# ICHA

PUNTA ARENAS · CHILE 2025

21st International Conference on HARMFUL ALGAE

# ABSTRACT BOOK 2025

From HAB Science to Environmental Resilience

# CONTENTS


| | Page |
|---|---|
| **Welcome Message from ICHA 2025 Chair** | 3 |
| **ICHA Proceedings Guidelines** | 4 |
| **Organizing Committees** | 5 |
| **Opening Lecture Plenary Talk** | 7 |
| **Oral Communications** | 17 |
| **Poster Communications** | 186 |
| **Index of Authors** | |

# Welcome Message from ICHA 2025 Chair

It is with great pleasure that we welcome you to the Twenty-First International Conference on Harmful Algae (ICHA 2025), held in Punta Arenas, Chile, at the southern tip of South America — in the heart of the Southern Hemisphere. This Book of Abstracts showcases the collective efforts of a diverse scientific community that, from multiple disciplines and regions, contributes to understanding and addressing one of the most complex and pressing challenges in aquatic ecosystems.

Harmful algal blooms are a global concern due to their impact on human health, marine resources, and coastal economies. However, they also provide an invaluable opportunity for scientific collaboration, technological innovation, and the strengthening of networks that connect researchers, managers, and communities.

Hosting this twenty-first edition of ICHA in the Southern Hemisphere carries a special significance. It reminds us that, although HABs are a shared global phenomenon, the conditions under which they occur — and the resources available to study and manage them — are unevenly distributed. Historical and economic asymmetries between the Northern and Southern Hemispheres continue to influence scientific capacity and research investment.

Nevertheless, it is essential to recognize that in many regions of the Southern Hemisphere now have research programs, infrastructure, and expertise that are fully comparable with those in the North. These achievements are the result of sustained local commitment, creative adaptation, and successful international cooperation. Together, they exemplify the growing maturity and diversity of global HAB science.

The theme of this conference — “From HAB Science to Environmental Resilience” — captures both the spirit and the responsibility of our community. Building resilience in the face of environmental change requires the integration of knowledge across ecosystems, disciplines, and nations. It demands that we bridge asymmetries and differences in capacity to ensure that every region, regardless of its level of development, can contribute to and benefit from scientific progress.

Recognizing both the contrasts and complementarities between hemispheres allows us to progress toward a more balanced and inclusive global scientific community, that is capable of transforming HAB science into tangible resilience for people and ecosystems.

We hope that the studies presented in these pages will inspire new questions, promote dialogue, and reinforced our collective dedication to sustainably and equitably managing of aquatic environments worldwide.

From the windswept shores and cold fjords of Chilean Patagonia, here at the end of the world, we extend to all of you a heartfelt welcome — a call to reflect, to collaborate, and to dream of oceans that remain vibrant and resilient for generations to come.

With gratitude, enthusiasm, and hope, we wish you a productive and inspiring conference



**Dr. Leonardo Guzmán-Méndez**
**President Organizer Committee**
**International Conference on Harmful Algae (ICHA 2025)**

# ICHA Proceedings Guidelines



# Local Organizing Committee



**Leonardo Guzmán**
Instituto de Fomento Pesquero (IFOP)
ICHA2025-CHAIR



**Máximo Frangopulos**
Universidad de Magallanes
1st Vive CHAIR



**Pamela Carbonell**
Instituto de Fomento Pesquero (IFOP)



**Catharina Alves-de-Souza**
Universidad de Concepción (UdeC)



**Patricio Díaz**
Universidad de Los Lagos
2nd Vice CHAIR



**Rodrigo Leiva**
Instituto de Fomento Pesquero (IFOP)

# Local Support Group

- **Alejandra Aguilera** – Universidad San Sebastián (USS).
- **Marisol Álvarez** – Subsecretaría de Pesca y Acuicultura (SUBPESCA).
- **Allisson Astuya** – Universidad de Concepción (UdeC).
- **César Alarcón** – Instituto de Fomento Pesquero (IFOP)
- **Gonzalo Álvarez** – Universidad Católica del Norte (UCN)
- **Patricia Álvarez** - Comité Oceanográfico Nacional (CONA)
- **Gressel Arancibia** – Servicio Nacional de Pesca y Acuicultura (SERNAPESCA).
- **Angela Baldrich** – Universidad de Los Lagos (ULA).
- **María Fernanda Barrera** – Universidad de Chile (UChile).
- **Patricia Beristain** – Universidad de Los Lagos (ULA).
- **Bruno Biso** – Instituto de Fomento Pesquero (IFOP).
- **Daniel Carrasco** – Universidad de Chile (UChile)
- **Alejandro Clément** – Plancton Andino Ltda.
- **Erik Daza** - Instituto de Fomento Pesquero (IFOP).
- **Daniela Díaz** – Instituto de Fomento Pesquero (IFOP).
- **Rosario Díaz** – Universidad de Los Lagos (ULA).
- **Christian Espinoza** – Instituto de Fomento Pesquero (IFOP).
- **Oscar Espinoza** – Instituto de Fomento Pesquero (IFOP).
- **Juan Fierro** – Comité Oceanográfico Nacional (CONA).
- **Carlos García** – Universidad de Chile (UChile).
- **Ricardo Haro** – Universidad de Magallanes (UMAG).
- **José Luis Iriarte** – Universidad Austral de Chile (UACh).
- **Alejandra Llanos** – Universidad de Concepción (UdeC).
- **Jorge Mardones** – Instituto de Fomento Pesquero (IFOP).
- **Rodrigo Martínez** – Instituto de Fomento Pesquero (IFOP).
- **Marco Morales** – Instituto de Fomento Pesquero (IFOP).
- **Alejandro Murillo** – Universidad de Atacama (UDA).
- **María Gabriela Nieves** – Universidad Católica del Norte (UCN).
- **Gemita Pizarro** – Instituto de Fomento Pesquero (IFOP).
- **Lorena Ramírez** – Instituto de Fomento Pesquero (IFOP)
- **Andrea Rivera** – Subsecretaria de Salud Pública.
- **Camilo Rodríguez** – Universidad de Los Lagos (ULA).
- **Ximena Rojas** – Instituto Tecnológico del Salmón (INTESAL).
- **Pablo Salgado** – Instituto de Fomento Pesquero (IFOP).
- **Miriam Seguel** - Universidad San Sebastián (USS).
- **Doris Soto** - Universidad de Valparaíso (UV).
- **Benjamín Suárez** – Universidad de Chile (UChile).
- **Daniel Varela** – Universidad de Los Lagos (ULA).
- **Paulina Vera** -Subsecretaria de Pesca y Acuicultura (SUBPESCA).

# Plenary Talks

Plenary Talk 01

# Managing Ciguatera Poisoning risk in light of contributions from “western” science and traditional knowledge

**Mireille Chinain**

Institut Louis Malardé (ILM), UMR 241-SECOPOL (IFREMER, ILM, IRD, University of French Polynesia), Laboratory of Marine Biotoxins, P.O. Box 30, 98713 Papeete, Tahiti, French Polynesia

Ciguatera Poisoning (CP) results from the consumption of seafood contaminated with lipid soluble toxins known as ciguatoxins (CTXs) that are produced by dinoflagellates in the genera Gambierdiscus and Fukuyoa. It is the most prevalent seafood-borne illness across the globe, affecting between 10,000 to 50,000 people annually, although it is common knowledge that CP cases are significantly underreported globally: in the Caribbean and the Pacific regions, it is estimated that statistics represent only 0.1 and 20 % of the actual cases, respectively. Ciguatera thus represents a major threat to food security and food sustainability in these CP endemic regions, a situation due in part to the strong reliance of local populations on marine resources. Therefore, ability to rely on effective risk management programs is pivotal for these small vulnerable island societies.
One significant sociocultural determinant likely to explain the high incidence rates consistently reported in CP-prone areas is the frequent banalization of CP risk by island communities, combined with marked risk-taking behaviors with regards to fish consumption habits. Conversely, other elements of CP cultural ramifications, namely traditional knowledge (TK) deeply rooted in the lifestyle of indigenous populations living in CP historical hotspots, can benefit risk monitoring and management programs. Indeed, numerous studies have acknowledged the ability of TK to e.g., identify potential problem areas for ciguatera. As commonly observed in other forms of poisonings, TK largely influences both individual and community responses to environmental changes and, in the case of CP, their perception of the poisoning risk and related management practices. Examples of CP-related TK include local ecological warning signs of CP outbreaks (some which foreshadow “western” science explanations), knowledge of local CP-prone fish species and fishing areas to avoid, a variety of folk tests to detect potentially toxic fish, adaptive fish consumption and/or meal preparation strategies to cope with the poisoning risk, and the use of traditional remedies to treat ciguatera whose recipes are transmitted across generations.

However, research advances achieved in the past decades in CP science have urged scientists to challenge/reconsider several of the early paradigms or common assumptions in ciguatera. This talk presents several examples where western science contributions have helped refine TK-based CP risk management practices established among French Polynesian island communities, highlighting the importance of integrating TK with science to improve community response and adaptation to environmental changes conducive to CP incidents. Additionally, efforts in bridging traditional and scientific knowledge can also have a positive impact on the effectiveness of public outreach and awareness campaigns, a key component of CP risk management programs, e.g., by promoting a higher community-wide acceptance of prevention messages and, consequently, a noticeable decrease in the number of CP cases, as accounted in some islands of French Polynesia.

**Keywords:**
Ciguatera poisoning, traditional knowledge, risk management

Plenary Talk 02

# After 25 years of the WHO guideline on toxic cyanobacteria: Advances achieved and main challenges from a public policy perspective

**Sandra M. F. O Azevedo**

Carlos Chagas Filho Biophysics Institute - Federal University of Rio de Janeiro IBCCF/UFRJ

The first WHO guideline on toxic cyanobacteria in water marked a significant advancement in recognizing the factors behind cyanobacterial dominance and recommending control measures. After 25 years, scientific progress has been made in understanding cyanobacterial issues, including their ecology, physiology, and management. Currently, at least 14 countries have guidelines or standards for acceptable cyanotoxin levels in drinking water, and some also for recreational water.

Despite this, toxic cyanobacterial blooms have become more frequent, persistent, and impactful globally. The causes of this mismatch between the knowledge generated and the effective use of this information to improve water quality must be analyzed. First, the occurrence of blooms is directly related to the degradation of aquatic ecosystems, and part of this degradation is a consequence of eutrophication and lack of sanitation. Stark disparities exist in sanitation access, from low levels in lower/middle-income countries (47.5%) to high-income countries (91.2%), contributing to regional differences in aquatic environment degradation and bloom occurrence

.

Additionally, growing attention is being paid to emerging contaminants like nanoplastics and pharmaceutical compounds. At the same time, cyanobacterial issues have become less attractive. Unlike traceable synthetic pollutants, toxic cyanobacteria lack identifiable sources, complicating mitigation. As a result, human exposure remains high, especially in low-income regions with weak environmental policies and limited water treatment infrastructure.

An overview of cyanotoxin occurrence and key challenges to mitigating environmental and public health impacts will be presented. Bridging the gaps between science and action will depend on political commitment and knowledge translation to empower communities and future researchers.

Plenary Talk 03

# From GEOHAB to GlobalHAB and beyond: 30 years of international coordination of research on Harmful Algal Blooms, lessons learnt and next steps

**Elisa Berdalet**

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

In the last decades of the 20th century, Harmful Algal Blooms (HABs) were considered a worldwide serious and increasing problem threatening human health, fisheries and coastal resources, and aquatic ecosystems. HABs were recognized as natural processes, also favoured by certain human activities. With the aim to prevent HABs impacts, research started to cover different issues, including identification of harmful species and toxins, their monitoring, prediction, etc. The scientific community was soon aware that HABs were a global and complex problem that could not be addressed by single efforts: an international coordination of individual and national research efforts was required.

As a response, the Scientific Committee on Oceanic Research (SCOR) and the Intergovernmental Oceanographic Commission (IOC) formed a partnership to developing and implementing a coordinated, multidisciplinary, international scientific program on HABs. In 2000, the SCOR-IOC GEOHAB program on the Global Ecology and Oceanography of Harmful Algal Blooms was born. Its mission was to foster international co-operative research on HABs in ecosystem types sharing common features, comparing the key species involved and the oceanographic processes that influence their population dynamics. The scientific goal of GEOHAB was to improve prediction of HABs by determining the ecological and oceanographic mechanisms underlying their population dynamics, integrating biological, chemical and physical studies supported by enhanced observation and modelling systems (GEOHAB 2000).

The GEOHAB Scientific Plan was implemented thanks to SCOR and IOC, and the engagement of the international community studying HABs, including scientists, endorsed projects and initiatives, stakeholders and local and international entities. Workshops, open science meetings, courses, experiments, were performed by international teams. Identification of noxious and toxic taxa progressed markedly along with a better scientific understanding of toxins, HABs forcings and dynamics in different ecosystems. This knowledge provided scientifically informed management tools and contributed to implement sound monitoring programs in different countries.

In 2013, at the sunset of GEOHAB, the international HABs community met in Paris to review the program. The community recognized that the objectives of GEOHAB had been partially accomplished and were still valid. It was recommended to launch a new program, the SCOR-IOC-GlobalHAB, building on the foundation provided by GEOHAB. GlobalHAB extended the GEOHAB objectives into brackish and freshwater systems and to a variety of harmful groups (benthic microalgae, cyanobacteria, macroalgae), addressing several issues related to the effects of HABs on human societies (health, socio-cultural aspects, economic impacts) and the potential trends of HABs and their impacts under climate change scenarios. With new tools, a wider multidisciplinary perspective and a similar support and engagement as in GEOHAB, GlobalHAB has contributed to new progresses to face the current and emerging HABs challenges.

GlobalHAB approaches its end. It is again time to look backwards and to the future. The rapid changes in our planet, with climate, ecological and social crisis, requires a new perspective for HABs research

and its international coordination. Since there are no magic solutions, I believe we can use ICHA2025 as an opportunity to start shaping this future together, by sharing ideas and envision our future steps together.

Plenary Talk 04

# The secret lives of plankton

**Manu Prakash**

Department of Bioengineering, Woods Institute for the Environment, Stanford University, USA

Tiny plankton play a huge role in regulating natural ecosystems, fuel life in the ocean but also cause harm when unchecked. Although plankton drive global carbon cycle, local fisheries - yet plankton behavior, dynamics, and reaction to the changing climate remain poorly understood. In this talk, we will share new tools to map plankton behavior in native habitats to understand phenotypic complexity encoded in plankton shapes and forms. By building a framework of Frugal Science - we will describe international efforts to develop innovative, low-cost tools like Planktoscope and Foldscope - that enable citizen scientists to monitor oceans including harmful algal blooms (HABs) and contribute to climate change solutions.

Plenary Talk 05

# Environmental drivers of neurotoxin BMAA production in marine diatoms and its biosynthesis pathway

**Aifeng Li**

College of Environmental Science and Engineering, Ocean University of China, Qingdao 266100, China

Neurodegenerative diseases like Alzheimer's disease (AD) and amyotrophic lateral sclerosis/ parkinsonism dementia complex (ALS/PDC) represent an increasing global health crisis. The neurotoxin β-N-methylamino-L-alanine (BMAA) produced by marine diatoms as a nonproteinogenic amino acid can potentially trigger AD and other neurodegenerative illnesses through the production of abnormal protein aggregates that are cytotoxic. The protein-bound BMAA as the main form was produced and exclusively located in the endoplasmic reticulum and Golgi organelles in marine diatoms. Our recent studies showed that different environmental factors could stimulate the production of BMAA-containing proteins in diverse species of marine diatoms. The co-culture with Cyanobacterium aponinum stimulated the production of BMAA in Thalassiosira minima up to seven times higher than that of the control group. Based on the expression changes of genes related to protein biosynthesis, ubiquitination and autophagy suppression, and limited COPII vesicles transport accuracy and efficiency were hypothesized to be responsible for biosynthesis of these error proteins in T. minima. The production of BMAA-containing proteins was significantly stimulated in diatoms under nitrogen limitation, e.g. up to 5.22-fold increase in T. andamanica. Non-targeted metabolomics analysis showed that a decrease in N-acetyl-D-glucosamine (GlcNAc) leads to an increase in N-glycan terminal modifications, which could increase the protein misfolding. The BMAA production was also strongly induced by iron (Fe) limitation in marine diatoms. Transcriptomic analyses suggested four identical and highly correlated KEGG pathways associated with the accumulation of misfolded proteins in diatoms, including ribosome, proteasome, SNARE interactions in vesicle transport, and protein processing in the endoplasmic reticulum. In addition, a reduction in the precision of ubiquitination-mediated protein hydrolysis and vesicular transport by the COPII system will exacerbate the accumulation of BMAA-containing proteins. Based on these findings, cysteine synthase (CysK) was suggested to be involved in BMAA synthesis in marine diatoms. The abolished BMAA production in CRISPR/Cas9-based CysK knockout diatoms strains and the restoration of BMAA synthesis by addition of the recombinant CysK to the mutant strains verified that CysK involves the biosynthesis of BMAA-containing proteins in marine diatoms. We hypothesized that the cysteine residues and methylamine are catalyzed by cysteine synthase to produce BMAA in marine diatoms. The biosynthesis pathway provides biomarkers for further investigation of BMAA production in marine diatoms and insights for understanding the pathological mechanism for human neurodegenerative diseases.

**Keywords:** βN-methylamino-L-alanine (BMAA); marine diatoms; neurodegenerative diseases; biosynthesis; iron limitation; nitrogen limitation

Plenary Talk 06

# Spatio-temporal expansion of HABs and marine biotoxins in Chile: 30 years of a country response through science, early warning strategies and management

**Benjamín A. Suárez Isla,** Fernanda Barrera, Daniel Carrasco, Ignacio Rubilar

Laboratory of Marine Toxins, Institute of Biomedical Sciences, Faculty of Medicine, University of Chile

Harmful algal blooms (HABs) pose a serious threat to public health, marine ecosystems, and the Chilean economy. Chile, the sixth-largest exporter of fishery products in the world, is heavily dependent on aquaculture. Mussel farming (Mytilus chilensis) contributes 76.7% of national mollusc production. The main toxins of concern include Paralytic Shellfish Poisoning (PSP) (saxitoxins) Amnesic Shellfish Poisoning (ASP) (domoic acid) and Lipophilic Marine Toxins (LMTs) (yessotoxins, pectenotoxins, okadaic acid and derivatives and azaspiracids). The economic losses caused by HABs are estimated at over $50 million since 2002 (Barría et al, 2022).

To minimize risks, Chile has implemented a cooperative and rigorous monitoring program for microalgae and biotoxins based in local scientific studies. The Shellfish Sanitation Program (PSMB) was established in 1995 under the National Fisheries and Aquaculture Service (Sernapesca). The program follows EU regulations (EC) N° 853/2004 and (EC) N°854/2004) ensuring compliance with international safety standards. It covers 105 aquaculture sites and 12 natural shellfish banks, primarily in Los Lagos region (94% of shellfish production). The PSMB includes weekly monitoring of biotoxins and phytoplankton, with additional controls for heavy metals and microbiological contamination. A real-time platform (mr-SAT) collects daily toxicological data, enables rapid decision-making 24/7, and can initiate emergency measures (e.g., harvest closures). The Regional Ministry of Health Services (SEREMIs) monitor shellfish production for domestic consumption. The Institute of Fisheries Research (IFOP) collects long-term HAB data with monthly records from over 200 stations on HABs occurrence in the Los Rios, Los Lagos, Aysén, and Magallanes regions.

In the Los Lagos region, HAB events occurred that led to precautionary closures. In the case of ASP, yearly HABs caused by Pseudonitzschia diatoms, with rapid domoic acid accumulation and detoxification, were observed between 2006 and 2024. During this period, only 92 (0.16%) of 58,000 ASP analyses were above 20 mg/kg, with no human intoxications. PSP in Chile is associated with the dinoflagellate Alexandrium catenella, which produces saxitoxins. In the southernmost regions (Los Lagos, Aysén, and Magallanes), 36 deaths and 497 poisonings have been reported since 1972. Of a total of 52,000 PSP analyses carried out in Chiloé (2006-2024), only 275 (0.52%) exceeded the regulatory limit of 800 µg STX equivalent/kg in blooms of 2002, 2009, and 2016. In 2016, during the largest PSP outbreak in history on Chiloé, toxicity reached 102,140 µg STX 2HCl Eq/kg, with only a few cases of intoxication. Prolonged closures (up to 211 days) caused major economic disruption and social unrest. LMTs such as yessotoxins (YTX) were most frequently detected (78%), followed by pectenotoxin-2 (PTX2) (20%). In contrast, diarrhetic toxins (okadaic acid and derivatives and azaspiracids) were rare (<1% of samples). Only 24 of 30,000 analyses in 2022 exceeded 3.75 mg Eq YTX/kg (0.08%) during 2021.

This presentation will explain how Chile's integrated surveillance system has successfully prevented ASP and LMTs intoxications and minimized mortality and poisoning risks from PSP, while ensuring seafood local consumption and exports. However, the data-driven, science-based approach, in line with international standards, remains critical for protecting public health, marine ecosystems, and the Chilean aquaculture industry.

**Keywords:** Marine biotoxins, early warning, management, public health

Plenary Talk 07

# What we know about ichthyotoxic microalgal species and their toxins

**Bernd Krock**

Alfred-Wegener Institut für Polar- und Meeresforschung, Am Handelshafen 12, 27570 Bremerhaven, Germany

Even though the knowledge about fish kills caused by microalgal is quite old, it has gained much more attention during the last two decades due to constantly growing marine fish aquaculture, which is particularly affected negatively by this phenomenon. In the last ten years, devastating ichthyotoxic blooms have occurred worldwide such as Pseudochatonella verriculosa and Alexandrium catenella blooms in Chile in March and May 2016 sociated with elevated seawater temperatures caused by a strong El Niño event, a Prymnesium parvum bloom in the Oder River (Germany/Poland) in August 2022 leading to more than 1,000 tons of dead biota associated with an extraordinarily hot and dry summer in addition to elevated salinity due to upstream mining activities, and a long lasting, more than 100 km long Karenia selliformis bloom along the East Australian coast in March-May 2025 associated with a marine heat wave and little precipitation, just to name three of the numerous events.

Despite of their dramatic effects and quite some scientific effort in the recent years, ichthyotoxic blooms are still not well understood and less is known about the ichthyotoxins being responsible for fish mortality. Several agents have been suggested to be involved in ichthyotoxicity such as reactive oxygen species (ROS), polyunsaturated fatty acids (PUFAs), short lived organic metal complexes, among others. However, none of these compounds could be confirmed in the environment at toxicologically active concentrations. In addition, in early works shellfish poisoning toxins have been erroneously associated with ichthyotoxicity as many shellfish poisoning toxin producing species are ichthyotoxic at the same, as several Alexandrium species, for example.

In the recent years the focus of ichthyotoxins has shifted to large polyketides produced by some ichthyotoxic marine plankton such as karlotoxins/karmitoxins (KmTx) produced by several pelagic Karlodinium species, amphidinols (including a group with different trivial names) that chemically belong to the karlotoxin group, but are produced by several benthic Amphidinium species, leadbeaterins produced by Chrysochromulina leadbeateri that are not yet fully characterized, but seem to be chemically related also with karlotoxins, and prymnesins (PRM) produced by the brackish water species Prymnesium parvum.

Even though KmTx and PRM are structurally very different molecules, they share some characteristics: they are 1) polyketides, 2) large compounds >1,000 Da, and 3) amphoteric, i.e., the presence of a large hydrophilic and a smaller lipophilic part within each molecule. Even tough structurally not yet elucidated due to their very large size, these characteristics also seem to apply to ichthyotoxins produced by several Alexandrium species. The conserved features of otherwise completely different compounds lead to the assumption that these characteristics are associated with ichthyotoxicity. Especially the amphoteric character of KmTx and PRM seems to be involved in their functionality, as the hydrophilic part of these large organic compounds enables their solubility in the aqueous environment, which is the prerequisite for any biological activity. On the other hand, the lipophilic part enables interactions with membranes of other marine organisms and is hypothesized as a predation and/or defense mechanism and also leads to gill membrane damage and finally to fish mortality.

# Oral Communications

Parallel Session 1: Ciguatera and Benthic HABs

O-001

# Giant moray eel, a long living apex predator that poses a food safety risk in the Pacific

**Sam Murray**[1], Emillie Passfield[1], Kirsty Smith[1], Joshua Fitzgerald[1], Jacob Thomson-Laing[1], Phoebe Argyle[2], Tim Harwood[1]

(1) Cawthron Institute, Private Bag 2, Nelson 7042, New Zealand
(2) Ministry of Marine Resources, P.O Box 85, Moss Rd, Avarua, Cook Islands

The giant moray eel (Gymnothorax javanicus) is an important marine species that plays a key ecological role in reef systems and is a valued food source for indigenous communities. However, it is well-known that giant moray eels pose a food safety risk due to their ability to accumulate high levels of ciguatoxins (CTXs), the toxins believed to cause ciguatera poisoning. This study assessed the age, CTX levels, elemental composition, and nutritional profile of seven specimens collected from Muri Lagoon, Rarotonga (Cook Islands), representing the most detailed investigation performed on this species. Age was determined for the three largest specimens, with the oldest being approximately 39 years. All specimens contained ciguatoxins, with Type I, Type II, algal-ciguatoxins and biotransformed metabolites. There was a higher ciguatoxin content in the liver compared to the flesh, with oldest-longest-heaviest specimen containing the most ciguatoxins. The CTX1B level observed in flesh samples of all specimens exceeded the recommended safe guidance level proposed by the USFDA. A similar ciguatoxin profile was observed across flesh sections, with the belly flap or anterior top loin containing the highest levels of CTXs in most specimens. Bioactive metabolites from co-occurring benthic harmful microalgae, including regulated shellfish toxins, were not detected. Elemental analysis determined the presence of 21 elements, including arsenic, low levels of mercury, and the volcanic elements rubidium and strontium. Nutritionally, the giant moray eel was shown to be a lean protein source, however, due to the ubiquitous bioaccumulation of CTXs, pose a significant food safety risk.

**Keywords:** Moray eel, ciguatera, food safety

Parallel Session 1: Ciguatera and Benthic HABs

O-002

# Ciguatera poisoning in Australian Waters: Investigating environmental, biological, and sociological drivers of risk

**Greta Gaiani**[1], Kate Barclay[2], Federico Davila[3], Carla Sbrocchi[2], Sam Murray[4], Tim Harwood[4,5], Andreas Seger[6], Alison Turnbull[6], Arjun Verma[1], Masahiro Hirama[7], Takeshi Tsumuraya[7], Monica Campas[8], Shauna Murray[1]

(1) University of Technology Sydney, School of Life Sciences, Faculty of Science, Broadway 2007, Sydney, Australia
(2) University of Technology Sydney, Faculty of Art and Social Sciences, Broadway 2007, Sydney, Australia
(3) University of Technology Sydney, Institute for Sustainable Futures, Broadway 2007, Sydney, Australia
(4) Cawthron Institute, Private Bag 2, Nelson, New Zealand
(5) Massey University, New Zealand Food Safety Science and Research Centre, Private Bag 11 2224442, Palmerston North, New Zealand
(6) University of Tasmania, Institute for Marine and Antarctic Studies, 15-21 Nubeena Crescent, Tasmania, Australia
(7) Osaka Metropolitan University, Department of Biological Chemistry, Graduate School of Science, 1-2 Gakuen-cho, Naka-ku, Sakai, Osaka 599-8570, Japan
8) IRTA, Marine and Continental Waters (AMiC) Programme, Ctra. Poble Nou del Delta, km. 5.5, 43540, La Ràpita, Spain

Ciguatera poisoning (CP) is the most prevalent form of non-bacterial seafood poisoning globally, with estimated annual incidence ranging from 50,000 to 500,000 cases. Approximately 80% of reported cases originate from the South Pacific region, including Australia, where CP presents a persistent public health challenge, particularly for coastal and Indigenous communities. In Australia, an estimated 300 cases occur annually, primarily in far north Queensland and other tropical regions; however, the true incidence is likely underrepresented due to frequent misdiagnosis and underreporting.

This study presents an integrated investigation into the occurrence and drivers of CP in Australian waters. Ciguatoxin (CTX) concentrations were measured in over 300 Spanish Mackerel (Scomberomorus commerson), a key vector species, collected across three fishing seasons, using liquid chromatography–mass spectrometry (LC-MS). A subset of samples was also analyzed using various CTX antibody-based techniques to assess their performance and comparability. Furthermore, the influence of environmental and biological variables on CTX concentrations in Spanish Mackerel was examined. In parallel, preliminary findings from a sociological assessment of CP awareness and knowledge among communities in far north Queensland are presented.

By combining ecological, biological, and sociological data, this research contributes to a more comprehensive understanding of CP dynamics in Australia. These findings are intended to support the development of improved monitoring frameworks, risk communication strategies, and evidence-based policy responses.

**Keywords:** Ciguatera, Spanish Mackerel, Sociological Assessment

**Financing:** Fisheries Research and Development Corporation (FRDC) Project No 2019-060 University of Technology Sydney Seed Funding scheme.

Parallel Session 1: Ciguatera and Benthic HABs

O-003

# New biogeographic records of *Gambierdiscus* spp. in Subtropical Eastern Atlantic: From the tropical Gulf of Guinea to the temperate Azores Islands

**Miguel Barbosa**[1,2], Catarina Churro[1,3], Bárbara Frazão[1], Sergei Danchenko[1], Pedro Afonso[4], Inês Gomes[4], Neide Gouveia[5], Viriato Timoteo[5], Rui Rosa[2,6,7], Jaquelino Varela[7], Maria Filomena Caeiro[8,9], Ana Amorim[2,9], Pedro Reis Costa[1,10]

(1) IPMA – Portuguese Institute for the Sea and Atmosphere, 1749-077, Lisboa, Portugal
(2) MARE – Marine and Environmental Sciences Centre/ARNET – Aquatic Research Network, Faculdade de Ciências, Universidade de Lisboa, 1749-016, Lisboa, Portugal
(3) CIIMAR – Blue Biotechnology Environment and Health - Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Terminal de Cruzeiros do Porto, Av. General Norton de Matos s/n, 4450-208 Matosinhos, Portugal
(4) Institute of Marine Sciences - Okeanos, University of the Azores and Instituto do Mar - IMAR, Rua Professor Doutor Frederico Machado 4, 9901-862, Horta, Portugal
(5) Laboratório Regional de Veterinária e Segurança Alimentar, Caminho das Quebradas de Baixo nº 79 S. Martinho, 9000-254, Funchal, Portugal
(6) Departamento de Biologia Animal, Faculdade de Ciências, Universidade de Lisboa, 1749-016, Lisboa, Portugal
(7) Sphyrna Association, Boa Vista Island, Cabo Verde
(8) Centre for Ecology Evolution and Environmental Changes (CE3C) & CHANGE – Global Change and Sustainability Institute, Faculdade de Ciências, Universidade de Lisboa, 1749-016, Lisboa, Portugal (9) Departamento de Biologia Vegetal, Faculdade de Ciências, Universidade de Lisboa, 1749-016, Lisboa, Portugal
(10) Centre of Marine Sciences (CCMAR/CIMAR LA), University of Algarve, Campus de Gambelas, 8005-139, Faro, Portugal

*Gambierdiscus* are benthic dinoflagellates responsible for producing potent toxins such as maitotoxins and ciguatoxin precursors, associated with Ciguatera Fish Poisoning (CFP). Originally considered from tropical regions, in recent years this genus has been increasingly reported from subtropical and temperate zones, including the Eastern Atlantic Islands of Macaronesia. This apparent geographic expansion has been linked to ocean warming and highlights the need for monitoring and risk assessment in new areas.

