employs genomic and bioinformatic approaches to investigate protist cell organization and function. Key research interests include the evolution and diversity of mitochondria and plastids in poorly studied protist lineages, the evolution of GTP-binding proteins (GTPases) in relation to the origin and diversification of eukaryotic cells, and evolutionary variation in molecular mechanisms of gene expression, particularly the genetic code. In addition, he contributes to mapping protist diversity through classical taxonomic studies, especially of green algae and eustigmatophytes. Marek has published over 100 peer-reviewed articles and is deeply committed to teaching, hands-on training, and the development of the University of Ostrava as a growing research institution.

Ryoma Kamikawa

Associate professor, Graduate School of Agreculture, Kyoto University

Lecture Title

Evolutionary gain and loss of light utilization in Stramenopiles

Biography

Ryoma is an Associate Professor at the Graduate School of Agriculture, Kyoto University. His research focuses on the evolutionary biology and genomics of eukaryotes, specifically investigating the fundamental mechanisms of organelle evolution and metabolic adaptation. By employing advanced comparative genomics and molecular phylogenetic approaches, his work elucidates the evolutionary principles governing the reduction and specialization of organellar functions.

Ryoma has extensively studied the transition from autotrophy to heterotrophy across diverse algal lineages, including diatoms and chrysophytes, uncovering how organelle genomes and cellular systems adapt during these evolutionary shifts. Beyond plastid evolution, he delves into the functional diversity of mitochondria-related organelles (MROs) in protists inhabiting oxygen-depleted environments. Through this integrative approach, his research not only sheds light on the vast diversity of the eukaryotic Tree of Life but also provides insights into the metabolic flexibility of microorganisms across diverse ecological niches, from marine to freshwater ecosystems.

Peter A. Siver

Becker Professor Emeritus, Department of Botany, Connecticut College, New London, Connecticut USA.

Lecture Title

Evolutionary history of chrysophytes: What have we learned from the fossil record.

Biography

Peter presented at each of the ten previous International Chrysophyte Symposia (ICS), co-organized the 5th and 7th symposia, and co-authored two of the ICS Proceedings volumes. Peter has broad research interests, including the biogeography, ecology and taxonomy of modern and fossil siliceous organisms, with a focus on scaled chrysophytes and diatoms. He has described over 100 new species and genera, and successfully used algal assemblages to reconstruct paleoenvironments over time scales ranging from hundreds to millions of years.

Peter has published over 180 peer-reviewed articles, three books on algae, one on lakes, and two edited volumes. He has received many honors, including the Darbaker Award (1990) from the Botanical Society of America, the North American Lakes Management Award (2000), two National Science Foundation OPUS awards (2011, 2025), the Gerald Prescott Award (2013) and the Award of Excellence from the Phycological Society of America (2021), and was elected into the Connecticut Academy of Science in 2023.

Louis Graf

Postdoctoral Researcher (CNRS), Institut de Biologie Paris-Seine (IBPS),
Sorbonne Université

Lecture Title

Using culture free methods to explore the diversity and ecological functions of oceanic Chrysophyceae biomes

Biography

Louis is a Postdoctoral Researcher within the Horizontal Evolution of Algal Lifestyles (HEAL) team at the Laboratory of Computational and Quantitative Biology (LCQB), Sorbonne Université, specializing in computational biology, algal evolution, and marine microbiology. His research focuses on the evolutionary genomics and population genetics of Stramenopiles, with a particular emphasis on brown seaweeds and Chrysophyceae. By employing high-throughput sequencing and functional genomic tools, his work elucidates the complex evolutionary histories and adaptive mechanisms of marine algal groups.

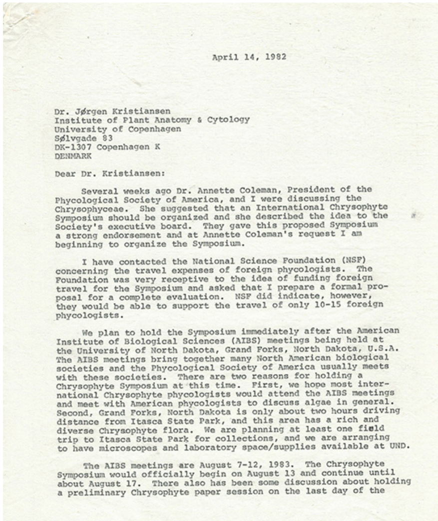
Louis has extensively studied the genomic architecture of Stramenopiles lineages. Through an integrative approach including culture-free metagenomic methods, his recent research seeks to uncover the hidden diversity and ecological roles of oceanic Chrysophyceae biomes, providing critical insights into the metabolic and functional flexibility of eukaryotes across global marine ecosystems.

Event Details

Dates: June 23 - 26, 2026

Venue: Sungkyunkwan University, Suwon, South Korea

Host: Sungkyunkwan University, Korean Society of Protistologists, Korean Phycological Society



April 14, 1982

Dr. Jørgen Kristiansen
Institute of Plant Anatomy & Cytology
University of Copenhagen
Sølvgade 83
DK-1307 Copenhagen K
DENMARK

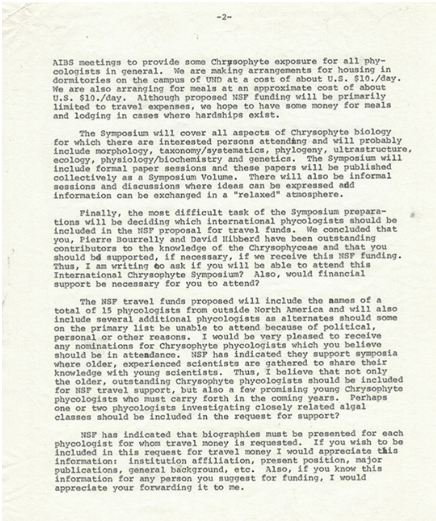
Dear Dr. Kristiansen:

Several weeks ago Dr. Annette Coleman, President of the Phycological Society of America, and I were discussing the Chrysophyceae. She suggested that an International Chrysophyte Symposium should be organized and she described the idea to the Society's executive board. They gave this proposed Symposium a strong endorsement and at Annette Coleman's request I am beginning to organize the Symposium.

I have contacted the National Science Foundation (NSF) concerning the travel expenses of foreign phycologists. The Foundation was very receptive to the idea of funding foreign travel for the Symposium and asked that I prepare a formal proposal for a complete evaluation. NSF did indicate, however, they would be able to support the travel of only 10-15 foreign phycologists.

We plan to hold the Symposium immediately after the American Institute of Biological Sciences (AIBS) meetings being held at the University of North Dakota, Grand Forks, North Dakota, U.S.A. The AIBS meetings bring together many North American biological societies and the Phycological Society of America usually meets with these societies. There are two reasons for holding a Chrysophyte Symposium at this time. First, we hope most international Chrysophyte phycologists would attend the AIBS meetings and meet with American phycologists to discuss algae in general. Second, Grand Forks, North Dakota is only about two hours driving distance from Itasca State Park, and this area has a rich and diverse Chrysophyte flora. We are planning at least one field trip to Itasca State Park for collections, and we are arranging to have microscopes and laboratory space/supplies available at UND.

The AIBS meetings are August 7-12, 1983. The Chrysophyte Symposium would officially begin on August 13 and continue until about August 17. There also has been some discussion about holding a preliminary Chrysophyte paper session on the last day of the



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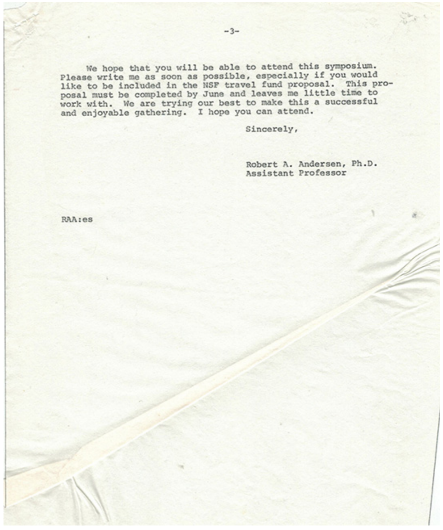
AIBS meetings to provide some Chrysophyte exposure for all phycologists in general. We are making arrangements for housing in dormitories on the campus of UND at a cost of about U.S. $10./day. We are also arranging for meals at an approximate cost of about U.S. $10./day. Although proposed NSF funding will be primarily limited to travel expenses, we hope to have some money for meals and lodging in cases where hardships exist.

The Symposium will cover all aspects of Chrysophyte biology for which there are interested persons attending and will probably include morphology, taxonomy/systematics, phylogeny, ultrastructure, ecology, physiology/biochemistry and genetics. The Symposium will include formal paper sessions and these papers will be published collectively as a Symposium Volume. There will also be informal sessions and discussions where ideas can be expressed and information can be exchanged in a "relaxed" atmosphere.

Finally, the most difficult task of the Symposium preparations will be deciding which international phycologists should be included in the NSF proposal for travel funds. We concluded that you, Pierre Bourrelly and David Hibberd have been outstanding contributors to the knowledge of the Chrysophyceae and that you should be supported, if necessary, if we receive this NSF funding. Thus, I am writing to ask if you will be able to attend this International Chrysophyte Symposium? Also, would financial support be necessary for you to attend?

The NSF travel funds proposed will include the names of a total of 15 phycologists from outside North America and will also include several additional phycologists as alternates should some on the primary list be unable to attend because of political, personal or other reasons. I would be very pleased to receive any nominations for Chrysophyte phycologists which you believe should be in attendance. NSF has indicated they support symposia where older, experienced scientists are gathered to share their knowledge with young scientists. Thus, I believe that not only the older, outstanding Chrysophyte phycologists should be included for NSF travel support, but also a few promising young Chrysophyte phycologists who must carry forth in the coming years. Perhaps one or two phycologists investigating closely related algal classes should be included in the request for support?

NSF has indicated that biographies must be presented for each phycologist for whom travel money is requested. If you wish to be included in this request for travel money I would appreciate this information: institution affiliation, present position, major publications, general background, etc. Also, if you know this information for any person you suggest for funding, I would appreciate your forwarding it to me.



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We hope that you will be able to attend this symposium. Please write me as soon as possible, especially if you would like to be included in the NSF travel fund proposal. This proposal must be completed by June and leaves me little time to work with. We are trying our best to make this a successful and enjoyable gathering. I hope you can attend.

Sincerely,

Robert A. Andersen, Ph.D.
Assistant Professor

RAA:es

The First International Chrysophyte Symposium was initiated by Annette Coleman, President of the Phycological Society of America in 1982, who asked Robert Andersen to organize a chrysophyte meeting in conjunction with the Botanical Society of America and the Phycological Society of America meetings to be held at the University of North Dakota in Grand Forks, North Dakota. Financial support was secured from the USA National Science Foundation (NSF), which provided a travel funds specifically for foreign attendees. This is an example invitation letter to Joergen Kristiansen.

1st International Chrysophyte Symposium, Grand Forks, ND, USA, 1983

Elliot Shubert & Robert Andersen

Helge Thomsen, Hans Preisig, David Hibberd & Barry Leadbeater

Paulette Gayral & Robert Andersen

• The 1st International Chrysophyte Symposium, Grand Forks, North Dakota, USA 1983

This photograph captures many of the pioneering scientists who attended the inaugural meeting, including Jeremy Pickett-Heaps, Frank Round, John Smol, Barry Leadbeater, and numerous others who helped shape early chrysophyte and protist research. The gathering brought together an extraordinary group of researchers whose work influenced phycology and protistology for decades to come.

Rick Meyer, Peter Siver, David (Paddy) Patterson

Paulette Gayral, Hans Preisig, Larry Hoffman Craig Sandgren, Larry Hoffman, Jim Wee and David Adam

Bob Guillard, Robert Andersen and Jørgen Kristiansen brave the Native American dance routine

• Informal discussions during the early days of ICS

Beyond formal sessions, the symposium was remembered for its lively and often humorous informal interactions. As recalled by participants, memorable moments included late-night fire alarms that turned into spontaneous protist discussions, and lighthearted toasts that reflected the close-knit and collegial atmosphere of the meeting.

Chantal Billard

Joergen Kristiansen

Monica Durrschmidt, Ken Stewart & Robert Andersen

• **Scientific exchange and the beginnings of long-term collaborations**

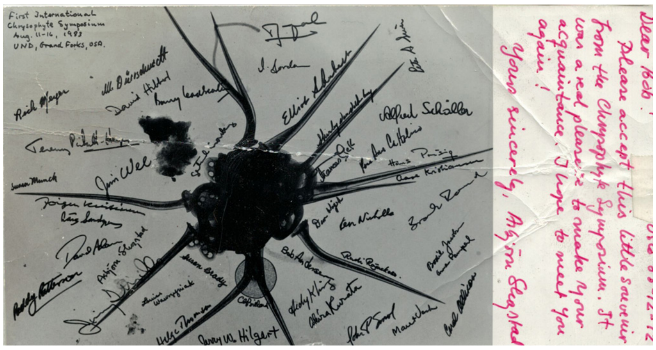
The first symposium fostered enduring scientific relationships and collaborations. Invited talks, such as Frank Round's presentation on heterokont phylogeny, led to future visits, collaborations, and divergent yet complementary research paths. Over time, figures such as Jørgen Kristiansen emerged as central contributors to the continuing International Chrysophyte Symposium tradition.


Name: Priscilla Sarai Dürrschmidt

geboren am: 19. August 1983

Geburtsort: Baraboo/Wisconsin, U S A

Where a Scientific Meeting Meets Life
The birth record of Priscilla Sarai Dürrschmidt, born on August 19, 1983, in Baraboo, Wisconsin.
ICS left behind more than research presentations; it intersected with the beginnings of lives.
This document symbolizes a time when science and everyday life were closely intertwined.



The Weight of a Final Written Line
As the first ICS drew to a close, participants wrote notes of thanks and reflections in a small booklet and presented it to Bob. I deliberately waited and wrote the final entry. I no longer remember exactly what I wrote, but I am certain that, over time, that booklet came to mean more than securing an NSF grant.

• **Field excursion to Lake Itasca during the First International Chrysophyte Symposium**

The field trip provided opportunities for informal interactions and lasting professional connections. It was here that participants met colleagues such as John "Platt" Bradbury, relationships that later developed into long-term collaborations in fields including paleolimnology. These excursions exemplified the hands-on and collegial spirit of the early ICS meetings.


Rudy Roijackers, Bob Guillard, Robert Andersen, Frank, Peter Heywood, Rudy Roijackers, Peter Heywood, Rick Meyer, Chantil Billard & Larry Hoffman.


Monica Durrschmidt, Robert Andersen, Joergen Kristiansen, Aase Kristiansen, David Adam & Rick Meyer


Joergen Kristiansen, Jim Craigie, Robert Andersen, Helge Thomsen, Barry Leadbeater & Ken Nicholls

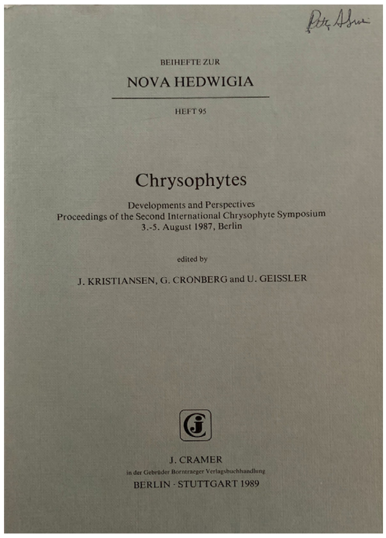
• **Informal moments reflecting mentorship, friendship, and shared memories.**

Beyond science, the 1st ICS was shaped by mentorship, student involvement, and memorable personal moments—from students hosting visiting scientists and organizing events, to friendships formed across generations. The symposium concluded with participants contributing personal messages to a commemorative booklet, a lasting reminder of the human connections that defined the meeting.

2nd International Chrysophyte Symposium, Berlin, Germany, 1987

Peter Siver, Robert Andersen & Monica Durrschmidt

2nd ICS Tyge Christiansen



BEIHEFTE ZUR

NOVA HEDWIGIA

HEFT 95

Chrysophytes

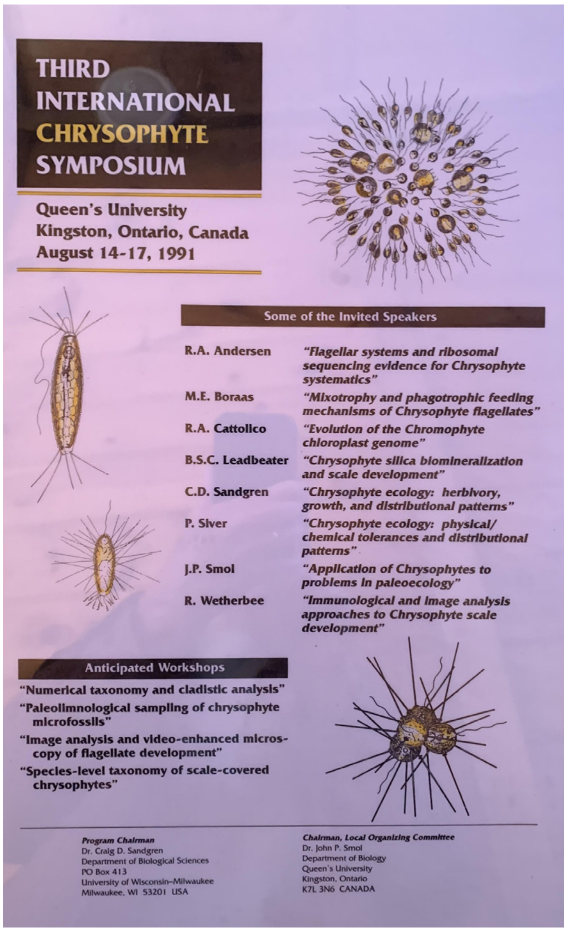
Developments and Perspectives
Proceedings of the Second International Chrysophyte Symposium
3.-5. August 1987, Berlin

edited by

J. KRISTIANSEN, G. CRONBERG and U. GEISSLER

J. CRAMER
in der Gebrüder Borntraeger Verlagsbuchhandlung
BERLIN · STUTTGART 1989

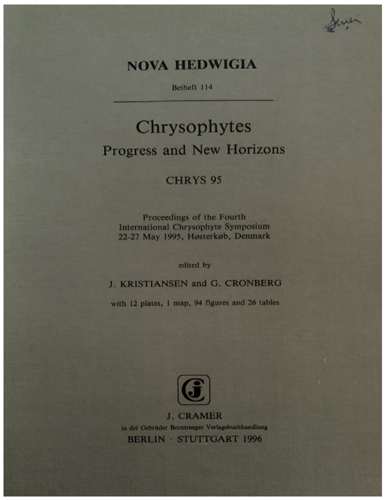
3rd International Chrysophyte Symposium, Kingston, Ontario, Canada 1991



4th International Chrysophyte Symposium, Høsterkøb, Denmark, 1995

4th ICS in Høsterkøb, Denmark. Jim Wee, Rick Wetherbee, Peter Siver

Barbara Zeeb, Sue Watson, Jørgen Kristiansen , Rick Wetherbee and Gertrud Cronberg.