Here, we present new data on the distribution and diversity of Gambierdiscus species across five Eastern Atlantic archipelagos: Azores, Madeira, Selvagens, Cabo Verde, and São Tomé and Príncipe. Sampling was conducted across multiple islands, from which *Gambierdiscus* cells were isolated, cultured and subsequently analyzed. Morphological characterization was performed using microscopy techniques, and molecular identification was based on LSU rRNA sequences (D1–D3 and D8–D10 regions). Five species were identified: *G. carolinianus*, *G. excentricus, G. australes*, and *G. caribaeus*. These findings represent the first report of Gambierdiscus in the Azores (*G. carolinianus*) and the highest latitude recorded so far for this genus (39°40'19"N), as well as the first record in São Tomé and Príncipe (*G. caribaeus*). We reported the presence of G. caribaeus for the first time in Cabo Verde, complementing previous records of *G. australes*. New isolates of *G. australes* (Selvagens) and *G. excentricus* (Madeira) were also obtained.

These results strengthen the expanding biogeographical range of benthic harmful algal species and support the need for early warning management in European waters.

**Keywords:** *Gambierdiscus*, Ciguatera, Benthic Harmful Algae

**Financing:** EFSA (EuroCigua projects: GP/EFSA/KNOW/2022/03)Pacto da Bioeconomia azul (C644915664-00000026)FCT (UID/04292 - Centro de Ciências do Mar e do Ambiente; LA/P/0069/2020; 2023.01759.BDANA)

Parallel Session 1: Ciguatera and Benthic HABs

O-004

# A high ciguatoxin-producing *Gambierdiscus* clade (Gonyaulacales, Dinophyceae) as a major source of ciguatera in the Pacific

Shauna Murray[1], Mona Hoppenrath[2], D Tim Harwood[3], J Sam Murray[3], Kirsty Smith[3], Richard Lewis[6], Sarah Finch[4], Shikder S Islam[5,7], Amna Ashfaq[1], Caroline Dornelles De Azevedo[1], Arjun Verma[1], **Christopher Bolch**[7]

(1) University of Technology Sydney, School of Life Sciences, PO Box 123 Broadway, Sydney, Australia
(2) Senckenberg am Meer, German Centre for Marine Biodiversity Research (DZMB), Südstrand 44, D-26382, Wilhelmshaven, Germany
(3) Cawthron Institute, 98 Halifax Street East, Nelson 7010, New Zealand
(4) AgResearch Ltd, Ruakura Research Centre, Private Bag 3123, Hamilton 3240, New Zealand
(5) Khulna University, Fisheries and Marine Resource Technology Discipline, Khulna, Bangladesh
(6) The University of Queensland, Institute for Molecular Bioscience, Brisbane, Australiax
(7) University of Tasmania, Institute for Marine and Antarctic Studies, Private Bag 129, Hobart, Australia

Ciguatera Poisoning (CP) is caused by neurotoxins (Ciguatoxins, CTXs) produced by benthic dinoflagellates of the genus *Gambierdiscus* and *Fukuyoa* that accumulate in seafood and can result in severe human illness. More than 80% of the world's CP occurs in the South Pacific, and climate change is projected to increase CP cases. However, which *Gambierdiscus* species are directly associated with CP remains uncertain. Most *Gambierdiscus*/*Fukuyoa* spp. demonstrate little or no CTX-like activity and therefore are unlikely to contribute to CP at scale. We used LM, SEM, morphometrics and phylogenomics to characterise several *Gambierdiscus* species from the Great Barrier Reef (Australia), a region with endemic CP, including a new species, *G. bagnisii* sp. nov. Using LC-MS/MS, we detected iso-P-CTX4A/B produced by cultures of *G. holmesii*, only the second taxon after *G. polynesiensis* with chemically detectable P-CTXs. Both G. bagnisii sp. nov. and G. holmesii produced an unknown compound previously found only in G. polynesiensis. These three species form a closely-related cluster within Clade III and are distributed from the far north to the southern Great Barrier Reef, and throughout the South Pacific. Our analyses indicate that CTXs produced by *Gambierdiscus* from Clade III may be responsible for the majority of CP in the South Pacific.

**Keywords:** Ciguatera, *Gambierdiscus*, ciguatoxins

**Financing:** This work was supported by Australian Research Council Grant DP180100001. The Hanse Wissenschaftskolleg (Delmenhorst, Germany) provided SM with a fellowship during manuscript preparation.

**Acknowledgments:** We thank Orpheus Island research station; Matt Tesoreiro for sample collection; Javier Perez-Burillo and Jacqui Stuart for assistance with Figures 1 and 5.

Parallel Session 1: Ciguatera and Benthic HABs

O-005

# Advancing knowledge on Caribbean ciguatoxin chemistry and development of critical reference materials

**Elizabeth M. Mudge[1],** Christopher O. Miles[2], Bruno Garrido[1], Nancy Lewis[1], Alison Robertson[3], Pearse McCarron[1]

(1) National Research Council of Canada, Biotoxin Metrology, Metrology Research Centre, 1411 Oxford St, Halifax, Canada
(2) Norwegian Veterinary Institute, Chemistry & Toxinology Research Group, Elizabeth Stephansens vei 1, Ås, Norway
(3) University of South Alabama, Stokes School of Marine & Environmental Sciences, 600 Clinic Drive, Mobile, USA

Ciguatera poisoning is endemic in subtropical and tropical regions from the consumption of ciguatoxin (CTX) contaminated fish. There are estimated to be up to 500 000 ciguatera poisoning cases annually, with increased occurrences in traditionally non-endemic, temperate regions. The lack of reference materials for CTXs has significantly hampered detection in fish implicated in CP outbreaks, and progress on pharmacology, environmental monitoring, regulations and long-term management. Ciguatoxins are tasteless, odorless, heat tolerant, large polyether compounds. As mobile vectors, toxicity in fish can be highly variable between individual fish, making purification of CTXs from fish tissues extremely challenging, impeding the development of calibration reference materials. The recent discovery of an algal produced analogue of Caribbean CTXs (C-CTX5) has enabled the development of reference materials for this toxin class. Following scaled-up culturing of a toxic strain of *Gambierdiscus silvae*, procedures were developed for isolation, elucidation and quantitation of C-CTX5. Considering both stereochemistry and yield, optimal conditions were assessed to convert C-CTX5 into C-CTX1, the most relevant analogue detected in fish and monitored by regulatory agencies in the Caribbean and Eastern Atlantic. Feasibility studies were performed to establish the optimal diluent, assess stability, and value-assignment for small batches of in-house prepared calibration solutions. In addition, fish tissues naturally contaminated with C-CTXs were used to prepare a small-scale batch matrix reference material. These studies established processes to prepare large-scale reference materials for ciguatoxins, which are essential to ensure accurate measurements for both research and regulatory frameworks.

**Keywords:** Caribbean ciguatoxin, reference materials, Gambierdiscus

Parallel Session 2: Ichthyotoxic HABs

O-006

# *Chrysochromulina leadbeateri* strikes again killing ≥2 mill fish in Northern Norway spring 2025

**Ingunn A. Samdal**[1], Kjersti Liv Eriksen Løvberg[1], Helena Michelsen[2], Tone Rasmussen[2], Christopher O. Miles[1]

(1) Veterinærinstituttet, Ås, Norway
(2) Sea Eco, Harstad, Norway

At the end of April and throughout May 2025, *Chrysochromulina leadbeateri* bloomed in the fjords of Nordland and Troms, in Northern Norway. So far, the bloom has caused an estimated loss of approximately 2 million farmed fish, with major consequences for the affected fish farms, inducing loss of income and layoffs of employees.

C. *leadbeateri* also bloomed in 2019 in the same area and killed 7.5 million farmed fish, with a direct economic loss of € 85 million, and indirect losses estimated between € 210-250 million.

Recently, we reported the finding of a new fish killing toxin named leadbeaterin-1 in the ToxANoWa project. Seawater collected from locations in fjords affected by the C. leadbeateri bloom in 2025, have been investigated using SPE clean-up and LC-HRMS. The new algal toxin leadbeaterin-1 (and several analogues) was detected in samples as small as 13 mL of seawater. The use of passive samplers (SPATTs) was also tested, and the same toxins were detected in these samples.

This confirms that leadbeaterins, the new algal toxins that we found in the algal cultures and samples from 2019, are also present in this year's bloom of C. *leadbeateri.* Thus, leadbeaterins are most likely also involved in the death of fish in fish farms during the 2025 bloom. The detection of Leadbeaterin-1 in water samples indicates potential for direct monitoring of the ichthyotoxins in the water column, which could save time and hence increase the timeframe available for taking mitigation measures to reduce fish mortality in the future.

**Keywords**: Fish kill, *Chrysochromulina leadbeateri*, leadbeaterin-1

**Financing:** Research Council of Norway for the project Toxic microalgae in Norwegian waters - Uncovering fish-killing mechanisms of phytoplankton from Scandinavian waters (ToxANoWa) (project no. 314861/E40).

Parallel Session 2: Ichthyotoxic HABs

O-007

# The cytotoxicity of the haptophyte *Chrysochromulina leadbeateri* towards gill cell lines

**Anita Solhaug**[1], Mathias Fon[1,3], Xinhui Wang[2], An Chen[1], Rosalie Ghesquiere[1], Aaron John Christian Andersen[2], Bruno Garrido[6], Elizabeth M. Mudge[6], Richard A Ingebrigtsen[4,5], Charlotte H. Gotfredsen[2], Per Juel Hansen[7], Silvio Uhlig[1], Christopher O. Miles[1], Thomas O. Larsen[2], Bente Edvardsen[3], Ingunn A. Samdal[1]

(1) Norwegian Veterinary Institute, Ås, Norway
(2) Technical University of Denmark, DTU Bioengineering, Lyngby, Denmark.
(3) University of Oslo, Department of Biosciences, Oslo, Norway.
(4) Cawthron Institute, Nelson, New Zealand.
(5) The Arctic University of Norway, Norwegian College of Fishery Science, Tromsø, Norway.
(6) National Research Counsil Canada, Halifax, Canada.
(7) University of Copenhagen, Marine Biological Section, Helsingør, Denmark.

Fish-killing harmful algal blooms (HABs) threaten fisheries and aquaculture globally. In May and June 2019, the haptophyte *Chrysochromulina leadbeateri* formed the most devastating fish-killing algal bloom ever recorded in Northern Norway. Despite the severe impact of HABs on farmed fish, our understanding of their toxic mechanisms is still limited. Here, we investigated the ichthyotoxicity of *C. leadbeateri* using gill cell lines from rainbow trout (RTgill-W1) and Atlantic salmon (ASG-10).

MeOH extracts of cultivated *C. leadbeateri* strains from the outbreak were highly toxic to both gill cell lines, with EC50-values (Alamar blue viability assay) of $2.9 \times 10^6$ and $3.3 \times 10^6$ algal cells/mL for the RTgill-W1 and the ASG-10 cell lines, respectively. Further work, involving bioassay-guided fractionation, allowed us to isolate a new fish-killing sterolysin, named leadbeaterin-1. Leadbeaterin-1, quantified by qNMR, impaired gill cell viability (Alamar Blue assay) after 4 hours of exposure, with EC50 values of 0.4 ± 0.1 µg/mL, and 0.5 ± 0.1 µg/mL, respectively, for RTgill-W1 and ASG-10. Next, we tested the impact of living *C. leadbeateri* algal cells on the ASG-10 cell line. Growth conditions for both ASG-10 and C. leadbeateri were optimized in order to allow co-exposure. After 4 hours of co-exposure, a slight reduction in ASG-10 cell viability was observed at higher concentrations of C. leadbeateri ($9 \times 10^6$ algal cells/mL). Interestingly, putrescine-treatment C. leadbeateri enhanced its toxicity towards ASG-10 cells.

Our results demonstrate that gill cell lines are a valuable tool to investigate the ichthyotoxicity of harmful algae.

Parallel Session 2: Ichthyotoxic HABs

O-008

# Structure elucidation of Leadbeaterin-1: The main fish-killing toxin from *Chrysochromulina leadbeateri* blooms in Northern Norwegian fjords

**Thomas O. Larsen**[1], Xinhui Wang[2], Inguun Samdal[3], Aaron Andersen[1], Anita Solhaug[3], Bruno Garrido[4], Elizabeth Mudge[4], Mathias Fon[3], Bente Edvardsen[5], Charlotte Gotfredsen[6], Per Juel Hansen[7], Christopher Miles[3]

(1) Technical University of Denmark, Dept. of Biotechnology and Bioengineering, Søltofts Plads, Kgs Lyngby, Denmark
(2) College of Food Science and Engineering, Nanjing University of Finance and Economics, Nanjing 210023, China
(3) Norwegian Veterinary Institute, ÅS, Norway
(4) National Research Council of Canada, Metrology Research Centre, 1411 Oxford Street, Halifax, NS, B3H 3Z1, Canada
(5) University of Oslo, Department of BiosciencesOslo, Norway
(6) Technical University of Denmark, Department of Chemistry, ,DK-2800 Kgs. Lyngby, Denmark
(7) University of Copenhagen, Department of Biology, Marine Biological Section,, Helsingør, Denmark

In May–June 2019, the haptophyte *Chrysochromulina leadbeateri* caused the most damaging fish-killing bloom in northern Europe to date, the species has also caused a massive bloom this year.[1] This study reports the isolation and structural characterization of a new fish-killing sterolysin, leadbeaterin-1 (1) from C. *leadbeateri*, using 1D/2D NMR and LC–HRMS/MS.[2] Although structurally related to karlotoxins, 1 has fewer double bonds, a chlorinated polyol side chain, and occurs as two diastereomeric forms, supporting the proposed ancestral link between Karlodinium and *Chrysochromulina*. Quantitative NMR (qNMR) of 1 established the first genuinely quantitative sterolysin standard, enabling precise toxin measurements. 1 was highly cytotoxic against RTgill-W1 cells ($EC_{50}$0.4 ± 0.1 µg/mL) and ASG-10 cells ($EC_{50}$ 0.5 ± 0.1 µg/mL). Unexpectedly, a high proportion of leadbeaterin-5 (5), identified as a glycolate ester of 1, was detected in freshly extracted cultures. This ester analogue was unstable to hydrolysis, likely converting to 1 during harvest and extraction.

**Keywords:** *Chrysochromulina leadbeateri*, Leadbeaterin-1 fish-killing toxin, Sterolysin

**Financing:** Norwegian Research Council

**Acknowledgments:** Norwegian Research Council

Parallel Session 2: Ichthyotoxic HABs

O-009

# Sterolysin diversity during fish-killing *Chrysochromulina leadbeateri* blooms in northern Norway

**Christopher O. Miles**[1], Kjersti L. E. Løvberg[1], Tone Rasmussen[2], Helena Michelsen[2], Oscar D. Rangel-Huerta[1], Thomas O. Larsen[3], Aaron C. Andersen[3], Bente Edvardsen[4], Mathias Fon[1,4], Xinhui Wang[3], Ingunn A. Samdal[1]

(1) Norwegian Veterinary Institute, Ås, Norway
(2) Sea Eco, Harstad, Norway
(3) Technical University of Denmark, Kgs. Lyngby, Denmark
(4) University of Oslo, Oslo, Norway

A major bloom of the haptophyte *C. leadbeateri* in 2019 killed 7.5 million farmed salmon, corresponding to a direct economic loss of €85 million, and indirect losses of €210–250 million. Very recently, we reported the isolation and structure elucidation by LC-HRMS/MS and NMR spectroscopy of a new fish-killing toxin, named leadbeaterin-1, in the ToxANoWa project. The presence of 5 other putative leadbeaterins was also revealed by LC–HRMS analyses of algal cultures. In May–June 2025, another *C. leadbeateri* bloom occurred in the same region, resulting in the deaths of ca. 2 million farmed salmon.

LC–HRMS/MS analyses of extracts from passive samplers (SPATT disks) and SPE of water from stored and fresh samples from the two blooms, and samples from cultures (including a culture from 1991), were performed, including targeted metabolomics approaches. These revealed a rich array of related compounds, including putative precursors, metabolites, and degradation products. Here, we report an update on findings from these studies and tentative structures for some of the major analogues. The implications of this sterolysin diversity for potential monitoring and early-warning strategies will also be discussed.

**Keywords**: Fish kill, *Chrysochromulina leadbeateri*, leadbeaterin

**Financing:** Research Council of Norway project Toxic microalgae in Norwegian waters - Uncovering fish-killing mechanisms of phytoplankton from Scandinavian waters (ToxANoWa) (project no. 314861/E40).

Parallel Session 2: Ichthyotoxic HABs

O-010

# From morphology to toxicity: First characterization of the fish-killing *Fibrocapsa japonica* (Raphidophyceae) from Argentina

**Delfina Aguiar Juárez**[1], Inés Sunesen[1], Ana Flores-Leñero[2], Luis Norambuena[3], Bernd Krock[4], Gonzalo Fuenzalida[5], Cecilia Gonano[1], Jorge I. Mardones[3,6]

(1) Universidad Nacional de La Plata, División Ficología, Facultad de Ciencias Naturales y Museo, Paseo del Bosque s/n, La Plata, Argentina
(2) Scottish Marine Institute, Scottish Association for Marine Science, Argyll, PA37 1QA, Oban, United Kingdom
(3) Instituto de Fomento Pesquero, Centro de Estudios de Algas Nocivas, Padre Harter 574, Puerto Montt, Chile
(4) Alfred Wegener Institut-Helmholtz Zentrum für Polar- und Meeresforschung, Bremerhaven 27570, Germany
(5) Universidad Santo Tomas, Departamento de Ciencias Básicas, Facultad de Ciencias, Ramon Picarte 1160, Valdivia, Chile
(6) Universidad Bernardo O´Higgins, Centro de Investigación en Recursos Naturales y Sustentabilidad, Santiago, Chile

*Fibrocapsa japonica* (Raphidophyceae) is a harmful algal species known for its ichthyotoxic effects and widespread distribution in coastal waters worldwide. While raphidophytes have been extensively studied in other regions, their diversity, distribution, and toxic potential remain unexplored in Argentina. This study presents the first characterization of *F. japonica* isolated from Argentinean coastal waters, consisting in five strains, analyzed by light (LM) and transmission electron microscopy (TEM), LSU rDNA-based phylogenetic analysis, pigment profiling via HPLC, cytotoxicity assays with RTgill-W1 cell lines under both intracellular and extracellular treatments, and brevetoxin screening by LC-MS/MS. Morphological observations revealed characteristic raphidophyte features and minor variations in cell size among strains. Phylogenetic analysis confirmed the clustering of most strains within the *F. japonica* clade (99% bootstrap). Pigment profiles were dominated by chlorophyll-a and fucoxanthin, as previously reported for this species. Cytotoxicity assays, performed on two strains, showed that both intra- and extracellular compounds were toxic to RTgill-W1 cells. The LPCc049 strain exhibited the highest toxicity, reducing cell viability down to 53% in the extracellular exposure at a concentration of $6.1\times10^{3}$ cells $ml^{-1}$. Despite this, the analysis by LC-MS7MS revealed the absence of brevetoxins (PbTx-1, -2, -3, -6). This study provides the first confirmed record and genetic identification of F. japonica in Argentina, as well as the first evidence of cytotoxicity in South American strains, offering novel insights for coastal monitoring and fisheries management in the region.

**Keywords:** Raphidophyceae, Ichthyotoxicity, Argentinean coastal waters

**Financing**: Universidad Nacional de La Plata 11/N 987; CONICET PIP 1920; Under-Secretariat for Fisheries and Aquacultureof Chile (SUBPESCA)

Parallel Session 2: Ichthyotoxic HABs

O-011

# Fish mortality event associated with harmful algal bloom in a Northern Tunisian Lagoon: A multifaceted crisis

**Afef Fathalli**[1], Nadia Besbes[4], Aida Ben Mansour[3], Bechir Bejaoui[2]

(1) National Institute of Marine Sciences and Technologies, Marine Environment Laboratory, Port de pêche La Goulette, Tunisia.
(2) National Institute of Marine Sciences and Technologies, Marine Environment Laboratory, 28 Street 2 March 1934 Carthage Salammbô 2025 Tunis, Tunisia.
(3) National Center for Nuclear Sciences and Technologies, Sidi Thabet, Tunisia.
(4) National Institute of Marine Sciences and Technologies, B3Aqua, Port de pêche La Goulette, Tunisia.

Bizerte Lagoon is also one of the most important aquaculture areas in Tunisia, recognized for its fisheries and shellfish producing activities such as mussels "*Mytilus galloprovincialis*", clams "*Ruditapes decussates*" and oysters "*Crassostrea gigas*" production. However, this economic and ecological resource is directly influenced by environmental factors, which are currently governed by climate change and the continuously deteriorating water quality due to land-based urban and agricultural inputs of chemical contaminants and nutrients. This can pose health risks to consumers, zoonotic threats to marine biodiversity, and result in significant economic losses.

In October 2024, a mass mortality event affecting fish and other marine organisms, including eels and cuttlefish, was observed in the lagoon. This event was correlated with a massive bloom of *Karenia* sp., which persisted for over three months. The bloom, reaching concentrations of 92 million cells per liter, caused severe hypoxic conditions throughout the lagoon. Moreover, the toxic analysis using Liquid Chromatography Tandem Mass Spectrometry (LC-MS/MS) reveals the detection of Gymnodimine A.

The Bizerte Lagoon, a major aquaculture hub in Tunisia, is increasingly vulnerable to the impacts of climate change and anthropogenic pollution. This event resulted in significant marine mortality and the detection of Gymnodimine A, raising serious ecological and public health concerns. It highlights the urgent need for strengthened environmental monitoring, the inclusion of currently unregulated toxins such as Gymnodimine A in national legislation, and the establishment or revision of health alert thresholds for harmful algal blooms.

**Keywords:** *Karenia* sp., Tunisian Lagoon, Fish mortality

Parallel Session 3: Microbiomes, Biological & Chemical Interactions

O-012

# Phenology of the toxic dinoflagellate *Dinophysis* along European coasts: Long-term observation networks reveal different phenoregions and confirm the key role of prey availability

**Victor Pochic**[1,2], Mathilde Schapira[2], Bede Davies[1], Maud Martinez Almoyna[3], Guillaume Charria[3], Marc Sourisseau[4], Elise Evrard[5], Paula Cohen[5], Thomas Lacour[5], Bruno Jesus[1], Pierre Gernez[1]

(1) ISOMER, UR2160, Nantes Université, F-44000 Nantes, France
(2) Ifremer COAST, F-44300 Nantes, France
(3) Ifremer LOPS, F-29280 Plouzané, France
(4) Ifremer DYNECO PELAGOS, F-29280 Plouzané, France
(5) Ifremer PHYTOX PHYSALG, F-44300 Nantes, France

The planktonic dinoflagellate *Dinophysis* is a major source of concern in various coastal regions worldwide, where it regularly contaminates edible shellfish with diarrhetic toxins. *Dinophysis* is also a peculiar biological model that relies on kleptoplastidy for photosynthetic growth.

Using data from decades-long observation networks, we studied the phenology of *Dinophysis* along the European Atlantic coastline. Based on cell counts from systematic microscope observation, we used Generalized Additive Models to model the seasonal dynamics of Dinophysis and, when data was available, of its prey *Mesodinium rubrum*.

We identified clear, region-specific seasonal patterns in *Dinophysis* phenology. In two distinct regions, periods of *Dinophysis* accumulation coincide with the presence of its prey in high concentration. This aligns with the detection of *Mesodinium* blooms on satellite images. This solidifies the notion that prey availability is a key factor in the onset of *Dinophysis* blooms.

Finally, we focused on periods of low-to-no growth, when *Dinophysis* is rarely observed in situ. Starvation experiments on laboratory cultures of Dinophysis acuminata, combined with measurements of environmental DNA in the field, helped us draw hypotheses on *Dinophysis* survival strategies during the unfavorable winter period. In the absence of prey, *Dinophysis* rapidly reduced its vegetative growth and photosynthetic activity. Nonetheless, *Dinophysis* was capable of surviving periods of starvation longer than 2 months and successfully resumed growth upon the return of its prey, as documented previously by other authors. Overall, our work offers new knowledge about the ecology of an elusive toxic dinoflagellate.

**Keywords:** *Dinophysis*, Phenology, *Mesodinium*

**Financing**: Funded by PPR project RiOMar (reference ANR 22 POCE 0006), Centre National d'Etudes Spatiales (CNES).

**Acknowledgments:** The Société Phycologique de France (SPF) is acknowledge for a financial support to V. Pochic.

Parallel Session 3: Microbiomes, Biological & Chemical Interactions

O-013

# The functional diversity of bacterial microbiota associated with toxigenic *Prorocentrum* species

**Lorena María Durán Riveroll**[1], Miguel A. Martínez-Mercado[2], Allan Douglas Cembella[3], Edna Sánchez-Castrejón[2], Anaid Saavedra-Flores[2], Clara E. Galindo-Sánchez[2]

(1) SECIHTI-Departamento de Biotecnología Marina, Centro de Investigación Científica y Educación Superior de Ensenada B.C., Ensenada, Mexico
(2) Departamento de Biotecnología Marina, Centro de Investigación Científica y Educación Superior de Ensenada B.C., Ensenada, Mexico
(3) Department of Ecological Chemistry, Alfred-Wegener Institut, Helmholtz-Zentrum für Polar-und Meeresforschung, Bremerhaven, Germany

Interactions between bacterial microbiota and epibenthic dinoflagellates such as *Prorocentrum* may influence the initiation, toxigenicity, and persistence of benthic harmful algal blooms (bHABs). These interactions likely involve complex chemical exchanges, including metabolites, toxins, and undefined bioactive compounds. This study characterized the bacterial diversity and core microbiota associated with 11 strains of three epibenthic Prorocentrum species from geographically distinct Mexican coastal waters. Using 16S rRNA gene (V3-V4) sequencing of monoclonal cultures, we identified 13 bacterial classes, with Alphaproteobacteria, Gammaproteobacteria, and Bacteroidia consistently dominant. Bacterial community structure varied significantly by dinoflagellate geographical origin but not between free-living (culture medium) and direct host-associated fractions. Twelve core bacterial taxa were identified, including *Algiphilus, Cohaesibacter, Labrenzia, Marinobacter*, and members of the Rhodobacteraceae. The bacterial profiles suggest mutualistic or commensal relationships with Prorocentrum. While these core members likely contribute to both primary and secondary metabolic functions, no direct link to dinoflagellate toxigenicity was identified. Further research on bacterial-dinoflagellate gene functions and interactions is essential to elucidate their roles in toxigenesis and bHAB dynamics.

**Keywords:** Benthic dinoflagellates, microbiome, phycosphere

**Financing:** CONACyT (now SECIHTI) Basic Science Project A-1S-8616 and Cátedras CONACyT, project 1009.

**Acknowledgments:** Yuri Okolodkov (U. Veracruzana), Manuel Victoria-Muguira. Functional Genomics Laboratory at CICESE.

Parallel Session 3: Microbiomes, Biological & Chemical Interactions

O-014

# A systematic quantitative review of the effects of PST toxins from *Alexandrium* on the copepod *Acartia*

**Aldo Barreiro**[1,5], Máximo Frangópulos Rivera[2,3,4], Vitor Vasconcelos[1,5]

(1) Centro Interdsiciplinar de Investigação Marinha e Ambiental (CIIMAR), Terminal de Cruzeiros do Porto de Leixões, Matosinhos, Portugal.
(2) Centro de Investigación GAIA Antártica (CIGA), Universidad de Magallanes, Avenida Bulnes 01855, Punta Arenas, Chile.
(3) Cape Horn International Center (CHIC), Puerto Williams, Chile.
(4) Millenium Institute Biodiversity of Antarctic and Subantarctic Ecosystems (BASE), Las Palmeras 3425, CP 780003, Santiago de Chile, Chile.
(5) Universidade do Porto, Faculty of Sciences, Rua do Campo Alegre, Porto, Portuga.l

The study of interactions between copepods of the genus *Acartia*, as one of the major components of marine mesozooplankton worldwide, and toxic dinoflagellates of the genus *Alexandrium*, as major producers of HABs associated with PST toxins, has been an important topic in recent decades. However, the results of the various studies have been contradictory. Recently, an evolutionary adaptation mechanism leading to improved tolerance of *Alexandrium* toxins by *Acartia* has been reported. In the present work, we tried to find a common framework that could explain all the results found for the interaction between *Alexandrium* and *Acartia* in terms of copepod reproductive responses. To this end, we collected data on feeding and reproductive parameters from all studies in which these two organisms were used. With these data, we conducted a systematic quantitative review consisting of general or generalized linear mixed models that weighted the data to account for variation found across studies. Our main findings were that the PST toxins do not have a clear inhibitory effect on *Acartia* egg production, but have a biphasic effect on hatching success that is inhibitory above a certain threshold. Our results also support the existence of the above-mentioned evolutionary adaptation mechanism across the Acartia populations studied.

**Keywords:** *Alexandrium*, *Acartia*, Review

**Financing:** The present work was supported by contract 2024_069_IA_TENURE_1 from FCT (Portugal) to ABF and by grant MEC80190094 from CONICYT- ANID (Chile) to MFR and ABF.

Parallel Session 3: Microbiomes, Biological & Chemical Interactions

O-015

# Nitrogen acquisition from co-occurring phytoplankton by the dinoflagellate *Alexandrium ostenfeldii*

**Elin Lindehoff**[1], Catherine Legrand[1], Anke Kremp[2]

(1) Linnaeus University, Biology and Environmental Science, Ecology and Evolution in Microbial Model Systems (EEMiS), SE-392 31, Kalmar, Sweden
(2) Leibniz Institute for Baltic Sea Research Warnemünde, Biological Oceanography, Seestraße 15, 18119, Rostock, Germany

The toxic dinoflagellate *Alexandrium ostenfeldii* forms dense blooms in shallow waters of the coastal Baltic Sea proper during late summer, a period marked by low concentrations of inorganic nitrogen (DIN) and elevated levels of dissolved organic nitrogen (DON). Its potential mixotrophic behaviour, i.e the ability to utilize DON, may contribute to the development of these blooms. In this study, phytoplankton-derived DON was generated from co-occurring cryptophyte *Rhinomonas nottbecki*, which was pre-cultivated with $^{15}NO_3$ and subsequently lysed by allelochemicals released by A. ostenfeldii. Uptake of $^{15}N$- labelled DON by *A. ostenfeldii* was visualized using second iron mass spectrometry (SIMS) and quantified in bulk using iron mass spectrometry (IRMS) across strain exhibiting varying allelopathic activity ($EC_{50}$). This approach enabled the investigation of a potential correlation between allelopathic activity, and the uptake of phytoplankton derived DON. Our findings support the concept that dense blooms of A. *ostenfeldii utilize* DON as N source and that its allelopathic activity facilitates N uptake.