NOVA HEDWIGIA

Beiheft 114

Chrysophytes

Progress and New Horizons

CHRYS 95

Proceedings of the Fourth
International Chrysophyte Symposium
22-27 May 1995, Høsterkøb, Denmark

edited by

J. KRISTIANSEN and G. CRONBERG

with 12 plates, 1 map, 94 figures and 26 tables

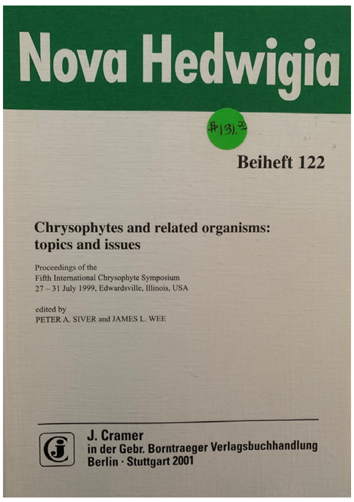
J. CRAMER
in der Gebrüder Borntraeger Verlagsbuchhandlung
BERLIN · STUTTGART 1996

Peter Siver, Rick Wetherbee

Gertrud Cronberg, Kate Duff, Barbara Zeeb

Jim Wee, Rick Wetherbee, Barbara Zeeb, Kate Duff

5th International Chrysophyte Symposium, Edwardsville, Illinois, USA, 1999



Nova Hedwigia

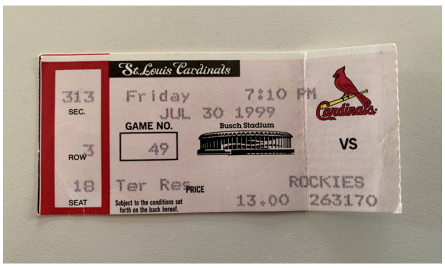
Beiheft 122

Chrysophytes and related organisms: topics and issues

Proceedings of the
Fifth International Chrysophyte Symposium
27 – 31 July 1999, Edwardsville, Illinois, USA

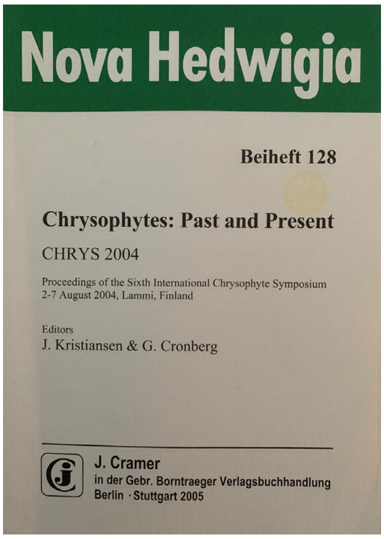
edited by
PETER A. SIVER and JAMES L. WEE

J. Cramer
in der Gebr. Borntraeger Verlagsbuchhandlung
Berlin · Stuttgart 2001



The fifth ICS in Edwardsville we arranged to bring everyone (especially the inter-national attendees) to St. Louis to a professional baseball game with the St. Louis Cardinals versus the Colorado Rockies. I (Peter siver) had been tracking the home run total for Mark McGwire during the summer hoping that he would hit his 500th home run of his career at the game. No luck, but he did hit #495. Attached is the ticket stub from that game.

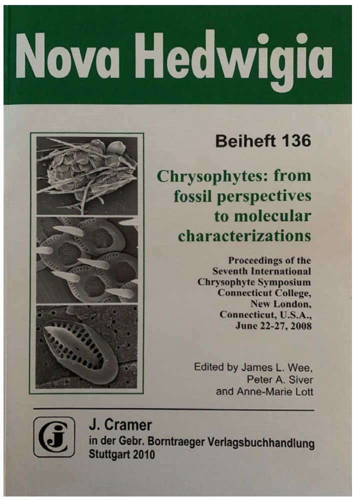
6th International Chrysophyte Symposium, Lammi, Finland, 2004



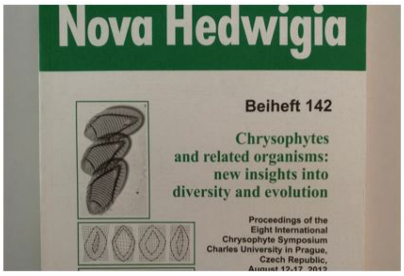
7th International Chrysophyte Symposium, New London, Connecticut, USA, 2008

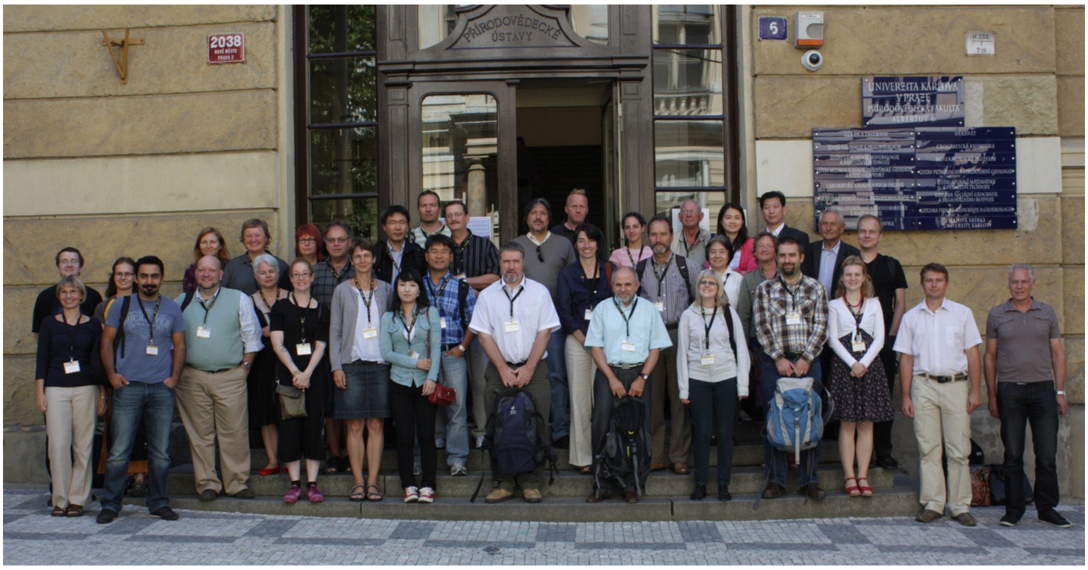
The lobster bake and the Taste and Odor "class" we had at the Seventh ICS at Connecticut College.

The lobster party at the Seventh ICS



8th International Chrysophyte Symposium, Prague, Czech Republic, 2012



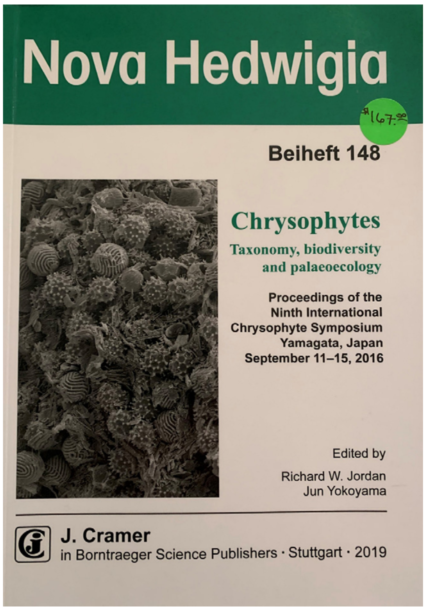


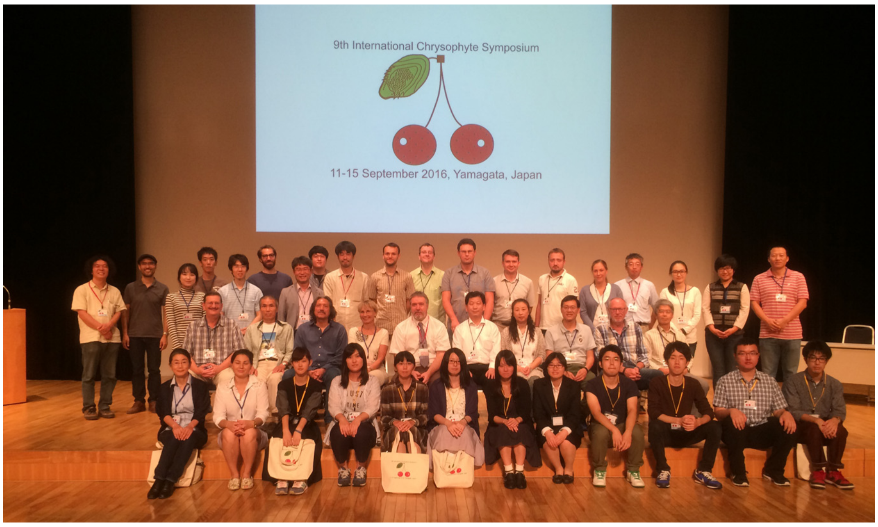
Group Photo for the 8th ICS in Prague

Jørgen Kristiansen & Anne-Marie Lott

Peter Siver & Jørgen Kristiansen

9th International Chrysophyte Symposium, Yamagata, Japan, 2016





Group Photo for the 9th ICS in Yamagata

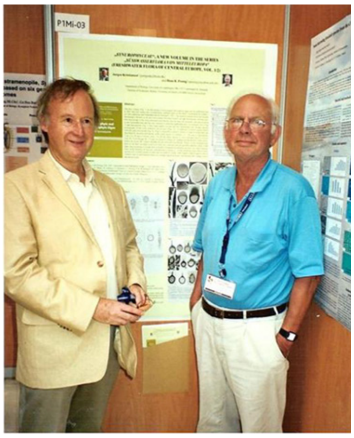
Train station in Yamagata

Peter Siver & Hwan Su Yoon

Louis Graf, David Hernandez, Peter Siver, Yvonne Nemcova

10th International Chrysophyte Symposium, Essen, Germany, 2022

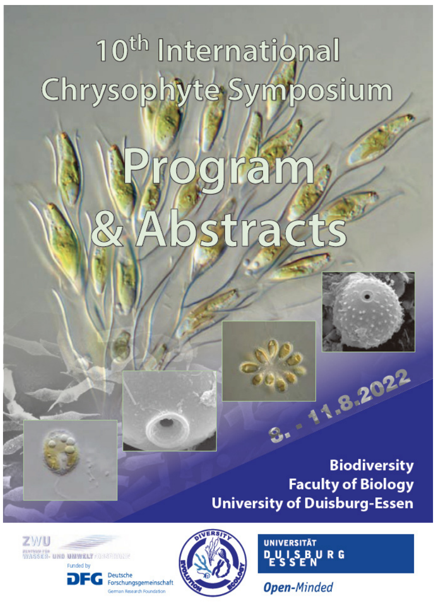
Praque meeting - Jørgen Kristiansen with son Peter and his grandson



Hans Preisig and Jørgen Kristiansen

Peter Siver made these frames out of birch bark.
These were donated to student auction at NEAS and raised $350.
Can you name the genera?

Chrysophyte cake.



https://www.uni-due.de/biodiversitaet/ics2020_welcome.php

CONTENTS

PROGRAM

11th International Chrysophyte Symposium & Korean Society of Protistologist Meeting 2026

Time	June 22 (Mon)	June 23 (Tue)	June 24 (Wed)	June 25 (Thu)	June 26 (Fri)	June 27 (Sat)
08:30–09:00		Registration				
09:00–09:50		Keynote Lecture Robert A. Andersen	Keynote Lecture Marek Elias		Keynote Lecture Peter A. Siver	
09:50–10:40		Keynote Lecture Ke Hu	Keynote Lecture Ryoma Kamiawa		Keynote Lecture Louise Graf	
10:40–11:00		Break	Break		Break	
11:00–12:20		Special Session I	Special Session II		Special Session III	
12:20–13:45		Lunch	Lunch	Field Trip	Lunch	
13:45–15:00		Best Student Oral Presentation	Best Student Oral Presentation		Special Session IV	Excursions
15:00–15:30		Break	Break			
15:30–17:00	Registration	Flash Talk Session	Best Student Oral Presentation		Colosing Ceremony	
17:00–18:00	Welcome Reception	Poster Session	Besst student presentation award/ ICS community Meeting/ KSOP Business Meeting			
18:30–		Banquet				

TIME TABLE

11th International Chrysophyte Symposium & Korean Society of Protistologist Meeting | Day 1 (Mon. Jun 22)

15:30~15:00	Registration
17:00~18:00	Registration / Welcome Reception

11th International Chrysophyte Symposium & Korean Society of Protistologist Meeting | Day 2 (Tue. Jun 23)

Plenary I — [Main Hall] Chair. Hwan Su Yoon

09:00~09:50	PL-01	Chrysophyte Symposia: Are we answering important questions? Robert A. Andersen
09:50~10:40	PL-02	The initiation, development, and evolution of apical-basal polarity of *Toxoplasma gondii* Ke Hu
10:40~11:00		Break

Special Session I — [Main Hall] Chair. Jong Soo Park

11:00~11:20	SS-I-01	Cryptic diversity in metopid ciliates: similar morphology but high molecular divergence (Metopida, Armophorea, Ciliophora) Novia Cahyani, Nanda Dwi Kristanti, Quoc Dung Nguyen, Mann Kyoon Shin
11:20~11:40	SS-I-02	Chemical mutagenesis and genome engineering of *Schizochytrium* sp. for enhanced docosahexaenoic acid (DHA) production Jin-Ho Yun, Sinyang Kim, Ji Won Park, Donghee Lee, Ain Choi, Hee-Sik Kim
11:40~12:00	SS-I-03	Core bacteria promote species-specific growth in the benthic toic dinoflagellate *Prorocentrum lima* Joo-Hwan Kim, Ro Young Park, Eui Seong Kim, Jeongwon Hailey Kim, Byung Don Joo, Naeun Yun, Jin Ho Kim, Bum Soo Park
12:00~12:20	SS-I-04	Independent Losses of Photosynthesis Drive Contrasting Genomic Outcomes among Free-Living Chlorophyceans Adrian Reyes-Prieto, Hocheol Kim, Ha Yeon Hwang, Hwan Su Yoon
12:20~13:45		Lunch

Student Presentation (Oral) I — [Main Hall] Chair. Hyeon Been Lee

13:45~14:00	SO-I-01	From hidden diversity to evolutionary insight: integrative perspectives on the genus *Mallomonas* Petr Knotek, Iva Jadrná, Martin Pusztai, Pavel Škaloud
14:00~14:15	SO-I-02	Deep-sea hydrothermal vent sediments are putative marine source localities for obligately halophilic eukaryotes unable to grow in normal seawater Hyeon Been Lee, Dong Hyuk Jeong, Young Ok Kim, Dongsung Kim, Jong Soo Park
14:15~14:30	SO-I-03	Phylogenomics and evolution of multicellularity and reproductive modes in yellow-green algae (Xanthophyceae, Heterokontophyta) Seok-Wan Choi, Robert A. Andersen, Hwan Su Yoon

14:30~14:45	SO-I-04	Toward understanding circadian mechanisms in dinoflagellates: evidence from *Alexandrium catenella* and *Lepidodinium chlorophorum* Na Yun Park, Bijoo Kim, An Suk Lim
14:45~15:00	SO-I-05	Exploring circadian clocks in red algae Yongsung Lee, Dongseok Kim, Min Kyun Han, Seong Wook Yang, Hwan Su Yoon
15:00~15:15	SO-I-06	Revealing survival strategy of dinoflagellates with transcriptomic approach Jeongah Shin, Kyung Ha Lee, Jiyeon Sung, Bum Soo Park
15:15~15:40	Break	

Flash Talk [Main Hall] Chair. Jong Im Kim

15:40~15:45	FT-01*	The core bacterium *Marinobacter adhaerens* improves trace metal access for the dinoflagellate *Prorocentrum lima* under trace metal limitation Jeongwon Hailey Kim, Bum Soo Park
15:45~15:50	FT-02*	High temperature alters the response of single harmful algal species and their interactions: *Gymnodinium impudicum* and *Heterocapsa pygmaea* Min Jun Park, Bijoo Kim, Jua Lee, Tae Gyu Park, An Suk Lim
15:50~15:55	FT-03*	Two novel parasitoids, *Pseudopirsonia longifila* sp. nov. and *Pseudopirsonia florifera* sp. nov (Imbricatea, Cercozoa), of marine diatoms from Korean coastal waters: morphological and genetic characterization Kyoungwon Cho, Sunju Kim
15:55~16:00	FT-04*	Early evolutionary history and diversification of sexual reproduction in the red algal class Compsopogonophyceae ShinYoung Kang, Min Ho Seo, Hwan Su Yoon
16:00~16:05	FT-05*	Species-specific patterns of glucose-induced color change in the genus *Galdieria* Jiwoo Kim, Yongsung Lee, Hwan Su Yoon
16:05~16:10	FT-06*	Comparative plastid genome evolution in the genus *Poterioochromonas* (Chrysophyceae) across photosynthetic and non-photosynthetic species Hyewon Kim, Minseok Jeong, Jong Im Kim, Woongghi Shin
16:10~16:15	FT-07*	The mitochondrial genome evolution of Synurales (Chrysophyceae) Nayoung Lee, Jong Im Kim, Pavel Škaloud, Woongghi Shin
16:15~16:20	FT-08*	Database on the distribution and ecology of silica-scaled chrysophytes of Siberia Anna Bessudova, Evgeniy Dolid
16:20~16:25	FT-09*	Morphological and molecular haracterization of *Apatococcus echinosporus* sp. nov. (Trebouxiophyceae), a green alga isolated from rainwater Minseok Jeong, Kyong Ha Han, Hyeon Ho Shin
16:25~16:30	FT-10*	Morphology, phylogeny, and host range of a phytomyxean parasitoid *Dinopallor comventus* n. gen., n. sp. (Endomyxa, Phytomyxea) infecting marine dinoflagellates Boo Seong Jeon, Ye Seul Jeong, Jun Su Jang, Myung Gil Park
16:30~16:35	FT-11*	*Mallomonas cucullata* and *M. tubulosa* (Chrysophyceae, Synurales) are conspecific Dmitry Kapustin, Maxim Kulikovskiy
16:35~16:40	FT-12*	Ultrastructure and elemental composition of loricae and stomatocysts of *Stenokalyx tubiformis* (Chrysophyceae) Dmitry Kapustin, Maxim Kulikovskiy

16:40~16:45	FT-13	Diversity of silica-scaled chrysophytes from waterbodies of the Kader bog Mire (Russia, Leningrad region) Svetlana Shadrina, Tatiana Safronova
16:45~16:50	FT-14	On stomatocysts of *Mallomonas silvicola* (Chrysophyedae) Svetlana Shadrina
16:50~16:55	FT-15	Performance of moving bed biofilm, periphyton, and halophyte biofilters in marine multi-trophic aquaculture systems Adam Bell, Sarina J. Ergas, Kevan Main, Nicole Rhody, Lior Guttman
16:55~17:00	FT-16	*Paraphysomonas* spp. and other benthic heterotrophic flagellates from the Songnim tidal flat, Seocheon, Korea Sun Young Kim, Seo Woo Son, Nam Seon Kang, Won Je Lee

Poster Session

17:00~18:00	PS-01	A xanthone O-glucoside isolated from *Iris setosa* Pall. ex Link exhibits promising anti-amoebic activity against brain-eating amoeba *Naegleria fowleri* Hương Giang Lê, Buyng Su Hwang, Ji-Su Choi, Yong Tae Jeong, Tuấn Cường Võ, Minkyoung Cho, Yeonchul Hong, Jungho Kim, Young Taek Oh, Byoung-Kuk Na
	PS-02	(−)-Epicatechin enhances the anti-*Acanthamoeba* activity of chlorhexidine through synergistic action Hương Giang Lê, Tuấn Cường Võ, Thu Hằng Nguyễn, Minkyoung Cho, Byoung-Kuk Na
	PS-03	The microalgal culture collection at the Freshwater Bioresources Culture Collection (FBCC): obtain microalgal cultures for phylogenetic classification and useful information. Jae Hak Lee, Yu Ho Kim, Ji Young Moon, Seung Won Nam
	PS-04	Optimization of cryopreservation conditions for *Tetradesmus dimorphus* and *T. lagerheimii* Ji Young Moon, Seung Won Nam
	PS-05	Morphological and molecular characterization of five newly recorded *Desmodesmus* species in Korean freshwater Yu Ho Kim, Minseok Jeong, Bok Yeon Jo, Jae Hak Lee, Seung Won Nam
	PS-06	Diversity and ecological differentiation of newly recorded benthic diatoms in Korean freshwaters: insights from pH and conductivity niches Suk Min Yun, Pyo Yun Cho, Chang Soo Lee
	PS-07	Utilizing nature-designed porous biosilica from diatoms for high-precision drug delivery platforms Suk Min Yun, Daeryul Kwon, Taek Lee, Yoseph Seo, Wonhwa Lee, Chung Hyeon Choi, Z-Hun Kim, Pyo Yun Cho, Chang Soo Lee
	PS-08	*Mychonastes homosphaera* MHSC24 isolated from brackish waters of Korea: taxonomic, physiological, and biochemical characterization Nam Seon Kang, Chang Rak Jo, Hyung June Kim
	PS-09	Taxonomical, physiological, and biochemical characteristics of *Dunaliella salina* DSTA20 from hypersaline environments of Taean salt pond, Republic of Korea Chang Rak Jo, Sun Young Kim, Nam Seon Kang
	PS-10	First report on the distribution of Acantharia (Radiolaria) in Korean coastal waters Young-Ok Kim, Jungmin Choi
18:30~20:30	Banquet	

11th International Chrysophyte Symposium & Korean Society of Protistologist Meeting | Day 3 (Wed. Jun 24)

Plenary II
[Main Hall] Chair. Louis Graf

09:00~09:50	PL-03	The complex evolutionary landscape of the organellar genomes in ochrophytes Marek Eliáš
09:50~10:40	PL-04	Retention and loss of chlorophyll biosynthesis in non-photosynthetic plastids Ryoma Kamikawa
10:40~11:00	Break	

Special Session II
[Main Hall] Chair. Hocheol Kim

11:00~11:20	SS-II-01	New insights into the taxonomy and ecological diversity of the genus *Poterioochromonas* (Chrysophyceae) Yingchun Gong
11:20~11:40	SS-II-02	Freshwater zooplankton selectivity with a focus on silica scaled chrysophytes Jonáš Lis, Petr Knotek, Radka Čablová, Pavel Škaloud
11:40~12:00	SS-II-03	From grazer to cell factory: rethinking the mixotrophic chrysophyte *Poterioochromonas malhamensis* Mingyang Ma, Bo Lu, Qiang Hu
12:00~12:20	SS-II-04	Genomic insights into the evolution of amoeboid movement in photosynthetic stramenopiles Hocheol Kim, Hwan Su Yoon
12:20~13:45	Lunch	

Student Presentation (Oral) II
[Main Hall] Chair. Sang Uk Kang

13:45~14:00	SO-II-01	Dot, dot, dot…deciphering the environmental drivers of papillae formation in *Mallomonas* Kateřina Tučková, Zuzana Hercíková, Pavel Škaloud
14:00~14:15	SO-II-02	DNA replication through multiple fission in green algal cells JiHeon Kang, JunMo Lee
14:15~14:30	SO-II-03	Genomic insights into morphological diversification in Xanthophyceae Min Ho Seo, Seok-Wan Choi, Sang-Yun Han, Jihoon Jo, Kang Shin Young, Hwan Su Yoon
14:30~14:45	SO-II-04	Marine plankton community structure and carbon biomass across contrasting hydrographic conditions in the South Sea of Korea Sang Uk Kang, Hyun Soo Choi, Na Yun Park, Hyun Jun yang, Se Hyeon Jang, Moo Joon Lee, Yeong Du Yoo, Suk Yeon Lee, An Suk Lim
14:45~15:00	SO-II-05	Hidden diversity of phototrophic *Paulinella*: two new brackish-water species uncover phylogenetic incongruence Sungpil Han, Julia Van Etten, Duckhyun Lhee, Hwan Su Yoon
15:00~15:30	Break	

Student Presentation (Oral) III		[Main Hall] Chair. YeongJun Jang
15:30~15:45	SO-III-01	Distinctive feeding behavior and global distribution of *Hexatilemonas jangsaensis*, a novel marine Apusomonad within the uncultured APU-30 clade Dong Hyuk Jeong, Hyeon Been Lee, Da Yeong Ji, Aaron A. Heiss, Jong Soo Park
15:45~16:00	SO-III-02	Organelle genomics of Ishigeales, the early-diverging lineage in brown algae Ha Yeon Hwang, Hocheol Kim, Seok-Wan Choi, Hiroshi Kawai, Hwan Su Yoon
16:00~16:15	SO-III-03	Taxonomic approaches for distinguishing intraspecific taxa within the genus *Desmodesmus* (Scenedesmaceae) YeongJun Jang, JunMo Lee
16:15~16:30	SO-III-04	A cryptic lineage within the *Pyropia dentata* complex (Bangiophyceae, Rhodophyta) and the description of *Pyropia eudentata* sp. nov. based on integrative evidence Namhyeok Kim, Hocheol Kim, Il-Ki Hwang, Hyung-Seop Kim, Ji-San Ha, Jin Suk Heo, Hyun Il Yoo, Sakurako Matsushita, Kyosuke Niwa, Hwan Su Yoon
16:30~16:45	SO-III-05	Morphological and phylogenetic analysis of *Pseudo-nitzschia* from the coastal waters of Jeju Island Xu Wang, Su-Min Kang, Sae-Hee Kim, Naeun Yun, Jin Ho Kim
16:45~17:00	SO-III-06	Global phylogeography reveals genetic homogeneity across the widespread *Asparagopsis taxiformis* Lineage-2 Jongwon Lee, Ga Hun Boo, Sang-Yun Han, Yongsung Lee, Kyeong Mi Kim, Il-Ki Hwang, Hwan Su Yoon
17:00~18:00	Besst student presentation award / ICS community Meeting / KSOP Business Meeting	

11th International Chrysophyte Symposium & Korean Society of Protistologist Meeting | Day 4 (Thu. Jun 25)

Field Trip

Wangsong lake, Bibong wetland

11th International Chrysophyte Symposium & Korean Society of Protistologist Meeting | Day 5 (Fri. Jun 26)

Plenary III		[Main Hall] Chair. Pavel Škaloud
09:00~09:50	PL-05	Evolutionary history of chrysophytes: What have we learned from the fossil record? Peter A. Siver, Pavel Škaloud
09:50~10:40	PL-06	Using culture free methods to explore the diversity and ecological functions of oceanic Chrysophyceae biomes Louis Graf, Emily Zajac, Ian Probert, Richard Dorrell
10:40~11:00	Break	

Special Session III		[Main Hall] Chair. Yvonne Nemcov
11:00~11:30	SS-III-01	Rapid Synurales dynamics and uneven morphological evolution revealed through high-resolution reference databases Pavel Škaloud, Kateřina Tučková, Petr Knotek, Iva Jadrná, Radka Čablová, Ivana Černajová
11:30~12:00	SS-III-02	Green red algae: pigment evolution in three *Porphyridium* species (Rhodophyta) Hwan Su Yoon
12:00~12:30	SS-III-03	Silica-scaled chrysophytes from temperate regions of the Southern Hemisphere (Tasmania and New Zealand), including three novel *Synura* species. Yvonne Nemcov, Iva Jadrna, Petr Knotek, Pavel Skaloud
12:30~14:00	Lunch	

Special Session IV		[Main Hall] Chair. Iva Jadrná
14:00~14:20	SS-IV-01	Beyond protist generalizations: different evolutionary trajectories in closely related *Synura* species Iva Jadrná, Zuzana Škvorová, Pavel Škaloud
14:20~14:40	SS-IV-02	Genomic framework of Red Algae Hildenbrandiophycidae to Identify Freshwater Adaptation and Fungal Symbiosis Sang-Yun Han, Christophe Vieira, Chung Hyun Cho, Hochoel Kim, Wendy A. Nelson, Myung Sook Kim, Hwan Su Yoon
14:40~15:00	SS-IV-03	Algal biofilter treatment and fish pathogen reservoirs in recirculating aquaculture systems Adam Bell, Kevan Main, Nicole Rhody, Andrea Tarnecki, Lior Guttman
15:00~15:20	SS-IV-04	Growth promotion of *Ochrosphaera neapolitana* by the phycospheric bacterium *Paraglaciecola chathamensis* Ji-San Ha, Sang-Yun Han, Che Ok Jeon, Hwan Su Yoon
15:20~16:00	Closing Ceremony	

11th International Chrysophyte Symposium & Korean Society of Protistologist Meeting | Day 6 (Sat. Jun 27)	
09:00 ~	Excursion SuwonHwaseong

11th International Chrysophyte Symposium & Korean Society of Protistologist Meeting I Day 2 (Tue. Jun 23)

Plenary I

PL-01

Chrysophyte Symposia: Are we answering important questions?

Robert A. Andersen

Friday Harbor Labs, University of Washington, Friday Harbor, WA USA

The First International Chrysophyte Symposium drew many famous phycologists and covered a broad array of topics, addressing important questions of the day. Now, as we participate in the 11th International Chrysophyte Symposium, I focus on questions that have been asked and possibly answered over the past 42 years. For example, in 1984 Frank Round discussed the Division Chrysophyta (classes Bacillariophyceae, Chrysophyceae, Xanthophyceae), and today we know that the three classes are unrelated and occupy positions in three separate branches of the Heterokontophyta. In 1984, the Chrysophyceae included silicoflagellates, pedinellids, *Olisthodiscus* and the marine Sarcinochrysidales, but today these taxa and several others have been removed from the class. At the time of the First Chrysophyte Symposium, the aflagellate/uniflagellate/biflagellate condition, which formed the basis for the Pascher and Bourrelly classification schemes, was being challenged by David Hibberd and others. Is flagellar length, as viewed in the light microscope better understood today? Have we answered important questions regarding chrysophyte biochemistry, sexuality, ecology and so forth? We know that some chrysophytes lack chloroplasts, and some plastid-containing chrysophytes will grow in the dark on organic media. Therefore, are chloroplasts necessary? From the work of John Raven and colleagues, we know that many chrysophytes lack carbonic anhydrase, forcing them to live in acidic waters where dissolved carbon dioxide is abundant or to absorb organic carbon as a carbon source for photosynthesis. Why have chrysophytes evolved in the absence of carbonic anhydrase? We have made no progress in better understanding whether cysts are formed sexually or asexually. Conversely, we have made considerable progress understanding the fossil history of chrysophytes because of the work of Peter Siver and colleagues. However, can we explain when, where, how and why chrysophytes appear seasonally in ponds and lakes? The literature is full of information regarding conductivity, pH and temperature relative to the distribution of scaled chrysophytes. Nevertheless, virtually every scaled species will grow in DY-V medium (pH 6.8, fixed conductivity) from 5-25°C temperature, so something else must be controlling their distribution. How important is morphology in these days of molecular phylogenetics? Finally, have our discoveries over the past 42 years generated new important questions that will require future Chrysophyte Symposia?

PL-02

The initiation, development, and evolution of apical-basal polarity of *Toxoplasma gondii*

Ke Hu

Arizona State University

Apicomplexa is a phylum of intracellular parasites responsible for many devastating diseases, including malaria, cryptosporidiosis, and toxoplasmosis. They are also rich in fascinating cell biology. The body plan of the human parasite *Toxoplasma gondii* has a well-defined polarity. The minus ends of the 22 cortical microtubules are anchored to the apical polar ring, a putative microtubule-organizing center. The basal complex caps and constricts the parasite posterior end, and is critical for cytokinesis. To determine how this apical-basal polarity is initiated, we examined the development of the apical polar ring and the basal complex using expansion microscopy. We found that substructures in the apical polar ring have different sensitivity to perturbations. In addition, apical-basal differentiation is already established upon nucleation of the cortical microtubule array: arc-shaped progenitors of the apical polar ring and basal complex associate with opposite ends of the microtubules. As the nascent daughter framework grows towards the centrioles, the apical and basal arcs co-develop ahead of the microtubule array.

The apical and basal complexes are shared among diverse apicomplexan lineages, indicating an ancient origin. To enable the study of the evolution of cellular architecture in apicomplexans, we recently developed transformation and expansion microscopy tools for *Chromera velia*, a photosynthetic, free-living alga closely related to the apicomplexans. The comparison of the cytoskeletal organization between *Chromera* and *Toxoplasma* suggests that the apical-basal polarity of the apicomplexans might have originated from structures associated with two flagella in their free-living ancestor.

References

Arias Padilla, L.F., J.M. Lopez, A. Shibata, J.M. Murray, and K. Hu, *The initiation and early development of apical-basal polarity in Toxoplasma gondii*. Journal of Cell Science, 2024: p. 263436.

Isadonna F. Tengganu, Ke Hu, *Transfection of the free-living alga Chromera velia enables direct comparisons with its parasitic apicomplexan relative, Toxoplasma gondii*. BioRxiv https://doi.org/10.1101/2025.08.26.672290

Special Session I

SS-I-01

Cryptic Diversity in Metopid Ciliates: Similar Morphology but High Molecular Divergence (Metopida, Armophorea, Ciliophora)

Novia Cahyani, Nanda Dwi Kristanti, Quoc Dung Nguyen, Mann Kyoon Shin

Department of Biological Sciences, University of Ulsan, Ulsan, Republic of Korea

The genus *Metopus*, described by Claparède and Lachmann in 1858, is a cornerstone of metopid taxonomy within Metopida. However, it has long been regarded as non-monophyletic, prompting a reevaluation of its morphological delimitation and phylogenetic relationships. We examined two morphospecies, *Metopus-like* sp. 1 and *M.-like* sp. 2, using an integrative approach combining detailed morphology with the nuclear small subunit (SSU) rRNA gene phylogeny. *Metopus-like* sp. 1 is characterized by an obpyriform body; a cytostome positioned anterodorsally; 8–11 dorsal kineties; a diplostichomonad-type paroral membrane; and five-rowed perizonal stripes (PS) arranged in non-false kineties. *Metopus-like* sp. 2 is identified by its barrel-shaped body, posteriorly positioned cytostome, adoral zone consisting of 30–38 membranelles, and PS invariably comprised of five kineties, with rows 1–3 segmented into 62–88 false kineties. SSU rRNA gene phylogenetic analyses indicate that the two morphospecies do not cluster together. *Metopus-like* sp. 1 forms a clade with *Parametopidium circumlabens*, though this is only supported by maximum likelihood (ML) analysis. *Metopus-like* sp. 2 branches basally to the genus *Pidimetopus*, with low nodal support (50% ML/0.40 BI). Despite sharing 96.5% nucleotide similarity (60 nucleotide differences), the two taxa occupy distinct positions in the phylogenetic tree. This incongruence between morphological affinity and molecular topology further underscores the non-monophyletic nature of *Metopus* and highlights the need to reassess generic boundaries within the Metopidae family.

SS-I-02

Chemical mutagenesis and genome engineering of *Schizochytrium* sp. for enhanced docosahexaenoic acid (DHA) production

Jin-Ho Yun, Sinyang Kim, Ji Won Park, Donghee Lee, Ain Choi, Hee-Sik Kim

Cell Factory Research Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon, Republic of Korea

Schizochytrium sp. is a marine thraustochytrid microorganism recognized as one of the most promising microbial cell factories for docosahexaenoic acid (DHA), an omega-3 fatty acid of critical importance in nutraceutical, pharmaceutical, and aquaculture industries. Despite its high natural DHA productivity, further strain improvement is necessary to meet the growing commercial demand. In this study, we report a multi-pronged strain engineering strategy combining chemical mutagenesis and genetic tools to enhance DHA titer and content in *Schizochytrium* sp. We first developed a high-DHA mutant strain through ethyl methanesulfonate (EMS)-based random mutagenesis. EMS treatment followed by high-throughput screening successfully identified mutant strains with significantly elevated DHA production compared to the wild-type parent, demonstrating a rapidly deployable approach for lipid overproduction. Building on this, we established a robust electroporation-based transformation platform using the pUC19-GZG vector system, which employs an endogenous GAPDH promoter/terminator and a Zeocin resistance marker. Successful genomic integration and stable expression were confirmed via colony PCR and fluorescent reporter assays. Using this system, we disrupted the phospholipase D (*PLD1*) gene via homologous recombination, resulting in increased DHA accumulation. Additionally, Cas9 expression was validated in *Schizochytrium* sp. as a foundation for future CRISPR-based targeted editing. Together, these results demonstrate the feasibility of combining random mutagenesis with targeted genome engineering for accelerated *Schizochytrium* strain development. Future efforts will focus on stacking beneficial mutations, developing auxotrophic selection markers independent of antibiotic resistance, and integrating cell sorting-based screening to further identify high-lipid producers.