**Keywords**: *Alexandrium ostenfeldii*, mixotrophy, 15N uptake

**Financing:** Research council FORMAS, SFO EcoChange, MSCA-IF EU commission

**Acknowledgments:** Emma Svahn (Linnaeus University) Jaqueline Jerney (Finnish Environment Institute).

Parallel Session 3: Microbiomes, Biological & Chemical Interactions

O-016

# How toxins and allelochemicals can shape phytoplankton communities, and example with Baltic *Synechococcus*

**Zofia Konarzewska**[1], Aldo Barreiro Felpeto[2,3], Sylwia Śliwińska-Wilczewska[1], Adam Latała[1], Vitor Vasconcelos[2,3]

(1) University of Gdańsk, Division of Marine Ecosystems Functioning, Oceanography and Geography, Av. Piłsudskiego 46, 81-378, Gdynia, Poland.
(2) CIIMAR, Centro Interdisciplinar de Investigação Marinha e Ambiental, Terminal de cruzeiros do porto de Leixões. Av. General Norton de Matos, s/n. 4450-208, Matosinhos, Portugal.
(3) Porto University, Department of Biology, Faculty of Sciences, Rua do Campo Alegre, 4069-007, Porto, Portugal.

Allelochemicals and toxins produced by phytoplankton can play a crucial role in shaping community structure by altering species interactions beyond classical resource competition. These compounds may inhibit or stimulate the growth of coexisting organisms, thereby influencing succession patterns, species dominance, and overall biodiversity. Although the ecological significance of such chemically driven interactions has been hypothesized for decades, experimental evidence—especially in complex aquatic communities—remains limited.

Seasonal surveys in the Baltic Sea revealed that *Synechococcus* is a consistent and abundant component of the picophytoplankton community, with distinct temporal patterns among its phenotypes. All three major phenotypes, distinguished by their specific pigment compositions, were present throughout the year, with the highest abundances typically recorded in spring and autumn.
All three *Synechococcus* phenotypes were found to produce the hepatotoxin microcystin-LR and a diverse spectrum of allelochemicals, including oximes, eicosane, and silanediol, with each strain exhibiting a distinct biochemical profile.

In simplified laboratory communities, we demonstrated that the allelopathic effects enabled stable coexistence through in-phase oscillations of population abundances. This supports the idea that chemical interactions can influence species diversity under single-nutrient limitation.

Moreover, in more complex phytoplankton assemblages from the Baltic, we found that intermediate allelopathy levels of *Synechococcus* led to significantly higher species diversity, while both low and high levels reduced it. These results highlight allelopathy as a key structuring force in phytoplankton communities and suggest its growing ecological relevance under future environmental change.

**Keywords:** *Synechococcus*, allelopathy, Baltic Sea

Parallel Session 3: Microbiomes, Biological & Chemical Interactions

O-017

# Exolymers and mucus in harmful algae: Composition, properties, and roles

**Ian R. Jenkinson[4,13],** Alenka Malej[1], Elisa Berdalet[14], Florence Elias[15], Hai-Bing Ding[2], Marina Ribas-Ribas[5], Igor Emri[21], Janina Rahlff[8,9], Magdalena Mrokowska[22], N.M. Aiswarya[12,17], Oscar Guadayol[18], Oliver Wurl[5], Rodrigo Gonçalves[10,11], Santosh Karn[19,20], Laurent Seuront[16], Jun Sun[6], Tim Wyatt[7], Wei-Chun Chin[3], Wu-Chang Zhang[13]

(1) Institut za Biologijo Ljubliana, Marine Biology Statoion, Piran, Slovenia
(2) Ocean University of China, Key Laboratory of Marine Chemsistry, Qingdao, China
(3) University of California, Department of Bioengineering, merced CA, USA
(4) Agency for Consultation and Research in Oceanography,, La Roche Canillac, France
(5) Carl von Ossietzky University Oldenburg,, Institute for Marine Chemistry and Biology,, Wilhelmshaven, Germany
(6) China University of Geosciences (Wuhan),, College of Marine Science and.Technology,, Wuhan, Chna
(7) Borreiros, Gondomar, Pntevedra Galciai, Spain
(8) Friedrich Schiller Universit, Aero-Aquatic Virus Research Group, Faculty of Mathematics and Computer Science, Jena, Germany
(9) Linnaeus Universityu, Centre for Ecology and Evolution in Microbial Model Systems (EEMiS), Biology and Environmental Science, Kalmar, Sweden
(10) Universidad de Granada, Departamento de Ecologia, Granada, Spain
(11) CONICET at CESUMAR, Puerto Madryn, Argentina
(12) Sardar Bhagwan Singh University, Department of Biochemistry and Biotechnology, Balawala Dehradun,, Uttarakhand, India
(13) Institute of Oceanology Chinese Academy of Sciernce, State Key laboratory of Marine Ecology and Environmental Science, Qingdao, China
(14) institute of Marine Sciences (icm-csic), Barcelona Catalonia, Spain
(15) Université Paris Diderot and CNRS, Laboratoire des Systèmes Compexes, Paris, France
(16) CNRS (UMR 8187), Laboratoire d'Océanologie et de Géoscience, Wimereux, France
(17) University of Tokyo, Department of Physics, Tokyo, Japan
(18) Mediterranean Institute of Advanced Studies, IMEDEA (UIB-C SIC), Esp)orles, Spain
(19) Sardar Bagwan Singh University, Department of Biochemistry and Biotechnology, Balawala Dehradun, Uttarakhand, India
(20) Institute of Oceanology Chinese Academy of Sciences, Key Laboratory of ERnvironmental Corrosion and Biofouling, Qingdao, China
(21) Universty of Ljubljana, Department of Mechanics, Polymers and Composites, Ljubljana, Slovenia
(22) Polish Academy of Sciences, Institute of Geophysics, Warsaw, Poland

For millennia, mariners have observed coloured water and the calming of ripples and waves by oil. In 1774, Benjamin Franklin showed that ~5 mL of oil could suppress ripples across ~10,000 m². By the 1980s, natural surface slicks were found to be enriched in dissolved organic matter (DOM) and more viscous than surrounding waters. Viscosity and elasticity were also detected in the surface microlayer (SML). DOM in the SML can inhibit air–sea gas exchange, including that of $CO_2$ and $CH_4$, with implications for climate models and toxic aerosols (e.g., Karenia, Ostreopsis).

In freshwater, surface cyanobacterial scums are common, yet their physical properties remain largely unmeasured. In three dimensions, rare "mucus events" can smother marine life or clog fishing gear. Rheological studies in the 1980s revealed that some harmful algal cultures are elastic and up to 400 times more viscous than culture medium, suggesting these algae engineer local water flow via exopolymers. Viscosity is also generally positively correlated with phytoplankton abundance.

Disulphide linkages (DSLs) contribute both to gelling in harmful algal bloom (HAB) mucus and to the production of reactive oxygen, indicating that DSL-rich mucus can be a toxic agent or co-agent. Conversely, mucus secreted by affected organisms may serve as a protective shield. Some HAB dinoflagellates also produce sticky, toxic mucus to trap and ingest other protists. Looking ahead, rheological tools—particularly at sub-10 µm scales—offer new ways to study mucus and surface properties as engineered traits in harmful algae.

**Keywords:** Exoplymers, Mucus, Rheology

**Financing:** The present review received no external funding.

**Acknowledgments**: IRJ thanks the Awards Committee of the International Society for the Study of Harmful Algae for a Retired Scientists Award to attend the ICHA.

Parallel Session 4: Ciguatera and Benthic HABs

O-018

# The emerging threat of Ciguatera in Brazil

**Silvia Nascimento**[1], Geovanna Borsato[1], Fabiano Salgueiro[1], Karoline Oliveira[1], Janaína Menezes[2], Nara Melo[3]

(1) Universidade Federal do Estado do Rio de Janeiro (UNIRIO), Av. Pasteur, 458, Rio de Janeiro, Brasil
(2) Ministério da Saúde, Departamento de Doenças Transmissíveis, Secretaria de Vigilância em Saúde e Ambiente, Brasília, Brasil
(3) Secretaria Estadual de Saúde de Pernambuco, Gerência de Vigilância das Doenças de Transmissão Hídrica e Alimentar, Recife, Brazil

Brazil was considered a ciguatera free area until March 2022, when the first suspected cases were reported at the Fernando de Noronha Archipelago (FN), located 345 km away from the Brazilian coast. Benthic dinoflagellate species composition and abundance have been studied at FN previously, since 2017, at three sites, on yearly scientific expeditions to this oceanic site. Mean *Gambierdiscus* abundance between 2017-2023 varied from 0 to 465 cells $FW^{-1}$macroalgae, with a peak of 703 cells $g^{-1}$FW. eDNA analysis revealed the presence of *Gambierdiscus belizeanus*, *G. carpenteri*, *G. excentricus*, *G. silvae* and G. ribotype 2 in field samples collected from FN in 2018. Between 2022 and 2025, 190 ciguatera cases (isolated and outbreaks) were recorded at FN. The intoxication was characterized by initial gastrointestinal symptoms (nausea, vomiting, diarrhea, abdominal pain) that were followed by cardiovascular signs (low blood pressure and slow heartbeat) and neurological symptoms, that included burning sensation, itching, changes in thermal perception and tingling of the tongue, lips, hands and feet. Motor symptoms such as pain in the joints and muscles, muscle weakness and asthenia were also reported. The main species of fish involved in the intoxications were *Caranx bartholomaei* and *Sphyraena barracuda*. Benthic dinoflagellates abundance and epidemiological data of ciguatera at FN will be presented. Besides the effects on human health, ciguatera has led to socio-economic impacts on fishermen income and compromised food safety, impacting the main protein source of this insular community.

**Keywords:** benthic harmful algae, ciguatoxins, One Health

**Financing:** Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) for the financial support to the project PELD-ILOC to C.E.L. Ferreira (441241/2016-6).

Parallel Session 4: Ciguatera and Benthic HABs

O-019

# Spatio-temporal dynamics of *Gambierdiscus* in the Balearic Islands

Sandra Gimeno-Monforte[1], Diana Dorado[1], Carles Alcaraz[1], Luisa Mangialajo[2], María Rey[1], Alba Garriga-Costa[1], **Jorge Diogène[1]**

(1) Institute of Agrifood Research and Technology (IRTA), Marine and Continental Waters, Carretera del Poble Nou, km 5.5, La Ràpita, Spain
(2) Université Côte d'Azur, CNRS, ECOMERS, Parc Valrose 28, Avenue Valrose, 06108 Nice, France

Driven by climate change and human activities, rising *Gambierdiscus* populations increase ciguatera poisoning risk from contaminated seafood. Despite *Gambierdiscus* being present in the temperate Balearic Islands since 2016, the understanding of its population dynamics and ciguatera potential in the area remains limited. This research modelled *Gambierdiscus* abundance and identified key drivers in the Balearic Islands using machine learning and feature selection. A holistic dataset from 2020-2024 integrated field, laboratory, and satellite data. Spatial analysis involved sampling across the Balearic Islands during autumn, while temporal analysis included year-round sampling at three Mallorca locations. Random Forest algorithms were applied to predict abundance and reveal influencing factors. A seasonal Random Forest model, combining field and open-source data, achieved the highest performance (Pearson correlation = 0.8), accurately capturing seasonal variability. Temperature, water movement, light, and dissolved oxygen were identified as primary environmental drivers. Gambierdiscus was present year-round with peaks occurring consistently in late September/early October, lagging behind peak temperatures and light. A spatial Random Forest model using open-source data performed strongly (Pearson correlation = 0.83), with phosphate and latitude explaining 42% of variability. Spatial abundance correlated with sampling location and macrophyte complexity; Digenea simplex and *Halopteris* sp. hosted higher densities, and the highest abundance was in Formentera (3113.02 cells·g w.w. macrophyte$^{-1}$). This study confirms *Gambierdiscus's* persistent, year-round presence across the Balearic Islands, demonstrating its adaptation to temperate conditions. The findings underscore the complex interplay of environmental factors in shaping abundance and highlight machine learning's potential for predicting and understanding regional harmful algal blooms.

**Keywords:** *Gambierdiscus*, West Mediterranean Sea, Random Forest

**Financing:** This work was founded by the EFSA through EUROCIGUA (GP/EFSA/AFSCO/2015/03) and EUROCIGUA 2 (GP/EFSA/KNOW/2022/03), and MICIN and EAI through the CIGUARISK (PID2019-108781RR-C21) and CIGUAADAPT (PID2022-137174OR-C21).

**Acknowledgments:** SGM acknowledges her PhD contract to the Ministry of Science, Innovation and Universities and the State Research Agency (MCINU/AEI) (PRE2020-096800).

Parallel Session 4: Ciguatera and Benthic HABs

O-020

# Comparative transcriptomic analysis of polyketide synthases genes from *Gambierdiscus polynesiensis* and *Gambierdiscus holmesii* to identify candidate genes potentially involved in ciguatoxin biosynthesis

**Amna Ashfaq[1],** Greta Gaiani[1], Kirsty F. Smith[2], Sam J. Murray[2], Shauna A. Murray[1]

(1) University of Technology Sydney, School of Life Sciences, Faculty of Science, PO Box 123 Broadway, Sydney, NSW, 2007, Australia
(2) Cawthron Institute, Molecular and Algal Ecology Group, 98 Halifax Street East, Nelson 7010, New Zealand

Ciguatera Poisoning (CP) is the most common non-bacterial seafood-borne disease affecting tropical/sub-tropical regional communities. CP is caused by consuming seafood contaminated with ciguatoxins (CTX) which are exclusively produced by dinoflagellates of genera *Gambierdiscus* and *Fukuyoa*. *Gambierdiscus* species are endemic to tropical and warm-temperate waters and are increasingly expanding to new areas due to changes in sea surface temperatures, nutrient loading, eutrophication and habitat disturbance. These environmental changes may affect CTX production in Gambierdiscus species, but there is lack of knowledge regarding the genetic regulation of CTX production by species of *Gambierdiscus*. Commonly, CTX are produced by polyketide synthases (PKS) enzymes. This study aimed to examine PKS related genes within two *Gambierdiscus* species, the high ciguatoxin producing *G. polynesiensis* and the non-ciguatoxin producing *G. holmesii* by applying de novo transcriptomics. A highly conserved region within identified PKS enzymes was also phylogenetically compared to bacteria, fungi and other dinoflagellates. Furthermore, the expression of genetic markers associated with CTX production in *Gambierdiscus* species under two different growth conditions, ambient nutrients and nitrogen enriched, were identified. Here, by utilizing transcriptomic analysis, differential gene expression of PKS genes in *G. polynesiensis* and *G. holmesii* were compared. The results from this study will help identify abiotic regulatory factors for toxin biosynthesis in G. polynesiensis. This study provides valuable knowledge of regulatory factors and genetic origin of CTX for future research to understand the complex mechanism of toxin production in *Gambierdiscus* species, which is essential for developing novel tools for characterizing CP risk in marine food webs.

**Keywords:** Ciguatoxins, de novo transcriptome, differential gene expression

**Financing:** The ARC project is supported and funded by Australian Research Council Linkage Project (PROJECT ID: LP180100001) and University of Technology Sydney.

Parallel Session 4: Ciguatera and Benthic HABs

O-021

# Sampling *Ostreopsis* cf. ovata along the Campania coastline (Italy). An unprecedented combination of sample preparation and LC-MS to mitigate ovatoxin-related health risks

**Chiara Melchiorre**[1,2], Valeria Tegola[1], Martina Carelli[1], Silvia Casabianca[3], Samuela Capellacci[3], Antonella Penna[3], Carmela Dell'Aversano[1]

(1) University of Naples Federico II, Department of Pharmacy, Via D. Montesano 49, Naples, Italy
(2) National Biodiversity Future Center, Palermo, Italy
(3) University of Urbino, Department of Biomolecular Sciences, Campus E. Mattei, Via Ca le Suore 2/4, 61029, Urbino (PU), Italy

*Ostreopsis* cf. *ovata*, a marine dinoflagellate native to tropical and subtropical regions, has gained increasing attention from scientists and public health authorities due to its expanding distribution and involvement in benthic harmful algal blooms. This species produces potent neurotoxins known as ovatoxins (OVTXs), with OVTX-a being the predominant variant in Mediterranean strains. Since the late 1990s, OVTXs have been associated with toxic outbreaks causing dermatitis and conjunctivitis through direct contact with contaminated seawater, and respiratory issues from inhaling aerosolized toxins. Their possible accumulation in seafood also poses significant health risks.

In Italy, *Ostreopsis* monitoring has been regulated since 2010, with seasonal occurrences documented in several regions, including Campania. Surveillance agencies track *O.* cf. *ovata* in seawater and notify local health authorities when concentrations exceed 10,000 cells/L. However, OVTX levels are not directly measured during this alert phase, limiting the ability to assess real health risks. Risk assessment remains incomplete due to insufficient data on toxin distribution in the environment and food chain, compounded by the lack of reference materials and standardized analytical methods.
This study presents results from a small-scale sampling campaign conducted in two Campanian marine protected areas under the BlueShellfish — HORIZON-MSCA-2021-SE-01 project. Six seaweed samples were collected from routine monitoring sites in waters classified as safe for bathing. Samples underwent an innovative treatment—intact and oxidative cleavage—prior to LC-MS analysis. OVTXs were quantified even at low cell densities, highlighting the urgent need for improved monitoring strategies to better protect public health.

**Keywords:** Ovatoxins, LC-MS, oxidative cleavage

**Financing:** European Union – NextGenerationEU. Project code CN_00000033, CUP E63C22000990007, Project title “National Biodiversity Future Center - NBFC”.BlueShellfish — HORIZON-MSCA-2021-SE-01.

Parallel Session 4: Ciguatera and Benthic HABs

O-022

# A study on the temporal dynamics and environmental drivers of harmful marine microalgae in Mauritius

**Manisha Curpen Mahadoo**[1], Sundev Parboteeah[1], Manoj Fakoo[1]

(1) Ministry of Agro-Industry, Food Security, Blue Economy and Fisheries, Fisheries Division, Albion Fisheries Research Centre, Petite Riviere, Albion, Mauritius

This study examined the diversity and temporal dynamics of harmful marine microalgal species at 10 established sites around the lagoons of Mauritius from 2014 to 2024. As per the established protocol, macroalgae samples were collected approximately 5 m from shore, processed within 24–48 hours, and shaken in seawater to dislodge epiphytic dinoflagellates. The resulting mixture was sieved through decreasing mesh sizes (150–20 µm) and fixed with Lugol's solution. Species identification and enumeration were performed using Sedgewick-Rafter chambers and inverted light microscopy. The most commonly occurring species of harmful marine microalgae were Amphidinium sp., Coolia sp., *Gambierdiscus sp., Ostreopsis sp., Prorocentrum* sp., and *Synophysis* sp.

The most prominent species were *Prorocentrum* sp. and *Ostreopsis* sp. A moderate positive correlation (r = 0.340) between those 2 species was more accentuated in monthly datasets, indicating concurrent responses to short-term environmental variations. Coolia sp. demonstrated a strong monthly association (r = 0.722) with other species, highlighting the role of seasonal and environmental factors in modulating community structure. The Kruskal-Wallis Test indicated that seasonality had an effect on microalgal density around Mauritius.

The south-east of Mauritius consistently showed the highest microalgal abundance. It is hypothesized that the influence of South East Trade Winds might have enhanced water mixing and movement of nutrients, leading to more favorable conditions for proliferation. Analysis of interspecific correlations revealed generally weak to moderate relationships. However, monthly and seasonal evaluations disclosed stronger pairwise associations, implying that environmental factors such as temperature, salinity, and nutrient availability considerably influence community dynamics.

**Keywords:** Harmful marine microalgae

**Financing:** Mauritius being a member state of the Project ME-INT7022-2406068, has requested IAEA for funding for participation to the ICHA 2025-still under process.

**Acknowledgments:** Mr. Fakoo for his insightful guidance and the team of the Laboratories Division for their collaborative spirit.

Parallel Session 4: Ciguatera and Benthic HABs

O-023

# SURVEY-TOX – A Pilot study on the monitoring of ciguatera poisoning and other emerging toxin risks for safer lagoon fisheries

**Hélène Taiana Darius[1],** Alexandra Grand[2], Kévin Henry[1], Taina Revel[1], André Ung[1], Jérôme Viallon[1], Mélanie Roue[3], Manoella Sibat[4], Vaihiti Teanininuraitemoana[5], Julien Rouxel[5], Serge Andrefouet[6], Mireille Chinain[1]

(1) Institut Louis Malardé (ILM), Laboratory of Marine Biotoxins, UMR 241-SECOPOL (IFREMER, ILM, IRD, UPF), P.O. Box 30, 98713 Papeete, Tahiti, French Polynesia
(2) Direction des Ressources Marines, Cellule Innovation et Valorisation, P.O. Box 20 98713 Papeete, Tahiti, French Polynesia
(3) Institut de Recherche pour le Développement (IRD), UMR 241-SECOPOL (IFREMER, ILM, IRD, UPF), P.O. Box 6570, 98702 Faa'a, Tahiti, French Polynesia
(4) Institut Français de la Mer (IFREMER), ODE/PHYTOX-METALG, Rue de l'île d'Yeu, F-44300 Nantes, France
(5) Ifremer, ILM, IRD, UPF, UMR 241-SECOPOL, P.O. Box 49, 98725 Vairao, Tahiti, French Polynesia
(6) Institut de Recherche pour le Développement (IRD), UMR ENTROPIE (IRD, Université de La Réunion, CNRS, IFREMER, Université de la Nouvelle-Calédonie), C/O Ifremer/Centre Océanographique du Pacifique, 98 725 Vairao, Tahiti, French Polynesia

In French Polynesia (FP, ~280,000 inhabitants), fish play an important role in the population's diet. However, lagoon fisheries and market-based economies are greatly affected by ciguatera poisoning (CP). Over the past five years, between 153 and 213 cases have been officially reported annually, although these statistics may represent only 20% of actual cases. The Arutua atoll, in the Tuamotu Archipelago, is one of the main fish providers, exporting approximately 80 tons annually to Tahiti, the main FP Island (Society Archipelago). In this context, the primary objective of the SURVEY-TOX program (2023-2026) is to provide an assessment of the risks associated with the consumption of reef fish originating from Arutua by establishing a CP risk map of the local population's main fishing grounds.

This presentation details the strategy and tools used to select the survey sites, to monitor CP organisms and ciguatoxin prevalence in two CP-prone fish species, i.e., the shortnose unicornfish and the marbled grouper, and to characterize the survey sites' habitats.

SURVEY-TOX's strength lies in its duration (three years), with two to three sampling expeditions per year to collect long-term datasets. Specifically, this program will measure fluctuations in benthic HAB species abundances and toxin levels in CP-prone fishes and the water column, across seasons and sites exposed to varying environmental and/or anthropogenic impacts (e.g., village, pearl farming). Additionally, SURVEY-TOX will evaluate whether regular monitoring of toxigenic microalgae and related toxins can provide an effective early warning system of toxin accumulation in fish, to reduce poisoning risks among local populations.

**Keywords:** Ciguatera poisoning, risk assessment, lagoon fish trade

**Financing:** This program is funded by the Institut Louis Malardé and the Direction of Marine Resources of French Polynesia.

**Acknowledgments:** We would like to thank the town council, the population, and the fishermen of the Arutua atoll for their support and assistance during field missions.

Parallel Session 5: Ichthyotoxic HABs

O-024

# Understanding the fish-killing mechanisms of harmful algal blooms (HABs) from multifaceted perspectives: Insights from observations of multiple dinoflagellate species

**Lixia Shang**[1]

(1) CAS Key Laboratory of Marine Ecology and Environmental Sciences, Institute of Oceanology, Chinese Academy of Sciences, Qingdao, 266071, China.

Harmful Algal Blooms (HABs) pose significant threats to marine ecosystems, fisheries, aquaculture, and human health. Dinoflagellates, responsible for ~75% of marine HABs, produce diverse toxins linked to aquatic animal and human harm. However, most ichthyotoxins (fish-killing toxins)—including those from common HAB-forming species—remain uncharacterized, with only rare compounds like karlotoxins confirmed. Consequently, the mechanisms driving fish mortality in most dinoflagellate-associated HABs remain unclear. This synthesis integrates recent findings on fish-killing toxicity in six dinoflagellate species (*Alexandrium leei*, *A. insuetum*, *Margalefidinium polykrikoides*, *M. fulvescens*, *Karlodinium veneficum* and *K. australe*), revealing three key insights: 1) Toxins as trophic tools: For some "toxic" dinoflagellates, toxin production may serve as an adaptive feeding strategy, integrating into both the process, and outcome of nutrient acquisition. 2) Non-toxic mortality drivers: Fish and organism deaths may arise from phagotrophy (micro-predation) rather than toxins in more HAB-forming species than previously recognized. 3) Ecological dual roles of phagotrophy: Phagotrophy influences dinoflagellate population dynamics through both top-down (predation) and bottom-up (nutrient cycling) mechanisms, potentially modulating HAB formation.

These multi-faceted perspectives redefine the ecological significance of ichthyotoxicity and phagotrophy in HAB-causing microalgae, emphasizing their roles in trophic interactions and bloom ecology.

**Keywords:** Harmful Algal Blooms (HABs); Dinoflagellates; Ichthyotoxicity

**Financing:** National Natural Science Foundation of China (42206215); Shandong Provincial Natural Science Foundation (ZR2021QD025); Open Research Fund Program of the Key Laboratory of Marine Ecosystem Dynamics (MED202304)

Parallel Session 5: Ichthyotoxic HABs

O-025

# Turbulence tames toxicity: Controlling the growth and toxicity of the rust tide alga, *Margalefidinium polykrikoides*

**Jiyeon Sung**[1], Christopher Gobler[1]

(1) Stony Brook University, School of Marine and Atmospheric Sciences, Stony Brook, USA

Harmful algal blooms (HABs) caused by the rust tide dinoflagellate *Margalefidinium polykrikoides* often lead to large-scale fish kills and severe ecological and economic damage. Despite the known impacts, effective and environmentally responsible mitigation strategies remain limited. While high turbulence generally inhibits dinoflagellate growth, species-specific responses to hydrodynamic stress are poorly understood. Some dinoflagellates show resilience or adaptation to turbulence, highlighting the need for targeted control methods that minimize ecological disruption. This study investigated whether artificially induced turbulence could mitigate the growth of *M. polykrikoides* by applying three treatments: shaking, nanobubble injection, and microbubble aeration. Microbubble treatment demonstrated the strongest and most consistent inhibition, significantly reducing cell growth and photosynthetic efficiency in two strains ($p < 0.0001$). Additionally, microbubble exposure mitigated ichthyotoxicity of *M. polykrikoides*, as shown by improved fish larvae survival in toxicity assays ($p < 0.0001$). In experiments with wild bloom populations, *M. polykrikoides* densities were significantly reduced while co-occurring, non-harmful dinoflagellates were not, indicating high species selectivity ($p < 0.05$, one-way ANOVA). Overall, microbubble-induced turbulence shows potential as an eco-friendly and targeted method for managing *M. polykrikoides* blooms. With climate change intensifying ocean stratification and eutrophication, scalable and selective mitigation tools like this will be crucial for effective coastal management.

**Keywords**: *Margalefidinium polykrikoides* (= *Cochlodinium polykrikoides*), Harmful algal bloom mitigation, Microbubble-induced turbulence

Parallel Session 5: Ichthyotoxic HABs

O-026

# *Heterosigma akashiwo* blooms and fish kills in San Francisco Bay, CA, USA: Remote sensing and lab-based experiments to understand the ecology and impacts

**Raphael Kudela**[1]

(1) University of California Santa Cruz, Ocean Sciences and Institute for Marine Sciences, UC Santa Cruz, 1156 High Street, Santa Cruz, USA

A massive bloom of the raphidophyte *Heterosigma akashiwo* occurred in summer 2022 in San Francisco Bay, causing widespread ecological impacts, including low dissolved oxygen events and mass fish kills. The rapidly evolving bloom required equally rapid management response, leading to the use of near-real-time image analysis of chlorophyll from the Ocean and Land Colour Instrument (OLCI) aboard Sentinel-3. Standard algorithms failed to adequately capture the bloom. An extensive dataset of in-water validation measurements from both bloom and non-bloom periods was used to develop and evaluate performance of a new chlorophyll algorithm. The final version of the algorithm successfully minimizes error for both non-bloom periods when chlorophyll is typically <30 mg $m^{-3}$, while also capturing bloom periods of >100 mg $m^{-3}$ chlorophyll a. Several strains of the alga were obtained in 2022 and 2023, and basic growth parameters (light, temperature, nutrients) were conducted. The combination of spatial information (remote sensing) and lab studies provides a "habitat envelope" that may help to predict future blooms. One key point is that this organism prefers nitrate as a nitrogen source, and is less robust when exposed to only urea or ammonium. There is also evidence for production of brevetoxin-like compounds which may explain the timing and extent of this ichthyotoxic event.

**Keywords:** *Heterosigma akashiwo*, Sentinel-3, brevetoxin

**Financing:** NOAA MERHAB Award NA23NOS4780288, California Delta Stewardship Council Award DSC-21003.

**Acknowledgments**: NOAA MERHAB Project Advancing technologies and interagency coordination for an integrated HABs detection and monitoring system across the SF Bay and Sacramento-San Joaquin Delta.