SS-I-03

Core bacteria promote species-specific growth in the benthic toxic dinoflagellate *Prorocentrum lima*

Joo-Hwan Kim[1], Ro Young Park[1], Eui Seong Kim[2], Jeongwon Hailey Kim[1], Byung Don Joo[1], Naeun Yun[1], Jin Ho Kim[3], Bum Soo Park[1]

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Harmful algal blooms (HABs) pose increasing threats to marine ecosystems under climate change, yet the microbial mechanisms underlying bloom-forming phytoplankton growth remain inadequately characterized. While host-microbiota interactions have been documented across various algal taxa, experimental evidence for growth-promoting effects in toxic benthic dinoflagellates remains limited. Here, we characterized the bacterial microbiota of six geographically distinct strains of the harmful benthic dinoflagellate *Prorocentrum lima* and identified conserved core bacterial taxa. Microbiota transplantation experiments into an axenic *P. lima* strain demonstrated that donor bacterial consortia significantly enhanced early-phase growth, with specific growth rates increasing by 51.1% relative to axenic controls. Co-culture experiments with *Marinobacter adhaerens*, a core taxon isolated from *P. lima*, revealed pronounced growth enhancement—up to 164.1% higher specific growth rates than axenic controls—with apparent species specificity, as no such enhancement was observed in other tested microalgal species. Nutrient limitation assays showed that growth promotion occurred specifically under trace metal-limited conditions, suggesting bacterial facilitation of metal bioavailability. Chrome Azurol S assays and genomic analyses of *M. adhaerens* revealed iron-chelating activity and extensive ferric iron uptake systems, supporting a role in trace metal mobilization for the host. These results provide experimental evidence that core bacterial lineages can promote toxic dinoflagellate proliferation through metal bioavailability mechanisms in a species-specific manner.

SS-I-04

Independent Losses of Photosynthesis Drive Contrasting Genomic Outcomes among Free-Living Chlorophyceans

Hocheol Kim[1], Ha Yeon Hwang[1], Hwan Su Yoon[1], Adrian Reyes-Prieto[1,2]

[1]*Department of Biological Sciences, Sungkyunkwan University, Republic of Korea*
[2]*Department of Biology, University of New Brunswick, Canada*

The loss of photosynthesis has occurred multiple times across chlorophytes. Plastome and transcriptome analyses have yielded key insights into evolutionary trajectories in parasitic and free-living lineages following this trophic transition. Comparative plastid genomics of free-living colorless chlorophytes reveals convergent reductions in coding capacity, with outcomes ranging from complete plastome loss (e.g., *Polytomella*) to expansion of non-coding regions (e.g., *Polytoma uvella*). Despite advances in plastome studies, comprehensive nuclear genome analyses remain scarce.

Here, we present a comparative analysis of the chlorophyceans *Polytoma uvella* and *Polytomella parva*, which independently lost photosynthesis. Using long-read sequencing and integrative annotation approaches, we generated high-quality nuclear genome assemblies for both taxa. The nuclear genome of *Polytoma uvella* is ~130 Mb (~13,000 genes), whereas *Polytomella parva* has a 50 Mb genome (~7,600 genes). These differences in genome size and gene content parallel document plastome-level patterns and indicate distinct nuclear evolutionary trajectories among nonphotosynthetic lineages. Compared to photosynthetic chlorophytes, *Polytoma uvella* has gained 289 gene families and lost 1,149, whereas *Polytomella parva* has gained 59 but lost 3,659. Both lineages share 644 gene family losses linked to heterotrophy, but *Polytomella parva* shows greater metabolic erosion, with 6.5 times more metabolism-related losses. Additionally, *Polytomella parva* has lost more gene families involved in cytoskeletal motility, intracellular trafficking, cell signaling, and membrane transport. Repeat landscape analyses indicate that *Polytomella parva* harbors fewer, older transposable elements (TE), whereas *Polytoma uvella* shows recent TE activity contributing to genome expansion. We further examine molecular and ecological mechanisms underlying these divergent patterns of genome reduction following independent loss of photosynthesis.

Student Presentation (Oral) I

SO-I-01

From hidden diversity to evolutionary insight: integrative perspectives on the genus *Mallomonas*

Petr Knotek, Iva Jadrná, Martin Pusztai, Pavel Škaloud

Department of Botany, Faculty of Science, Charles University, Praha, Czech Republic

The silica-scaled chrysophyte genus *Mallomonas* represents an exceptional model for studying protist evolution, combining remarkable morphological complexity, high species richness, pronounced biogeographic structure, and a fossil record that links recent diversity with deep evolutionary history. Despite long-standing taxonomic interest, many lineages remain insufficiently understood, and the evolutionary significance of key morphological traits is still unresolved.

In this presentation, I highlight how integrative research on *Mallomonas* can uncover overlooked diversity, refine species boundaries, and place morphological variation into an evolutionary framework. By combining detailed morphology with molecular phylogeny, biogeographic evidence, experimental data, and fossil information, it becomes possible to distinguish stable diagnostic characters from environmentally induced phenotypic variation, recognize previously hidden evolutionary lineages, and reconstruct the history of important scale traits through time.

Together, these findings show that hidden diversity in *Mallomonas* is still substantial, that morphology alone may both reveal and mislead, and that only an integrative approach can reliably delimit species and clarify their evolutionary history. More broadly, *Mallomonas* provides a powerful system for understanding how protist diversity is discovered, interpreted, and linked to evolutionary processes across temporal and spatial scales.

SO-I-02

Deep-sea hydrothermal vent sediments are putative marine source localities for obligately halophilic eukaryotes unable to grow in normal seawater

Hyeon Been Lee[1], Dong Hyuk Jeong[1], Young Ok Kim[2], Dongsung Kim[2], Jong Soo Park[1]

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Halophilic protists, defined as those showing optimal growth at 90 practical salinity units (PSU) or higher, are found across diverse lineages, including Heterolobosea, Stramenopiles, Ciliophora, and Chlorophyta. Heterolobosea comprises numerous halophilic genera (e.g., *Tulamoeba*, *Pleurostomum*, *Aurem*, *Halosymphonia*, *Euplaesiobystra*, and *Pharyngomonas*) representing a core halophilic radiation of eukaryotes unable to grow in normal seawater. While these taxa are widely distributed as ecological generalists in marine-derived hypersaline environments (>40 PSU), their distribution and source localities in normal marine environments remain poorly understood. To assess their natural seawater presence, we examined their vertical distribution across the marine water column using two large-scale global datasets: the Tara Oceans and the Malaspina 2010. Known halophilic heteroloboseans were largely undetected, except for *Pharyngomonas* in the Indian Ocean epipelagic zone. Although Heterolobosea are generally rare in the pelagic water column, previous studies indicate they are abundant in deep-sea sediments. We hypothesized that deep-sea hydrothermal vent sediments, which harbor distinct biological communities, might act as source localities. To test this hypothesis, we investigated eukaryotic communities in sediments from three hydrothermal vent sites (Onnuri, Onnare, and Onbada) along the Central Indian Ridge using metabarcoding. These sediment communities exhibited high heterogeneity, with Onnare showing peak diversity. Intriguingly, diverse sequences affiliated with core obligately halophilic genera (including *Tulamoeba*, *Euplaesiobystra*, and *Pharyngomonas*) were identified at Onnuri and Onnare. These findings suggest that obligately halophilic heteroloboseans persist in deep-sea hydrothermal vent sediments. Our results reveal for the first time that deep-sea hydrothermal vents at normal salinity levels in the Indian Ocean serve as cryptic source localities for diverse obligately halophilic eukaryotes.

SO-I-03

Phylogenomics and evolution of multicellularity and reproductive modes in yellow-green algae (Xanthophyceae, Heterokontophyta)

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The evolution of multicellularity has long been linked to reproductive strategies, particularly the role of single-cell bottlenecks in stabilizing multicellular individuality, although alternative strategies using multicellular propagules may also be favored under different ecological and evolutionary conditions. Protist lineages showing transitions from unicellular to simple multicellular forms therefore provide important systems for investigating these evolutionary relationships. Xanthophyceae is the only photosynthetic stramenopile class that has undergone both terrestrialization and the evolution of multicellular forms, exhibiting morphologies ranging from unicellular coccoid cells to macroscopic filamentous and coenocytic thalli. Reproductive modes are also diverse, including motile zoospores and immotile autospores, aplanospores, and akinetes. Here, we present a phylogenomic framework based on a nuclear dataset of 680 genes from 18 species, including 17 newly generated transcriptomes. Nuclear phylogenies robustly resolve all inter-ordinal and inter-familial relationships with full concordance between concatenation and coalescent analyses, while plastid (141 genes) and mitochondrial (31 genes) datasets from 33 species recover identical topologies. Based on these results, we establish one new order (Pseudopleurochloridales), emend Heterococcales, and propose five new families. Ancestral character reconstruction indicates at least four independent transitions from unicellular ancestors to simple multicellularity. Bayesian analyses show that these transitions were consistently accompanied by shifts from multiple autospore-type propagules toward single aplanospore- and akinete-type propagules, whereas reversions to unicellularity were associated with the reappearance of autospore-based reproduction. The results provide a phylogenomic framework for understanding multicellular evolution in Xanthophyceae and shed light on the correlation between reproductive modes and the emergence of simple multicellularity.

SO-I-04

Toward Understanding Circadian Mechanisms in Dinoflagellates: Evidence from *Alexandrium catenella* and *Lepidodinium chlorophorum*

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Driven by the Earth's rotation, organisms have evolved circadian clock systems with an approximately 24-hour periodicity, enabling them to anticipate and adapt to daily environmental fluctuations. These rhythms are generally regulated by an endogenous circadian clock, and various mechanisms have been proposed across a wide range of organisms. However, the molecular mechanism of the circadian clock in dinoflagellates remains largely unknown. In this study, we investigated whether cell division, photosynthesis, and bioluminescence maintain circadian rhythmicity under constant environmental conditions in two dinoflagellate, *Alexandrium catenella* and *Lepidodinium chlorophorum*. Our results showed that photosynthetic parameters did not maintain rhythmicity under constant light (LL) conditions. In contrast, bioluminescence exhibited robust circadian rhythms under constant light conditions. To explore the molecular factors underlying this rhythmicity, we performed differential gene expression analysis on samples collected at midday and midnight, revealing distinct patterns between *A. catenella* and *L. chlorophorum*. Our findings offer a potential approach to uncovering the molecular mechanisms underlying the circadian clock in dinoflagellates.

SO-I-05

Transposable element as a driver of evolution in red algae *Porphyridium*

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Freshwater habitats impose distinct physiological and metabolic challenges on organisms compared to marine environments, which are generally more stable in terms of light and nutrient availability. Interestingly, many freshwater red and brown algae tend to appear green, rather than the colors that they are named for, indicating that the transition to a green color is an adaptive strategy of photosynthetic organisms in freshwater environments. Here, we studied the underlying genomic changes associated with this phenomenon using the red algal genus *Porphyridium*, which displays different habitats and corresponding colorations (e.g., red, purple, green). Through comparative genomic analysis of three *Porphyridium* species, massive transposable element (TE) expansion was uniquely observed in the green species (*P. aerugineum*), which prefers freshwater habitats. We provide direct evidence that TE insertions disrupt phycobilisome linker protein genes, thereby driving adaptive shifts in pigmentation. Comparative analyses show that *P. aerugineum* possesses a distinct repertoire of TE-suppression genes and, notably, exhibits substantially reduced small RNA (sRNA) levels. In vitro functional assays demonstrate that this reduction stems from reduced DICER processivity, linking impaired sRNA biogenesis to unchecked TE activity and consequent color adaptation. Consequently, TE expansion has driven a remarkable genomic remodeling in the freshwater species, facilitating the adaptation. Our findings establish a mechanistic connection between TE dynamics and adaptive phenotypic evolution in red algae, shedding light on how genomic and molecular factors shape the diversity and environmental success of photosynthetic life on Earth.

SO-I-06

Revealing survival strategy of dinoflagellates with transcriptomic approach

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Marine dinoflagellates exhibit high environmental adaptability, yet the molecular basis of strain-specific stress responses remains elusive. We compared the physiological and transcriptomic responses of Prorocentrum cordatum and Heterocapsa steinii under optimal and cold conditions. Despite high genetic similarity in rRNA sequences, strains displayed distinct 'well-growing' and 'defensive' phenotypes characterized by significant divergence in chlorophyll-a dynamics and growth.

Transcriptomic analysis revealed that strain identity, rather than temperature, primarily governed cellular responses. Under optimal conditions, well-growing phenotypes prioritized translational efficiency while suppressing energy-intensive nutrient acquisition pathways, such as cellulase activity and transmembrane transport.

Under cold stress, defensive strains shared a universal initiation via nitric oxide synthase (NOS) up-regulation. Despite this shared trigger, downstream execution was entirely divergent. P. cordatum focused on NO-mediated protein quality control through the proteasome core complex. In contrast, H. steinii redirected resources toward redox buffering via SAM/methionine metabolism and nucleotide pool stabilization through ribonucleoside-diphosphate reductase (RNR) activity to protect its massive genome from cold-induced damage.

These findings demonstrate that dinoflagellate resilience is driven by specialized, phenotype-specific regulatory signatures. While overarching strategies like energy trade-offs and NOS-mediated defense initiation are conserved, the genetic blueprints for execution are uniquely shaped at the strain level, ensuring survival across fluctuating global oceans.

Flash Talk

FT-01

The core bacterium *Marinobacter adhaerens* improves trace metal access for the dinoflagellate *Prorocentrum lima* under trace metal limitation

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Trace metals are essential micronutrients that regulate the growth, metabolism, and physiological performance of marine dinoflagellates. However, their bioavailability is often limited in natural environments. Increasing evidence suggests that dinoflagellate-associated microbiomes are not merely co-occurring communities but critical players in mediating host nutrient acquisition. In particular, core bacterial members with high prevalence and abundance within the microbiome are more likely to contribute to host fitness. In this study, we investigated whether *Marinobacter adhaerens*, the core bacterium associated with the benthic dinoflagellate *Prorocentrum lima*, supports growth of the host under trace metal-depleted conditions. Axenic and bacterized cultures of *P. lima* were compared under metal-replete and metal-limited conditions. Growth performance was assessed by cell counting, and physiological responses will be further examined by transcriptomic analyses and complementary assays. Under trace metal limitation, co-culture with *M. adhaerens* significantly enhanced the specific growth rate (μ) of *P. lima* compared to the axenic control. Notably, the growth rate of the metal-limited co-culture was restored to a level statistically equivalent to that of metal-replete controls. This result indicates that M. adhaerens may enhance host access to trace metals, either by increasing metal bioavailability in the extracellular environment or by facilitating processes associated with host metal uptake and utilization. These possibilities will be explored further by ongoing transcriptomic analyses. Overall, our findings highlight the functional importance of core members within the microbiome in supporting dinoflagellate survival under trace metal depletion. Moreover, these findings suggest that algae-bacteria interactions play a key role in shaping trace metal dynamics in marine ecosystems.

FT-02

High temperature alters the response of single harmful algal species and their interactions: *Gymnodinium impudicum* and *Heterocapsa pygmaea*

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Effects of climate change, especially the rise in marine temperatures, are expected to affect the physiology and competitive dynamics of harmful algal species. Yet, it lacks an analysis of how high temperatures differentially affect dinoflagellates. To understand these complex responses, this study investigated the impacts of simulated ocean warming on the growth, physiological traits, and interspecific interactions of two co-occurring harmful dinoflagellates, *Gymnodinium impudicum* and *Heterocapsa pygmaea*. We assessed alterations in their growth kinetics, morphological plasticity, and species-specific bioactivities under a gradient of elevated temperatures. Our findings demonstrate that warming significantly alters individual growth dynamics, thermal tolerances, and the expression of species-specific harmful traits. Furthermore, co-cultivation experiments revealed that elevated temperatures strongly disrupt their competitive balance, potentially altering species interactions. Ultimately, these shifts suggest that future ocean warming could profoundly reshape the ecological dominance and environmental impacts of harmful algal blooms.

FT-03

Two novel parasitoids, *Pseudopirsonia longifila* sp. nov. and *Pseudopirsonia florifera* sp. nov (Imbricatea, Cercozoa), of marine diatoms from Korean coastal waters: Morphological and Genetic Characterization

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Marine diatoms are primary producers that account for approximately 20–25% of global annual carbon fixation and play pivotal roles in marine biogeochemical cycling. The cercozoan parasitoid genus *Pseudopirsonia* is an ecologically important regulator of these marine diatom populations, but its diversity and biology remain poorly documented. Here, we describe two novel species, *Pseudopirsonia longifila* sp. nov. and *Pseudopirsonia florifera* sp. nov., isolated from infected marine diatoms in the coastal waters of Busan, Republic of Korea. Both species share the characteristic developmental pattern of the genus, including pseudopodial attachment to the host, formation of an auxosome, and a trophosome. Both species possess subapically inserted flagella that are not completely retracted during development and form an Alcian blue-positive mucilaginous envelope. However, they differ in key morphological and developmental traits. *P. longifila* is distinguished by a significantly longer posterior flagellum and a simpler FMC division pattern, whereas *P. florifera* shows repeated FMC divisions, forming a conspicuous morula-shaped stage and producing up to eight zoospores. Cross-infection experiments revealed relatively broad but phylogenetically bounded host ranges restricted to diatoms, with clear differences in host susceptibility and exploitation dynamics between the two species. Phylogenetic analyses of SSU, ITS, and LSU rRNA gene sequences supported their recognition as distinct taxa within Pseudopirsonia and separated them from previously described congeners. Together, these results demonstrate that species delimitation in *Pseudopirsonia* requires an integrative framework combining morphology, development, host range, and multigene phylogeny.

FT-04

Early Evolutionary History and Diversification of Sexual Reproduction in the Red Algal Class Compsopogonophyceae

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Sexual reproduction is an ancestral eukaryotic trait that generates genetic diversity through meiosis and recombination. Red algae (Rhodophyta) display unique sexual systems, including UV sex chromosomes that determine sex in the haploid gametophyte phase. However, the early evolution and diversification of these mechanisms remain poorly understood. Compsopogonophyceae, an early-diverging class within Rhodophyta, provides an ideal model. Freshwater Compsopogonales reproduce almost exclusively asexually via monospores, whereas marine Erythropeltidales and Rhodochaetales exhibit monoecious sexual reproduction. Previous knowledge of Compsopogonophyceae reproduction has relied almost entirely on morphological observations, with little molecular data available. In this study, we have completed PacBio HiFi-based chromosome-level genome assemblies for representative species across Compsopogonales and Erythropeltidales. Using these high-quality reference genomes, we are performing comparative genomics analyses—including gene presence/absence, synteny comparisons, and searches for potential UV-specific regions—together with stage-specific transcriptomics (RNA-seq of gametophyte and sporophyte phases under sexual-inducing conditions) to identify candidate sex-determination genes and sex-linked genomic feature. This work will provide the first molecular insights into the early evolution of sexual reproduction in Rhodophyta and establish a foundation for future functional studies.

FT-05

Species-Specific Patterns of Glucose-Induced Color Change in the Genus *Galdieria*

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Among the four orders of Cyanidiophyceae, only Galdieriales exhibits both a thermoacidophilic and mixotrophic lifestyle. A notable characteristic of the genus *Galdieria* is trophic mode-associated color change. They appear green under phototrophic conditions but undergo bleaching when photosynthesis is suppressed in the presence of glucose. Recently, taxonomic revisions within *Galdieria* have changed the interpretation of this trait at the species level, leaving *G. sulphuraria* as the only species reported not to show glucose-induced color change. This highlights the need for a comparative survey of color change patterns across species.

In this study, we investigated glucose-induced color change in five distinct species: *G. javensis, G. phlegrea, G. sulphuraria, G. yellowstonensis*, and *G. partita*. We also performed a time-course analysis to identify the time point at which color change was most pronounced. While the timing of color change did not vary significantly among species, the pattern of color change showed clear interspecific differences. In *G. javensis* and *G. phlegrea*, color change occurred in the presence of glucose regardless of concentration, whereas in *G. yellowstonensis* and *G. partita*, it varied depending on glucose concentration. Interestingly, *G. sulphuraria* largely maintained photosynthetic pigments and exhibited faster growth in the presence of glucose. These findings suggest that glucose-induced color change in *Galdieria* can be categorized into three species-specific patterns and *G. sulphuraria* may follow a distinct regulatory mode from the other species.

FT-06

Comparative plastid genome evolution in the genus *Poterioochromonas* (Chrysophyceae) across photosynthetic and non-photosynthetic species

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Poterioochromonas is a genus within the class Chrysophyceae that includes both photosynthetic and non-photosynthetic species. To investigate plastid genome evolution associated with the loss of photosynthesis within a single lineage, we sequenced the plastid genomes of one photosynthetic species (*P. andersenii*) and two non-photosynthetic species (*P. amplexa* and *P. communis*). Despite the loss of photosynthetic ability, plastid genome was retained in non-photosynthetic species. The three plastid genomes were compared with 11 previously reported chrysophycean plastid genomes (7 photosynthetic and 4 non-photosynthetic species), including the photosynthetic species *Poterioochromonas malhamensis*. The plastid genome size of non-photosynthetic species (68–75 kb) is approximately half that of photosynthetic species (126–134 kb), in *Poterioochromonas* species. This size reduction is mainly due to the loss of photosynthesis-related genes in non-photosynthetic lineages. Plastid gene order is generally conserved in almost all chrysophyte plastid genomes, whereas gene order is rearranged in *Poterioochromonas* species. This study provides insights into the evolutionary dynamics of plastid genomes in chrysophytes including photosynthetic and non-photosynthetic *Poterioochromonas* species.

FT-07

The mitochondrial genome evolution of Synurales (Chrysophyceae)

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The order Synurales comprises photosynthetic unicellular or colonial flagellates characterized by siliceous scales and bristles. Despite sustained taxonomic studies based on scale ultrastructure and molecular phylogeny, genomic information on Synurales remains limited; in particular, only a single mitochondrial genome (mtDNA) has been reported for the genus *Synura*. To elucidate general characteristics and investigate genomic variation of mtDNAs in Synurales, we sequenced the mtDNAs of 40 species from the three genera *Mallomonas*, *Synura* and *Neotessella*, and performed comparative analyses of 42 mtDNAs, including those of previously reported chrysophycean species, *Synura synuroidea* and *Chlorochromonas danica* (Ochromonadales). The mtDNA size ranged from approximately 32 kbp to 54 kbp and comprised of two rRNAs, 20-28 tRNAs, and 34 core protein-coding genes (PCGs). Overall gene content was largely conserved across synuralean mtDNAs, whereas the arrangement of PCGs differed substantially among taxa. Phylogenetic analysis based on 18 concatenated mitochondrial PCGs supported the monophyly of each genus. Pairwise rearrangement distances ranged from 0 to 13, indicating varying degrees of structural divergence. Comparisons of gene order revealed distinct genus-level arrangement patterns among synuralean mtDNAs that were consistent with phylogenetic relationships. Notably, two major clades within *Mallomonas* exhibited pronounced differences in gene arrangement. Furthermore, gene rearrangements within each clade contributed to lineage-specific gene arrangement patterns. Our results provide important insights into structural evolution and gene rearrangement dynamics of mtDNAs in Synurales.

FT-08

Database on the distribution and ecology of silica-scaled chrysophytes of Siberia

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One of the key tasks of biology is to study biological diversity in order to develop effective strategies for its conservation. Chrysophytes, which have solid cellular structures, convert silicic acid dissolved in water into silica elements unique to each species, such as scales, bristles, and spines. These elements form a mobile shell that disintegrates when environmental conditions change or when cell growth ends. Due to the species-specific structure of silica elements, which can be observed using electron microscopy, even after the destruction of cells, it is possible to determine which species they belonged to. This makes silica-scaled chrysophytes a promising object for monitoring freshwater reservoirs. For these purposes, there is already an online database https://chrysophytes.eu/ “Silica-scaled chrysophytes of Europe. Distribution, morphology, ecology” developed by the Department of Charles University in Prague, Czech Republic. However, given the significant amount of accumulated information about silica-scaled chrysophytes found in Siberian reservoirs, it became necessary to create a similar database. The Limnological Institute in Irkutsk, Russia, is developing a database https://lin.irk.ru/chrysophytes-siberia similar to the European one, which will allow saving, cataloging and adding new information about the species of silica-scaled chrysophytes found in the reservoirs of Siberia. The data on each species will be accompanied by micrographs, as well as contain information about the location, including geographical coordinates (linked to an online map), date, and basic parameters of the water at which the species was detected, such as temperature, pH, and electrical conductivity. The database will include data on 194 species already discovered, including 43 potentially new ones from 7 genera, *Chrysosphaerella* Lauterborn, *Spiniferomonas* Takahashi, *Paraphysomonas* de Saedeler, *Lepidochromonas* (Kristiansen 1980) Kapustin et Guiry 2019, *Polylepidomonas* Preisig et Hibberd, *Mallomonas* Perty, and *Synura* Ehrenberg. This online database will allow all interested researchers to obtain data on the distribution of a particular species and its ecological ranges in the reservoirs of Siberia. The database will also be useful for monitoring, paleolimnological and biogeographic studies, for studying biodiversity and the mechanisms of its formation.

Acknowledgements

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FT-09

Morphological and molecular characterization of *Apatococcus echinosporus* sp. nov. (Trebouxiophyceae), a green alga isolated from rainwater

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This study describes a new species, *Apatococcus echinosporus sp. nov.*, collected from rainwater representing atmospheric wet deposition. *A. echinosporus* was characterized by spherical vegetative cells with thick cell walls and shallowly lobed, parietal chloroplasts lacking pyrenoids, distinguishing it from other *Apatococcus* species. Autospores were covered with numerous blunt spines distributed over approximately half of the spore surface. Molecular phylogenetic analyses revealed that *A. echinosporus* forms a well-supported monophyletic clade including isolates from rainwater, the surface of a polyethylene waste container, and house dust. The occurrence of this species across these diverse environments is consistent with the capacity of aerophytic microalgae to undergo atmospheric dispersal via wet deposition. This finding also provides observational support for the role of rainwater in the colonization of terrestrial surfaces by aeroterrestrial algae.

FT-10

Morphology, phylogeny, and host range of a phytomyxean parasitoid *Dinopallor comventus* n. gen., n. sp. (Endomyxa, Phytomyxea) infecting marine dinoflagellates

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Phytomyxea represents a class of obligate biotrophic parasites partitioned into the terrestrial Plasmodiophorida and the marine Phagomyxida. Despite the ecological prominence of marine Phagomyxida, they remain understudied in contrast to the economically significant Plasmodiophorida. In this study, 23 isolates of a novel dinoflagellate-infecting parasitoid were recovered from 10 coastal stations in Korea. While the infection process and plasmodial development mirror those of *Phagomyxa*, this taxon possesses a unique sporangiosorus wall and lacks resting spores, with each zoosporangium consistently releasing three biflagellate zoospores. Molecular phylogeny using SSU rDNA sequences confirmed its placement in a distinct clade shared with *Marinomyxa* and the TAGIRI-5 environmental sequence, with which it shares 99.87% identity. Furthermore, cross-infection assays revealed a restricted host range limited to five specific dinoflagellate genera. Consequently, we propose the establishment of *Dinopallor comventus* n. gen., n. sp. as a novel member of the Phagomyxida.

FT-11

Mallomonas cucullata and *M. tubulosa* (Chrysophyceae, Synurales) are conspecific

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Both *Mallomonas cucullata* and *M. tubulosa* have been described from small ponds in the Visegrád Mountains (North Hungary). Their descriptions were based on the isolated scales. *Mallomonas cucullata* is characterized by the domeless, somewhat irregular scales. The shield is densely covered with papillae which fuse to form a hexagonal reticulum with a central papilla on the anterior part of the shield. The most striking morphological trait of this species is a V-rib, which is broad, thin and hooded, and it covers a big portion of the shield. *Mallomonas tubulosa* has three types of scales: domeless scales, domed scales with a wing-like projection and domed scales without such projection. In some domed scales the dome has a chimney-like form. The shield of all scale types is covered with a hexagonal reticulum with a central papilla.

Mallomonas tubulosa was placed into the section *Annulatae* Asmund & Kristiansen, whereas a new section *Cucullatae* Barreto was established to accommodate *M. cucullata*.

During the study of the silica-scaled chrysophytes from the Moscow Region (Russia) the intact cells bearing scales of both *M. cucullata* and *M. tubulosa* were recorded. Thus, both taxa should be considered to be conspecific. Since the description of *M. tubulosa* is fuller and the molecular data are available, we propose to keep this name and synonymize *M. cucullata* with it.

Acknowledgements

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FT-12

Ultrastructure and elemental composition of loricae and stomatocysts of *Stenokalyx tubiformis* (Chrysophyceae)

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Stenokalyx tubiformis (Fott) Fott (≡*Kephyrion tubiforme* Fott) is a rarely reported loricate chrysophyte. We recorded it from the Myachkovo quarry (Moscow Region) and studied the morphology and elemental composition of its loricae and zygotic stomatocysts using light and scanning electron microscopy and energy-dispersive X-ray spectroscopy.

The loricae of *Stenokalyx tubiformis* are cylindrical with helical ribs. It was believed that *Stenokalyx tubiformis* differs from all other members of the genus in the lorica being open at both ends. We revealed that the lorica aperture at the posterior end is not open but covered by a thin membrane. Zygotic stomatocysts are spherical with a regular pore and a rough cyst surface.

EDS microanalysis showed that carbon and oxygen are predominant elements of both loricae and stomatocysts. In contrast to other loricate chrysophytes, like *Pseudokephyrion pseudospirale* Bourrelly and *Kephyrion rubri-claustri* Conrad, neither manganese, nor iron were detected in the loricae of *Stenokalyx tubiformis*. Also, loricae contain aluminum and low amounts of calcium. Remarkably that zygotic stomatocysts contain rather low amounts (11,5%) of silicium. This may indicate that silicification of stomatocyst is unfinished.

Acknowledgements

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FT-13

Diversity of silica-scaled chrysophytes from waterbodies of the Kader bog Mire (Russia, Leningrad Region)

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Peat bogs represent one of the widespread landscape types at middle and higher latitudes of the Northern Hemisphere. Silica-scaled chrysophytes are common components of the bog biota in Leningrad Region (Russia). The flora of scaled chrysophytes was examined at 25 sites in the Kader Mire, located in the southwest of the Leningrad Region. Fifty-three taxa were noted in total, with *Mallomonas* (25) and *Spiniferomonas* (11) showing the greatest diversity. The remaining genera included no more than five taxa: *Paraphysomonas* (5), Synura (5), *Chrysosphaerella* (2), and *Lepidochromonas* (1). In our research, we recorded species new to Russia: *Paraphysomonas ovalis*, *Mallomonas favosa*, *M. multisetigera*, *M. teres* (Safronova & Shadrina 2020; Kotkova et al 2025). Also, eight species are reported for the first time for the Leningrad Region: *M. maculata, M. pillula f. latimarginalis*, *M. pillula f. valdiviana*, *M. transsylvanica*, *M. vannigera*, *Spiniferomonas abei*, *Spiniferomonas conica*, *Spiniferomonas takahashii*. Two unidentified *Mallomonas* species and one unidentified species of Spiniferomonas may probably be new to science. Overall, the species composition is typical for northern temperate areas. The most common species were *M. canina*, *M. paludosa*, and *Synura sphagnicola*.

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FT-14

On stomatocysts of *Mallomonas silvicola* (Chrysophyceae)

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Cyst development of *Mallomonas silvicola*, a species endemic to Europe, was studied using scanning electron microscopy. The material was collected from a temporary water body on the coast of the Gulf of Finland (St. Petersburg, Russia). Stomatocysts are described following the guidelines of the International Statospore Working Group (ISWG) and illustrated with SEM micrographs. The ultrastructure of stomatocysts is known for only a few *Mallomonas* taxa, and this study provides the first detailed description of cysts for *M. silvicola*. Since chrysophyte cysts have species-specific morphology and are well preserved in sediments, they are valuable indicators for paleolimnological reconstructions. However, their application is limited because most cyst morphotypes have not been linked to vegetative stages. The obtained results allow the identification of *M. silvicola* stomatocysts in fossil assemblages and their use for monitoring temporary water bodies.

FT-15

Performance of Moving Bed Biofilm, Periphyton, and Halophyte Biofilters in Marine Multi-Trophic Aquaculture Systems

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Combining multi-trophic recirculating aquaculture system (MT-RAS) biofilter types leverages the strengths of different ecological biomes, benefits water treatment, resource recovery, economics, and environmental sustainability. The overall goal of this study was to determine the effects of different aquaculture biofilter combinations on MT-RAS. Three duplicate biofilter combinations were tested in a pilot scale MT-RAS with red drum (*Sciaenops ocellatus*): 1) periphyton (algae and bacterial biofilm) with halophytes (P+H), 2) periphyton with moving bed biofilm reactors (P+M), and 3) periphyton only (P^2). Experiments were performed in two trials (spring and summer) with four replicates. Water quality tests validated that NH_3/NH_4^+, NO_2^-, NO_3^-, and CO_2 were below fish toxic limits for all biofilter combinations. Fish mortalities were low, with food conversion ratios between 1.1 and 2.0. In all trials, periphyton added dissolved oxygen (DO) to the water (at an average of +3.95 ± 6.52 mg/(L*d)), thus reducing energy costs. Periphyton was also found to include valuable lipid content (4.55 ± 2.24% of dry weight) with the detection of Ω-3 fatty acids. The P^2 trials maintained a stable alkalinity and pH balance. The M+P trials removed NH_3/NH_4^+ at a high rate; however, they also required more energy for DO. Edible sea purslane growth rates (1.0431 ± 0.3361 g/day/plant) were efficient in all P+H trials. The microbiome revealed abundance of *Ignavibacterium* bacteria, Chrysophyceae, Cyanobacteria, Haptophytes, *Navicula* and *Chlorella* algae, *Nitrospira*, *Nitrospirae*, *Nitrosospharota*, and *Nitrosoarchaeum* nitrogen cyclers. Overall, periphyton biofilter combinations nitrify, denitrify, stabilize pH, photosynthesize, and produce oxygen and a value-added product.

FT-16

Paraphysomonas spp. and Other Benthic Heterotrophic Flagellates from the Songnim Tidal Flat, Seocheon, Korea

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Free-living heterotrophic flagellates are important components of benthic microbial communities, yet their taxonomic diversity in Korean intertidal sediments remains incompletely documented. In this study, we examined heterotrophic flagellates from marine intertidal sediment samples collected at the Songnim tidal flat, Seocheon, Chungnam, Korea, in March 2026, with particular focus on the genus *Paraphysomonas*.

Heterotrophic flagellates were isolated from sediment samples and maintained in culture. Species identification was conducted primarily based on light-microscopic morphology. Two *Paraphysomonas*-like isolates were further examined using scanning electron microscopy (SEM) to observe diagnostic siliceous scale morphology, and molecular analyses are currently underway to confirm their taxonomic identities.

Meanwhile, the benthic microflagellates identified from the Songnim tidal flat comprised 18 previously recorded Korean species representing 16 genera. These included 1 species of Apusomonadida, 2 of Bicosoecophyceae, 1 of Choanoflagellatea, 1 of Developayellales, 5 of Euglenoida, 1 of Euglenoidea incertae sedis, 1 of Goniomonadales, 1 of Imbricatea, 1 of Jakobea, 3 of Kinetoplastea, and 1 of Metromonadea. In addition, two *Paraphysomonas* spp. (Chrysophyceae), which may represent taxa not previously reported from Korea, were isolated and established in culture. SEM observations revealed scale morphologies similar to those of *Paraphysomonas imperforata* and taxa historically treated as *P. butcheri*.

This study provides additional distributional and morphological information on benthic heterotrophic flagellates from Korean tidal-flat sediments and highlights the occurrence of *Paraphysomonas* spp. in the Songnim tidal flat. Ongoing molecular analyses will help clarify the taxonomic identities and Korean record status of the *Paraphysomonas* isolates.