Parallel Session 5: Ichthyotoxic HABs

O-027

# Large scale bloom of *Karenia* species in South Australia associated with extensive deaths of marine life

**Shauna Murray[1],** Kirsty Smith[3], Tim Harwood[3], Steve Brett[5], Clinton Wilkinson[2], Mark Doubell[2], Ian Moody[2], Greta Gaiani[1], Christopher Bolch[4]

(1) University of Technology Sydney, School of Life Sciences, PO Box 123 Broadway, Sydney, NSW 2007, Australia. https://orcid.org/0000-0001-7096-1307
(2) PIRSA/SARDI
(3) Cawthron Institute, 98 Halifax Street East, Nelson 7010, New Zealand
(4) Institute for Marine and Antarctic Studies (IMAS), University of Tasmania, Private Bag 129, Hobart, 7001, Tasmania Australia
(5) Microalgal Services, 308 Tucker Rd, Ormond 3204, Australia

Beginning in March 2025, a fish-killing harmful algal bloom consisting of an abundance of species of *Karenia*, primarily *K. mikimotoi*, began impacting marine life off the Fleurieu Peninsula south of Adelaide in South Australia. Over more than 10 weeks, the area impacted by the bloom increased to ~150 km, including Kangaroo Island and the coast of Coorong in the south-east of the state. Using a combination of light microscopy observation, quantitative PCR and long-read MinIon sequencing, the diversity and identities of *Karenia* species present are being elucidated. Single cell isolation has been used to obtain unialgal cultures for further genetic and toxin analysis.

**Keywords:** *Karenia*, fish deaths

**Financing:** none

**Acknowledgments:** None

Parallel Session 6: Modeling, Early Warning and Forecasting

O-028

# A decade of HABreports: early warning of HABs and biotoxins for the aquaculture industry

**Keith Davidson[1],** Dimitry Aleynik[1], Gregg Arthur[2], Andrew Duncan[3], Steve Gontarek[1], Gary Groves[1], Po Teen Lim[4], Chuipin Leaw[4], Alan MacDonald[1], Tim Szewczyk[1], Callum Whyte[1]

(1) Scottish Association for Marine Science (SAMS), Dunbeg, Oban, Scotland
(2) University of the Highlands and Islands, UHI Shetland, Port Arthur, Scalloway, Scotland
(3) University of the Highlands and Islands, UHI Inverness, Inverness, Scotland
(4) University of Malaya, Bachok Marine Research Station, Institute of Ocean and Earth Sciences, Bachok, Kelantan 16310, Malaysia

Since 2015, SAMS has produced early warning and risk assessments of HABs and associated biotoxins in Scottish waters for the shellfish and finfish aquaculture industries. Since 2017, these have been provided on the www.HABreports.org website, with a parallel Malaysian (My-HABs) alerts system being developed in 2021/2. This presentation will discuss the development and content of HABreports including its traffic light alerts, FVCOM based model forecasts of HAB advection, and development of a mobile phone-based App for those users who do not routinely sit at a desktop. Recent developments including incorporation of real time Imaging FlowCytobot data from two sites in the Shetland Islands, and true site- specific forecasts of HAB risk using ensemble modelling approaches will also be reviewed.

**Keywords:** risk assessment, modelling, early warning

Parallel Session 6: Modeling, Early Warning and Forecasting

O-029

# A three-dimensional mechanistic model for predicting *Karenia brevis* blooms on the West Florida Shelf

**Ming Li**[1], Yuren Chen[2]

(1) Horn Point Laboratory, University of Maryland Center for Environment Science, Cambridge, Maryland, U.S.A.
(2) University of Maryland Center for Environmental Science, Horn Point Lab, 2020 Horn Point Road, Cambridge, United States

Blooms of the toxic dinoflagellate *Karenia brevis* occur almost annually on the West Florida Shelf, but blooms vary widely in intensity and duration from year to year, from brief and localized, to temporally and spatially expansive and ecologically devastating. The brevetoxins produced by *K. brevis* blooms can pose significant risks to human health and may lead to mass mortality of fish and marine mammals. It has been challenging to predict *K. brevis* blooms on seasonal and longer time scales due to a wide range of physical, biogeochemical and physiological processes that were shown to affect the initiation, development and termination of the blooms in laboratory experiments and field surveys. Here, we report the development of a three-dimensional mechanistic model of *K. brevis* that integrates physics, nutrient cycling, and plankton physiology including mixotrophy. We use this coupled model to hindcast three blooms: (1) a summer bloom following an emergency nutrient release from a phosphorus mine in 2021; (2) an expanded fall-winter bloom following the passage of Hurricane Ian in 2022; (3) a long-duration bloom that extended for over 1 year in 2002-2003. We discuss how this mechanistic model may complement the existing statistical models in expanding the capability in forecasting *K. brevis* blooms on the West Florida Shelf. We also discuss *K. brevis*' nutrition acquisition strategy in comparison with other mixotrophic harmful algal species.

**Keywords:** harmful algal blooms, modeling, *Karenia brevis*

**Financing:** National Oceanic and Atmospheric Administration National Centers for Coastal Ocean Science Competitive Research Program under Award NA19NOS4780183

Parallel Session 6: Modeling, Early Warning and Forecasting

O-030

# Empirical Dynamic Modeling applied to Chilean fjords phytoplankton assemblages: An approach to identify causal relationships among harmful algal species and other microalgae species

**Matías Volke**[1], Leonardo Guzmán[2], Ishara Perera[4], Gemita Pizarro[3], Oscar Espinoza[2]

(1) Instituto de Fomento Pesquero, Centro de Investigación Putemún, camino Ten Ten s/n, Castro CHILE, Castro, Chile
(2) Instituto de Fomento Pesquero, Centro de Estudios de Algas Nocivas (CREAN), Padre Harter 574, Puerto Montt, Chile
(3) Instituto de Fomento Pesquero (IFOP), Centro de Estudios de Algas Nocivas (CREAN), Enrique Abello 0552, Punta Arenas, Chile
(4) University of Yamaguchi, International Research Center for one Welfare, Yamaguchi, Japan

Harmful algal blooms are a major global environmental concern, impacting human health, marine ecosystems, and coastal economies. In Chilean fjords (41°–55°S), these events have particularly severe consequences for fisheries, aquaculture, and local communities.

A methodological framework is presented for analyzing the dynamics of causality among harmful microalgae and other co-occurring phytoplankton species, with focus on *Alexandrium catenella*, *Protoceratium reticulatum* and *Dinophysis acuminata* as HAB species. The analysis is based on quantitative phytoplankton data from 146 locations and sampled monthly between October 2007 and February 2024.

We apply Empirical Dynamic Modeling (EDM), combining CCM to identify statistically significant causal relationships, and S-Map to quantify their strength and temporal variation. Results reveal distinct positive causal interaction involving harmful algae and co-occurring species, varying by taxa and region. Positive causal interactions primarily originate from other dinoflagellates and diatoms. *Protoceratium reticulatum* showed consistent causal links with *Gyrodinium* spp. and *Protoperidinium steinii*. *Alexandrium catenella* was significantly influenced by *Chaetoceros* debilis, *Thalassionema nitzschioides* and *Protoperidinium punctulatum*. In turn, *Dinophysis acuminata* was affected by *Chaetoceros debilis*, *Ditylum brightwellii*, *Dictyocha speculum*, and several species of the genus Protoperidinium. These patterns suggest ecologically relevant roles among species, with potential trophic, physiological, or environmental implications.

EDM enables the detection of nonlinear, time-varying species interactions, overcoming limitations of traditional correlation-based approaches. Overall, this demonstrates a significant advance in the ecological understanding of the distribution and abundance of harmful algae in fjords and contributes to the development of early warning systems and management strategies applicable to regions highly vulnerable to climate change.

**Keywords:** Empirical Dynamic Modeling (EDM), Harmful Algal Blooms (HABs), Phytoplankton interactions

**Financing:** Fisheries and Aquaculture Undersecretary, Chile

**Acknowledgments:** We thank the Undersecretariat for Fisheries and Aquaculture (Chile), CREAN, and the Centro de Investigación Putemún–IFOP for supporting this research on harmful algal blooms.

Parallel Session 6: Modeling, Early Warning and Forecasting

O-031

# A machine-learning based, shellfish biotoxin forecasting method: Successes from Maine, USA and opportunities for other regions

**Johnathan Evanilla**[1], Nicholas Record[1], Benjamin Tupper[1], Stephen Archer[2], Kohl Kanwit[3]

(1) Bigelow Laboratory for Ocean Sciences, Tandy Center for Ocean Forecasting, East Boothbay, USA
(2) Bigelow Laboratory for Ocean Sciences, Bigelow Analytical Services, East Boothbay, USA
(3) Maine Department of Marine Resources, Bureau of Public Health, West Boothbay Harbor, USA

Paralytic shellfish toxins are detected in seafood around the world. There are multiple methods of measuring their levels in shellfish in order to protect public health and manage seafood harvest. Maine, USA has a long-term monitoring program dating back to 1958, containing >100,000 observations of shellfish toxicity across >150 stations. A switch in 2014 in the method used for PST monitoring, from the mouse bioassay to high performance liquid chromatography (HPLC), has led to the development of a machine learning based forecast system that is in its fifth year of operation. Stations where routine monitoring is taking place can now receive predictions of the probability that they will exceed the toxicity threshold that makes their shellfish dangerous for human consumption. The forecast has been co-developed with its end users, both regional resource managers who implement harvesting closures and shellfish industry members who must make day-to-day decisions. While Maine is currently the only US state leveraging HPLC for PST monitoring, many other countries have implemented it. Our forecasting software is being released as an open-source package built in R, and we encourage its use within other monitoring programs. The model shows high potential for transfer learning. We would like to answer questions around transferability, such as: How does a model trained on data from one region perform in other regions? Does joining monitoring data from multiple regions to train a model yield an increase in skill? Results from a case study in a novel region will be shared.

Parallel Session 7: Modeling, Early Warning and Forecasting

O-032

# A pilot program towards an early warning system for harmful algal blooms in Bahía de La Paz, Gulf of California, Mexico

**Christine Johanna Band-Schmidt**[1], José Reyes Hernández-Alfonso[1], Ignacio Leyva-Valencia[1,2], Víctor Hugo Cruz-Escalona[1], Brenda Ávila-Engrande[1], Francisco E. Hernández-Sandoval[3], Leyberth Fernández-Herrera[3], Erick J. Núñez-Vázquez[3], Cotsikayala Pacheco-Ramírez[4], Armando Trasviña-Castro[4], Romeo Saldivar-Lucio[4], Arturo del Pino Machado[5], Ernesto García-Mendoza[6]

(1) Instituto Politécnico Nacional (IPN), Centro Interdisciplinario de Ciencias Marinas (CICIMAR), Avenida Instituto Politécnico Nacional s/n, Col. Playa Palo de Sta. Rita, 23096, La Paz, BCS, Mexico
(2) Secretaría de Ciencia, Humanidades, Tecnología e Innovación (SECIHTI), Av. Insurgentes Sur 1582, Col. Crédito Constructor, Demarcación Territorial Benito Juárez, 03940, Mexico City, Mexico
(3) Centro de Investigaciones Biológicas del Noroeste (CIBNOR), Ave. Instituto Politécnico Nacional s/n, Col. Playa Palo de Sta. Rita, 23096, La Paz, B.C.S., Mexico
(4) Centro de Investigación Científica y Educación Superior de Ensenada (CICESE), Unidad Académica La Paz (UALP), Calle Miraflores 334, Col. Bellavista, 23050, La Paz, B.C.S., Mexico
(5) Habana Consultoría, Miguel Venegas 4, Col. Borrego Cimarrón, 27090, La Paz, B.C.S., Mexico
(6) Centro de Investigación Científica y Educación Superior de Ensenada (CICESE), Carr. Tijuana-Ensenada 3918, Zona Playitas, 22860, Ensenada, B.C., Mexico

In 2023, a pilot program for an Early Warning System (EWS) for harmful algal blooms was launched in Bahía de La Paz, Gulf of California with the main purpose to monitor harmful phytoplankton and reduce their impact in artisanal fishing, tourism, wildlife, and aquaculture. For this reason, by-weekly samplings have been conducted. Physicochemical parameters and paralytic toxins have been recorded; abundance of phytoplankton species has been determined by Uthermöl, and live cells have been collected with a 20 µm mesh phytoplankton net to isolate and cultivate phytoplankton species. Superficial temperature ranged from 20°C from October 2023 to June 2024, to 30°C from July 2024 to October 2024; salinity oscillated from 35.4 in February 2023 to 37.9 in October 2024. In general, the phytoplankton community is dominated by diatoms, however, in the colder months of 2023, silicoflagellates dominated, and in the warmer months of 2023 and 2024, high abundances of cyanobacteria were found. In July 2024 an extensive bloom of the diatoms *Guinardia striata* and *Leptocylindrus danicus* was reported that lasted over a month, reaching maximum abundances of 144,500 and 3,625,000 cel $L^{-1}$, respectively, causing bad odors in local beaches. In April 2025, a bloom of Chattonella sp. occurred reaching 541,600 cel $L^{-1}$. The highest abundances of *Gymnodinium catenatum* were recorded in May 2025 with 1,903 cel $L^{-1}$. Other harmful species reported have been: *Akashiwo sanguinea*, *Alexandrium* spp., *Dinophysis* spp., *Gambierdiscus* sp., *Gonyaulax polygramma*, *G. spinifera*, *Margalefidinium polykrikoides*, *Oscillatoria* sp., *Vulcanodinium rugosum* and *Pseudo-nitzschia* spp.

**Keywords:** Bahía de La Paz, Mexico, Phytoplankton

**Financing:** Institutional project SIP, 2025-1372CONAHCyT PRONAII, PRONACES SSyS No. 319104

**Acknowledgments:** Rojas-Montiel, B., Meza-Castro, D.R. (CONANP-La Paz); Comité Representante del Tiburón Ballena, A.C., La Paz, B.C.S.; Cerpa G. (IPN-CICIMAR) for their sampling and technical support.

Parallel Session 7: Modeling, Early Warning and Forecasting

O-033

# Early warnings and predictions according to *Alexandrium catenella* abundances, mussels' toxicity by paralytic toxins and hydrographical and meteorological conditions in Chilean fjords

**Leonardo Guzmán**[1], Valentina Besoaín[2], Pablo Reche[3], Oscar Espinoza-González[1], Pamela Carbonell[1], Rodrigo Martínez[1], Javier Paredes-Mella[1], Osvaldo Artal[4,5], Cristina Hernández[6], María Angélica Tocornal[7], Paulina Solar[8]

(1) Instituto de Fomento Pesquero, Centro de Estudios de Algas Nocivas (CREAN), División de Investigación en Acuicultura, Padre Harter 574, Puerto Montt, Chile
(2) Instituto de Fomento Pesquero, Centro de Investigación Putemún, División de Investigación en Acuicultura, camino Ten Ten s/n, Castro, Chile
(3) Plataforma Oceánica de Islas Canarias (PLOCAN), Telde, Spain
(4) Universidad de La Frontera, Departamento de Ingeniería en Obras Civiles (Geodel Laboratory), Facultad de Ingeniería y Ciencias, Temuco, Chile
(5) Universidad de Concepción, Centro de Investigación Oceanográfica COPAS COASTAL, Concepción, Chile
(6) Secretaría Regional Ministerial de Salud, región de Los Lagos, Laboratorio de Salud Pública, Puerto Montt, Chile
(7) Secretaría Regional Ministerial, región de Aysén, Laboratorio de Salud Pública, Puerto Aysén, Chile
(8) Secretaría Regional Ministerial, región de Magallanes, Laboratorio de Salud Pública, Punta Arenas, Chile

*Alexandrium catenella* and Paralytic Shellfish Toxins (PST) have caused marked effects to public health and productive activities in Chilean fjords. Although *A. catenella* and PST can be tracked to year 1884, since October 1972, when a severe bloom occurred in the Strait of Magellan, an apparently northward expansion has occurred, and today the vegetative cells are distributed from -55° to -36°, including the Pacific Ocean north of the fjords, although much less abundant.

*A. catenella* relative abundance (RA) is estimated from net samples, counting the motile stage in 0,1 mL (three drops) and without comparison to other species abundances. RA is expressed in a scale from 1 to 10, and the range of each step limits are defined using a 4X geometric progression. RA and density are exponentially correlated ($r^2$=0.966), so 1 represents 130 cells $L^{-1}$ and 10 are 301,251 cells $L^{-1}$. RA estimations correct biases due to patchiness distribution and low densities. Mussels' toxicity is estimated by mouse bioassay.

Regardless the seasonal and interannual variations, and the fjords geographical sectors with higher probability detections of *A. catenella* and PST, the monthly frequency time series from 146 sites from October 2007 to February 2024, and modeling development, allow hydrodynamic models, particle tracking and individual based models, through cross-correlations,, a) to predict PST public health risk levels in mussels, b) anticipate the areas potentially affected by PST and c) the ending of *A. catenella* blooms, using meteorological and hydrographic 10 days forecasts, when physical factors are determining.

**Keywords:** early warning, *Alexandrium catenella*, Paralytic Shellfish Toxins

**Financing**: Fisheries and Aquaculture Undersecretary, Chile; Public Health Under-Secretariat, Chile

Parallel Session 7: Modeling, Early Warning and Forecasting

O-034

# Modeling anthropogenic and oceanographic drivers of domoic acid production in the Southern California Bight

**Marco Sandoval-Belmar[1],** Faycal Kessouri[1,2], Jayme Smith[2], Allison R. Moreno[3], Clarissa Anderson[4], Raphael M. Kudela[3], Martha Sutula[2], Minna Ho[1], Pierre Damien[1], Claudia Benitez-Nelson[5], James McWilliams[1], Daniele Bianchi[1]

(1) University of California, Los Angeles, Department of Atmospheric and Oceanic Sciences, Los Angeles, CA 90095-1565, Los Angeles, United States of America
(2) Southern California Coastal Water Research Project, 3535 Harbor Blvd, Suite 110, Costa Mesa, CA 92626, Los Angeles, United States of America
(3) University of California Santa Cruz, Ocean Sciences Department, Santa Cruz, CA 95064, Santa Cruz, United States of America
(4) Scripps Institution of Oceanography, University of California, San Diego, La Jolla, CA, San Diego, United States of America
(5) University of South Carolina, School of the Earth, Ocean, and Environment, Columbia, SC 29208, Columbia, United States of America

Domoic acid (DA), produced by toxigenic diatoms of the genus *Pseudo-nitzschia*, poses a recurring threat to marine ecosystems, fisheries, and public health along the California coast and worldwide. However, the interaction between natural and anthropogenic sources of nutrients, physical transport, and environmental conditions has not been systematically evaluated. Here, we introduce a novel mechanistic parameterization of DA production, based on nutrient limitation and temperature effects, into a high-resolution 3D coupled physical-biogeochemical model of the Southern California Bight. The model is validated against long-term observations and used to simulate DA HAB dynamics from 2006 to 2017 under two scenarios: one representing natural ocean variability with nutrient input from rivers and wastewater discharges (ANTH), and a control simulation including only natural and freshwater inputs (CTRL). The ANTH simulation more accurately reproduces the observed magnitudes and spatial patterns of particulate DA (pDA), particularly in nearshore zones adjacent to urban areas. Enhanced nitrogen delivery from land sources stimulates diatom productivity and shifts nutrient limitation from nitrogen to silica, favoring conditions for DA synthesis. As a result, the coastal intensity of DA-producing blooms increases by approximately 25% on average when anthropogenic inputs are included. This study underscores the importance of incorporating land-sea nutrient coupling into predictive HAB models and provides a transferable framework for modeling DA events in other coastal systems.

**Keywords:** Domoic acid, Biogeochemical modeling, Anthropogenic nutrients

**Financing:** Funded by NOAA NA18NOS4780174, OPC C0831014, and ANID/DOCTORADO BECAS CHILE/2019–72200138 (Chilean National Agency for Research and Development).

**Acknowledgments:** National Agency for Research and Development (ANID) / Scholarship Program / DOCTORADO BECAS CHILE/2019 - 72200138.

Parallel Session 7: Modeling, Early Warning and Forecasting

O-035

# Influences of bottom temperature on *Alexandrium catenella* cyst dynamics in the Gulf of Maine

**David Ralston**[1], Michael Brosnahan[1], Nate Spada[1], Vanessa Haggans[1]

(1) Woods Hole Oceanographic Institution, Woods Hole, USA

The Gulf of Maine is a region with recurrent harmful algal blooms of the dinoflagellate *Alexandrium catenella* that cause closures of shellfish beds in coastal and offshore waters. *A. catenella*, like many HABs, has a life cycle that includes a benthic resting cyst stage. The distribution of cysts in the sediment and the cycle of germination and encystment affect the location and timing blooms in the Gulf of Maine. Prior studies pointed to an endogenous clock as the primary control on the seasonal germination, but recent work has shown instead that temperature has the main influence on cyst maturation and dormancy cycling. We apply this revised conceptual model for temperature-driven cyst dynamics to a realistic physical-biological model of *A. catenella* in the Gulf of Maine. Cyst distributions are established based on annual shipboard surveys. Near-bottom water temperatures are from a multi-decadal simulation that has been evaluated against observations. Cyst conditions are initialized stochastically, and dormancy cycling and germination are simulated based on local bottom-water temperature for multiple hindcast years. Spatial variability in the annual cycle of bottom-water temperature, due to gradients in water depth and mixing, correspond to differences in cyst germination timing. We characterize discrepancies in dormancy cycling between coastal and deep-water cyst populations and evaluate links between temperature and endogenous dormancy rhythms. Warming trends in the Gulf of Maine are among the fastest in the global ocean, making accurate representation of cyst dynamics crucial for projections of future blooms and toxicity.

**Keywords:** cysts, dormancy, warming

**Financing:** US National Science Foundation and National Institute of Environmental Health Sciences.

Parallel Session 7: Modeling, Early Warning and Forecasting

O-036

# Ocean warming reduces risk of paralytic shellfish toxin events from *Alexandrium catenella* in Tasmania, Australia

**Lael Wakamatsu**[1,3,4], Gregory Britten[3,4], Christopher Bolch[2], Andy Fischer[2,5]

(1) Japan Agency for Marine-Earth Science and Technology, Advanced Institute for Marine Ecosystem Change
(2) Institute for Marine and Antarctic Studies, Ecology & Biodiversity
(3) Massachusetts Institute of Technology, Earth, Atmospheric, and Planetary Sciences
(4) Woods Hole Oceanographic Institution, Biology
(5) Australian Maritime College

Paralytic shellfish toxins (PSTs) produced by *Alexandrium catenella* have caused repeated shellfish harvesting closures along the east coast of Tasmania. Between 2012 and 2017, especially high toxin levels were recorded in the north and central regions. To identify environmental conditions linked to these events, we analyzed long-term data from marine farms and applied a machine learning approach (random forest) to determine key environmental and climate predictors of high toxin levels. Results showed that cooler sea surface temperatures (SST), along with large-scale climate indices such as the Southern Oscillation Index (SOI) and Pacific Decadal Oscillation (PDO), were the strongest predictors of high toxin events in the north and central regions. In the southern region, wind, solar exposure, and indices such as the Trans-Niño Index (TNI) and Southern Annular Mode (SAM) were more influential. A clear SST threshold of 12°C emerged for the north and central regions. When temperatures dropped below this threshold, the likelihood of high toxin events increased significantly —two-fold in the north and five-fold in the central region. Following the high-toxin period ending in 2017, the number of days below this threshold declined, coinciding with a marked decrease in toxin events, particularly in the central region. This study highlights the importance of environmental conditions, especially SST, in driving high toxin events and suggests that warming trends in the region may reduce the future risk of PST outbreaks and shellfish farm closures.

**Keywords:** Random Forest Modeling, Sea Surface Temperature, *Alexandrium*

**Financing:** Funding provided by the Institute for Marine and Antarctic Studies, Massachusetts Institute of Technology, and Woods Hole Oceanographic Institution

**Acknowledgments:** Thanks to Andy Fischer, Chris Bolch, and Greg Britten for guidance, and to the Shellfish Market Access Program (ShellMAP) for providing biotoxin data.

Parallel Session 7: Modeling, Early Warning and Forecasting

O-037

# Bridging morphological traits and model attention for improved phytoplankton classification and forecasting

**Paul Samuel Ignacio**[1,4], Bryan Miguel Tul-ao[2], Lance Oliver Licnachan[2], Arnel Malubay[3], Deo Florence Onda[2]

(1) University of the Philippines Baguio, Department of Mathematics and Computer Science, College of Science, Baguio City, Philippines
(2) University of the Philippines Diliman, Marine Science Institute, College of Science, Quezon City, Philippines
(3) Ateneo de Manila University, Department of Information Systems and Computer Science, School of Science and Engineering, Quezon City, Philippines
(4) Intelligent Systems Center, University of the Philippines, Quezon City, Philippines

Effective monitoring and forecasting of harmful algal blooms (HABs) require timely, species-level identification of phytoplankton, particularly those known to trigger disruptive events. While automated classification using machine learning (ML) and deep learning (DL) models has become increasingly viable, these models often lack transparency, limiting their integration into ecological forecasting pipelines. In this study, we present a trait-focused interpretability framework that links learned model attention to biologically meaningful morphological features—supporting more ecologically grounded and model-compatible outputs. We trained both ML and DL models on a curated image dataset of phytoplankton species relevant to HAB dynamics. Using SHapley Additive exPlanations (SHAP) for ML and Gradient-weighted Class Activation Mapping (Grad-CAM) for DL, we identified and compared key image regions associated with classification decisions. Our analysis reveals strong spatial correlations between biologically interpretable traits and model attention, particularly for morphologically distinctive taxa. Importantly, we also assess how consistently these image-based methods focus on biologically relevant traits, providing a way to gauge confidence in their outputs—an essential step for integrating such data into ecological models and forecasting tools. By connecting classification outputs to interpretable traits, our approach enhances the ecological relevance of automated pipelines and lays the groundwork for incorporating image-derived trait metrics into dynamic HAB models. This supports a shift from black-box classification toward biologically informed forecasting, offering valuable tools for early warning systems and operational monitoring of phytoplankton communities.

**Keywords:** Phytoplankton Trait Classification, Interpretable Machine Learning, Harmful Algal Bloom Forecasting

**Financing:** Commission on Higher Education

Parallel Session 8: Ecology, Biology and Biogeography

O-038

# Evolutionary insights into polyketide synthases in *Amphidinium carterae*

**Armando Mendoza-Flores**[1], Clara Elizabeth Galindo-Sánchez[2], M. del Pilar Sánchez-Saavedra[1]

(1) Centro de Investigación Científica y de Educación Superior de Ensenada, Baja California, Department of Aquaculture, Carretera Ensenada - Tijuana No. 3918, Zona Playitas, Ensenada, Mexico
(2) Centro de Investigación Científica y de Educación Superior de Ensenada, Baja California, Department of Marine Biotechnology, Carretera Ensenada - Tijuana No. 3918, Zona Playitas, Ensenada, Mexico

Polyketide biosynthesis in dinoflagellates is a complex process, yet crucial due to its ecological and pharmacological relevance. This study aimed to identify and analyze polyketide synthases (PKS) in the transcriptome of *Amphidinium carterae*, focusing on their structural organization and evolutionary origin. A total of 24 transcripts with a single KS domain structure and seven muti-domain PKSs transcripts were identified in *A. carterae*, including a triple KS domain (previously reported in dinoflagellates) and a nine-module PKS representing the largest PKS described in dinoflagellates to date. Phylogenetic analyses reveal a distinct clade separates single-domain and multi-domain PKS in dinoflagellates, all resembling type I PKS. The observed modular architecture is similar to that of Gambierdiscus polynesiensis and other dinoflagellates, suggesting a conserved domain structure likely shaped by gene duplication events. Gene duplications, which are common in dinoflagellates, may have driven the diversification of polyketide structures and toxin production. Moreover, the modular PKSs may also operate iteratively, similar to bacteria systems, enabling the synthesis of structurally diverse polyketides. Notably, transcripts related to bacterial BurA and ZmaK were identified, phylogenetically clustering with sequences from Escherichia coli and Streptomyces, supporting the hypothesis that horizontal gene transfer (HGT) as a key evolutionary mechanism. These bacterial-like sequences, classified as hybrid NRPS/PKS, may have been acquired early in dinoflagellate evolution. In conclusion, the results underscore the importance of gene duplication and HGT in the evolution and functional expansion of PKS gene families in dinoflagellates, with implications for future studies on polyketide biosynthesis and the development of novel biotechnological applications.

**Keywords:** Polyketide synthase, gene duplication, horizontal gene transfer.

Parallel Session 8: Ecology, Biology and Biogeography

O-039

# Intra- and inter-specific transcriptomic profiling of *Alexandrium* strains from Irish waters and the North Sea to identify novel molecular markers associated with toxin production

**Francesca Cucchi**[1], Amna Ashfaq[2], Amanda Curtin[3], Dave Clarke[3], Fiona Kavanagh[1], Patrick Costello[3], Francis Butler[4], Shauna Murray[2], Greta Gaiani[2], Luca mirimin[1]

(1) Atlantic Technological University, Natural Resources & the Environment, School of Science and Computing, Dublin Road, H91 T8NW, Galway, Ireland
(2) University of Technology Sydney, Climate Change Cluster, School of Life Sciences, Ultimo, NSW, 2007, Sydney, Australia
(3) Marine Institute, Shellfish Safety, Marine Environment & Food Safety, Rinville, H91 R673, Oranmore, Ireland
(4) University College Dublin, Biosystems Engineering, School of Agriculture, Food Science and Veterinary Medicine, UCD Belfield Dublin 4, Dublin, Ireland

The dinoflagellate *Alexandrium* is a known producer of Paralytic Shellfish Toxins (PSTs), posing risks to public health and the shellfish aquaculture sector. While the sxtA gene has been linked to PSTs biosynthesis, the broader genetic architecture of toxins production in dinoflagellates remains poorly understood. This study performed intra- and inter-specific transcriptomic profiling of Alexandrium strains isolated from Irish waters and the North Sea to identify novel molecular markers associated with PSTs production. Twenty *Alexandrium* spp. strains (*A. minutum*, *A. tamarense, A. catenella, A. ostenfeldii*, and *A. tamutum*) were selected and screened for toxin profiles. A subset of 11 PSTs-producing and non-producing strains of A. minutum, the primary species responsible for PSTs events in Irish waters, were selected for mRNA sequencing in biological triplicates, resulting in 33 stranded mRNA libraries sequenced using Illumina NovaSeq technology. Differential gene expression analysis identified candidate genes potentially involved in PSTs biosynthesis. Based on their sequences, qPCR assays targeting differentially expressed genes were developed. High-throughput qPCR (HT-qPCR) was applied to cDNA synthesized from all 20 *Alexandrium* spp. strains in biological triplicates to validate potential PSTs biomarkers. Results will be discussed to showcase how combining mRNA sequencing and gene expression profiling provides new insights into intra- and inter-specific variability in toxins production pathways. The further understanding of genetic markers associated with PSTs biosynthesis will contribute to the development of molecular diagnostic tools, expected to enhance early warning systems and support more effective risk management strategies for food safety in shellfish production areas.

**Keywords:** mRNA Sequencing, *Alexandrium*, Gene Expression

**Financing:** The PSPSafe Project is supported and funded by the Irish Department of Agriculture, Food and the Marine (DAFM, Project Ref 2021R578).

Parallel Session 8: Ecology, Biology and Biogeography

O-040

# Comparison of microscopy and metabarcoding for long-term monitoring of harmful algae taxa in the Western English Channel

**Keelan Lawlor[1],** Loïck Kléparski[1], Joanne Warrick-Dugdale[1], Claire Widdicombe[2], Michael Cunliffe[1,3]

(1) The Marine Biological Association, The Laboratory, Citadel Hill, Plymouth, PL1 2PB, United Kingdom
(2) Plymouth Marine Laboratory, Prospect Place, Plymouth, PL1 3DH, United Kingdom
(3) University of Plymouth, Plymouth, PL4 8AA, United Kingdom

Harmful algal blooms (HABs) are naturally occurring high biomass and/or toxin-producing events caused by specific taxa which pose a threat to aquaculture and human health. Current HAB monitoring relies on microscopy which has limited potential for implementation at scale. Conversely, metabarcoding is scalable and cost-effective, however shifting to primarily molecular approaches for large scale phytoplankton monitoring presents challenges.

A comparison of microscopy and molecular datasets from a unique twenty-year time-series was performed. The seasonal community of key HAB taxa at the Western Channel Observatory Station L4 was compared, abundance visualized over time and environmental data incorporated to characterize ecological niches.

In the two datasets, potential HAB species comprised between 0.1 – 6.8 % (microscopy) and 5.6 –7.6 % (molecular) of the total phytoplankton. The HAB community was mostly comprised of a small number of taxa, with a more diverse community in the molecular dataset. In both datasets, Phaeocystis spp. was the primary HAB taxa during at least one season. Ecological niches were generally characterized by low nutrient conditions and high temperatures. However, those derived from molecular data show larger amplitudes, making niche characterization difficult for some taxa.

Despite such challenges, application of molecular tools for monitoring is desirable but currently requires an integrated approach utilizing both methods to facilitate further comparative studies. Finally, the adoption of standardized metabarcoding methodology and investigation into potential impacts of molecular data utilization in downstream ecological assessment requires further consideration.

**Keywords:** Metabarcoding, Ecological Niche, Long-Term Ecological Research (LTER)

**Financing**: This work was conducted as part of the project ACTNOW (www.actnow-project.eu), funded by the Horizon Europe Research and Innovation Programme (Grant agreement No. 101060072).

Parallel Session 8: Ecology, Biology and Biogeography

O-041

# Phylogenetic diversity and yessotoxin variation of the marine dinoflagellate *Lingulaulax polyedra* from a western Sweden (Skagerrak) fjord system

**Allan Cembella**[1,2], Daniela Voss[3], Bengt Karlson[4], Bernd Krock[1], Jan Tebben[1], Lorena María Durán-Riveroll[5], Uwe John[1]

(1) Alfred-Wegener-Institut, Helmholtz Zentrum für Polar-und Meeresforschung, Ecological Chemistry, Am Handelshafen 12, 27570 Bremerhaven, Germany
(2) Centro de Investigación Científica y de Educación Superior de Ensenada, Departamento de Biotecnología Marina, Carretera Ensenada-Tijuana 3918, Zona Playitas, C.P. 22860, Ensenada, Baja California, Mexico
(3) Institute for Chemistry and Biology of the Marine Environment (ICBM), University of Oldenburg, 26129 Oldenburg, Germany
(4) Swedish Meteorological and Hydrological Institute (SMHI), Research & Development, Oceanography, Göteborgseskaderns plats 3 SE – 426 71 Västra Frölunda, Sweden
(5) Secretaría de Ciencia, Humanidades, Tecnología e Innovación (SECIHTI), Departamento de Biotecnología Marina, Centro de Investigación Científica y de Educación Superior de Ensenada, Carretera Ensenada-Tijuana 3918, Zona Playitas, C.P. 22860, Ensenada, Mexico.

*Lingulaulax polyedra* is a frequently toxigenic dinoflagellate capable of forming massive harmful blooms, particularly in temperate coastal waters subject to upwelling. Oceanographic sampling was conducted along a longitudinal transect within the Orust fjord system on the Skagerrak coast to evaluate mesoscale variation in rDNA sequences and polyketide toxin composition. Multiple clonal cultures were established from net tow samples and compared with characteristics of corresponding taxa harvested directly from field populations in the water column. Sanger sequencing of the regions D1/D2 28S rDNA and ITS revealed tight phylogenetic clustering consistent with *L. polyedra*. This taxon was most closely related to other gonyaulacoid dinoflagellates, *Protoceratium reticulatum* and *Gonyaulax spinifera*, as alternative sources of yessotoxins (YTXs) in the Skagerrak. Analysis of selected polyketide toxins by liquid chromatography-tandem mass spectrometry (LC-MS/MS) detected YTXs in 20 of 21 *L. polyedra* isolates. The YTX spectrum was unusually diverse, comprising YTX and numerous analogs, including trinor-, homo-, hydroxyl- and keto-YTX, as well as incompletely characterized putative YTXs. Total YTX cell yield among isolates (0 to 0.76 pg/cell), was low compared to maximum values for YTX-producing gonyaulacoids from global locations. The diverse YTX profiles were not consistent with the limited variation of the conservative rDNA gene marker. There was no significant rDNA genetic differentiation of geographical populations along the fjord, nor clustering of YTX chemotypes according to stations of origin. Toxin chemotype is apparently not a reliable discriminator of biogeographical populations of *L. polyedra* in the Skagerrak, although the YTX profile remains genetically fixed and stable in culture.

**Keywords:** rDNA genotyping, gonyaulacoid dinoflagellates, polyketide toxins

**Financing:** Helmholtz research program “Changing Earth, Sustaining our Future” (Sub-topic 6.2 Adaptation of marine life) of the Alfred-Wegener-Institut, Helmholtz Zentrum für Polar- und Meeresforschung, Germany

Parallel Session 8: Ecology, Biology and Biogeography

O-042

# Domoic acid biosynthesis and genome expansion in *Nitzschia navis-varingica*

**Steffaney Wood-Rocca**[1,2]

(1) University of California San Diego, Scripps Institution of Oceanography, Center for Marine Biotechnology and Biomedicine, La Jolla, USA
(2) J. Craig Venter Institute, Environmental Genomics Group, La Jolla, USA

Production of the neurotoxin domoic acid (DA) by benthic diatom *Nitzschia navis-varingica* poses considerable health and economic concerns. In this study, we employed whole genome sequencing and transcriptomic analyses of regionally distinct *N. navis-varingica* strains to unravel the genomic underpinnings of DA biosynthesis. Our analyses revealed sizable genomes—characterized by an abundance of repetitive elements and noncoding DNA—that exceed the size of any other pennate diatoms. Central to our findings is the discovery of an expanded domoic acid biosynthesis (dab) gene cluster, spanning over 60 kb and marked by a unique organization that includes core genes interspersed with additional genetic elements. Phylogenetic and syntenic comparisons indicate that transposition events may have driven the expansion and reorganization of this cluster. Biochemical assays validated that the kainoid synthase encoded by dabC catalyzes the formation of isodomoic acid B, thereby establishing a distinct chemotype in contrast to the DA profiles of planktonic diatoms. These results highlight the evolutionary trajectory of DA biosynthesis in diatoms and potential advantages conferred by genome expansion and enzyme diversification in dynamic marine environments.

**Keywords:** domoic acid, genomics

Parallel Session 8: Ecology, Biology and Biogeography

O-043

# Comparative genomics of harmful bloom-forming diatoms *Pseudo-nitzschia*

**Zoltan Fuessy**[1], Andrew Allen[1], Steffaney Wood Rocca[1]

(1) University of California, San Diego, Scripps Institution of Oceanography, San Diego, CA, United States

As major primary producers and toxic algal bloom formers, the members of the genus Pseudo-nitzschia are one of the most ecologically relevant diatom taxa in the California Current Ecosystem. Yet, we have limited genome sequence data for the group. Using long-read sequencing we assembled high-quality genomes of diverse lineages of *Pseudo-nitzschia* local to both West and East coast. The genome sizes vary substantially, with the difference occupied by repetitive sequences. We discuss gene family evolution and transcriptomic variation that drives the differences in niche occupation in these cohabiting, yet ecologically divergent species.

**Keywords:** comparative genomics, biogeography, toxin production

**Financing:** Simons Collaboration on Principles of Microbial Ecosystems (PriME) (Grant ID: 970820 to Andrew E Allen).

Parallel Session 9: Prevention, Control and Mitigation (PCM – HABs)
O-044

# A sustainable and innovative management system for toxic cyanobacteria blooming of surface waters with combined energy production, sustainable agriculture, and food safety (CYANOTECH)

**Maria G. Antoniou[1],** Nikoletta Tsiarta[1], Efthymia Chatziathanasiou[1], Andreas P. Hadjicosti[1], Giannis P. Neofytou[4], Yixin Yan[2], Ioannis Fotidis[3], Antonios Chrysargyris[4], Nikolaos Tzortzakis[4], Robert Konkel[5], Hanna Mazur Marzec[5]

(1) Cyprus University of Technology, Chemical Engineering, Faculty of Geotechnical Sciences and Environmental Management, 30 Arch. Kyprianos Str. 3036 Limassol, Lemesos, Cyprus
(2) Southeast University, Civil Engineering, School of Civil Engineering, Nanjing, 210096, Nanjing, China
(3) Aristotle University of Thessaloniki, Department of Agriculture, School of Agriculture, University Campus 54124, Thessaloniki, Greece
(4) Cyprus University of Technology, Department of Agricultural Sciences, Biotechnology and Food Science, Faculty of Geotechnical Sciences and Environmental Management, 30 Arch. Kyprianos Str. 3036 Limassol, Lemesos, Cyprus
(5) University of Gdańsk, Department of Marine Biology and Biotechnology, Faculty of Oceanography and Geography, ul. Jana Bażyńskiego 8, Gdynia, Poland

Increase of persistent and prevalent cyanobacteria harmful blooms globally, is a direct result of increased inputs of nutrient-rich waste into aquatic systems, increasing temperatures, and CO2 emission. Besides the aesthetic and environmental effects of cyano-HABs, a number of economic sectors including tourism, fishery, food, health, and water industries, experience annual losses in the range of millions USD. With so many diverse sectors of modern living being affected by the same problem, it is crucial to develop and apply innovative and sustainable management systems that can be easily adapted into current infrastructures. The CYanoTech project applied an innovative approach for safeguarding surface water quality from further deterioration, while utilizing harmful waste as raw materials for the production of fertilizers, food, and energy. Specifically, the CYanoTech approach comprises of the removal of the excess aquatic biomass (cyanobacteria cells and algae) from water with a low-energy non-mechanical separation technology. The collected harmful biomass was successfully co-digested with livestock waste and doubled methane yield production. The digested effluent underwent alkaline precipitation were nutrients converted into a high value biofertilizer (struvite) that was applied in along with treated and untreated cyanobacterial water in hydroponic cultures to ensure the production of cyanotoxins-free crops. Finally, ozonolysis was employed as a pre-treatment step for the removal of both the cells and toxins for DWTPs, to prove under which conditions this can help protect both the treatment plant and water quality. Finally, a Life-Cycle Analysis confirmed that the CYanoTech approach significantly reduces the environmental impact of cyano-HABs.

**Keywords:** cyanobacteria, energy, crops

**Financing:** The Project CYANOTECH-EXCELLENCE/ 0421/0212 is co-financed by the European Union and the Republic of Cyprus through the Research and Innovation Foundation.

Parallel Session 9: Prevention, Control and Mitigation (PCM – HABs)

O-045

# Novel light-guided photocatalytic treatment for in situ control of harmful algal blooms

**Diana S. Moura**[1], Indira Menezes[1], Christine Edwards[1], Francisca Vermeulen[2], Linda Lawton[1]

(1) Robert Gordon University, School of Pharmacy, Applied Sciences and Public Health, Garthdee Road, AB10 7GJ, Aberdeen, United Kingdom
(2) Scottish Association for Marine Science, Dunbeg, PA37 1QA, Oban, United Kingdom

Harmful algal blooms (HABs) are an increasing issue to marine ecosystems and industries, particularly causing substantial financial losses to salmon farming. While water treatment methods are being developed to remove harmful algae and their toxins, applying these solutions in situ remains challenging. Photocatalysis has been reported to be a promising method. Our previous studies demonstrated success in removing *Alexandrium catenella*, a paralytic shellfish toxins (PSTs) producer that is a key contributor to salmon mortality, using a protective photocatalytic curtain. This curtain, composed of graphitic carbon nitride (g-$C_3N_4$) coated beads activated by UV-A LEDs, significantly reduced PSTs uptake in mussels compared to unprotected controls. However, deploying such photocatalytic barriers in open salmon farm environments is limited due to their extensive water volume. Recent findings show that harmful algae can be attracted to specific wavelengths. Advances in LED technology allow precise control of wavelength and light intensity across the visible spectrum. The current study introduces a novel targeted approach: combining photocatalysis with light-induced luring. Promising results showed that *Scrippsiella trochoidea*, a marine dinoflagellate, actively swims toward blue LED lights (wavelength pending) at 200-400 µm/min speed. Additionally, g-$C_3N_4$ coated beads activated by low-cost UV-A LEDs (£0.075/LED) completely degraded a PST producer cyanobacteria and its toxins, *Raphidiopsis raciborskii* (ITEP-A1) within 24 hours (initial concentrations: intracellular saxitoxin 6 µg/L, neosaxitoxin 35 µg/L; extracellular saxitoxin 10 µg/L, neosaxitoxin 50 µg/L). This integrated strategy may offer a groundbreaking, targeted, and cost-effective solution to mitigate the impacts of HABs on salmon farming, reducing both environmental and economic harm.

**Keywords**: Aquaculture, Salmon farms, Paralytic shellfish toxins.

**Financing**: Natural Environment Research Council (NERC) [NE/X015459/1].

Parallel Session 9: Prevention, Control and Mitigation (PCM – HABs)

O-046

# Towards scalable photocatalytic water treatment: Simplified preparation of g-$C_3N_4$ coated glass beads for microcystin-LR removal

**Indira Menezes**[1], Diana Souza Moura[1], Christine Edwards[1], Linda A. Lawton[1]

(1) Robert Gordon University, School of Pharmacy, Applied Sciences and Public Health, Garthdee Road, Aberdeen

Cyanobacterial blooms can produce microcystins, which are potent hepatotoxins. As conventional water treatment processes may be ineffective in fully removing cyanotoxins, especially during bloom events, there is an increasing need for complementary technologies that can be applied at source. Photocatalysis can be used for the removal of cyanotoxins, however, the recovery of the powdered catalyst from water represents a challenge for the application of photocatalysis at source. To overcome this issue, beads made of recycled glass were previously used as photocatalyst immobilization matrix in a successful mesocosms-study in a drinking water reservoir for the removal of cyanobacteria.

In the current study, the same type of glass beads was coated with graphitic carbon nitrite (g-$C_3N_4$) and activated by low-cost LEDs (£0.075/LED) to remove microcystin-LR (2 mg/L). The photocatalytic system was effective in the removal of microcystin-LR, however, scaling up this technology requires a fast, simple, accessible, and environmentally friendly coating protocol. The standard preparation method involved multiple steps: acetone washing, pre-calcination and calcination in an alumina crucible at 500°C in the muffle furnace, and another wash with deionised water. All these steps make the coating process time-consuming and costly. A new simplified protocol was developed using accessible materials. Glazed plant pots, pottery studio kilns, and tap water replaced the need for specialized lab equipment and reagents. These modifications reduced the production costs from £500 to £100 and made the preparation time eight times faster than the standard process. This approach supports the application of photocatalysis for mitigating cyanotoxin contamination at source.

**Keywords:** Photocatalysis, Cyanotoxins, Graphitic carbon nitride

**Financing:** Natural Environment Research Council (NERC) [NE/X015459/1].

**Acknowledgments:** The authors would like to thank the Natural Environment Research Council (NERC) [NE/X015459/1].

Parallel Session 9: Prevention, Control and Mitigation (PCM – HABs)

O-047

# Development of surfactant-based foams for targeted control of harmful algal blooms

**Vincent Lovko**[1], Vijay John[2], Srinivasa Raghavan[3]

(1) Mote Marine Laboratory, Phytoplankton Ecology Research Program, Senior Scientist, 1600 Ken Thompson Parkway, Sarasota, United States of America
(2) Tulane University, Department of Chemical and Biomolecular Engineering, Professor, 6823 St. Charles Avenue, New Orleans, LA, United States of America
(3) University of Maryland, Department of Chemical and Biomolecular Engineering, Professor, 4418 Stadium Drive, College Park, MD, United States of America

The control and mitigation of harmful algal blooms (HABs) can involve physical, chemical, or biological approaches. However, the practical application of these technologies in-situ is often limited by challenges such as cost, scalability and regulatory constraints. Chemical and biologically derived algaecides, in particular, may require high surface application rates to achieve effective concentrations throughout the water column, reducing efficiency and increasing environmental risks. Scalable delivery methods that ensure uniform coverage and gradual dispersal of active compounds are essential for the successful implementation of HAB control strategies at larger scales. Here, we describe the development and evaluation of surfactant-based foams as a novel delivery system for algaecides and other mitigation agents targeting both marine and freshwater HABs. These foams consist of surfactant-stabilized air bubbles separated by interconnected aqueous microchannels. When applied to the water surface, the foam forms a cohesive layer that facilitates the uniform release of embedded algaecides or other materials through gravitational drainage from the microchannels, enabling broad-area distribution into the underlying water column. We demonstrate that foams formulated with the commonly used surfactant polysorbate 80 effectively delivered a sodium percarbonate-based algaecide (PAK27), achieving >90% mortality of cultured *Microcystis aeruginosa* at concentrations as low as 12.5 mg/L within 24 hours. Ongoing work investigates the performance of foams generated with additional surfactants—polysorbate 80, sodium dodecyl sulfate, and sodium oleate—for the delivery of algaecides and flocculants in both marine and freshwater systems.

**Keywords:** Control, HABs, Foams

**Financing:** This work is funded through the US ACE ERDC Harmful Algal Bloom Demonstration Program and the US HAB-CTI.

Parallel Session 9: Prevention, Control and Mitigation (PCM – HABs)

O-048

# Harmful algal bloom mitigation of dinoflagellate, *Karenia brevis*, Using Lake Guard® Oxy

**Jessica R. Frost**[1], Cynthia Heil[2], Rich Pierce[2], Emily Hall[2], Jennifer Toyoda[2], Todd Lundell[1]

(1) BlueGreen Water Technologies, 2233 NW 41st Street Suite 500, Gainesville, United States
(2) Mote Marine Laboratory, 1600 Ken Thompson Pkwy, Sarasota, United States

BlueGreen Water Technologies partnered with Mote Marine Laboratory to assess the efficacy of Lake Guard® Oxy against Karenia brevis. Studies included a 1.6m column migration experiment, a 1.5L beaker Tier 1 range-finder experiment, and a 1,400L mesocosm Tier 2 experiment. Lake Guard® Oxy was applied at concentrations up to 36 $mgL^{-1}$. *K. brevis* cell concentrations, photosynthetic physiology (PAM), brevetoxin levels, water quality (pH, dissolved oxygen, salinity, temperature, nutrients, turbidity), and marine invertebrate impacts (hard clams, sea urchins) were monitored for up to 72 hours. Results consistently showed Lake Guard® Oxy effectively reduced and eliminated *K. brevis* cells. In columns, cell concentrations dropped significantly within 1 hour, with no viable cells detected after 3 hours. Tier 1 achieved 100% cell elimination by 24 hours, with physiological decline noted at 2-4 hours. Tier 2 demonstrated an 84.4% *K. brevis* reduction within 3 hours and 100% elimination by 24 hours. Brevetoxin concentrations declined by up to 60% within 4 hours in Tier 1. Tier 2 revealed brevetoxin accumulation reduced by approximately 46% in clam tissue and 85% in urchins over 72 hours. Water quality analyses indicated temporary increases in pH and dissolved oxygen in treated tanks. Crucially, no mortalities occurred in hard clams or sea urchins in Tier 2, indicating low acute lethality. However, some sublethal behavioral effects, such as increased urchin righting time and spine loss, were observed. These findings confirm Lake Guard® Oxy is highly effective at rapidly eliminating *K. brevis* cells, with minimal acute impact on tested marine invertebrates.

**Keywords:** Dinoflagellates, Mitigation, Algaecide

**Financing:** Mote Red Tide Initiative

**Acknowledgments:** Sarah Klass, Victoria Devillier, Jessica Frankle, Gad Weiss, Alon Goldman, Sara Turner.

Parallel Session 10: Toxins & Other Microalgal Metabolite

O-049

# Isolation of polyketide toxins from free-living and symbiotic Symbiodiniaceae

**Emily Jolly[1],** Phillip Cleves[2], Jennifer Sneed[3], Valerie Paul[3], Cody Dickinson[4], Mark Hamann[4], Allen Place[1]

(1) University of Maryland Center for Environmental Science, Institute of Marine and Environmental Technology, 701 E Pratt Street, Baltimore, United States
(2) Carnegie Institution for Science, Department of Embryology, 3520 San Martin Drive, Baltimore, United States
(3) Smithsonian Marine Station at Fort Pierce, 701 Seaway Drive, Fort Pierce, United States
(4) Medical University of South Carolina, Department of Drug Discovery and Biomedical Sciences, College of Pharmacy, 70 President Street, Charleston, United States

Dinoflagellates are a taxonomic group of single-celled eukaryotes in the Alveolate lineage and are the major toxin-producing algae affecting humans. Toxin-producing dinoflagellates are often widely characterized as harmful algae or associated with harmful algal bloom (HAB) formations, yet Symbiodiniaceae, a charismatic family of dinoflagellates capable of forming endosymbiotic relationships with invertebrates, can also produce toxins. Polyketides zooxanthellamides and zooxanthellatoxins have been isolated from two free-living Symbiodiniaceae— *Symbiodinium pilosum* (strain no. Y-6) and *S. natans* (strain HA3-5)— but whether symbiotic species also possess this trait has remained largely unexplored. To address this research gap, we isolated material from free-living S. natans CCMP 2548 as well as symbiotic species *S. linucheae* (SSA01) and *Breviolum minutum* (SSB01) via a standard lipid extraction and a methanol gradient elution. HPLC revealed a high abundance of material absorbing at UV 225 nm in each of the 60% MeOH fractions. Time-of-flight mass spectrometry analyses further revealed the most abundant neutral monoisotopic masses produced by *S. natans* were Peak 1 2805 amu ($C_{138}H_{212}O_{57}$) and Peak 2 2959 amu ($C_{138}H_{238}O_{63}$). SSA01 was found to produce two smaller polyketides with parent masses Peak 1 964.5 amu ($C_{44}H_{84}O_{22}$) and Peak 2 920.5 amu ($C_{42}H_{80}O_{21}$). SSB01, however, does not appear to produce any major polyketides. Coral larvae were collected from the Florida Keys to finally assess the bioactivity of these compounds. Settlement assays conducted with whole algal cells, whole cell extracts, and isolated toxins demonstrated settlement and/or mortality of the larvae is species dependent.

**Keywords:** Polyketides, Toxins, Dinoflagellates

**Financing:** Smithsonian Marine Station; Institute of Marine and Environmental Technology; University of Maryland Center for Environmental Science; Marine, Estuarine, and Environmental Science Program University of Maryland.

**Acknowledgments:** Special thanks to Joanne Salzer and Jonathan Deeds for performing additional HPLC runs.

Parallel Session 10: Toxins & Other Microalgal Metabolite

O-050

# Untargeted metabolomics of cytotoxic extracts of the benthic dinoflagellate *Amphidinium eilatiense*

**María del Carmen Osorio-Ramírez**[1], Alan Gerardo Hernández-Melgar[2], Allan D. Cembella[1,3], Benjamin H. Maskrey[4], Lorena María Durán-Riveroll[5]

(1) Departamento de Biotecnología Marina, Centro de Investigación Científica y de Educación Superior de Ensenada, Ensenada, Baja California, Mexico
(2) Departamento de Innovación Biomédica, Centro de Investigación Científica y de Educación Superior de Ensenada, Ensenada, Baja California, Mexico
(3) Department of Ecological Chemistry, Alfred-Wegener-Institut, Helmholtz-Zentrum für Polar-und Meeresforschung, Bremerhaven, Germany
(4) Centre for Environment, Fisheries and Aquaculture Science (CEFAS), Barrack Road, The Nothe, Weymouth, UK
(5) SECIHTI-Departamento de Biotecnología Marina, Centro de Investigación Científica y de Educación Superior de Ensenada, Ensenada, Baja California, Mexico

Benthic dinoflagellates of the genus *Amphidinium* are rich sources of secondary metabolites. The chemical characterization of these metabolites is essential for understanding their structures and mechanisms of action, enabling the assessment of their therapeutic potential in treating various diseases. Several analytical techniques are employed, including mass spectrometry, infrared spectroscopy, and nuclear magnetic resonance. However, one of the main challenges in this field is the limited availability of pure compounds for analysis. To address this limitation, complementary approaches such as untargeted metabolomics on the fractions that showed the highest cytotoxic activity allow the identification and characterization of virtually all the metabolites produced by the organism, which could facilitate the discovery of new bioactive compounds with therapeutic potential. For this reason, in this study, two non-polar cytotoxic fractions (FNP-5 and FNP-6) from methanolic extracts of *A. eilatiense* cultures were analyzed. Untargeted metabolomic profiling was performed using LC-MS/MS in positive and negative ionization modes. Over 5000 features were detected, and ~1500 were annotated at level 2 and 3 of the MSI (Metabolomics Standard Initiative), revealing a broad chemical diversity landscape including molecules such as fatty acid, alkaloid, polyketide, and flavonoid biosynthetic pathways. The sub-fraction FNP-6 exhibited a higher abundance of unique metabolites and greater differential cytotoxic activity on cancerous and healthy cells. Identified compounds included erucamide, linoleamide, and 2',3'-dihydroxyflavone, all previously reported for their antitumor properties. These findings support *A. eilatiense* as a promising source of marine-derived compounds for oncological applications and underscore the value of untargeted metabolomics for discovering novel bioactive molecules.

**Keywords:** Antitumor compounds; cancer research; OMICS; phytobenthic, secondary metabolites

**Financing:** A1-S-8616/Consejo Nacional de Humanidades, Ciencias y Tecnologías Project 1009/Consejo Nacional de Humanidades, Ciencias y Tecnologías.

**Acknowledgments:** We thank Andrew Turner, Centre of Environment Fisheries and Aquaculture Science, for analyzing the samples.

Parallel Session 10: Toxins & Other Microalgal Metabolite

O-051

# Acquisition and evolution of the neurotoxin domoic acid biosynthesis genes in diatoms

**Nansheng Chen[1,2,4],** Ziyan He[1,2,3,4], Qing Xu[1,2,4,5], Shuya Liu[1,2,4], Huiyin Song[1,2,4], Hui Wang[1,2,3,4], Chui Pin Leaw[6], Zongmei Cui[1,2,4], Po Teen Lim[6], Suh Nih Tan[7], Yuichi Kotaki[8]

(1) Institute of Oceanology, Chinese Academy of Sciences, CAS Key Laboratory of Marine Ecology and Environmental Sciences
(2) Qingdao National Laboratory for Marine Science and Technology, Laboratory of Marine Ecology and Environmental Science
(3) University of Chinese Academy of Sciences, College of Marine Science
(4) Chinese Academy of Sciences, Center for Ocean Mega-Science
(5) China Three Gorges University, Hubei Key Laboratory of Tumor Microenvironment and Immunotherapy, College of Basic Medical Sciences
(6) University of Malaya, Bachok Marine Research Station, Institute of Ocean and Earth Sciences
(7) Xiamen University Malaysia, China-ASEAN College of Marine Sciences
(8) Tohoku University, Graduate School of Agricultural Science

Of the hitherto over 60 taxonomically identified *Pseudo-nitzschia* species, 26 have been confirmed to be toxigenic and/or be capable of producing the neurotoxin domoic acid (DA). In addition, an increasing number of non-*Pseudo-nitzschia* diatom species, including *Nitzschia navis-varingica*, have been found to be toxigenic and produce DA. Nevertheless, the acquisition and evolution of the toxin biosynthesis genes by this growing group of diatom species remains unclear. Through constructing high-quality chromosome-level genomes of more than 10 toxigenic diatom species of multiple genera and comparative genomics analysis, putative genomic integration sites for toxin biosynthesis genes in diatom species were explored. A “single acquisition, multiple independent losses (SAMIL)” model is proposed to explain the acquisition and evolution of the toxigenic genes in *Pseudo-nitzschia* species, and multiple independent acquisitions of toxin biosynthesis genes have been proposed to occur in the evolutionary history in diatom species of different genera.

**Keywords:** Domoic acid, Acquisition and evolution, Comparative genomics

**Financing:** The Strategic Priority Research Program of Chinese Academy of Sciences (XDB42000000).

Parallel Session 10: Toxins & Other Microalgal Metabolite

O-052

# Lipophilic cholinergic ligands from the marine cyanobacterium *Oscillatoria* cf. *bonnemaisonii*

**Rómulo Aráoz[1],** Edouard Nkogue-Andène[1], Denis Servent[1], Nicolas Elie[2], Dominique Laurent[3], Iñaki J. Guijarro[4], Muriel Delepierre[4]

(1) CEA-Saclay, DMTS, SIMOS, Bâtiment 152, 91191 Gif sur Yvette, France, 91191 Gif sur Yvette, France
(2) CNRS, Institute de Chimie des Substances Naturelles, 1 Av. de la Terrasse, 91191 Gif sur Yvette, France, France
(3) University Paul Sabatier Toulouse 3, UMR 152, BP 529, F-98713 Tahiti, French Polynesia, France
(4) Institut Pasteur, Université Paris Cité, CNRS UMR3528, Biological NMR and HDX-MS Technological Platform, 25 rue du Docteur Roux, 75015 Paris, France

Anthropogenic impact on the reef ecosystems in Raivavae Island (French Polynesia) was associated with the proliferation of benthic marine *Oscillatoria*. Human health issues have emerged following consumption of giant clams of the genus *Tridacna* in the areas where massive growth of benthic marine cyanobacteria was reported. Methanolic extracts of *Oscillatoria* cf. *bonnemaisonii*, which were collected from Raivavae Island reefs, were shown to block nerve-evoked muscle twitch and synaptic transmission in frog isolated neuromuscular preparations. The blockade of the amplitude of miniature-endplate potentials pointed the muscle nicotinic acetylcholine receptor as a potential target. Microplate receptor-binding assay, using *Torpedo marmorata* electrocyte membranes rich in nicotinic acetylcholine receptor of muscle type and biotinylated α-bungarotoxin as toxin tracer, was used for bio-guided purification of the marine lipophilic nicotinic ligands by preparative HPLC. High resolution mass spectrometry analyses of the active fraction showed a series of structure-related lipophilic molecules with overlapping elution times. NMR analyses confirmed the complexity of the mix. However, the exact masses and the fragmentation patterns obtained by high resolution mass spectrometry allowed the annotation of the bioactive molecules. The blockade of muscle nicotinic acetylcholine receptors by these lipophilic molecules was confirmed by two-electrodes voltage clamp electrophysiology using *Xenopus laevis* oocytes which were previously micro-transplanted with purified electrocyte membranes from *T. marmorata*. This study summarizes state-of-the-art methodologies for the discovery of bioactive molecules and their structural and functional characterization. Marine cyanobacteria are a valuable source of novel bioactive molecules.