Acknowledgements

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Poster Session

PS-01

A xanthone O-glucoside isolated from *Iris setosa* Pall. ex Link exhibits promising anti-amoebic activity against brain-eating amoeba *Naegleria fowleri*

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Primary amoebic meningoencephalitis (PAM), caused by *Naegleria fowleri*, poses a significant challenge in humans owing to its high mortality rate, exceeding 97%. Current therapeutics have been unable to deliver satisfactory treatment outcomes, due to suboptimal efficacy and toxicity, highlighting the critical need for efficacious drug development. In this study, we identified a natural compound, 3,5-Dihydroxy-8-methoxy-1-O-β-D-glucopyranosyl xanthone (DX), which exhibited promising anti-*N. fowleri* activity, and investigated its underlying anti-*N. fowleri* mechanisms. The anti-amoebic activity of DX against *N. fowleri* trophozoites and its cytotoxicity against C6 glial cells were evaluated using a cell viability assay. The anti-*N. fowleri* mechanism of DX involved analyses of apoptosis-necrosis, TUNEL, caspase-3, ROS production, mitochondrial dysfunction, ATP production, qRT-PCR, and actin integrity. The efficacy of DX in protecting C6 glial cells from the amoebae was assessed using a co-culture method. DX, isolated from *Iris setosa* Pall. ex Link, demonstrated significant anti-*N. fowleri* activity with an IC_{50} of 55.37 ± 2.58 μM, exhibiting a high selectivity index (> 9.03) and negligible cytotoxicity to C6 glial cells. DX induced apoptosis-like programmed cell death in the amoebae, characterized by DNA fragmentation, increased caspase-3 activity, and mitochondrial dysfunction. DX also disrupted actin cytoskeletal integrity in the amoebae. DX significantly protected C6 glial cells against phagocytosis of *N. fowleri* trophozoites. The selective anti-amoebic activity of DX for *N. fowleri* underscores its potential as a promising candidate drug or a supplemental compound in the development or optimization of therapeutic drugs for PAM.

PS-02

(−)-Epicatechin enhances the anti-*Acanthamoeba* activity of chlorhexidine through synergistic action

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Acanthamoeba species are causative agents of the sight-threatening ocular disease, *Acanthamoeba* keratitis (AK). (−)-Epicatechin (EC) has been reported to exhibit anti-amoebic activity against laboratory strains of *A. castellanii* and *A. polyphaga*, suggesting its potential as an AK drug alternative. However, its efficacy against clinical isolates of *Acanthamoeba* species and its feasibility as a treatment for AK have not yet been investigated. In this study, we analyzed the anti-amoebic activity of EC against *Acanthamoeba* clinical isolates and its synergistic effect with chlorhexidine (CHX) to validate its potential in developing or optimizing AK treatment regimes. The anti-amoebic activity of EC against trophozoites and cysts of 10 clinical isolates of *Acanthamoeba* species was analyzed. The synergistic anti-amoebic effect of EC and CHX was also investigated. EC exhibited anti-amoebic activity against clinical isolates of *Acanthamoeba*, but showed varying efficacy, with IC_{50} values ranging from 43.24 to 271.30 μM against trophozoites. EC induced apoptosis-like programmed cell death in the trophozoites of these clinical isolates, and also had partial cysticidal activity. Co-treatment with EC and CHX exhibited prominent *in vitro* synergistic anti-amoebic activity against *Acanthamoeba* trophozoites and cysts, and co-treatment with EC and a subclinical dose of CHX (0.001 and 0.002%) revealed a dose-dependent anti-amoebic effect on both trophozoites and cysts equivalent to or greater than a clinical dose of CHX (0.02%). The promising anti-amoebic activity of EC against *Acanthamoeba* clinical isolates, along with the observed synergistic effect with CHX, highlights its potential as a drug candidate or an adjunctive treatment for AK.

PS-03

The Microalgal Culture Collection at The Freshwater Bioresources Culture Collection (FBCC): Obtain Microalgal Cultures For Phylogenetic Classification and Useful Information.

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Phytoplankton isolated from the natural environment can be maintained for extended periods under nutrient-sufficient conditions and proper culture settings. The collected cultures can provide users with high-quality materials, certified biological materials that are consistent and safe. Additionally, it allows for the immediate use of culture strains without the need for subsequent efforts to explore growth conditions and adapt phytoplankton to culture conditions in a controlled laboratory environment. This study aimed to preserve and manage phytoplankton isolated from Korean water bodies, to acquire morphological and various molecular marker information of the culture strains held by the Freshwater Bioresources Culture Collection (FBCC), to establish an integrated biodiversity database, a taxonomic system, and to assess their usability. FBCC of the NakdonggangNational Institute of Biological Resources preserves and maintains phytoplankton culture strains. It has secured a total of 491 species and 1,650 culture strains of microalgae, Major groups include green algae (931 strains, 56.4%), cyanobacteria (301 strains, 18.2%), and others such as chrysophytes, dinoflagellates, diatoms, cryptophytes, euglenoids, and protozoa (combined 25.4%). Morphological information on 88 culture strains preserved and maintained in the collection was intended to be provided.

PS-04

Optimization of cryopreservation conditions for *Tetradesmus dimorphus* and *T. lagerheimii*

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Preservation of microalgae, an important biological resource, poses significant challenges owing to the limitations of subculturing, including contamination, high costs, and time consumption. Cryopreservation offers an effective strategy for long-term storage. This study aimed to establish suitable cryopreservation conditions for two *Tetradesmus* species, *T. dimorphus* and *T. lagerheimii*. Prior to cryopreservation, optimal light intensity and temperature conditions were evaluated to enhance microalgal growth. The effects of cell density, post-thaw light exposure, freezing methods, final storage temperatures, and cryoprotectant type and concentration on post-thaw recovery were subsequently assessed. The highest recovery rates for both species were obtained when cells were cryopreserved at 1×10^7 cells mL^{-1} by direct immersion in liquid nitrogen using 5% methanol (MeOH) as the cryoprotectant. These findings provide an effective cryopreservation protocol for *Tetradesmus* species and contribute to the long-term preservation and industrial utilization of microalgae.

PS-05

Morphological and molecular characterization of five newly recorded *Desmodesmus* species in Korean freshwater

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Desmodesmus (Scenedesmaceae) is a freshwater green algal genus that generally forms four-celled coenobia characterized by distinct spines and diverse ultrastructural features such as ribs, warts, and rosettes. Due to morphological similarities among species, molecular approaches are essential for accurate identification. To improve our understanding of species diversity, we conducted a taxonomic review of Korean freshwater *Desmodesmus* species based on light and electron microscopy, together with molecular phylogenetic analysis. The clade comprising the five species was divided into three subclades based on spine morphology: a long-spined group (*D. pseudoperforatus, D. dohacommunis, D. pseudocommunis*), a short-spined group (*D. lamellatus*), and a mixed group (*D. perdix*) with both short and long spines. As a result, we report five unrecorded Desmodesmus speices in Korea. Their taxonomic classification is as follows: Order Sphaeropleales Luerssen 1877 - Family Scenedesmaceae Oltmanns 1904 - Genus *Desmodesmus* An, Friedl and Hegewald, 1999 - *D. pseudoperforatus* Hegedüs and Dragos 2024; *D. dohacommunis* Demura 2022; *D. pseudocommunis* Hegewald 2017; *D. lamellatus* Demura 2024; *D. perdix* Fawley, Fawley and Hegewald 2011.

PS-06

Diversity and Ecological Differentiation of Newly Recorded Benthic Diatoms in Korean Freshwaters: Insights from pH and Conductivity Niches

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We conducted a survey of indigenous microalgal species at four freshwater sites in Cheongsong-gun, Gyeongsangbuk-do, Korea, from April 2022 to February 2024. A total of eight diatom species new to Korea were identified, belonging to two classes, five orders, six families, and eight genera. The taxa include *Cymbopleura incerta*, *Gomphonema pseudosubtile*, *Eunotia latitaenia*, *Caloneis latiuscula* var. *subholstei*, *Pinnularia subrostrata*, *Iconella angusta*, *Surirella apiculata* var. *constricta*, and *Pseudostaurosira brevistriata* var. *nipponica*. For each species, nomenclature, references, morphological characteristics, ecology, and distribution are provided. The newly recorded taxa exhibited distinct ecological niches associated with substrate preference and environmental gradients. Stalk-forming and attached taxa (e.g., *Gomphonema*) were primarily found in low-flow stream environments, whereas motile epipelic taxa (e.g., *Pinnularia*, *Caloneis*, and *Surirella*) were associated with fine sediments in lentic or slow-flowing habitats. Acidophilous tendencies were observed in *Eunotia*, while most other taxa occurred under neutral to alkaline conditions. All species were distributed along relatively low to moderate conductivity ranges, indicating adaptation to freshwater systems with varying ionic conditions. These findings demonstrate clear niche differentiation among benthic diatoms in relation to pH and conductivity gradients, as well as functional strategies such as attachment and motility. The results expand current knowledge of diatom diversity in Korea and provide essential baseline data for ecological assessment and biomonitoring of freshwater ecosystems.

PS-07

Utilizing Nature-Designed Porous Biosilica from Diatoms for High-Precision Drug Delivery Platforms

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This study presents the rational design of a high-performance drug delivery platform leveraging the hierarchical nano-architecture of freshwater diatom biosilica. By strategically exploiting its species-specific porous ultrastructure, we engineered a biogenic carrier that surpasses conventional synthetic silica in both structural complexity and intrinsic biodegradability. To ensure scalability, a comprehensive upstream-to-downstream process was established, integrating a modified FDMed medium to maximize biosilica yield and a precision purification protocol to maintain structural integrity.The system was functionalized through interfacial electrostatic assembly, hybridizing purified biosilica with nanostructured lipid carriers (NLC) to form a robust Diatom Biosilica-Nanolipid Carrier (DBNC) complex. Physicochemical characterization confirmed a stable hybrid matrix with tunable pore loading capacity. In vitro assays demonstrated superior intracellular retention and minimal cytotoxicity for hydrophobic anticancer and anti-inflammatory payloads. Furthermore, in vivo imaging revealed route-dependent pulmonary accumulation and prolonged systemic circulation.Dynamic release analysis quantified a pH-responsive kinetic with minimized burst effects and high encapsulation efficiency. These results underscore the potential of diatom-based nano-architectures as a sustainable, precision-engineered alternative for advanced therapeutic delivery.

PS-08

Mychonastes homosphaera MHSC24 Isolated from Brackish Waters of Korea: Taxonomic, Physiological, and Biochemical Characterization

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Mychonastes homosphaera MHSC24 is a green microalga newly isolated from a brackish coastal site in Korea. This study represents the first indigenous record of this species in the country. It provides a comprehensive characterization of its morphological, molecular, physiological, and biochemical characteristics. This microalga was identified through morphological observations and multilocus phylogenetic analyses. Strain MHSC24 exhibited robust growth under mesophilic temperatures (15–27°C), moderate light intensities (88–300 μmol photons m^{-2} s^{-1}), and low salinity levels (0–10 PSU). Optimal growth was observed at 27°C, 193 μmol photons m^{-2} s^{-1}, and 0 PSU. Under standard cultivation, the strain exhibited high protein levels (~54% of dry weight, DW) and accumulated substantial amounts of canthaxanthin (5.59 mg g^{-1} DW), the predominant carotenoid in its pigment profile. Thus, MHSC24 is a promising candidate for sustainable protein- and carotenoid-based applications. Palmitic acid (11.95 mg g^{-1} DW) and galactose (2.07 mg g^{-1} DW) were the predominant fatty acid and monosaccharide, respectively. The physiological resilience, high protein yield, and substantial canthaxanthin accumulation of MHSC24 support its potential utilization in the functional food, feed, and nutraceutical sectors. Therefore, this study provides a basis for optimized cultivation strategies and industrial exploitation of indigenous Korean microalgae.

PS-09

Taxonomical, Physiological, and Biochemical Characteristics of *Dunaliella salina* DSTA20 from Hypersaline Environments of Taean Salt Pond, Republic of Korea

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Dunaliella salina, a halophilic unicellular chlorophyte, produces bioactive compounds and biofuels applicable to various industries. Despite its industrial significance, comprehensive studies on the morphological, physiological, and biochemical characteristics of the genus *Dunaliella* remain challenging. In this study, we characterized an axenically isolated green alga from a salt pond in Taean, Republic of Korea, and assessed its industrially relevant traits. The morphological characteristics were typical of *D. salina*, and molecular phylogenetic analysis of the SSU, ITS1-5.8S-ITS, LSU regions of rDNA, and rbcL gene confirmed the isolate as *D. salina* strain DSTA20. The optimal temperature, salinity, and photon flux density required for its growth were determined to be 21°C, 0.5 M NaCl, and 88 μmol m^{-2} s^{-1}, respectively. Dried biomass analysis revealed 42.87% total lipids, with major fatty acids, including α-linolenic acid (31.55%) and palmitic acid (21.06%). The alga produced high-value carotenoids, including β-carotene (2.47 mg g^{-1} dry weight (DW)) and lutein (1.39 mg g^{-1} DW), with peak levels at 0.25 M salinity. Glucose (195.5 mg g^{-1} DW) was the predominant monosaccharide. These findings highlight the potential of *D. salina* DSTA20 for biodiesel production and as a source of ω-3 fatty acids, carotenoids, and glucose. Morphological traits provide insights relevant to the industrial potential of the species.

PS-10

First report on the distribution of Acantharia (Radiolaria) in Korean coastal waters

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Acantharia, a major group of microzooplankton inhabiting warm open-ocean waters, have not previously been studied in Korean coastal regions, despite these areas being frequently influenced by warm-water intrusions from the East China Sea and the Kuroshio Current. This study investigated the distribution of Acantharia in southern Korean coastal waters through a summer field survey. At the coastal site, high abundances of Acantharia observed in surface waters. Large acantharian cells, with endoplasm diameter exceeding 50 µm, were concentrated in the upper water layer, coinciding with abrupt increases in temperature and decreases in salinity. Peaks in acantharian abundance did not coincide vertically with layers of high chlorophyll concentration. Satellite-derived chlorophyll maps indicate that the dense occurrence of acantharian cells in the Korean coastal waters may be associated with an immigration-driven hotspot along the eastern boundary of the Changjiang diluted water plume. Further studies across the waters surrounding the Korea Peninsula are required to better understand the distribution patterns and ecological roles of Acantharia in this region.

11th International Chrysophyte Symposium & Korean Society of Protistologist Meeting I Day 3 (Wed. Jun 24)

Plenary II

PL-03

The complex evolutionary landscape of the organellar genomes in ochrophytes

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Ochrophyta represent the most speciose and phenotypically diverse algal phylum, encompassing such familiar groups as diatoms, chrysophytes, or brown seaweeds. As algae, ochrophytes possess not only the mitochondrion omnipresent in eukaryotes, but most of them also harbour another endosymbiotically evolved organelle, specifically a "second-hand" plastid acquired by the stramenopile ancestor of ochrophytes and ultimately derived from a red algal source. Visual appearance of different ochrophytes immediately points to substantial evolutionary diversification of the plastid during the ochrophyte phylogeny, manifested by the broad colour spectrum of ochrophyte plastids stemming from differences in their photosynthetic pigment content, up to their complete absence in multiple lineages of secondarily non-photosynthetic ochrophytes. Further documents of the structural variation of the plastids across ochrophytes has been provided by electron microscopy, but the it is the molecular level where the range of evolutionary diversification is expected to be most broadly pronounced. While full-scale comparative molecular studies of ochrophyte plastids are in their infancy, a considerable body of knowledge has been gathered about the diversity of ochrophyte plastid genomes. In my talk I will briefly review some of the main themes of ochrophyte plastid genomics, including but not restricted to: (1) the current status of the sampling across the ochrophyte phylogenetic diversity; (2) the progress in metagenomics bringing into the picture uncultivated ochrophyte lineages; (3) the contribution of plastid genomics to the refinement of our understanding of the ochrophyte phylogeny; (4) reconstruction of the plastid gene content in the last ochrophyte common ancestor and the role of gene loss and gain in shaping the plastid genome in diverse ochrophyte lineages; (5) the special case of plastid genomes in non-photosynthetic ochrophytes. I will complement the discussion of the ochrophyte plastid genomics by summarizing the current status of the exploration of ochrophyte mitochondrial genomes, which has long lagged behind but is recently witnessing significant progress, partly thanks to the effort of my group and our collaborators. I will focus on a few particularly notable points: (1) the still unexplained conflict between the phylogenies inferred from mitochondrial and plastid genomes regarding the phylogenetic position of eustigmatophytes; (2) the origin and function of unassigned mitogenomic *orfs*; (3) unexpected cases of genetic code variation in ochrophyte mitochondria. I will conclude by defining the most urgent needs of the ochrophyte organellar genomics and outlining its future prospects.

PL-04

Retention and loss of chlorophyll biosynthesis in non-photosynthetic plastids

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Photosynthesis, a hallmark function for autotrophic lifestyles in eukaryotes, converts solar energy into biochemical energy carriers, such as ATP and NADPH. Eukaryotic photosynthesis and associated metabolic processes, such as carbon fixation, occur within plastids. Despite the inherent benefits of autotrophy, photosynthesis has been lost multiple times independently throughout the evolution of eukaryotes. Although the loss of photosynthesis does not necessarily result in the loss of the plastid or its genome, it triggers the divergence of plastid genome sequences and metabolic pathways, and can even lead to the complete loss of certain plastid functions. Given the independent losses, the functions retained in non-photosynthetic plastids vary significantly across species. One of the most functionally reduced non-photosynthetic plastids appears to lack almost all well-known metabolic pathways, retaining only the heme biosynthetic pathway. In contrast, some non-photosynthetic "algae" still retain genes for the chlorophyll biosynthesis pathway (*chl* genes) in addition to those for the synthesis of various metabolites, including heme, amino acids, fatty acids, and lipids. However, it has remained unclear whether these *chl* genes are functionally active and if these eukaryotes continue to biosynthesize chlorophyll-related compounds after losing their photosynthetic capacity. In this talk, I will present biochemical evidence showing that non-photosynthetic plastids in two independently evolved lineages still biosynthesize chlorophyll-related porphyrin compounds. Time-course high-performance liquid chromatography (HPLC) analysis unveiled an ecological strategy that enables these organisms to mitigate the potential cytotoxicity caused by the photosensitivity of porphyrins in the absence of photosystems and antenna proteins. Our findings suggest a detailed evolutionary route toward the complete loss of the chlorophyll biosynthesis pathway, regardless of whether the porphyrin compounds still serve ecophysiological or biochemical functions.