**Keywords:** nicotinic acetylcholine receptors, Marine cyanobacteria harmful blooms, Toxin discovery

**Financing:** We acknowledge the French National Research Agency (ANR-21-CE34-0024 ICH-NEURO-MET to RA and JIG) and the INTERREG Atlantic Area (EAPA-0032/2022 BEAP_MAR to DS).

Parallel Session 10: Toxins & Other Microalgal Metabolite

O-053

# Chemical stability of prymnesins

**Tobias Mueller**[1], Urban Tillmann[1], Bernd Krock[1], Jan Tebben[1]

(1) Alfred Wegener Institut, Ecological Chemistry, Am Handelshafen 12, Bremerhaven, Deutschland

The haptophyte *Prymnesium parvum* is globally distributed and cause for massive fish kills, such as the Oder/Odra River incident in 2022, where 1000 tons of fish were killed by the prymnesins (PRMs) produced by *P. parvum*. The alga and its ichthyotoxic compounds have been studied for decades but little is known about the chemical properties and mode of action of the PRMs. Several studies found varying toxic effects of *P. parvum* and PRMs under different conditions but the effective concentrations of PRMs have not been quantified, due to a lack of standard and missing information about the stability of the compounds. PRMs are assumed to be unstable in aqueous environments. The chemical reactions of PRMs in water and the role of the quantity and composition of various water constituents for PRM stability are presumably essential for the toxic effects in natural ecosystems. In this work, HPLC-MS/MS measurements were conducted to quantify the chemical degradation of PRMs in aqueous conditions. The degradation products of PRMs will be identified and the influence of factors like pH, light exposure and temperature on PRM degradation will be evaluated. Whether chemical degradation via hydrolysis is the only or the main loss factor of PRMs will be evaluated. Adsorption experiments based on the Solid-Phase-Adsorption-Toxin-Tracking (SPATT) method reliably detected PRMs in aqueous media. This work fills a gap in the knowledge about the chemical properties of PRMs and their stability that is essential to consider when working with PRMs in a scientific framework.

**Keywords:** *Prymnesium parvum*, LC-MS/MS, SPATT

**Financing:** This work is funded by the German Federal Ministry of Education and Research (BMBF), grant number 16LW0561k.

Parallel Session 11: Ecology, Biology and Biogeography

O-054

# Blue holes and red tides: Underwater sink holes on the West Florida Shelf serve as a nutrient source for *Karenia brevis*

**Patricia Glibert**[1], Cynthia Heil[2], Emily Hall[2]

(1) University of Maryland Center for Environmental Science, Horn Point Laboratory, 2020 Horns Point Rd., Cambridge, MD, USA
(2) Mote Marine Laboratory, 1600 Ken Thompson Parkway, Sarasota, FL, USA

Blooms of the toxigenic dinoflagellate *Karenia brevis* are an almost annual occurrence in the eastern Gulf of Mexico, typically initiating in late summer and early fall months and terminating in late spring or earlier. Various nutrient sources have been proposed and measured to support these blooms, ranging from land based nutrient pollution to upwelling and in situ nutrient recycling. Although submarine ground water sources have been previously suggested as a potential nutrient source, mechanisms and fluxes have been rarely reported. Here, blue holes, the underwater sink hole features of the West Florida Shelf, were identified and nitrogen isotopic signatures of particulate material monitored monthly for several years, yielding new insight into the processes of nitrogen cycling that may occur within these holes and that may contribute new nitrogen in support of these blooms. Previously reported direct measurements within the holes of nitrogen concentrations and analysis of genes for metabolism suggested high rates of denitrification (nar, nir, nor, nos), and dissimilatory nitrate reduction to ammonia (DNRA, nrf). The del-15N record of particulate material was directly related to river flow with a few months lag; low flow led to more enriched del-15N, implying more time for N processing to occur. Historical reports of *Karenia* within 10 km of known blue holes show that *K. brevis* can concentrate in these locations, and these holes appear also to be hot spots for a diversity of *Karenia* species.

**Keywords:** *Karenia brevis*, nutrient fluxes, groundwater

**Financing:** NOAA ECOHAB Award NA19NOS4780183, NSF OCE2309082

**Acknowledgments:** We thank the Mote Marine Laboratory field crew for sample collection and Victoria Devillier for assistance with sample processing.

Parallel Session 11: Ecology, Biology and Biogeography

O-055

# Dead or alive? How dinoflagellate HABs shift the coastal hypoxia paradigm

**Christopher Gobler**[1]

(1) Stony Brook University, School of Marine and Atmospheric Sciences, SUNY Distinguished Professor, 239 Montauk HWY, Southampton, United States

Harmful algal blooms and hypoxia are common environmental phenomena in coastal zones that can be promoted by eutrophication. In large estuarine and coastal ocean systems, hypoxia is traditionally viewed as the outcome of a seasonal succession of events beginning with an increase in pelagic primary productivity followed by algal bloom senescence, the sinking of bloom-derived organic matter, and the respiration of that organic matter causing low dissolved oxygen (DO) conditions in bottom waters. In shallower estuaries prone to dinoflagellate HABs, however, evidence is accumulating that hypoxia can occur during HABs, begging the question: are hypoxia events always driven by algal bloom senescence or can it be caused by dinoflagellates and associated plankton communities during HABs? Answers to this question have critical implications to understand the true risk that HABs pose to coastal ecosystems. This presentation will review the classical view of how hypoxic zones are established, often by diatom blooms in large estuarine or coastal systems including the Gulf of Mexico, Chesapeake Bay, the Baltic Sea, and Eastern Coastal Boundary Systems. This will be contrasted with evidence from shallower, high retention, eutrophic, estuaries where hypoxia can be a nightly-occurrence during HABs. For example, data will be presented from *Dinophysis acuminata* and *Margalefidinium polykrikoides* blooms in NY, USA, that co-occur with extended nocturnal hypoxia (>12 hours/day) including DO levels < 1 mg/L. The co-occurrence of nocturnal hypoxia and HABs coupled with strong diel cycling of DO may be a more significant threat to marine life than chronic hypoxia without HABs.

**Keywords:** hypoxia, paradigm shift, risk assessment

**Financing**: This work was funded by NOAA's National Centers for Coastal Ocean Science (NCCOS) programs.

**Acknowledgments**: The author acknowledges the assistance of graduate students Adrienne Tracy and Mairead Farrell.

Parallel Session 11: Ecology, Biology and Biogeography

O-056

# Microplastics and microalgae-phycotoxins: A synergistic toxicological risk in marine aquaculture environments

**Jorge I. Mardones**[1], Valentina Giraldó[2], Lara Marcus[3], Maria José Nariño[4], Caroline Montes[1]

(1) Instituto de Fomento Pesquero (IFOP), Centro de Estudios de Algas Nocivas (CREAN), Padre Harter 574, Puerto Montt, Chile
(2) Universidad de Bogotá Jorge Tadéo Lozano, Facultad de Ciencias Naturales e Ingeniería, Santa Marta, Colombia
(3) Universidad San Sebastián, Facultad de Ciencias, Puerto Montt, Chile
(4) Universidad Austral de Chile, Doctorado en Ciencias de la Acuicultura, Puerto Montt, Chile

The interaction between aquaculture-derived microplastics (MPs) and harmful algal bloom (HAB)-related toxins remains a poorly understood but emerging concern in marine ecotoxicology. This study explores the isolated and combined effects of high-density polyethylene (HDPE) and polypropylene (PP) microplastics—commonly derived from buoys and ropes—on the toxic dinoflagellate *Karenia selliformis* and their subsequent impacts on RTgill-W1 fish gill cell lines. Fragmented MPs were characterized and introduced into *K. selliformis* cultures at environmentally relevant concentrations (50–2000 mg/L) over 30 days, with and without polarity alteration using Tween 80. Supernatants from algal cultures were filtered and exposed to RTgill-W1 cells for cytotoxicity analysis via metabolic and lysosomal activity assays. Results revealed that HDPE-MPs significantly suppressed *K. selliformis* cell densities by up to 39%, while the presence of Tween 80 modulated the growth response in both inhibitory and stimulatory ways. Critically, RTgill-W1 cells exposed to the microalgae-MP supernatants exhibited marked declines in viability, particularly at longer exposure times and in the absence of Tween 80, suggesting cumulative cytotoxic effects due to MP-adsorbed phycotoxins. These findings underscore a dual biological threat: MPs may not only influence toxin-producing microalgae, but also potentiate the toxicity of their exudates to aquaculture-relevant species such as *Oncorhynchus mykiss*. Our work highlights the importance of evaluating MP-phycotoxin co-exposures in ecotoxicological risk assessments and suggests that common aquaculture materials may exacerbate the biological impact of HABs in marine ecosystems.

**Keywords:** Microplastics-Phycotoxin Interactions, *Karenia selliformis*, Toxicity, Aquaculture Ecotoxicology

Parallel Session 11: Ecology, Biology and Biogeography

O-057

# Realized niche of *Pseudo-nitzschia* spp. in a coastal upwelling center off Central Chile

**Catharina Alves-de-Souza[1,2],** Fabián J. Tapia[1,2], Marcelo H. Gutiérrez[1,2], Valentina Valdés-Castro[2], Bárbara Jacob[3,4], Humberto E. González[5]

(1) Universidad de Concepción, Departamento de Oceanografía, Facultad de Ciencias Naturales y Oceanográficas, Concepción, Chile
(2) Universidad de Concepción, Centro de Investigación Oceanográfica COPAS Coastal, Concepción, Chile
(3) Centro de Investigación en Ecosistemas de la Patagonia (CIEP), Coyhaique, Chile
(4) Centro de Estudios Avanzados en Zonas Áridas (CEAZA), Coquimbo, Chile
(5) Universidad Austral de Chile, Centro de Investigación en Dinámica de Ecosistemas Marinos de Altas Latitudes (UACh-IDEAL), Valdivia y Punta Arenas, Chile

Harmful algal blooms caused by diatoms of the genus *Pseudo-nitzschia* have considerable ecological and economic consequences due to their production of domoic acid (DA), a potent neurotoxin harmful to marine organisms and human health. While *Pseudo-nitzschia* species have not yet been observed forming blooms in the coastal upwelling zone off Central Chile, toxic DA levels have been frequently detected in shellfish, raising concerns about the latent potential for future bloom events. Here, we assess the realized niche of *Pseudo-nitzschia* spp. during the upwelling season (October to March), based on a 10-year dataset obtained from "Station 18" (36°30.80'S, 73°07.75'W), a long-term time-series site located approximately 18 nautical miles (~30 km) off Central Chile. Outlying Mean Index (OMI) analysis revealed that *Pseudo-nitzschia* occupies a narrower and more marginal realized niche compared to dominant diatoms in the region (i.e., *Skeletonema*, *Chaetoceros*, and *Thalassiosira* species). Specifically, *Pseudo-nitzschia* spp. exhibited higher abundances under elevated temperatures (13–15 °C), stratified conditions (Brunt-Väisälä frequency = 0.1–0.2), reduced riverine discharge (>5,000 $m^3$ $s^{-1}$), and lower silicate concentrations (10–30 µM). Documented trends over the past two decades—declining silicate availability and diminished river flow—combined with marine heatwave events observed in this area, may create favorable conditions for high-density *Pseudo-nitzschia* blooms. Future research should focus on resolving species-level dynamics within the *Pseudo-nitzschia* complex, improving early warning models by integrating oceanographic and biogeochemical drivers, and assessing the influence of climate variability on bloom potential in this ecologically sensitive upwelling system.

**Keywords:** Upwelling, *Pseudo-nitzschia*, Realized niche

**Acknowledgments:** We are grateful to the Department of Oceanography UdeC, for providing access to the "Station 18" long-term dataset.

Parallel Session 12: Cyanobacteria & Freshwater HABs

O-058

# Uncovering intraspecific trait plasticity in harmful cyanobacteria: A functional trait approach to understand bloom dynamics

**Arnaud P. Louchart**[1], Annemieke M. Drost[1,2], Chaohong Lin[1,2], Suzanne M.H. Naus-Wiezer[1], Zhipeng Duan[3], Elena Litchman[4], Dedmer Van de Waal[1,2]

(1) Department of Aquatic Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, The Netherlands
(2) Department of Freshwater and Marine Ecology, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, Amsterdam, The Netherlands
(3) College of Environment, Hohai University, 1 Xikang Road, Nanjing, Jiangsu 210098, China
(4) Kellogg Biological Station, Michigan State University, MI 49060, Hickory Corners, USA

Trait-based approaches offer a mechanistic framework for understanding how individual phytoplankton respond to their environment, with implications for population and community dynamics. These approaches often consider traits being fixed at an organism level, overlooking intraspecific variation and phenotypic plasticity. To address this, we applied a functional trait approach at the cellular level using high-throughput flow cytometry to capture traits of harmful cyanobacteria at the individual level. We assessed the trait plasticity of Microcystis spp. in laboratory cultures exposed to gradients of light, nitrogen, and phosphorus. This allowed us to quantify intraspecific trait variation and examine how these traits respond to resource limitation. We then extended these findings to natural communities by applying a novel data analysis framework that uses trait-response patterns as ecological fingerprints. This approach enabled us to explore how resource availability influences the distribution and prevalence of cyanobacteria in lakes. Our results reveal that trait plasticity is a key factor in shaping cyanobacterial community structure and may help explain the conditions under which blooms emerge. This trait-based perspective offers new insights into the ecological mechanisms underlying harmful cyanobacterial blooms, providing a potential framework for assessing lake ecological status and informing management strategies.

**Keywords:** Cyanobacteria, Harmful algal bloom, Trait plasticity

Parallel Session 12: Cyanobacteria & Freshwater HABs

O-059

# Microdiversity of *Microcystis aeruginosa* complex shows an incredible diversity of ecotypes

**Gabriela Martínez de la Escalera**[1], Carla Kruk[2], Angel Segura[3], Frederick M. Cohan[4], Claudia Piccini[1]

(1) Laboratorio de Ecología Microbiana Acuática, Departamento de Microbiología, Instituto de Investigaciones Biológicas Clemente Estable (IIBCE), Montevideo, Uruguay
(2) Sección Limnología, Instituto de Ecología y Ciencias Ambientales, Facultad de Ciencias, UdelaR, Montevideo, Uruguay
(3) Departamento de Modelación Estadística de Datos e Inteligencia Artificial, Centro Universitario Regional del Este, UdelaR, Rocha, Uruguay
(4) Department of Biology, Wesleyan University, Middletown, Connecticut, USA

The species of the *Microcystis aeruginosa* complex (MAC) have been defined according to the morphology of their colonies (morpho-species). However, the morpho-species are not always phylogenetically coherent and can be the results of phenotypic plasticity. This masks the microdiversity of this group. In previous studies we demonstrated that there are different ecotypes adapted to local environmental conditions. However, the method used to detect ecotypes (qPCR-HRMA of community samples) did not allow us to individualize the sequences corresponding to each one. In this work, we used a complementary approach to identify the ecotypes adapted to each environmental condition. To this purpose, we obtained and analyzed MicrocystismcyJ sequences from water samples (Uruguay river-Río de la Plata estuary) to obtain phylogenetic information that was applied to the Ecotype Simulation v.2 program. This software was designed to delimit ecotypes and to evaluate their relationship with the environment. A total of 27 ecotypes were detected with an abundance higher than 1500 reads. The relative abundance of each ecotype varied according to different environmental conditions such as season and ecosystem type. We defined ecotypes with different environmental preferences for temperature, conductivity and turbidity. This work proposes a new way of analyzing the microdiversity of toxic MAC based on phylogenetic and ecological traits, which allows a better understanding of the environmental mechanisms that determine the community assemblage. This will contribute not only to the construction of the theoretical framework, but also to the understanding of the dynamics of organisms that constitute a serious environmental problem.

**Keywords:** *Microcystis aeruginosa* complex, Microdiversity, ecotypes

**Financing:** Agencia Nacional de Investigación e Innovación, proyecto Fondo Clemente Estable.

Parallel Session 12: Cyanobacteria & Freshwater HABs

O-060

# Functional and genetic diversity of bloom-forming cyanobacteria in the Laurentian Great Lakes

**Carol Waldmann Rosenbaum[1],** Elena Litchman[1], Anders Kiledal[2]

(1) Michigan State University, Integrative Biology
(2) University of Michigan

Cyanobacterial harmful algal blooms' (cHABs) frequency and severity in the Laurentian Great Lakes (LGL) are both on the rise. Despite diverse environments across the LGLs, the same bloom-forming taxa are present in all five lakes, suggesting that these cyanobacterial genera have adapted to a broad range of conditions. Although blooms are dominated by few cyanobacterial genera, there is great inter- and intraspecific genetic and functional diversity within these genera, which may aid cyanobacterial adaptation to local conditions. We explore the breadth of bloom-forming cyanobacterial genetic diversity in the LGL by sequencing over 300 strains isolated from Lakes Superior, Huron, Michigan, and Erie in 2022 and 2023. We used trait bioassays to investigate how temperature and nutrient traits vary across and within cyanobacterial populations in the LGLs. We found that *Dolichospermum* and *Aphanizomenon* strains had higher nitrogen and phosphorus affinities than *Microcystis*, except for Green Bay strains, where Microcystis strains had higher phosphorus affinity. Across lakes, *Microcystis* strains had higher temperature optima than the other genera. In general, trait diversity is higher between genera than across lakes. Our results contribute to evidence of great inter- and intraspecific functional diversity within and across cyanobacterial LGLs populations. Further comparing genetic and functional traits with environmental data would contribute to mechanistic explanations of community dynamics and help us understand species abundance and succession across environmental gradients such as in the LGLs.

**Keywords:** Cyanobacteria, Traits, Great-Lakes

**Financing:** Cooperative Institute for Great Lakes Research (CIGLR), Michigan State Ecology, Evolution, and Behavior Program.

Parallel Session 12: Cyanobacteria & Freshwater HABs

O-061

# Characterizing the freshwater cyanobacterium, *Microcystis aeruginosa*, using digital holography

**Madison Bennett**[1,3], Olivia Ruchti[1,3], Karuna Agarwal[1], Addison Ryne[4], Aditya Nayak[1,2]

(1) Florida Atlantic University, Harbor Branch Oceanographic Institute, 5600 US-1 N, Fort Pierce, FL 34946, Fort Pierce, United States
(2) Florida Atlantic University, Ocean and Mechanical Engineering, 777 Glades Rd, Boca Raton, FL 33431, Boca Raton, United States
(3) Florida Atlantic University, Biological Sciences, 777 Glades Rd, Boca Raton, FL 33431, Boca Raton, United States
(4) California State University-Monterey Bay, Marine Science, 100 Campus Ctr, Seaside, CA 93955, Seaside, United States

*Microcystis aeruginosa* is a bloom-forming freshwater colonial cyanobacterium, which can significantly impact freshwater and estuarine ecosystems. Quantifying the cell number and spatial arrangement within colonies is crucial to understanding bloom dynamics and toxicology. Digital holography, a non-invasive volumetric imaging approach, can enable in situ characterization of 3-D distributions of *Microcystis* colony sizes and abundances. Holography encodes depth to high-resolution images by illuminating a sample volume with a laser and recording the diffraction patterns as holograms, which can then be reconstructed numerically to focus on 2D planes at varying depths. However, while colony abundances are easily obtained, cell counts are considerably more challenging to quantify, leading to a critical gap in existing methodologies.

Here, we present laboratory experiments using holography to establish an empirical correlation between *Microcystis* colony size and cell counts. Morphologically diverse strains of *M. aeruginosa* colonies isolated and cultured from Lake Okeechobee and Lake Erie, two large freshwater bodies in the US, are used. Each experiment involves: (i) holographic imaging of a single colony; (ii) sonication to separate colonies into individual cells; and (iii) cell counts using flow cytometry and holography. Numerous replicates across colony sizes and shapes are analyzed. Separately, confocal microscopy is used to scan colonies plane-by-plane in depth for high resolution three-dimensional information. This technique enables measurement of average colony thickness and porosity for each strain, which is incorporated into data processing. Successful development of this empirical relationship will support rapid in situ cell quantification using a custom-built holographic system deployable during different bloom conditions.

**Keywords:** *Microcystis aeruginosa*, In Situ Instrumentation, Freshwater HAB Monitoring

Parallel Session 12: Cyanobacteria & Freshwater HABs
O-062

# Silent stress: Iron limitation suppresses cyanobacterial growth but elevates toxin risk

**Charlie Trick**[1], Sathya Ganegoda[1], Kevin Erratt[1], Irena Creed[1]

(1) University of Toronto, Department of Physical and Environmental Sciences, DPES, Toronto, Canada

The Prairie Pothole Region of North America is experiencing widespread and intensifying cyanobacterial blooms. Yet, the drivers of bloom persistence and toxigenicity in these shallow, nutrient-rich lakes remain incompletely understood. We surveyed over 100 lakes spanning oligotrophic to hypereutrophic conditions and a broad salinity gradient (~100 to >100,000 µS/cm) to assess how macro- (phosphorus [P], nitrogen [N]) and micronutrient (iron [Fe]) availability interact to constrain cyanobacterial growth. Contrary to the long-standing assumption that macronutrients alone govern cyanobacterial limitation, we identified 32 eutrophic lakes that were neither P- nor N-limited. In these systems, modelled free ferric iron ($Fe^{'}$) levels exceeded the threshold for biological limitation (pFe > 20), suggesting that Fe availability emerged as a key bottleneck to further biomass accumulation. Although cyanobacteria can produce Fe-scavenging siderophores to overcome macro-nutrient limitation, cell biomass in Fe-limited lakes was not correlated with the concentration of siderophores, indicating that even these adaptive mechanisms were insufficient under extreme Fe scarcity. Across the salinity gradient, Fe-limitation was most pronounced in moderately to highly saline lakes, where ionic strength and sulphate likely reduced Fe bioavailability via precipitation and speciation shifts. These Fe-limited lakes also showed a strong positive association with cyanotoxin production, implicating Fe stress, not only as a brake on biomass, but also as a trigger for increased toxigenicity—potentially mediated by siderophore-linked regulatory pathways. These findings challenge classical paradigms of nutrient control in eutrophic systems and highlight a micronutrient-mediated paradox: cyanobacteria constrained by Fe in nutrient-rich, saline lakes exhibit slow growth yet elevated toxin risk.

**Keywords:** cyanotoxins, salinity, siderophores

**Financing:** Natural Sciences and Engineering Research Council of Canada (NSERC) Discovery Grant (05265-2019) awarded to Irena Creed.

Parallel Session 12: Cyanobacteria & Freshwater HABs

O-063

# Salinity thresholds drive nonlinear cyanobacterial toxin responses in prairie lakes

**Irena Creed**[1], Kevin Erratt[1], Daniel Beach[2], Charles Trick[1]

(1) University of Toronto, Department of Physical and Environmental Sciences, 1065 Military Trail, Toronto, Canada
(2) National Research Council Cana, Metrology Research Centre, 1411 Oxford Street, Halifax, Canada

Rising salinity is reshaping the dynamics of cyanobacterial blooms across Canada's Prairie Pothole Region. By integrating historical salinity records with contemporary surveys from 100+ lakes, we reveal high interannual variability in lake salinity—ranging from 100 to 100,000 µS/cm. Using phycocyanin fluorescence as a proxy for cyanobacterial biomass, FlowCAM imaging for community composition, and LC–MS/MS for toxin profiling, we identified two distinct salinity thresholds—around 1,000 µS/cm and 10,000 µS/cm—associated with elevated hepatotoxin concentrations.

At the freshwater-to-brackish threshold (~1,000 µS/cm), mixed cyanobacterial assemblages—including *Aphanizomenon*, *Dolichospermum*, *Planktothrix*, and *Microcystis*—produced elevated concentrations of microcystins (up to 500 µg/L), primarily MC-LR and MC-LA. At the brackish-to-saline threshold (~10,000 µS/cm), dominance shifted to *Microcystis* and *Nodularia*, which produced even higher concentrations toxins (up to 2,000 µg/L) of more potent toxins, including [Leu$^1$]MC-LR, [Leu$^1$]MC-LY, and nodularin-R.

Our findings reveal that bloom risk peaks not at the highest salinity levels, but at intermediate thresholds where cyanobacteria exhibit nonlinear and intensified toxin production. This elevated toxin synthesis is likely not merely a consequence of physiological stress, but part of a broader suite of adaptive strategies that enhance cyanobacterial fitness under fluctuating environmental conditions. These bimodal dynamics challenge traditional nutrient-centric bloom models and highlight the importance of incorporating salinity regimes into forecasting frameworks. As climate change accelerates salinization–desalinization cycles in freshwater lakes, pinpointing when and where these thresholds are crossed will be essential for proactive and effective management of cyanobacterial bloom risks.

**Keywords:** salinity, toxin, prairie lakes

**Financing:** Natural Sciences and Engineering Research Council of Canada (NSERC) Discovery Grant (05265-2019) awarded to Irena Creed.

Parallel Session 13: Toxins & Other Microalgal Metabolites

O-064

# Cyanotoxins in marine and freshwater cyanobacteria from LEGE-CC, Portugal

**Flavio Luis de Oliveira**[1,2], Joana Azevedo[1], Raquel Silva[1], Guilherme Scotta Hentschke[1], Joao Morais[1], Pedro Cruz[1,2], Gabriela Alves Moreira[1,3], Carlos Pinheiro[1], Vitor Vasconcelos[1,2]

(1) CIIMAR/CIMAR LA – Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Avenida General Norton Matos s/n, 4450-208, Matosinhos, Portugal
(2) University of Porto, Department of Biology, Faculty of Science, Rua do Campo Alegre 1021, 4169-007, Porto, Portugal
(3) E2S, Polytechnic of Porto, Rua Dr. Roberto Frias, 712, 4200-072, Porto, Portugal

Culture collections play a crucial role in preserving cyanobacterial diversity, supporting toxicological and biotechnological research. The Blue Biotechnology and Ecotoxicology Culture Collection (LEGE-CC) is one of the world's significant repositories of cyanobacterial and microalgal strains located at the Interdisciplinary Centre of Marine and Environmental Research (CIIMAR) in Portugal, with over 1500 strains. This study aimed to screen LEGE-CC cyanobacterial strains from different environments for cyanotoxin biosynthesis genes and production. PCR-based molecular assays targeting gene clusters associated with cylindrospermopsin (CYN), saxitoxin (STX), anatoxin (ANA), microcystin (MC), and β-N-methylamino-L-alanine (BMAA) production were performed, and sequencing of amplicons of the expected sizes was done. Strains testing positive were cultivated, and their cyanotoxin production was confirmed using liquid chromatography–mass spectrometry (LC-MS). Molecular screening revealed the presence of cyanotoxin biosynthesis genes in 56 strains out of 1200 strains, with 5 strains for CYN (8.8%), 7 for STX (12.3%), 12 for ANA (21.0%), 14 for MC (26.3%), and 18 for BMAA (35.6%). LC-MS analyses confirmed cyanotoxin production for some strains. A notable higher frequency of cyanotoxin-producing strains was observed in freshwater/terrestrial isolates (91%), with Portugal (including Azores Island) strains represented 87.7% of all cyanotoxins producing strains. This work highlights the importance of systematic cyanotoxin screening in culture collections. The integration of molecular and chemical approaches, such PCR and LC-MS confirmation, ensures accurate detection of cyanotoxin producers and expands our understanding of cyanotoxin distribution across diverse cyanobacterial taxa and environments. These findings will support future ecological, toxicological, and biotechnological studies involving cyanobacteria from the LEGE-CC.

**Keywords:** Molecular screening, LC-MS analysis, Culture collection

**Financing:** This research was funded by FCT Projects UIDB/04423/2020, UIDP/04423/2020, WP9-Portuguese Blue Biobank (C644915664-00000026), and FO thanks to FCT scholarship UI/BD/06241/2021.

**Acknowledgments:** We thank LEGE-CC for providing the data and strains for this study.

Parallel Session 13: Toxins & Other Microalgal Metabolites

O-065

# Toxin profiles of *Alexandrium ostenfeldii* (Dinophyceae) strains isolated from the Beagle Channel: Spirolide diversity

**Luis Norambuena**[1], Pablo Salgado[2], Bernd Krock[3,4], Alexander Brevis[4,5], Gemita Pizarro[2], Máximo Frangópulos[6,7,8], José Luis Iriarte[9]

(1) Instituto de Fomento Pesquero, Padre Harter 574, Puerto, Chile
(2) Instituto de Fomento Pesquero, Enrique Abello 0552, Punta Arenas, Chile
(3) Alfred Wegener Institut-Helmholtz Zentrum für Polar- und Meeresforschung (AWI), Bremerhaven 27570, Bremerhaven, Germany
(4) Universidad de Concepción, Centro de Investigación Oceanográfica COPAS Coastal, Concepción, Chile
(5) Laboratorio de Biotoxinas Marinas de la U. de Concepción (LBTx-UdeC), Victor Lamas 1290, P.O. Box 160-C, Concepción, Chile
(6) Centro de Investigación GAIA Antártica (CIGA), Universidad de Magallanes, Av Bulnes 01855, Punta Arenas, Chile
7) Cape Horn International Center (CHIC), Universidad de Magallanes, Puerto Williams, Chile
(8) Millenium Institute Biodiversity of Antarctic and Subantarctic Ecosystem (BASE), Las Palmeras 3425, Santiago, Chile
(9) Centro FONDAP de Investigación en Dinámica de Ecosistemas Marinos de Altas Latitudes (IDEAL), Instituto de Acuicultura y Ciencias Ambientales, UACh, Puerto Montt, Chile

*Alexandrium ostenfeldii* (Dinophyceae) is the only known toxin-producing dinoflagellate that can produce paralytic shellfish toxins (PSTs), spirolides (SPXs) and gymnodimines (GYMs). We studied the toxin-producing capacity of three strains of *A. ostenfeldii*, germinated from resting cysts collected in Yendegaia Bay (central Beagle Channel), during the EXOFAN survey. PSTs were quantified by HILIC-UHPLC MS. The presence of PSTs GTX 2/3, C 1/2 and saxitoxin (STX) could be determined in all the three strains. Various mass spectrometric experiments were applied to study gymnodimines and spirolides, including Selected Reaction Monitoring (SRM), precursor ion and product ion analysis. We were unable to detect any GYM analogue in the studied strains. In contrast, we detected a large number of spirolides in all three strains. The main spirolide was 13-desmethyl-spirolide C (SPX1). Other potential spirolides were found at m/z 618 and m/z 592, which putatively are identical to spirolides, which were recently detected in waters of the northern part of the Atlantic Patagonian Shelf and in the Eastern Beagle Channel. Additionally, other low abundant spirolides were detected, including some not yet reported variants. This study demonstrates the great diversity of spirolides produced by *A. ostenfeldii* strains in subantarctic waters and is in line with the high variability of toxin production by this dinoflagellate species.