Special Session II

SS-II-01

New insights into the taxonomy and ecological diversity of the genus *Poterioochromonas* (Chrysophyceae)

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Poterioochromonas is a typical mixotrophic chrysophyte that plays an important ecological role in natural aquatic environments. It has received particular attention from a morphological and ecological perspectives over the last few decades because of its peculiar mode of feeding and relevance for practical applications. However, the taxonomic classification of this genus remains controversial, and the true extent of their diversity remains largely unknown. Here, we use a complementary approach of culturing, morphological and phylogenetic analyses, and sequence database mining to address this issue. We collected 16 cultures of *Poterioochromonas* to determine the essential morphological characteristics and clarify the taxonomy and phylogeny of the genus. Our results confirmed that all *Poterioochromonas* strains produce lorica, which is the diagnostic character for the genus. We suggest that the shape of the lorica cup and the morphology of the cyst could be used as diagnostic characteristics to differentiate different species within the genus. Molecular phylogenetic analysis based on the SSU rRNA and rbcL gene sequences confirmed the monophyly of *Poterioochromonas*, which is subdivided into heterotrophic and mixotrophic clades. Comparative analysis of six molecular markers revealed that the COI gene is the most sensitive for distinguishing both inter- and intraspecific relationships. An exhaustive screening of the NCBI GenBank database and publicly available amplicon sequencing datasets revealed 100 SSU rDNA gene sequences for *Poterioochromonas.* The results showed that many soil-derived environmental sequences grouped with heterotrophic *Poterioochromonas* and indicated that the heterotrophic representatives of the genus are abundant in the soil environment. The results also revealed that many environmental sequences did not group with any reference sequences of known species, indicating that the genus *Poterioochromonas* is much more diverse than previously thought. This study contributes to a clearer taxonomic and distributional framework for *Poterioochromonas*, thereby facilitating future basic and applied research on this genus and similar mixotrophic chrysophytes.

SS-II-02

Freshwater zooplankton selectivity with a focus on silica scaled chrysophytes

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There is an ongoing debate over the function of chrysophyte scales and bristles. To determine whether these silica structures serve as a defence mechanism against planktonic predators, we investigated the *in situ* feeding selectivity of Cladocera, Copepoda and Rotifera species in freshwater ponds, swamps and small lakes of the Třeboňsko region (Czech Republic) in the autumn peak of chrysophyte abundance. By combining DNA metabarcoding and transmission electron microscopy (TEM) of both zooplankton specimens and open-water samples, we obtained their feeding preferences for chrysophyte species, as well as for various other planktonic organisms. Preliminary data suggest that chrysophytes are preferred over diatoms, which are generally considered a favored food source of zooplankton. Single cells with spines (e.g., the genus *Mallomonas*) provide a relatively effective defensive morphology against rotifers. However, larger zooplankton grazers are not repelled by them. Against these larger predators, the only effective strategy appears to be the formation of large colonies with bristles, as seen in *Synura sphagnicola*. Avoidance of *S. sphagnicola* may also be influenced by the presence of potentially toxic red droplets. Overall, a pattern emerges suggesting that silica scales and bristles may serve as a defense against smaller zooplankton, such as rotifers and small cladocerans.

SS-II-03

From grazer to cell factory: rethinking the mixotrophic chrysophyte *Poterioochromonas malhamensis*

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This presentation summarizes our evolving research on the mixotrophic chrysophyte *Poterioochromonas malhamensis*. Initially, this organism was regarded as a problematic contaminant in microalgal mass cultures due to its strong grazing activity on microalgae. Our early work therefore focused on elucidating its grazing behavior and developing strategies to control contamination in algal cultivation systems. A shift in perspective later revealed its potential as a valuable biotechnological resource. By establishing high-density heterotrophic fermentation platforms, we developed *P. malhamensis* as a microbial cell factory capable of producing high-value bioactive compounds. These include the immunomodulatory β-1,3-glucan chrysolaminarin and the carotenoid fucoxanthin, both of which have promising biomedical and nutritional applications. More recently, our research has turned to fundamental biological questions, particularly the development and regulation of chloroplasts in this mixotrophic organism. Investigating the interplay between heterotrophic metabolism and photosynthesis provides new insights into mixotrophic physiology and organelle function. Together, these studies highlight the transformation of *P. malhamensis* from a harmful grazer into a promising model organism and biotechnological platform, offering new opportunities for both basic research and metabolic engineering.

SS-II-04

Genomic insights into the evolution of amoeboid movement in photosynthetic stramenopiles

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Photosynthetic stramenopiles exhibit diverse morphologies, ranging from unicellular forms to colonial organizations. Interestingly, some taxa, particularly within Synchromophyceae, Chrysophyceae, and Dictyochophyceae, display amoeboid movement during their life cycles. Although the functional roles of this behavior remain poorly understood, it has been associated with phagocytosis, substrate or symbiont attachment, and, in some cases, reproductive strategies. These movements are largely mediated by cytoskeletal components such as actin filaments and microtubules. Nevertheless, the genomic basis of amoeboid movement in photosynthetic stramenopiles remains largely unexplored. Here, we generated *de novo* nuclear genome assemblies for two representative species, *Chlamydomyxa montana* SAG36.96 (Synchromophyceae) and *Rhizochromulina marina* A13,803 (Dictyochophyceae), and performed comparative analyses with other stramenopiles including Chrysophycean species and amoeboid lineages to gain genomic insights into the evolution and mechanisms of amoeboid movement. The assembled genome sizes of *C. montana* and *R. marina* are 69.3 Mbp and 65.9 Mbp, respectively, with 20,991 and 17,887 predicted genes. Genome completeness was estimated at 93.7% and 97.3%, respectively, based on the stramenopile odb12 database. Orthologue analysis identified gene ontology (GO) terms associated with amoeboid movement in both species. In *C. montana*, genes related to GPCR-mediated signaling and extracellular degradation pathways are enriched, suggesting chemotactic amoeboid movement with enhanced environmental interaction. In addition, the presence of genes associated with extracellular matrix-like components indicates a potential role in substrate interaction and adhesion during movement. In contrast, *R. marina* shows enrichment in calcium-dependent signaling, phospholipid remodeling, and septin-associated cytoskeletal organization, indicative of a contractility-driven mode of movement. These differences suggest that the two species may have acquired amoeboid motility through distinct evolutionary strategies, potentially independent of those observed in amoebae and other stramenopile lineages.

Student Presentation (Oral) II

SO-II-01

Dot, dot, dot···Deciphering the Environmental Drivers of Papillae Formation in *Mallomonas*

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Papillae are small siliceous protuberances frequently observed on the scales and cysts of many chrysophyte algae. Although these structures are widespread among microscopic taxa, their ecological function and the environmental drivers of their formation remain poorly understood.

This contribution focuses on the environmental drivers of papillae formation in the genus *Mallomonas*. To identify these drivers, we combined two datasets: a long-term pan-European dataset of Chrysophyte species occurrences (Chrysophyte.eu database) and a high-resolution local dataset based on intensive sampling in the Czech Republic.

Our results show that the presence of papillae is not random but follows a consistent ecological pattern shaped by both broad-scale climatic gradients and local environmental conditions. Across both spatial scales, pH emerged as the primary environmental filter, with acidic conditions consistently favouring a higher proportion of papillae-forming species. Papillae structures may provide a selective advantage in low-pH environments, for example by acting as a physical barrier against toxic metal ions. Furthermore, our results highlight the scale-dependent nature of these environmental drivers. While climatic variables, such as mean annual temperature, influence the occurrence of papillae-forming *Mallomonas* species at the continental scale, local patterns are more strongly determined by immediate chemical conditions, particularly pH and dissolved silica availability.

SO-II-02

DNA replication through multiple fission in green algal cells

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Eukaryotes generally produce two daughter cells through cell division, but several green algal species show an alternative cell division strategy, such as multiple fission. This process comprises successive rounds of DNA replication and nuclear division within a single cell, followed by the generation of multiple daughter cells. Although multiple fission is relatively uncommon, it has been reported in several green species. Moreover, slightly different patterns of multiple fission are shown among green algae, including differences in the number of nuclear division cycles, cytokinesis, and division timing. However, this topic has primarily been studied in the model species *Chlamydomonas*, and knowledge of cell cycle progression associated with multiple fission in non-model green algal species therefore remains limited.

In this study, variations in DNA content were analyzed using flow cytometry to characterize the cell cycle progression associated with multiple fission in six green algal species (Scenedesmaceae; Sphaeropleales). Our results show that multiple fission occurs in all six green algal species and reveal diverse patterns of cell cycle progression through multiple fission within this family. This study provides evidence that cell cycle patterns are diverse and that multiple fission occurs frequently in non-model green algal species.

SO-II-03

Genomic insights into morphological diversification in Xanthophyceae

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The genomic basis of cellular complexity remains a fundamental question in eukaryotic evolution. The Xanthophyceae (yellow-green algae) provide a unique system to address this question, encompassing a wide range of cellular organizations—from unicellular forms to multinucleate coenocytes and filamentous architectures—within a relatively compact genomic framework. In this study, we generated high-quality genomes for nine species across seven genera using PacBio HiFi sequencing, combined with RNA-seq and Iso-seq-based gene annotation. Comparative analyses across these genomes revealed extensive lineage-specific variation in genome architecture, including differences in gene content, repeat composition, and structural organization. Notably, species exhibiting increased cellular complexity—such as multinucleation and filamentous growth—show distinct genomic signatures compared to simpler forms. These include shifts in repeat landscapes and potential changes in regulatory and structural gene components, suggesting multiple evolutionary routes toward complex cellular organization. Together, our results highlight that cellular complexity in Xanthophyceae is associated with diverse genomic configurations rather than a single conserved mechanism. Ongoing functional analyses in *Vaucheria* and *Ophiocytium* aim to further resolve the molecular basis of these transitions. This work establishes Xanthophyceae as an emerging model for studying the evolution of cellular complexity and provides a comparative genomic framework for understanding how diverse genomic features contribute to morphological innovation.

Keywords: Xanthophyceae, cellular complexity, comparative genomics, evolution

SO-II-04

Marine plankton community structure and carbon biomass across contrasting hydrographic conditions in the South Sea of Korea

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Marine plankton communities and carbon biomass distribution in regions affected by interacting water masses are still not fully understood. This study investigated how hydrographic variability influences plankton community structure in the South Sea of Korea. Sampling was carried out in August 2023 at 10 stations distributed from the southern coastal area to the Korea Strait, covering depths between 0 and 100 m. Plankton assemblages were examined morphologically, and carbon-based estimates were used to assess biomass structure. In parallel, microbial community composition was analyzed using 18S and 16S rRNA gene metabarcoding, and correlation analyses were applied to explore the main environmental drivers of community variation. Environmental conditions displayed marked spatial and vertical gradients, indicating the presence of multiple water masses across the study area. Phytoplankton biomass was relatively high in coastal-influenced waters, whereas zooplankton contributed a larger proportion of total biomass in offshore areas under stronger Tsushima Warm Current influence. Metabarcoding results also showed clear differences in taxonomic composition with both station and depth. Overall, these results highlight the importance of hydrographic structure in shaping plankton trophic organization and microbial community variability in the South Sea of Korea.

SO-II-05

Hidden diversity of phototrophic *Paulinella*: two new brackish-water species uncover phylogenetic incongruence

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Photosynthetic *Paulinella* provides a valuable model for investigating the early evolution of photosynthetic organelles derived from primary endosymbiosis. Nevertheless, its diversity and evolutionary history remain insufficiently understood, largely because these organisms are rarely encountered in nature and are difficult to maintain in culture. In this study, we discovered two previously undescribed photosynthetic *Paulinella* species from a brackish-water habitat in North Carolina, USA, and examined their morphological, molecular, and genomic characteristics. The two species showed clear differences in cell size, surface morphology, and lifestyle. Although the gene repertoires of their chromatophore and mitochondrial genomes were largely conserved relative to those of other photosynthetic *Paulinella*, genome structural variation was detected. Notably, the chromatophore genomes of the two species were distinguished by a single inversion. Phylogenetic analyses showed discordance between nuclear ribosomal and organelle-based trees, as well as conflicts among individual gene trees. In particular, evidence of substitution saturation in rbcL suggests that this gene may partly explain the observed phylogenetic incongruence. Overall, our findings broaden the known diversity of photosynthetic *Paulinella* and emphasize the importance of expanded taxon sampling and multilocus analyses for resolving evolutionary relationships within this lineage.

Student Presentation (Oral) III

SO-III-01

Distinctive feeding behavior and global distribution of *Hexatilemonas jangsaensis,* a novel marine Apusomonad within the uncultured APU-30 clade

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Heterotrophic nanoflagellates (HNFs; 2–20 μm in size) are widely distributed across aquatic and terrestrial ecosystems, where they play major roles as bacterial grazers in microbial food webs and also serve as prey for higher trophic-level organisms. HNFs have traditionally been classified into three feeding behaviours: raptorial feeders, filter feeders, and interception feeders, but their actual feeding behaviours are more complex than previously thought. Such variation in feeding behavior is likely linked to differences in bacterial grazing efficiency and is therefore important for understanding the structure and function of marine microbial food webs. Here, we describe a novel apusomonad isolated from the Korean coast as *Hexatilemonas jangsaensis* gen. n. et sp. n. based on morphological and molecular phylogenetic analyses. We further investigated its feeding behavior and ecological potential. The isolate resembled *Chelonemonas* in morphology but differed in its dorsal pellicle, and phylogenetic analyses placed it within the uncultured APU-30 clade, a lineage composed primarily of environmental sequences. Notably, it exhibited a distinctive feeding behavior characterized by the grasping and ingestion of bacterial assemblages using lateral pseudopodia. Interestingly, environmental DNA surveys (Tara Oceans expedition) revealed that the genus *Hexatilemonas* is widely distributed across global marine environments, occurring in 29.2% of epipelagic and 47.7% of mesopelagic samples. Our results suggest that *Hexatilemonas* may prefer to feed on particle-associated bacteria. Our findings expand the known diversity of Apusomonadida by describing a novel lineage and provide insights into its morphological distinctiveness, phylogenetic position, and ecological role in marine ecosystems.

SO-III-02

Organelle genomics of Ishigeales, the early-diverging lineage in brown algae

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Brown algae (Phaeophyceae) are one of the few eukaryotic lineages that have evolved complex multicellularity. Over their 450-million-year evolutionary history, brown algae have developed remarkable morphological and size diversity, ranging from simple filamentous forms to massive kelp with highly complex thallus structures. Interestingly, a similar pattern of morphological diversity is observed in Ishigeales, an early-diverging lineage of brown algae. Ishigeales exhibit a morphological progression from simple filamentous forms (*Pilinia rimosa* and *Petroderma maculiforme*) to more complex structures, including branched (*Ishige okamurae*) and foliose (*Ishige foliacea*) forms. Thus, Ishigeales provides a valuable model for understanding the evolutionary transition from simple to complex multicellularity in brown algae. In this primary study of Ishigeales, we assembled the organelle genomes of four species to investigate whether organelle genome structure and genetic differences correspond to morphological complexity. Phylogenetic analysis confirmed that the *P. rimosa* diverged first, followed by the *P. maculiforme*, *I. okamurae*, and *I. foliacea*. However, there was a phylogenetic conflict regarding the placement of *P. maculiforme* between the species tree and the plastid and mitochondrial gene trees, indicating filamentous species have complex gene histories. We also observed a distinct increase in mitochodrial genome size in the filamentous species. The genomic expansion was attributed to an increase of tandem repeats in non-coding regions and gene duplications, including *cox2* and *nad1*. Notably, we identified amplification of the *cox2* gene, likely triggered by the tandem repeat-mediated genomic recombination. Excluding the original copy, the duplicated *cox2* copies exhibited relatively elevated Ka/Ks values compared with other mitochondrial genes, potentially reflecting relaxed purifying selection. Consequently, we identified that simple filamentous species (*P. maculiforme* and *P. rimosa*) exhibit more intricate gene histories and genomic variation than two *Ishige* species with more developed morphologies.

SO-III-03

Taxonomic approaches for distinguishing intraspecific taxa within the genus *Desmodesmus* (Scenedesmaceae)

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Desmodesmus species (Scenedesmaceae) are typically identified by comparing marker genes (e.g., 18S rRNA, ITS2, *rbc*L, and *tuf*A), because their morphology is difficult to distinguish under light microscopy. However, several *Desmodesmus* taxa, morphologically similar under light microscopy but ultrastructurally distinct, have conserved marker gene sequences. Therefore, despite ultrastructural feature differences, phylogenetic relationships based on marker genes remain indistinct, supporting their recognition as intraspecific taxa. Therefore, recent studies suggest that the identifying intraspecific taxa within *Desmodesmus* requires both distinct ultrastructural morphological characteristics and notable genetic variation among genetically closely related taxa that are phylogenetically indistinguishable (i.e., under the phylogenetic species concept).

In this study, we established well-supported phylogenetic relationships among *Desmodesmus* taxa and compared their interspecific and intraspecific genetic variation using ribosomal RNA sequences and organelle genomes. We suggest that comprehensive patterns of notable genetic variation represent taxon-specific genetic mutations, thereby providing useful markers for recognizing intraspecific diversification. Our results contribute to understanding of intraspecific variation within this family.

SO-III-04

A cryptic lineage within the *Pyropia dentata* complex (Bangiophyceae, Rhodophyta) and the description of *Pyropia eudentata* sp. nov. based on integrative evidence

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Pyropia dentata is a commercially significant seaweed species that is extensively cultivated in Korea. However, its taxonomic identity has long been confounded by an overreliance on morphological characteristics, resulting in frequent misidentifications. Although recent studies have examined the taxonomy of the *P. dentata* complex, these investigations have primarily focused on Japanese populations and have largely depended on a single molecular marker (*rbc*L), leaving the status of Korean populations unresolved. In this study, we evaluated cryptic diversity within the *P. dentata* complex by integrating multilocus phylogenetic analyses based on de novo assembled organelle genomes, along with morphological and biogeographic evidence. Our results revealed a genetically distinct lineage occurring in Korea, northern Japan, and Chile, which is clearly differentiated from the type specimen of *P. dentata*. Based on this integrative evidence, we propose that this lineage constitutes a new species, described here as *Pyropia eudentata* sp. nov. This taxonomic revision provides important insights for aquaculture practices, species delimitation, and the management of biological data in *Pyropia*.