**Keywords:** LC MS/MS; PST; Patagonia

**Financing:** CONICYT/ANID-PIA AUB2000006Convenio desempeño IFOP-MINECON y EMT 2024

**Acknowledgments:** Biotoxin Laboratory Concepción University (LBTx-UdeC), COPAS-COASTAL ANID FB210021, and FONDEQUIP EQM210168 ASSOCIATIVE Research Program PIA-CONICIT/ANID.

Parallel Session 13: Toxins & Other Microalgal Metabolites

O-066

# Prevalence and distribution of dissolved phycotoxins in seawater in the Yellow Sea and the Bohai Sea, China

**Jiangbing Qiu**[1], Xiaoyun Wang[1], Dongyue Li[1], Aifeng Li[1]

(1) Ocean University of China, Environmental Science, College of Environmental Science and Engineering, No. 238 Songling Road, Qingdao, China

Phycotoxins could be secreted by toxin-producing microalgae or released by ruptured cells in seawater. In this study, the distribution of dissolved paralytic shellfish toxins (PSTs) and lipophilic shellfish toxins (LSTs) in the Yellow Sea and the Bohai Sea, China, was investigated by two surveys in April and July 2023. Seawater samples were collected from the surface, middle and bottom layers, and the profiles of PSTs were analyzed by liquid chromatography-tandem mass spectrometry (LC-MS/MS), and the spatial distribution characteristics of dissolved phycotoxins and their correlation with environmental factors were explored. Results showed that C1/2, GTX1/4, GTX2/3, dcGTX2/3, OA, DTX1 and PTX2 were detected in seawater samples in both spring and summer. The detection rates of PSTs and LSTs in spring and summer seawater samples were more than 97%. The concentrations of total PST and LSTs in seawater varied across different layers and seasons, with PSTs ranging from 12-590 pmol/L (spring surface), 9.3-546 pmol/L (spring middle), 12-2,452 pmol/L (spring bottom), and not detected (nd)–188 pmol/L (summer surface), and LSTs ranging from nd-13.86, 1.60-17.03, 2.73-17.39, and 1.26-30.21 pmol/L in the corresponding layers. Significant differences in phycotoxin concentrations were observed in the vertical water column across different sea areas, and notably lower toxin levels were found in surface waters during summer than in spring. These results indicate that phycotoxins were prevalent in the Yellow Sea and the Bohai Sea, of which the potential hazard to marine organisms should be highly concerned.

**Keywords:** Phycotoxins, Seawater, Spatial distribution

**Financing:** The National Natural Science Foundation of China-Shandong Joint Fund (grant No. U2106205), and the Special Foundation for Taishan Scholar of Shandong Province (grant No. tstp20231216).

Acknowledgments: Data and samples were collected onboard the "Lanhai 101" implementing the open research cruise NORC2023-01 supported by NSFC Shiptime Sharing Project (grant No. 42249901).

Parallel Session 13: Toxins & Other Microalgal Metabolites

O-067

# 10-year study of the occurrence and distribution of lipophilic marine toxins in shellfish from production areas in Chile

Benjamín A Suárez-Isla[1], Daniel Carrasco[1], **Fernanda Barrera[1],** Leonardo Cigarra[1], Ignacio Rubilar[1]

(1) University of Chile, Laboratory of Marine Toxins Institute of Biomedical Sciences, Faculty of Medicine, Av. Independencia 1027, Santiago, Chile

Lipophilic marine biotoxins accumulate in shellfish and can have a negative impact on human health and the local economy. An important mussel aquaculture area has developed in the Los Lagos region (41°-43°30'LS), where over 400,000 tons of mussels (*Mytilus chilensis*) were landed in 2024. The application of a UHPLC-MS/MS method for lipophilic toxins, as part of a national shellfish sanitation program from 2015 to 2025 (PSMB-Sernapesca) led to a detailed overview of toxin occurrence and distribution in over 100 sampling stations. During this period, toxins were detected in 14.8% of all samples (4422 of 29680). Yessotoxin accounted for 78% of all detected samples and this correlated well with the abundance of *Protoceratium reticulatum* at some sites. Pectenotoxin-2 was detected in 20.7 % of the detected samples and correlated with the presence of *Dinophysis acuminata*. Significantly fewer samples contained okadaic acid, dinophysistoxin-1 and -2 (0.4 %) and azaspiracid-1, 2 and 3 (0.7 %). The toxin levels did not exceed the maximum levels, except for one *P. reticulatum* bloom in 2022 with YTX (5.93 mg Eq YTX/kg) that led to precautionary closures. The number of detections of YTX, the abundance of *P. reticulatum* and the toxicity values showed a clear north-south gradient decreasing with latitude. A similar trend was observed for PTX2 and *D. acuminata*. These results indicate that the Los Lagos region is characterized by a very low prevalence of diarrheagenic lipophilic toxins (AO, DTX and AZA) and a low accumulation of these toxins in mussels.

**Keywords:** early warning, monitoring, lipophilic toxins

**Financing:** IAEA Projects RLA7022, RLA 7025, RLA7028, CHI7014 and analysis proceeds

**Acknowledgments:** We are grateful to IAEA Technical Cooperation Program and Comisión Chilena de Energía Nuclear (CCHEN) for their support.

Parallel Session 14: Taxonomy and Phylogeny

O-068

# Revisiting the taxonomy of *Prymnesium parvum*: Historical challenges

**Urban Tillmann**[1], Øjvind Moestrup[2]

(1) 1Alfred Wegener Institute, Helmholtz Center for Polar and Marine Research, Bremerhaven, Germany
(2) University of Copenhagen, Department of Biology, Marine Biological Section, Universitetsparken 4, DK-2100 Copenhagen Ø, Denmark

The haptophyte genus *Prymnesium* includes important ichthyotoxic species responsible for harmful algal blooms (HABs) in marine and brackish ecosystems. Among these, *Prymnesium parvum* Carter is the most well-studied due to its ecological impact and toxin production. However, significant issues persist in the formal taxonomy of the genus, which may complicate ecological and regulatory work. A primary concern is the type species, *Prymnesium saltans* Massart, which remains poorly characterized morphologically and genetically. This undermines the stability of the genus and hampers efforts to delineate species boundaries, especially between *P. saltans*, *P. minutum* and *P. parvum*.

For *P. parvum*, ITS sequence data and prymnesin profiles recently revealed the existence of at least three distinct clades, raising questions about species boundaries and potential cryptic diversity. However, a major taxonomic complication arises from the original description of *P. parvum* by Nelly Carter in 1937. In her work, Carter listed *Wyssotzkia gladiociliata* Büttner as a synonym of *P. parvum*, stating it was "probably identical" with her newly described species. This ambiguous synonymization introduces uncertainty into the historical and taxonomic lineage of *P. parvum,* raising questions about its true identity and the status of earlier taxa.
This presentation examines these issues through a historical and taxonomic lens. Addressing taxonomic ambiguities is essential for accurate species identification, environmental monitoring, and bloom management strategies. The case of *Prymnesium* illustrates broader challenges in algal taxonomy where ecological relevance and nomenclatural stability must be reconciled.

**Keywords:** *Prymnesium*, taxonomy

**Financing:** This work was funded by the Federal Ministry of Education and Research (BMBF), grant number 16LW0561k.

Parallel Session 14: Taxonomy and Phylogeny

O-069

# The critical role of biological sample curation in advancing research on *Eutreptiella* (Euglenophyceae/Euglenozoa)

**Sinuhé Hernández Márquez**[1,2], María Eugenia Zamudio Resendiz[2], María Luisa Núñez Resendiz[3], Laura Margarita Márquez Valdelamar[5], Nelly María López Ortiz[5], Montserrat Murrieta Alarcón[2], Kurt M. Dreckmann[3], Ricardo Caballero Fuentes[4], Abel Sentíes[3]

(1) Universidad Autónoma Metropolitana, Doctorado en Ciencias Biológicas y de la Salud, Ciudad de México, México
(2) Universidad Autónoma Metropolitana Iztapalapa, Laboratorio de Fitoplancton Marino y Salobre, Departamento de Hidrobiología, Ciudad de México, México
(3) Universidad Autónoma Metropolitana Iztapalapa, Laboratorio de Macroalgas Marinas y Salobres, Departamento de Hidrobiología, Ciudad de México, México
(4) Universidad Autónoma de Guerrero, Facultad de Ecología Marina, Acapulco de Juárez, México
(5) Universidad Nacional Autónoma de México, Instituto de Biología, Pabellón de la Biodiversidad, Laboratorio de Secuenciación Genómica de la Biodiversidad, Ciudad de México, México

The genus *Eutreptiella* is widely distributed in marine and brackish environments and plays a key role in microbial food webs. Despite its ecological importance, its taxonomy remains problematic due to frequent misidentifications. Many sequences in GenBank are incorrectly assigned, as species are often identified based solely on molecular data without proper morphological validation. This leads to errors in phylogenetic analyses and misinterpretations of biodiversity and species distribution, ultimately affecting ecological studies. Additionally, the genus *Eutreptiella* is known to form harmful algal blooms (HABs), which further underscores the need for accurate species identification. Our results confirm these inconsistencies. Morphological analyses of studied strains reveal differences in cell size, flagellar structure, periplast morphology, and intracellular features compared to previously described species. Phylogenetic trees based on SSU and LSU rDNA sequences show that several strains do not cluster with their supposed species, indicating misclassification. These errors likely stem from the fact that many identifications are made by non-taxonomists, leading to the propagation of inaccurate data in ecological and evolutionary studies worldwide. Misclassifications in public databases not only distort phylogenetic relationships but also affect ecological studies by misrepresenting species diversity and distribution. Our findings highlight the urgent need for a rigorous taxonomic reassessment of the genus *Eutreptiella*, integrating morphological and molecular approaches to ensure accurate classification and restructure the genus. In conclusion, correcting misidentifications will improve our understanding of *Eutreptiella* biodiversity, aid in the reorganization and restructuring of the genus, and provide a clearer framework for studying its role in HABs and ecosystem dynamics.

**Keywords:** Euglenoids, Marine, Herbarium

**Financing:** This work was supported by the projects: UAMI-CBS2023-2026: session 84.22-211222 and UAMI-CA-117. SECIHTI scholarship granted to study postgraduate 1141580.

Parallel Session 14: Taxonomy and Phylogeny

O-070

# Intracellular ultrastructure comparison of seven toxigenic and non-toxigenic *Amphidoma* and *Azadinium* species (Amphidomataceae, Dinophyceae) isolated from the North Pacific

**Koyo Kuwata[1],** Wai Mun Lum[2], Kazuya Takahashi[3], Garry Benico[4], David U. Hernández-Becerril[5], Mayu Ozawa[6], Hajime Uchida[6], Toshiyuki Suzuki[7], Mitsunori Iwataki[1]

(1) University of Tokyo, Graduate School of Agricultural and Life Sciences, 1-1-1 Yayoi, Bunkyo, Japan
(2) Mie University, Graduate School of Bioresources, 1577 Kurimamachiya, Tsu, Japan
(3) Institute of Parasitology, Biology Center CAS, 1160/31 Branišovská, České Budějovice, Czech Republic
(4) Central Luzon State University, Department of Biological Sciences, Science City of Muñoz, Nueva Ecija, Philippines
(5) Universidad Nacional Autónoma de México, Avenida Universidad 3000, Ciudad Universitaria, Coyoacán, Mexico City, Mexico
(6) Fisheries Technology Institute, Environment and Fisheries Applied Research Department, 2-12-4 Fukuura, Yokohama, Japan
(7) Kitasato University, School of Marine Biosciences, 1-15-1 Kitasato, Minami, Sagamihara, Japan

Small marine dinoflagellates within the family Amphidomataceae, including the lipophilic toxin azaspiracid (AZA)-producing species of genera *Amphidoma* and *Azadinium*, have been classified mainly based on thecal morphology, such as ventral pore and antapical spine, using SEM. For further exploration of morpho-characters distinguishing the amphidomatacean dinoflagellates, in this study, intracellular ultrastructure was observed by TEM and compared using unialgal cultures of seven species, including toxigenic (*Am. languida*, *Az. poporum*, and *Az. spinosum*) and non-toxigenic species (*Am. fulgens*, *Az.* cf. *dexteroporum*, *Az. dalianense*, and *Az. zhuanum*) isolated from the North Pacific. In the seven amphidomataceans, organelles common in dinoflagellates, such as the dinokaryotic nucleus, mitochondria with tubular cristae, parietal chloroplasts surrounded by three membranes, fibrous bodies, and trichocysts, were observed. Vesicles containing crystalline structures positioned in the periphery of the cell were newly discovered in amphidomataceans. Structural differences were also found in pyrenoids: a single stalked pyrenoid (*Am. fulgens*, *Am. languida*, and *Az. spinosum*), several bulged or sometimes stalked pyrenoids (*Az. poporum*, *Az. dalianense*, and *Az.* cf. *dexteroporum*), and several embedded pyrenoids (*Az. zhuanum*). The stalked and bulged types were covered by a starch sheath. Cytoplasmic invaginations into the pyrenoid matrix, present in *Amphidoma*, but absent in *Azadinium*, were probably a character distinguishing these genera. Oil droplets and lipid-associated multilayered membranes were found in the toxigenic *Am. languida* but not in the non-toxigenic *Am. fulgens*; however, they were observed in all five *Azadinium* species, including non-toxigenic species.

**Keywords:** *Amphidoma*, *Azadinium*, shellfish poisoning

Parallel Session 14: Taxonomy and Phylogeny

O-071

# Species diversity of amphidomatacean dinoflagellates in Japan based on morphological and molecular identification

**Mitsunori Iwataki[1],** Koyo Kuwata[1], Kazuma Nakano[1], Wai Mun Lum[2], Kazuya Takahashi[3], Garry Benico[4]

(1) University of Tokyo, Graduate School of Agricultural and Life Sciences, 1-1-1 Yayoi, Bunkyo, Tokyo, Japan
(2) Mie University, Graduate School of Bioresources, 1577 Kurimamachiya, Tsu, Japan
(3) Institute of Parasitology, Biology Center CAS, 1160/31 Branišovská,, České Budějovice, Czach Republic
(4) Central Luzon State University, Department of Biological Sciences, Science City of Muñoz, Philippines

Species diversity of amphidomatacean dinoflagellates belonging to *Azadinium* and *Amphidoma* was examined by ITS- and LSU rDNA-based phylogeny and microscopic observation, using 81 culture strains and two uncultured cells from Japanese waters during 2016–2024. In total, 10 species were found in Japanese waters. Of these, *Azadinium caudatum*, *Az. cuneatum*, *Az. dexteroporum*, and *Az. spinosum* were newly found in the Northwest Pacific, *Az. dalianense* was first reported in Japan, and several other unidentified species separately branched from known *Azadinium* species were found in this study. *Azadinium* sp.1 had several unique morphological characters, i.e., spindle-shaped cell with an ellipsoidal nucleus, a spherical pyrenoid at the antapex, a ventral pore in the left lateral of the 1' plate, and a conspicuous antapical spine. *Azadinium* sp.2 independently branched in the clade of *Az. dexteroporum*/ *Az. galwayense*/ *Az. perfusorium*, but differed from *Az. dexteroporum* in the shape of the Po plate (absence vs. presence of the finger-like protrusion), from *Az. galwayense* in the shape of the 2a plate (four- vs. five-sided), and from *Az. perfusorium* in the position of pyrenoid (in the episome vs. at the antapex). Among 81 cultures examined, 47 cultures were assigned to *Az. poporum* that belonged to four intraspecific ribotypes, suggesting the species is the major AZA-producer in the Japanese coastal waters. These results expand the known distribution and taxonomic resolution of amphidomatacean dinoflagellates in the Northwest Pacific, highlighting their ecological significance and potential toxin production.

**Keywords:** *Amphidoma*, *Azadinium*, shellfish poisoning

Parallel Session 14: Taxonomy and Phylogeny

O-072

# New toxins and harmful species. Updates from the IOC-taxonomic task team

Shauna Murray[1], Cécile Bernard[1], **Catarina Churro[1],** Laura Escalera[1], Mona Hoppenrath[1], Mitsunori Iwataki[1], Jacob Larsen[1], Kenneth Neil Mertens[1], Øjvind Moestrup[1], Nina Lundholm[1], Rafael Salas[1], Urban Tillmann[1], Adriana Zingone[1]

(1) Without Affiliation

The number of species that can produce toxins is steadily growing, and so does the IOC taxonomic reference list of harmful species. Newly described species are added and for some species toxin production has recently been verified, e.g in genera such as *Prorocentrum*, *Alexandrium*, *Centrodinium*, *Gonyaulax*, *Ostreopsis*, *Heterocapsa*, *Chattonella* and *Pseudo-nitzschia*. Moreover, the list of toxic cyanobacteria—both freshwater and marine—has been updated, now comprising over 100 described toxigenic species.

Taxonomic revisions are ongoing in several taxa, leading to frequent name changes. However, there are active efforts to conserve certain widely used names, such as *Alexandrium*, to maintain consistency in the literature. The reference list is continuously being updated, with the exclusion of some species for which toxin production is not soundly demonstrated (e.g., *Aureococcus anophagefferens* and *Alexandrium balechii*). Current work focuses on the inclusion of verified DNA sequences.

Based on HAEDAT and literature search, a list of 54 species that do not produce toxins but still cause health impairment or kills of marine animals has been compiled and is available on the site. Mechanisms are often unknown, but oxygen depletion (e.g., *Tripos*), mechanical damages to fish gill by spines (e.g., some *Chaetoceros* and *Octactis speculum*) or mucous clogging (e.g., *Thalassiosira mala*) are the most common causes for these harmful events. Another list is being compiled with non-toxigenic species producing discolorations or mucilage event with impacts on tourism and recreational use of coastal waters or other economic losses.

Parallel Session 15: Cyanobacteria & Freshwater HABs

O-073

# Cyanobacterial toxin profiling of 40 lakes in a temperate northern region

**Malin Olofsson**[1], Ana Cekol[1], Lauren Davies[1], Stina Drakare[1], Aida Zuberovic Muratovic[2]

(1) Swedish University of Agricultural Sciences, Department of Aquatic Sciences and Assessment, Uppsala, Sweden
(2) Swedish Food Agency, Box 622, 751 26, Uppsala, Sweden

Cyanobacterial blooms are believed to be associated to high temperatures, but surprisingly often they are also found at high latitude and even under ice during winter. To explore the cyanobacterial diversity and their toxins in temperate lakes, samples from more than 40 lakes all over Sweden were analyzed across season (latitudes of 55°N to 64°N), to record various toxins and species, and to map their prevalence and the diversity. Collaboration with municipalities across Sweden enabled collection of lake water samples when blooms occurred at bathing locations, whereafter the knowledge was provided back to municipalities for guidance of their bathing sites. Samples were also received from ongoing monitoring and field surveys. Using a combination of enzyme-linked immunoassay (ELISA), liquid chromatography mass spectrometry (LC-MS), quantitative polymerase chain reaction (qPCR), and microscopy-based community composition measurements, the toxin concentrations were mapped in cells and in the dissolved fraction, with species presence and their potential toxin production. Both ELISA and LC-MS, and ELISA and qPCR, correlated significantly, indicating their usefulness as proxies for each other. Overall, we found various types of microcystins, nodularin, anatoxin, cylindrospermopsins, and saxitoxins. The lake blooms consisted of species like *Dolichospermum*, *Microcystis*, and *Aphanizomenon*, with toxin concentrations up to 10,000 µg $L^{-1}$ and the proportion between the fraction found in the cells and in the dissolved fraction varied largely. Temperate lakes are at risk for increased blooms and toxin exposure as a result of climate change and anthropogenic impact, with negative outcome on tourism, drinking water production, aquaculture, and irrigation.

**Keywords:** Cyanobacteria, Temperate lakes, Cyanotoxins

**Financing**: Swedish Board of Agriculture

Parallel Session 15: Cyanobacteria & Freshwater HABs

O-074

# Predicting cyanobacteria blooms in U.S. lakes using national scale data

**Kendall Ash**[1,2], Patrick Hanly[1], Kendra Cheruvelil[1,3]

(1) Michigan State University, Fisheries and Wildlife, Natural Resources Building 480 Wilson Road, East Lansing, Michigan, USA
(2) Michigan State University, Ecology, Evolution, and Behavior, Giltner Hall, 293 Farm Ln, East Lansing, Michigan, USA
(3) Michigan State University, Lyman Briggs College, 919 E Shaw Ln, East Lansing, Michigan, USA

Harmful algal blooms of toxin-producing cyanobacteria (cyanoHABs) are a major threat to freshwater lakes as they contaminate drinking water, harm aquatic organisms, and cause economic losses due to decreased recreation. Prediction of cyanoHABs for their mitigation and management has been difficult due to their complex drivers in combination with limited spatial data coverage. We leverage the U.S. Environmental Protection Agency's National Lakes Assessment data for >8,000 lakes, the LAGOS research platform, and recent advances in machine learning to forecast bloom events based on multi-scaled predictors including chemical, physical, biological, climate, and human. We present three gradient boosting models that predict different indicators of cyanoHAB harmfulness: 1) microcystin toxin concentration, 2) chlorophyll-a, and 3) cyanobacteria biovolume. Model one achieved 81% accuracy on unseen test data and identified chlorophyll-a, turbidity, dissolved organic carbon, and pH as key predictors of microcystin concentration. The second model yielded an $R^2$ of 0.38 on test data, with turbidity, total phosphorus, pH, and total nitrogen as important drivers of chlorophyll-a. Model three had an $R^2$ of 0.32 on test data, highlighting temperature, latitude, turbidity, and total phosphorus as key predictors of cyanobacteria biovolume across sites. With this framework, we are able to both predict cyanoHABs in U.S. lakes and better describe which combinations of drivers lead to bloom formation and harmfulness. Our model can be extrapolated to lakes with limited data to enhance prediction and management of cyanoHABs in understudied regions, which will greatly aid lake managers in their fight against cyanoHABs.

**Keywords**: cyanoHAB, Prediction, Machine learning

**Financing:** National Science Foundation, Robert C. Ball and Betty A. Ball Fisheries and Wildlife Fellowship.

**Acknowledgments:** Thank you to the LAGOS team and the Fisheries & Wildlife and EEB departments at Michigan State University for their guidance and support.

Parallel Session 15: Cyanobacteria & Freshwater HABs

O-075

# Recovery and characterization of potentially toxin-producing cyanobacteria from a century-old reservoir

Alex Hoke[1], D. Quynh Nguyen[1], W. Leighton Petty[1], J. Thad Scott[1,2], **Katelyn McKindles[1,2]**

(1) Baylor University, Biology
(2) Baylor University, Center for Reservoir and Aquatic Systems Research, 101 Bagby Avenue, Waco, United States

While regular monitoring is critical for tracking harmful cyanobacteria blooms in water reservoirs, many programs are relatively new and lack high-resolution, long-term data. To address this gap for Lake Waco (Texas, USA), sediment cores were analyzed to uncover the reservoir's cyanobacterial history. Certain cyanobacteria, such as those in the Order Nostocales, form dormant cells called akinetes during unfavorable conditions. These cells can remain in sediments and germinate to initiate new blooms, making their quantification and germination experiments key to understanding bloom potential. Six sediment cores were collected from the reservoir's arms and main body, which were sectioned based on sediment characteristics and subsampled for physiochemical and DNA analyses. Additionally, subsamples were used in germination experiments. After 28 days of incubation in BG-11 media, cyanobacterial populations that had been recovered and/or germinated from the sediment cores were assessed using FlowCam imagery and DNA analyses. Core sections closest to the sediment-water interface (0 – 5 cm) were dominated by green algae and common bloom forming species such as *Planktothrix* and *Dolichospermum*. *Cyanobium* and *Nostoc* were found across multiple cores at greater depths (up to 190 cm from sediment-water interface). Select cyanobacterial groups were then isolated to generate unialgal cultures. Successful isolates included members of *Planktothrix*, *Dolichospermum*, and *Nostoc*. Further characterization of these isolates includes toxin production capabilities and phylogenetic relatedness to known species. These experiments lend insight into recoverability of potential toxin-producing cyanobacteria from the sediments of reservoirs.

**Keywords:** Sediment Core, Germination, Reservoir

**Acknowledgments:** We would like to thank the Texas Water Development Board for providing us access to their sediment cores.

Parallel Session 15: Cyanobacteria & Freshwater HABs

O-076

# Global change impacts on cyanobacterial bloom toxicity: Scaling from traits to threats

**Dedmer B. Van de Waal[1,2],** Annemieke Drost[1,2], Chaohong Lin[1,2,3], Arnaud Louchart[1], Savannah Sarkis[1,2]

(1) Netherlands Institute of Ecology (NIOO-KNAW), Aquatic Ecology, Droevendaalsesteeg 10, 6708 PB, Wageningen, The Netherlands
(2) University of Amsterdam, Freshwater and Marine Ecology, Institute for Biodiversity and Ecosystem Dynamics (IBED), Sciencepark 904, 1098 XH, Amsterdam, The Netherlands
(3) University of Twente, MESA+ Institute for Nanotechnology, Hallenweg 15, 7522 NH, Enschede, The Netherlands

Harmful cyanobacterial blooms have a major impact on water quality worldwide. The risks associated with these blooms not only depend on the cyanobacterial biomass in the water, but also on the community composition, population structure and the amounts and types of toxins produced by the cells. To effectively assess and predict these risks, it is crucial to understand how cellular-level processes influence broader ecological patterns. Understanding bloom toxicity thus requires scaling from cellular processes to ecosystem dynamics. Bridging this gap, functional traits provide a unifying framework to link cellular processes and ecological interactions, as traits determine growth, resource competition, and grazing defense. A trait-based approach, therefore, may support our understanding on cyanobacterial bloom toxicity across scales. Here, we explore various key cyanobacterial traits, their responses to global change factors such as eutrophication, warming and elevated $pCO_2$, and how they can support our understanding of ecological interactions. Specifically, this talk will highlight outcomes from review syntheses, experiments, and field observations to assess how traits involved in nutrient acquisition, colony formation, $N_2$ fixation and toxin synthesis underlie changes in bloom toxicity across environmental gradients.

**Keywords**: Global environmental change, Trait-based ecology, Harmful cyanobacteria

**Financing:** ERC Consolidator Grant (BLOOMTOX; 101044452)

Parallel Session 15: Cyanobacteria & Freshwater HABs

O-077

# A freestream in situ digital holographic imaging system for monitoring cyanobacterial blooms in freshwater lakes

Ahammad Abdullah[1,2], **Aditya R. Nayak[1,2]**

(1) Florida Atlantic University, Ocean and Mechanical Engineering, 777 Glades Road, Boca Raton, FL 33431, USA
(2) Florida Atlantic University, Harbor Branch Oceanographic Institute, 5600 US 1 North, Fort Pierce, FL 34946, USA

Cyanobacterial harmful algal blooms (cHABs) are increasingly impacting freshwater systems across the globe. Early detection and monitoring play an important role in mitigating harmful impacts, as well as understanding cHAB ecology; thus, it is imperative to push the envelope towards adaptation of new methodologies for rapid and accurate characterization of cHAB abundance. Digital holography is a freestream, non-intrusive, imaging technique that can detect particles and planktonic organisms in situ in a relatively undisturbed manner, over sizes ranging from microns to centimeters in diverse aquatic systems. Here, we present a multi-year field study to test the performance of a new generation holographic imaging system (AUTOHOLO), developed in-house at Florida Atlantic University, to characterize cyanobacterial species (e.g., *Microcystis* sp.) and the general plankton community composition in Lake Erie, one of the Laurentian Great Lakes.

Over the course of three seasons, the AUTOHOLO was vertically profiled across multiple stations in pre and peak-bloom conditions to obtain fine-scale plankton community distributions, with a particular focus on *Microcystis*. Additionally, the system was also deployed on a buoy to obtain time series of these distributions across several days. Results from these deployments, including horizontal and vertical variations in particle size distributions and *Microcystis* colony sizes and abundance will be discussed, highlighting how this technology could potentially open new avenues in bloom monitoring and cyanobacterial ecology studies. Future long-term deployments of this instrument can support the examination of individual stages of bloom and the understanding of the life cycle in each phase.

**Keywords**: Lake Erie, Cyanobacterial blooms, Digital holography.

**Financing**: Great Lakes Observing System (GLOS) FAU subcontract - National Oceanic and Atmospheric Administration (NOAA) Grant NA21NOS0120098

Parallel Session 15: Cyanobacteria & Freshwater HABs

O-078

# Cyanotoxins diversity and their biotechnological potential

**Vitor Vasconcelos**[1,2]

(1) CIIMAR, Terminal de Cruzeiros do Porto de Leixões, Matosinhos, Portugal
(2) University of Porto, Biology, Sciences, Rua do Campo ALegre, Porto, Portugal

Cyanotoxins, though primarily recognized for their toxicological and ecotoxicological effects, possess significant biotechnological potential across diverse fields. These secondary metabolites, including microcystins, cylindrospermopsins, saxitoxins and anatoxins, have unique biochemical properties that can be harnessed for pharmaceutical, biomedical, and agricultural applications. Microcystins, for instance, are valuable tools in cancer research due to their selective inhibition of protein phosphatases, aiding cell signaling studies and drug development. Anatoxins and saxitoxins, as potent neurotoxins, offer models for neurological research, anti-pain drugs and biosensor development. Furthermore, cyanotoxins hold promise in pesticide and antimicrobial agent design, leveraging their high specificity and potency. Advancements in synthetic biology and metabolic engineering enable the controlled production and modification of these compounds, transforming toxic natural products into valuable bioresources with significant commercial and scientific utility. Culture collections such as LEGE-CC are unique biodiversity reservoirs that are essential for the preservation of biodiversity, ecosystem recovery and biotechnological applications.

**Keywords:** cyanotoxins, biotechnological potential, culture collections.

**Financing:** The Portuguese Foundation for Science and Technology (FCT) Projects UIDB/04423/2020 and UIDP/04423/2020.

**Acknowledgments:** WP9- Portuguese Blue Biobank under the Blue Economy Pact - Project N°. C644915664-00000026 co-funded by PRR, The Portuguese Republic and the European Union.