SO-III-05

Morphological and phylogenetic analysis of *Pseudo-nitzschia* from the coastal waters of Jeju Island

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The genus *Pseudo-nitzschia* is one of the major contributors to harmful algal blooms (HABs) and is known to produce domoic acid (DA), a neurotoxin that can affect marine ecosystems. However, the diversity of potentially toxigenic *Pseudo-nitzschia* species and their toxin production remain poorly understood in Korean coastal waters, particularly around Jeju Island. In this study, *Pseudo-nitzschia* species occurring in the coastal waters of Jeju Island were identified through morphological and molecular analyses, species diversity was investigated using NGS analysis, and toxin production was analyzed. Samples were collected from 12 coastal stations around Jeju Island from March 2022 to April 2024, and monoclonal cultures of *Pseudo-nitzschia* were established. Morphological identification was conducted using light microscopy (LM) and scanning electron microscopy (SEM). Molecular phylogenetic analysis was performed based on ITS rDNA sequences using the maximum likelihood (ML) method. In addition, toxin production was analyzed, and next-generation sequencing (NGS) was used to examine species diversity and spatial and temporal distribution patterns. A total of seven species were identified during the study period, including *P. brasiliana*, *P. calliantha*, *P. cuspidata*, *P. delicatissima*, *P. multiseries, P. multistriata* and *Pseudo-nitzschia jejuensis* sp. nov. Morphological observations indicated that the six identified species, excluding *Pseudo-nitzschia jejuensis* sp. nov., were consistent with previous reported descriptions. Likewise, phylogenetic analysis showed that these species clustered with previously reported sequences, whereas *Pseudo-nitzschia jejuensis* sp. nov. formed a distinct clade, suggesting that it is a new species. NGS analysis revealed a total of 15 *Pseudo-nitzschia* species. Among them, *P. americana* (5.96%), *P. delicatissima* (23.47%), *P. galaxiae* (36.17%), and *P. multistriata* (6.05%) were considered dominant species, each accounting for more than 5% of occurrence proportion. *P. delicatissima* was consistently abundant from March to August. Seasonal variation in species composition was observed, with the highest number of species recorded in August (10 species). Toxin analysis revealed that three species produced domoic acid during different growth phases, including *P. lundholmiae* (1.89 fg $cell^{-1}$), *P. multiseries* (6.85 fg $cell^{-1}$), and *Pseudo-nitzschia jejuensis* sp. nov. (3.84 fg $cell^{-1}$). This study provides taxonomic information on the newly discovered *Pseudo-nitzschia* species in Jeju Island and contributes to the development of future HAB warning and management strategies.

SO-III-06

Global phylogeography reveals genetic homogeneity across the widespread *Asparagopsis taxiformis* Lineage-2

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The red alga *Asparagopsis taxiformis* comprises six cryptic mitochondrial lineages (L1−L6) that are genetically distinct but morphologically cryptic. While these lineages occur across tropical and subtropical oceans worldwide, the phylogeographic structure of Korean populations has remained poorly understood. In this study, 39 individuals were collected from eight coastal localities in Korea and analyzed together with global samples. Phylogenetic analyses of concatenated *cox*2-3 spacer and partial *cox*1 sequences revealed that all Korean *A. taxiformis* samples belong to Lineage-2 (L2), a cosmopolitan lineage distributed across multiple ocean basins. Within Lineage-2, the *cox*2-3 spacer network displayed a consistent global pattern where the H1 haplotype predominated worldwide, including in Korea, whereas private haplotypes were primarily concentrated in Mediterranean populations, especially in Italy. The *cox*1 network provided higher resolution, resolving three dominant haplotypes (H1-H3) with distinct geographic ranges in East Asia: H1 mainly in the East Sea and Jeju Island; H2 mainly along the south and west coasts of Korea and Jeju Island; and H3 largely in the Ryukyu Islands. Despite this geographic structure, only one to three mutational steps separate these three haplotypes. Organelle genomic analysis of Korean, Italian, and American individuals further demonstrates that Lineage-2 exhibits low to intermediate divergences, a conserved trait despite its broad global distribution compared to other Rhodymeniophycidae species. Demographic and palaeoceanographic reconstructions suggest that the eastern Italian and southern Korean Peninsula served as refugial areas for Lineage-2, although the mechanisms maintaining this conserved, widespread structure remain unknown.

11th International Chrysophyte Symposium & Korean Society of Protistologist Meeting I Day 5 (Fri. Jun 26)

Plenary III

PL-05

Evolutionary history of chrysophytes: What have we learned from the fossil record?

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Although remains of fossil cysts belonging to the Chrysophyceae extend ~230 Ma to the Late Triassic, the oldest definitive specimens of scale-bearing chrysophytes date to the upper Cretaceous, with numerous taxa appearing soon after in the early Cenozoic. Much of the evolutionary history of the group took place under a warm Greenhouse Earth lacking a cryosphere and under elevated atmospheric [CO_2] concentrations, and only recently during the transition to a cool Icehouse Earth with declining [CO_2]. Given this environmental framework, and based on remains of over 200 fossil cyst and scale morphotypes, multiple conclusions with respect to evolutionary history can be made. First, most of the major scale-bearing genera known today, including *Mallomonas*, *Synura*, *Chrysosphaerella*, *Spiniferomonas*, *Paraphysomonas* and *Lepidochromonas*, had evolved by the late Cretaceous. Second, the most significant differences in scale structure were found between the Cretaceous and the Eocene, while multiple lineages display evolutionary stasis in siliceous structures since the onset of the Cenozoic. Third, there has been a clear trend towards decreasing scale and cell size in specific lineages. Fourth, many of the fossil taxa were uncovered in waterbodies inferred to be shallow, acidic, and with elevated levels of CDOM. Fifth, there is a connection between a group of fossil species uncovered from localities close to the Arctic Circle, and modern congeners described from tropical waters. Sixth, the fossil record harbors an impressive array of cyst morphotypes, many still with attached parent scales, and others hinting at formation of a cyst-related type of scale. The fossil dataset with respect to the genus *Mallomonas* was coupled with an extensive molecular dataset, and used to develop a highly-resolved phylogeny aligned with geologic time. The resulting phylogeny provides a framework from which rates of change in morphological traits can be estimated and traced over time (~200 Ma), and hypotheses based on the fossil record can be tested. Examples will be discussed.

PL-06

Using culture free methods to explore the diversity and ecological functions of oceanic Chrysophyceae biomes

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Marine planktonic eukaryotes play critical roles in global biogeochemical cycles and climate. However, their poor representation in culture collections limits our understanding of the evolutionary history and genomic underpinnings of planktonic ecosystems. This lack of representation exists both at the lineage level or at the ecosystem level. Today, the generation of culture free methods and the extent of new expeditions starts to fill this gap.

In that context, the Chrysophyceae are being revealed as an important lineage of marine ecosystems. They are an emerging evolutionary cell biology system due to recurrent variations of their morphology, lifestyles and nutrition modes linked to environmental adaptations. However, historically they have been known and studied almost exclusively from freshwater environments and much less is known on the taxonomy, biogeography or metabolism of the diverse chrysophyte lineages found in the marine environment.

I will present how the combination of modern approaches can help to fill this knowledge gap. In my investigation of the marine Chrysophyceae. I will present results on oceanic metagenomic data and Metagenome Assembled Genomes (MAGs) and newly established marine cultures. From understanding their phylogenetic diversity and its link to freshwater lineages, mapping and analyzing their distribution in the global ocean and finally using comparative genomics to provide a glimpse into their functions and ecological roles. This pioneer work is also supported by the establishment of new cultures from marine environment, notably of cryophilic marine Chrysophyceae that hole promises to study freshwater to marine transitions.

I advocate that unraveling this unsuspected complexity of the marine diversity of the Chrysophyceae constitute a fundamental development in our understanding of this lineage and is an important research avenue for the future.

Special Session III

SS-III-01

Rapid Synurales dynamics and uneven morphological evolution revealed through high-resolution reference databases

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Phytoplankton of the order Synurales (Chrysophyceae) play a key role in freshwater ecosystems, yet the temporal scale of their ecological and morphological dynamics remains poorly understood. Here, we combined high-frequency (3-day) sampling over 70 days with DNA metabarcoding and a uniquely complete ITS1 reference database covering all common species and 64% of all Synurales taxa ever recorded in Europe. This database enabled near-complete assignment of high throughput sequencing reads to individual species or genetically distinct lineages and allowed us to link each sequence to detailed morphological traits. Community changes in colonial species were influenced by abiotic drivers such as silica concentration and wind speed. By contrast, shifts in unicellular species communities were mainly driven by Cladocera predators, influencing the occurrence of bristle-bearing species.

We further show a striking mismatch between genetic and phenotypic patterns of diversity. Some lineages exhibit deep genetic divergence while remaining morphologically nearly indistinguishable, whereas others show clear morphological differentiation despite minimal SSU rDNA variation. These contrasting evolutionary tempos demonstrate that morphological and molecular evolution proceed at highly unequal rates across Synurales. Our results highlight that only high-resolution reference databases allow us to detect this hidden complexity and to accurately interpret ecological dynamics, evolutionary patterns, and true diversity within this ecologically important group.

SS-III-02

Green red algae: pigment evolution in three *Porphyridium* species (Rhodophyta)

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Phycobilisomes are complex light-harvesting antenna proteins anchored to the thylakoid membrane of plastids, playing a crucial role in light absorption for photosynthesis in cyanobacteria, glaucophytes, and rhodophytes. Three species of unicellular red algal genus Porphyridium (P. purpureum, P. sordidum and P. aerugineum) show different colors; red, purple, green, respectively, and they are inhabiting mainly in marine water (P. purpureum), brackish-freshwater (P. sordidum), and freshwater habitats (P. aerugineum). To better understand phycobilisome evolution and chromatic adaptation, we sequenced chromosome-level of genomes of these three Porphyridium species. Genome analysis showed that P. purpureum contains 28 phycobilisome genes, including 20 linker proteins, while P. sordidum and P. aerugineum (loss of cpeA) retain only 8 and 6 linker proteins, respectively. Loss of linker proteins were directly correlated with TE insertions, therefore, these genomes feature directly support different color of three species that were adapted in different habitats in which different wavelengths of light are available. Our findings offer novel insights into the diverse evolutionary pathways of phycobilisomes and the intricate mechanisms of chromatic adaptation within the Porphyridium.

SS-III-03

Silica-scaled chrysophytes from temperate regions of the Southern Hemisphere (Tasmania and New Zealand), including three novel *Synura* species.

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While hundreds of records of Synurales exist from temperate regions of the Northern Hemisphere, the Southern Hemisphere has received considerably less attention. During the 1980s and 1990s, only about a dozen studies were published from southern Australia (including Tasmania), New Zealand, and the southernmost regions of South America. Species identifications in these studies were based primarily on TEM and SEM analyses of silica scale morphology. Recent advances in molecular systematics using DNA sequence data have revealed substantial genetic diversity within Synurales worldwide. However, molecular data from temperate regions of the Southern Hemisphere are lacking. Here, we present a survey of species diversity based on two sampling campaigns conducted in Tasmania and New Zealand in August 2023. We identified 37 species in Tasmania and 48 in New Zealand, significantly expanding current knowledge of both morphological and molecular diversity. This study has shown that silica-scaled chrysophytes comprise a mixture of cosmopolitan species and regionally restricted or initially presumed endemic taxa. Three new *Synura* species are described based on detailed morphological and molecular analyses. First *Synura* species belonging to section Curtispinae, is closely related to *S. longitubularis* and was detected at multiple localities in both Tasmania and New Zealand. Second *Synura* species was found to be identical to strain CCAC0052, previously isolated in Germany. The last novel *Synura* species morphologically resembles *S. australiensis*, forming distinctive large colonies composed of elongate club-shaped cells; however, it differs in its phylogenetic position, representing a more derived species. Despite the progress achieved in Tasmania and New Zealand, several gaps remain. Seasonal coverage is still limited, and many habitats, particularly remote dystrophic lagoons and meromictic lakes, remain insufficiently sampled. A secondary aim of this study was to isolate previously described species from their type localities. This objective was only partially successful. We suggest that biodiversity loss in these regions may be linked to environmental changes, including the transformation of mosaic open vegetation into degraded, pasture-dominated landscapes, as well as the widespread loss of wetlands due to anthropogenic drainage.

Special Session IV

SS-IV-01

Beyond protist generalizations: different evolutionary trajectories in closely related *Synura* species

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The processes underlying microbial diversity are inherently complex, so it is highly challenging to establish universal explanations and theoretical models of speciation. Using a population genetic approach, our study reveals that even closely related protist taxa with similar distributions, inhabiting overlapping ecological niches and comparable abundances, employ distinct speciation strategies. We investigated the population structure of freshwater algae, two related species, *Synura petersenii* and *S. glabra* (Chrysophyceae, Stramenopiles), across Europe. Using single-digest RAD sequencing, we analyzed genomes of both species from a total of 43 distinct water bodies. A population pattern was present in both *Synura* species, demonstrating their recent divergence and ongoing speciation. Nevertheless, the underlying drivers of genetic differentiation varied substantially. *Synura petersenii* exhibited a population pattern primarily associated with environmental factors, with conductivity emerging as the strongest habitat predictor of genetic structuring. In contrast, *Synura glabra* demonstrated strict geographical boundaries and formed populations primarily according to geographical distance. We propose that divergences in population patterns between the two studied species arise due to differing mechanisms of distribution. By maintaining a balanced design, our study provides unique insights into the intricacy of speciation and highlights the special nature of diversification processes.

SS-IV-02

Genomic framework of Red Algae Hildenbrandiophycidae to Identify Freshwater Adaptation and Fungal Symbiosis

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Within Florideophyceae, a class of red algae characterized by diverse upright multicellular morphologies, the subclass Hildenbrandiophycidae has been regarded as one of the earliest-diverging lineages. It also represents a distinctive taxonomic group with remarkable tolerance to environmental stresses, including ultraviolet radiation, salinity fluctuations, and desiccation. Although Hildenbrandiophycidae currently comprises only three recognized genera, *Hildenbrandia*, *Riverina*, and *Apophlaea*, recent molecular marker studies have revealed substantial hidden biodiversity and deep genetic divergence within the group, indicating the need for taxonomic re-evaluation at the order, family, and genus levels. Among these genera, *Riverina* is particularly notable as the only freshwater-adapted lineage, providing an opportunity to directly compare freshwater and marine relatives. In contrast, *Apophlaea* represents a unique evolutionary model because, unlike other members of the subclass, it develops the upright thallus morphology characteristic of Florideophyceae through an obligate symbiosis with the fungus *Stigmidium apophlaeae*. However, the genomic changes associated with the transition from marine to freshwater habitats and from an independent lifestyle to obligate fungal symbiosis remain largely unresolved. In this project, we are conducting comparative genomic analyses using the freshwater red alga *Riverina jigongshanensis*, the upright symbiotic marine red algae *Apophlaea lyallii* and *A. darchnoae*, and its associated symbiotic fungus *Stigmidium apophlaeae* as key experimental taxa. We further aim to include additional marine *Hildenbrandia* species as control taxa representing diverse phylogenetic positions within Hildenbrandiophycidae. This expanded taxon sampling will provide a robust comparative framework for identifying the genomic innovations associated with freshwater adaptation, environmental stress tolerance, and symbiosis-dependent thallus evolution in Hildenbrandiophycidae.

SS-IV-03

Algal Biofilter Treatment and Fish Pathogen Reservoirs in Recirculating Aquaculture Systems

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Fish pathogens are a significant cause of loss and cost in aquaculture. Frequently, pathogens accumulate in high nutrient areas such as in the microbial community of the nitrifying biofilter in recirculating aquaculture systems (RAS). On the other hand, algal biofilms can also enhance the disease resistance and growth of the cultured species and increase water quality. Previous research at Mote shows that microbial communities of periphyton (algae, bacteria, and archaea in an attached submerged biofilm) may help to reduce the number of pathogens in the system, preventing their establishment in the RAS biofilms. Validation of the effect of biofilter combination is necessary to establish where pathogens are residing within the RAS and if periphyton is useful for remediating fish pathogens. Two trials were carried out on two separate 2500 L pilot scale RAS for different biofilter combinations with samples taken over two different time periods per trial. The combinations tested in trials were periphyton only and periphyton in combination with a nitrifying biofilter. Samples were extracted with Qiagen EarthSoil Kits and validated on a Nanopore Nanodrop. High resolution classification of fish pathogens using the hsp70 gene and next generation sequencing was carried out to precisely examine fish pathogens in periphyton biofilters and nitrifying biofilters. Results will be compiled by OTU and into stacked bar charts, then compared for significant differences. The results will show where pathogens are residing in the biofilter as well as if the pathogens are in the biofilter effluent. The results may be explained by the microbial ecology relating different clades such as Chrysophytes, *Vibrios,* nitrogen cyclers, and Cyanobacteria. The importance of this experiment is that it shows where pathogens reside in RAS biofilter and if they are influenced by different microbial communities such as periphyton.

SS-IV-04

Growth promotion of *Ochrosphaera neapolitana* by the phycospheric bacterium *Paraglaciecola chathamensis*

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Algae play a pivotal role in aquatic ecosystems, particularly in global carbon cycling and climate regulation. Among them, haptophytes are major contributors to marine ecosystem functioning. In natural environments, algae interact with diverse biotic and abiotic factors, including phycosphere bacteria that influence algal growth and survival. To investigate these interactions, we examined the haptophyte alga *Ochrosphaera neapolitana* and its associated bacterium *Paraglaciecola chathamensis* B15. A total of 22 bacterial strains were isolated from *O. neapolitana* cultures and screened for their effects on algal growth in co-culture. Among these, *P. chathamensis* B15 markedly enhanced algal growth, while its abundance declined over time. Similar growth-promoting effects were observed across representative taxa of Rhodophyta, Viridiplantae, and Stramenopiles. The growth-promoting effect originated from non-viable bacterial biomass. Transcriptomic analyses combined with nutrient-depletion assays identified bacterially derived inorganic phosphate (Pi) as the primary factor underlying growth enhancement, with additional contributions from riboflavin and sulfur-related processes. These changes were accompanied by transcriptional activation of metabolic and nutrient acquisition pathways in *O. neapolitana*. These results indicate that bacterial biomass can serve as a nutrient source for algal growth, providing mechanistic insight into algae–bacteria interactions and their roles in marine ecosystems under nutrient-limited conditions.

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