Parallel Session 16: Ecology, Biology and Biogeography

O-079

# The role of G protein-coupled receptors in red tide dinoflagellate bioluminescence

Aidan McFarland[1], Malissa Fenton[1], Jesper Madsen[2], **Libin Ye[1,3]**

(1) Department of Molecular Biosciences, University of South Florida, 4202 E Folwer Ave, Tampa, USA
(2) Department of Molecular Medicine, University of South Florida, 4202 E Fowler Ave, Tampa, USA
(3) Moffitt Cancer Center & Research Institute, 12902 USF Magnolia Drive, Tampa, USA

G protein-coupled receptors (GPCRs) are ubiquitous transmembrane proteins in multicellular life. Human vision, taste, and neuron activity are all mediated by GPCRs, and a large percentage of currently approved drugs target GPCRs. However, our understanding of GPCRs in single-celled eukaryotes is incomplete, and many of the components of GPCR signal transduction have not been identified in unicellular eukaryotes. Previous works studying bioluminescent dinoflagellates—single-celled algae involved in coral reef endosymbiosis and toxic red tide blooms—implicate GPCRs in a signaling pathway for bioluminescence but have not elucidated the individual components comprising the pathway. Herein, we identified a novel GPCR in dinoflagellates—Bioluminescence-Inducing Receptor 1 (BIR1)—which plays a significant role in the signaling pathway for bioluminescence in red tide blooms in response to wave turbulence. Additionally, we identified a full endogenous G-protein complex and downstream effectors that are integral to known calcium signaling networks. Based on these identifications, we used knockdown and knockout techniques to demonstrate the integral role of BIR1 in bioluminescence and highlight its role in predator response and shear force-elicited GPCR signaling in red tide blooms. This advance opens avenues for red tide control and supports the existence of similar GPCR pathways involved in bloom toxicity dynamics.

**Keywords**: GPCR, bioluminescence, red tide blooms

**Financing:** National Institute of Health, USA

**Acknowledgments**: N/A

Parallel Session 16: Ecology, Biology and Biogeography

O-080

# Rapid sexual reproduction in *Dinophysis acuminata* revealed through temporal partitioning of cellular processes

**Serena Sung-Clarke**[1,2], Nour Ayache[1], Wenguang Zhang[3], Mengmeng Tong[3], Juliette Smith[4], Michael Brosnahan[1]

(1) Woods Hole Oceanographic Institution, Biology Department, 266 Woods Hole Rd., Woods Hole, United States
(2) MIT-WHOI Joint Program in Applied Ocean Sciences and Engineering, Biological Oceanography, 77 Massachusetts Ave., Cambridge, United States
(3) Zhejiang University, Ocean College, 1 Zheda Rd, Zhoushan, China
(4) Virginia Institute of Marine Sciences (William and Mary), Ecosystem Health, 1370 Greate Rd, Gloucester Point, United States

Sexual reproduction is fundamental to the ecology and evolution of eukaryotes, yet its dynamics in microbial eukaryotes are often cryptic. *Dinophysis* are specialist mixotrophs that must balance prey capture, cell division, and sexual recombination during blooms, but relatively little is known about the occurrence and role of sex in their ecology. Here, mating was investigated in *D. acuminata* through continuous automated microscopy of natural blooms and cultured cells. Vegetative division and mating were phased on a diel timescale, occurring primarily at night and near dawn, regardless of prey availability. Mating and division were determined to be linked based on the sequencing of their phases, the correlation of their daily amplitudes, and their reestablishment following a two-day light block. Mating, though frequent (up to 14% $day^{-1}$ in culture), was not associated with zygote accumulation or resting stage formation, but rather with rapid cell reproduction via meiosis. Confinement of division and mating to nighttime and early morning may minimize conflict with photosynthesis-related metabolism and/or predator exposure. Sexual reproduction was the dominant mode of proliferation during the observed blooms, accounting for 71% and 64% of their new cell production. Because it is dependent on gamete encounters, sexual reproduction is increasingly accessible as blooms intensify. This sexual mode of proliferation may also reduce blooms' susceptibility to pathogens, parasites, and other threats via genetic recombination, an example of Red Queen dynamics.

**Keywords**: sexual reproduction, mixotrophy, Red Queen

**Financing:** NOAA National Centers for Coastal Ocean Science.

Parallel Session 16: Ecology, Biology and Biogeography

O-081

# Distribution dynamics of vitamin B12, *Pseudo-nitzschia* sp. and domoic acid in the Northwest Passage

**Elisabeth Rosselli**[1], Fuat Dursun[2], Simon Tulatz[1], Marina Arregui[1], Urban Tillmann[1], Bernd Krock[1], Scarlett Trimborn[1], Florian Koch[1]

(1) Alfred Wegener Institute for Polar and Marine research, Ecological Chemistry Department, Am Handelshafen 12, 27570 Bremerhaven, Germany
(2) Istanbul University, Physical Oceanography and Marine Biology Department, Institute of Marine Sciences and Management, Mollahüsrev mah. Molla Şemsettin Camii sok. No:1/1 Süleymaniye 34134 Fatih, Istanbul, Türkiye

There has been an increase in the frequency of harmful algal blooms (HAB) worldwide, including the domoic acid (DA) producing diatom *Pseudo-nitzschia* sp., the causative agent of amnesic shellfish poisoning in humans and marine mammals. Vitamin $B_{12}$, also known as cobalamin, has been linked to the bloom dynamics of some HABs and laboratory studies found that *Pseudo-nitzschia* is auxotrophic for this micronutrient. To date, however, the relationship between $B_{12}$ distribution, abundances of *Pseudo-nitzschia* and DA are unknown. On an expedition through the Northwest Passage (Reykjavik, Iceland to Seattle, USA), in the late summer, water samples were collected and analyzed for plankton biomass, dissolved and particulate $B_{12}$ *Pseudo-nitzschia* sp. abundance and domoic acid. Concentrations of dissolved $B_{12}$ were highest in the Bering Sea and North Pacific, and lowest around Greenland, ranging from 0,02-2,46 pmol $L^{-1}$ and displaying an east-west gradient. The plankton biomass was heterogeneously distributed, with low concentrations of both, chlorophyll a and particulate organic carbon observed at the northernmost stations. *Pseudo-nitzschia* abundances were higher at the eastern stations and associated with high concentrations of DA. Multidimensional scaling resulted in stations clustering into 5 regions, primarily driven by temperature. The inverse correlation between dissolved $B_{12}$ and DA and the higher particulate $B_{12}$ in the eastern stations where *Pseudo-nitzschia* was most abundant, suggests a higher $B_{12}$ requirement for-, and utilization by plankton communities harboring these toxic species.

For the first time, theseresults provide an interesting insight of the relationships between DA and $B_{12}$ concentrations in the field.

**Keywords**: Diatom, Domoic Acid, Cobalamin

Parallel Session 16: Ecology, Biology and Biogeography

O-082

# A year long in situ survey of HAB species and their respective metabolic activities in the Northern Adriatic Sea

**Daniela Maric Pfannkuchen[1],** Mirta Smodlaka Tanković[1], Mia Knjaz[1], Ivan Vlašićek[1], Ana Baricevic[1], Lana Grizancic[1], Ariana Turkovic[1], Ivan Podolsak[1], Martin Pfannkuchen[1]

(1) Rudjer Boskovic Institute, Center for marine research, G. Paliaga 5, Rovinj, Croatia

The Northern Adriatic (NA) is a highly dynamic marine ecosystem, in which multiple environmental stressors, particularly phosphorus limitation, shape phytoplankton communities.
A metatranscriptomic approach was used to investigate the taxonomic and functional dynamics of the NA phytoplankton community, focusing on toxic and potentially toxic species. Based on observed patterns of ecologically relevant molecular mechanisms and underlying physiological responses to environmental conditions, we unveiled contrasting life strategies and adaptations to ecological conditions. Monthly sampling from April 2021 to March 2022 was conducted at two stations, one coastal and one offshore. Metatranscriptomes were extracted from the collected samples, alongside the measurement of various environmental parameters. Analysis of annual patterns in taxonomic and functional community succession revealed an unexpected year-round dominance of dinoflagellates in terms of metabolic activity. Peaks in the metabolic activity of other studied groups aligned with the typical seasonal succession of species, as previously reported. Notably, the expected spring diatom bloom was not observed, whereas an autumn bloom dominated by *Pseudo-nitzschia* species was consistently detected.

6 *Pseudo-nitzschia* species were recorded by metatranscriptome, more than 30 toxic and potentially toxic dinoflagelates and 6 Haptophyta were found. This study provides critical new insights into the inventory of toxic species and their metabolic activities in the NA. However, the results also underscore the need for further multi-method research to fully understand the ongoing dramatic ecological changes in NA ecosystem, particularly with respect to HAB species.

**Keywords:** Metatranscriptomics; HABs; Phytoplankton

**Acknowledgments:** Croatian Science Foundation (HRZZ): UIP-2014-09-6563, ADRILife (UIP-2020-02-7868), DOK-2021-02-5104.

Parallel Session 17: Prevention, Control and Mitigation (PCM) - HABs

O-083

# Controlling harmful algal blooms (HABs) in marine waters: current status and future prospects

**Vera Trainer**[1], Donald Anderson[2], Mark Wells[3], Kevin Claridge[4], Kathryn Coyne[5], Quay Dortch[6], Chris Gobler[7], Cynthia Heil[4] , Nobuharu Inaba[8], H. Dail Laughinghouse[9], Jorge I. Mardones[10], Natsuko Nakayama[11], Taegyu Park[12], Melissa Peacock[13], Kaytee Pokrzywinski[14], Heather Raymond[15], Jennifer Toyoda[4], Dean Trethwey[16], Petra Visser[17], Yanfei Wang[5], Yongquan Yuan[18], Marc Suddleson[19]

(1) University of Washington, Olympic Natural Resources Center, 1411 S Forks Ave, Forks, WA, USA
(2) Woods Hole Oceanographic Institution, Woods Hole, MA, USA
(3) University of Maine, School of Marine Sciences, Orono, ME, USA
(4) Mote Marine Laboratory, 1600 Ken Thompson Parkway, Sarasota, FL, USA
(5) University of Delaware, School of Marine Science and Policy, 1440 College Dr, Lewes, DE, USA
(6) CSS Inc under contract to NOAA, Competitive Research Program, NCCOS, NOS, 1305 East-West Hwy, Silver Spring, MD, USA
(7) Stony Brook University, School of Marine and Atmospheric Sciences, Stony Book, NY, USA
(8) Public Works Research Institute, Civil Engineering Research Institute for Cold Region, Hiragishi 1-3-1-34, Tohohira-ku, Sapporo, Hokkaido, Japan
(9) University of Florida, Agronomy Department, Ft. Lauderdale Research and Education Center, 3205 College Ave, Davie, FL, USA
(10) Instituto de Fomento Pesquero, Centro de Estudios de Algas Nocivas, Padre Harter 574, Puerto Montt, Chile
(11) Japan Fisheries Research and Education Agency, Fisheries Technology Institute, 2-17-5 Maruishi, Hatsukaichi, Hiroshima, Japan
(12) National Institute of Fisheries Science (NIFS), Busan, Korea
(13) Northwest Indian College, 2522 Kwina Rd., Bellingham, WA, USA
(14) NOAA NCCOS, 101 Pivers Island Rd., Beaufort, NC, USA
(15) The Ohio State University, Office of Research and Graduate Education, College of Food, Agricultural, and Environmental Sciences, 2120 Fyffe Rd., Columbus, OH, USA
(16) Akvafuture Canada, 1040 Cedar St., Campbell River, British Columbia, Canada
(17) University of Amsterdam, Department of Freshwater and Marine Ecology, Institute for Biodiversity and Ecosystem Dynamics, P.O. Box 94240, Amsterdam, The Netherlands
(18) Chinese Academy of Sciences, CAS Key Laboratory of Marine Ecology and Environmental Sciences, Institute of Oceanology, Qingdao, China
(19) NOAA, CRP, NCCOS, NOS, 1305 East-West Hwy, Silver Spring, MD, USA

The societal, economic, geographic, and environmental impacts from marine Harmful Algal Blooms (HABs) have increased in many regions around the world. The growing array of impacts is large and varied, threatening human health, marine and freshwater wildlife, and ecosystems upon which many nations rely on for food, recreation, tourism, and a plethora of other goods and services. Although the HAB burden has grown substantially over the past few decades, marine and estuarine HAB control remains one of the least developed areas of HAB science. The disconnect between HAB control needs and solutions stems in part from public, stakeholder, and scientific uncertainties about the balance between benefits and potentially undesirable environmental consequences.

Other more practical challenges can include substantial regulation of in situ testing, scaling up laboratory-proven technologies to attack widespread blooms that can move in three dimensions in open marine waters, and an immature commercial market. Here we describe the current status of control strategies targeting marine coastal and estuarine HABs, in particular those few approaches that have been tested on mesocosm to larger scale field applications. We identify the regulatory support, targeted science, investments, and public outreach that will be needed to accelerate the availability of applications for controlling HABs in marine waters worldwide.

**Keywords**: Control, Marine, HAB

**Financing:** Funds were provided by the NOAA PCMHAB program, PICES, GlobalHAB, and a FL Fish and Wildlife Conservation Commission grant to Mote Marine Laboratory.

Parallel Session 17: Prevention, Control and Mitigation (PCM) - HABs

O-084

# In situ impacts of modified clay on *Karenia brevis* cell concentrations, water quality, and microbial communities

**John Kristoffer Andres**[1], Victoria Devillier[2], Emily Hall[2], Jessica Frankle[2], Julianna Martin[1], Michelle Gaither[1], Robert Fitak[1], Donald Anderson[3], Kristy Lewis[4]

(1) University of Central Florida, Biology, 4110 Libra Dr., Orlando, United States
(2) Mote Marine Laboratory, 1600 Ken Thompson Parkway, Sarasota, United States of America
(3) Woods Hole Oceanographic Institution, 86 Water Street, Falmouth, Massachusetts, United States of America
(4) University of Rhode Island, Graduate School of Oceanography, 215 S Ferry Road, Narragansett, Rhode Island, United States of America

In Florida, USA, algal blooms of *Karenia brevis* are a common disturbance with widespread impacts on coastal communities and the local ecosystem. To address this problem, a surge of research is ongoing to develop mitigation techniques to reduce the concentration of toxic cells to minimize the effects of ongoing blooms. Clay-based compounds are one of the most widely studied mitigation techniques and are now being considered for use in the United States. In this study, poly-aluminum chloride (PAC) Modified Clay (MCII) was investigated for its efficacy at removing cells within large scale in situ mesocosms (i.e., limnocorrals) in Sarasota Bay, Florida. Water samples were collected before modified clay application and then at three time points after application (4-, 24-, and 48-hours). Samples were analyzed to determine cell concentration, microbial community composition, physico-chemical parameters, nutrient, and carbonate chemistry. *K. brevis* cell concentrations ranged from 37,500 ± 10,380 - 60,000 ± 14,616 cells/L in control limnocorrals. Cell concentrations were reduced by 60% after 4 hours and 100% for succeeding sampling periods in modified clay-treated limnocorrals. Physico-chemical parameters such as $pH_{NBS}$ and dissolved oxygen (DO) were significantly lower after clay application and remained at low levels until time 48. Nutrient concentrations were impacted after modified clay application at time 4, but returned to normal levels in later time periods. No changes in the microbial community structure were observed. These results indicate the potential of modified clay II to be applied on natural waters with limited effects on physico-chemical parameters, nutrients, and non-targeted microbial organisms.

**Keywords:** Clay, *Karenia brevis*, Mitigation

**Financing:** Florida Sea Grant

**Acknowledgments:** Mote Marine Laboratory, University of Rhode Island Graduate School of Oceanography, and UCF Gaither Lab (Molecular Ecology and Evolution Laboratory).

Parallel Session 17: Prevention, Control and Mitigation (PCM) - HABs

O-085

# Using modified clay to mitigate fjord HAB taxa: Laboratory results using species from Chile, Scotland, and Norway

**Anita Flores Lenero**[1], Jorge I. Mardones[3,4], Marco Antonio Pinto Torres[6], Javier Paredes[3], Sonia Rey Planellas[5], Francisca Vermeulen[1], Michael Ross[1,2], Keith Davidson[1]

(1) Scottish Association for Marine Science (SAMS), Scottish Marine Institute, PA37 1QA, Oban, Scotland, UK
(2) Culture Collection of Algae and Protozoa (CCAP), Scottish Marine Institute, PA37 1QA, Oban, Scotland, UK
(3) Centro de Estudios de Algas Nocivas (CREAN), Instituto de Fomento Pesquero (IFOP), Aquaculture, 5501679, Puerto Montt, Chile
(4) Centro de Investigación en Recursos Naturales y Sustentabilidad (CIRENYS), Universidad Bernardo O´Higgins, 8370993, Santiago, Chile
(5) Institute of Aquaculture, University of Stirling, FK9 4LA, Stirling, Scotland, UK.
(6) Ciencias de la Acuicultura, Universidad Austral de Chile, Puerto Montt, Chile

Understanding the mechanisms involved in the inactivation and control of the main microalgal species responsible for Harmful Algal Blooms (HABs) in fjord systems is a priority for developing effective mitigation strategies. HAB species present in the waters of Chile, Scotland, and Norway pose a threat not only to local food security, but also to the global aquaculture industry. Modified clay (MC) is a promising method that may reduce the impact of HABs in fjord aquaculture, as it has been reported to effectively flocculate algal cells and adsorb their toxins. This study investigated the efficiency of MC in removing 10 HAB species through a series of laboratory flocculation experiments using commercial MC under fjord-relevant temperature and salinity conditions. We evaluated cell removal, cell viability, and toxin adsorption. These experiments targeted HAB species that cause physical damage to farmed fish: *Pseudo-nitzschia fraudulenta* and *Chaetoceros curvisetus*, and toxic species: *Alexandrium catenella*, *Alexandrium minutum*, *Karenia selliformis, Karenia mikimotoi, Karlodinium veneficum, Chrysochromulina leadbeateri, Pseudochattonella verruculosa,* and *Prymnesium parvum*. The results showed that on a laboratory scale, MC reduced at least 50% of the cell density in the water column for all taxa. However, removal efficiency varied significantly among species. Additionally, toxic compounds from *Karenia selliformis* were not effectively adsorbed, as indicated by RTgill-W1 bioassays. MC presents a potential control method against several HAB species affecting fjord aquaculture, but further experiments are necessary to fully understand its effects and potential environmental impacts.

**Keywords:** Mitigation, Fjords, Aquaculture

**Financing:** 1) SUPERDTP-NERC UK2) Aquaculture HUB scheme (SARF-UHI)3) UHI Research Conference & Training FUND

**Acknowledgments**: We thank our collaborators, institutions, and funding from FIPA-2020 (Chile-Subpesca) and SUPER DTP (UK-NERC) for supporting this research.

Parallel Session 17: Prevention, Control and Mitigation (PCM) - HABs

O-086

# Synchronous removal of the potent marine algal toxins in mitigating harmful algal blooms using modified clay

**Lianbao Chi**[1], Xiaona Zhang[1], Xiuxian Song[1], Zhiming Yu[1]

(1) Institute of Oceanology, Chinese Academy of Sciences, Key Laboratory of Marine Ecology and Environmental Sciences, Assocaite Researcher, Nanhai road, Qingdao, China, Qingdao, China

The global surge in harmful algal blooms (HABs), driven by ocean warming and eutrophication, has intensified ecological and public health risks, particularly through the production of marine algal toxins. Given their ubiquitous occurrence and multiple adverse effects on marine ecosystems, increasing efforts have been dedicated to the study of HABs and associated algal toxins. Modified clay (MC) has been proven effective in controlling HABs and is becoming a widespread practice in coastal waters due to its low cost, high efficiency, and environmental friendliness. Nevertheless, the fates of marine algal toxins following MC treatment remain unclear. To address this issue, this study explored the effects of MC on the removal of typical algal toxins. The results indicated that MC effectively removed toxic algal cells, including *A. pacificum* and *K. brevis*. The application of MC significantly reduced the content and toxicity of PSTs and BTXs. On one hand, MC effectively inhibited total intracellular toxin synthesis by removing toxic algal cells. On the other hand, MC promoted the transformation of highly toxic components (STX) into less toxic components (GTX2&3 and C1&2). Furthermore, MC was found to oxidize and degrade the PSTs and BTXs, with the oxidant products (OPs) identified via high-resolution liquid chromatography-mass spectrometry. Most OPs underwent substantial structural modifications with significant mass reductions. In silico predictions indicated that, compared to the parent toxins, the biodegradability of most OPs significantly increased while their toxicities decreased. Overall, this study presents an efficient method for the simultaneous removal of HABs and algal toxin pollution.

**Keywords**: Toxic algal blooms; Modified clay; Synchronous removal

**Financing:** National Natural Science Foundation of China (Grant Nos. 42376210 and 42276220).

Parallel Session 17: Prevention, Control and Mitigation (PCM) - HABs

O-087

# Development of HAB mitigation using modified clays in China

**Zhiming Yu[1],** Xiuxian Song[1], Xihua Cao[1], Yongquan Yuan[1]

(1) Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

The impacts of harmful algal blooms (HABs) on economies, public health, ecosystems, and aquaculture across the globe have all increased in recent decades, and this has been acutely the case in China. Flocculation is an essential approach to control HABs in the ocean, compared to other means. However, the application of traditional flocculants in marine environment is limited, due toinsufficient aggregation and their slow settlement to HAB organisms caused by hydrodynamic influence, wave disturbance, etc. Such limitations can be overcome by Modified Clay (MC) technology. Using natural clay particles as a carrier, the surface of which is physically modified to enhance the electrical neutralization, to strengthen the function of absorption bridging and sweep netting, and to improve the algicidal ability. As a result, the HAB organisms can be aggregated effectively and settled down to the bottom rapidly. The technology was first used in the field in 2005 and has been developed for about twenty years in China. Up to date, it is the most accepted method and widely used technology in China. A comprehensive MC based technology system for HAB control has been established, including development of functional MC products and supporting equipment, eco- and environmental evaluations of MC, standards and protocols for on-site applications, etc. Within this presentation, the research, development, and application of MC technology in China would be generally introduced, focusing on the principle and theory, safety assessments, and application cases. This also provides a reference for HAB mitigation in other countries of the world.

**Keywords:** HAB control; Modified Clay; Principle and theory ; Safety assessments; Application case

**Financing:** This work was financially supported by Laoshan Laboratory (LSKJ202203700), the National Key Research and Development Program of China (2024YFF0506902).

**Acknowledgments:** Thanks for all members of the research team of mitigation and control of HABs from Institute of Oceanology, Chinese Academy of Sciences.

Parallel Session 17: Prevention, Control and Mitigation (PCM) - HABs

O-088

# Enhancing carbon sequestration through flocculation of harmful algal blooms by modified clay

**Xiuxian Song[1],** Lianbao Chi[1], Jing Chen[1], Tianhao Zheng[1], Xin Feng[1], Wentao Wang[1], Zhiming Yu[1]

(1) Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

Abstract: Marine microalgae play a key role in carbon sequestration, but their overgrowth often results in harmful algal blooms (HABs). Notably, the rapid mineralization of alga-derived organic carbon poses significant ecological hazards and severely diminishes carbon sequestration potential. Modified clay (MC) has been proven effective in controlling HABs. Nevertheless, the fates of alga-derived organic carbon following the dissipation of HABs and MC treatment remain unclear. To this end, our study explored the enhancing effects of MC on organic carbon sequestration and the underlying mechanism. Results indicated the mineralization rate of alga-derived organic carbon was time-dependent and postulated to occur in two stages, averaging 0.68 mg/(L·d) for S. costatum and 0.80 mg/(L·d) P. donghaiense. The treatment of MC significantly reduced the mineralization rate to 0.09 mg/(L·d) for both species, enhancing carbon sequestration potential. Multiple lines of evidence suggested MC reduced the bioavailability of alga-derived organic carbon by rapidly flocculating and effectively encapsulating it, limiting bacterial-mediated mineralization. Moreover, it also inhibited heterotrophic bacterial growth, reducing bacterial abundance by about 60% compared to the control. FAPROTAX analysis showed a 50% decrease in microbial mineralization-related functional genes in the MC treatment group. These findings enhance quantitative and mechanistic understanding regarding the fate of alga-derived organic carbon and provide further insights into the potential for enhancing carbon sequestration by MC.

**Keywords:** Harmful algal blooms; Mineralization; Modified clay; Mineral-enhanced Carbon sequestration

**Financing:** This work was financially supported by Laoshan Laboratory (LSKJ202203700), the National Key Research and Development Program of China (2024YFF0506902).

**Acknowledgments:** The authors thank all members of the research team of mitigation and control of HABs from Institute of Oceanology, Chinese Academy of Sciences.

Parallel Session 18: Modelling, Early Warning and Forecasting
O-089

# Are we in an unprecedented era of HAB-driven marine mammal mortality events in coastal California?

**Clarissa Anderson[1],** Jayme Smith[2], Kasia Kenitz[1], Alissa Deming[3], Ruth Dover[12], Jeni Smith[4], Melissa Carter[1], Rebecca Shipe[5], Nathalie Guillocheau[6], Amber Briesach[6], Alexis Pasulka[7], Kathi Lefebvre[8], Raphael Kudela[9], Kendra Hayahsi[9], Andrew Thompson[10], Mattison Peters[11], Nathali Cordero Quiros[1]

(1) University of California San Diego, Scripps Institution of Oceanography, 9500 Gilman Dr., La Jolla, California, USA
(2) Southern California Coastal Water Research Project, 3535 Harbor Blvd., Suite 110, Costa Mesa, California, USA
(3) Pacific Marine Mammal Center, 20612 Laguna Canyon Rd, Laguna Beach, California, USA
(4) Sea World, 500 Sea World Dr., San Diego, California, USA
(5) University of California Los Angeles, Institute of the Environment and Sustainability, 405 Hilgard Ave, Los Angeles, California, USA
(6) University of California Santa Barbara, Earth Research Institute, 1210 Cheadle Hall Santa Barbara, California, USA
(7) California Polytechnic State University, San Luis Obispo, 1 Grand Ave., San Luis Obispo, California, USA
(8) Northwest Fisheries Science Center, 2725 Montlake Blvd., Seattle, Washington, USA
(9) University of California Sant Cruz, 1156 High St., Santa Cruz, California, USA
(10) Southwest Fisheries Science Center, 8901 La Jolla Shores Dr., La Jolla, California, USA
(11) Marine Mammal Care Center Los Angeles, 3601 S. Gaffey, San Pedro, California, USA
(12) Channel Islands Marine and Wildlife Institute, P.O. Box 4250, Santa Barbara, California, USA

This presentation reviews four years of successive domoic acid (DA) events along the central and southern California coast. From 2022 to 2025, there have been an onslaught of marine mammal mortality events caused by phycotoxins associated with strengthening upwelling and abundant anchovy populations. The strongest DA event in recent years occurred in 2025 in conjunction with La Niña conditions that moved from Baja, California to southern, central, and then northern California over the winter/spring transition. In fact, the longest, nearshore cold-water episode since the La Niña year of 2010/2011 likely contributed to the origin of this bloom period as early as December 2024 and sustained it through April 2025, by supplying new nutrients for algal growth. Macronutrient levels at nearshore stations have indeed been anomalous the last three years, and in 2025, devastating wildfires potentially brought additional allochthonous nutrients to the coastal zone via ash and runoff. Very high levels of DA detected in sardine tissue prompted state agencies to recommend recreational and commercial fishing restrictions in Southern California. Animal stranding numbers over 1500 far exceeded those reported in any of the toxic events over the past four years. This was followed by the emergence of several other HAB taxa, most notably an extensive toxic *Alexandrium* bloom that caused a rare and prolonged saxitoxin advisory for shellfish throughout Southern California, and positive detection of saxitoxins in marine wildlife tissue. We discuss the role of early warning systems and possible causative pathways to this new ear of HABs in California.

**Keywords:** domoic acid, saxitoxin, La Niña

Parallel Session 18: Modelling, Early Warning and Forecasting

O-090

# Investigation of phytoplankton blooms at a reference station in Algoa Bay, South Africa

**Brishan Kalyan**[1,2,3], Thomas Bornman[1,2,3]

(1) Nelson Mandela University, Department of Atmospheric and Oceanographic Science, Science, 4 Gomery avenue, Gqeberha, South Africa
(2) South African Environmental Observation Network, Elwandle Coastal Node, 4 Gomery avenue, Gqeberha, South Africa
(3) Nelson Mandela University, Institute for Coastal and Marine Research, 4 Gomery avenue, Gqeberha, South Africa

The South African coast provides a unique area of study, bounded by two powerful currents, the Benguela on the west and the Agulhas on the east. Algoa Bay, a log-spiral shaped bay that is eastward facing located on the warm, temperate, south-eastern coast is a Sentinel Site of Long-Term Ecological Research. A reference station within this site was used to evaluate bloom detection methods, 1) in-situ chlorophyll-a and 2) phytoplankton relative abundance thresholds for bloom detection. A total of 65 events were detected using chlorophyll-a refined to 18 events and additionally 24 events using relative abundance. This resulted in 42 events detected between 2010 and 2024 within Algoa Bay. A total of 18 taxa were identified as bloom forming taxa. A conical correspondence analysis identified that the majority of the variance was explained by the first 2 axis (CCA1: 0.799; CCA2: 0.624). Bloom forming taxa, *Chaetoceros*, *Leptocylindrus*, Dinoflagellate spp, *Skeletonema*, *Ditylum*, *Rhizosolenia* and species *Chaetoceros socialis*, *Pseudo-nitzschia* spp., *Leptocylindrus minimus* and *Gonyaulax polyedra* were greatly influenced by temperature. *Thalassiosira, Noctiluca scintillans* and *Lithodesmium* were influenced by dissolved oxygen, and *Lithodesmium* was influenced by the ratio of nitrogen to orthophosphate. *Detonula* was also influenced by this ratio together with *Bacteriastrum* and *Thalassionema* which were additionally influenced by pH. The orthosilicate to nitrogen ratio had an influence on *Asterionellopsis* blooms identified. This study provides an overview of blooms detected by in-situ monitoring over a 14-year period additionally, it also provided an indication of the associated biogeochemical environment during the bloom detection.

**Keywords:** biogeochemistry, diatoms, dinoflagellates

**Financing:** South African Environmental Observation Network

**Acknowledgments:** Nelson Mandela University, South African Environmental Observation Network, Shallow Marine Coastal Research Infrastructure.

Parallel Session 18: Modelling, Early Warning and Forecasting

O-091

# Characterization of HAB-associated microplankton around Karachi coast and the Indus River Estuary (IRE)

**Sher Khan**[1], Nadeem Yaqoob[2], Ume Robab[2]

(1) University of Karachi, Centre of Excellence in Marine Biology, Science, University Road Karachi, Karachi, Pakistan
(2) 2Pakistan Institute of Nuclear Science and Technology, Isotop Applicaiton Division, NILORE, ISLAMABAD, Islamabad, Pakistan

Marine ecosystems rely greatly on microplankton, but even slight environmental changes can reduce their abundance and growth, ultimately diminishing food quality and threatening human health. A significant outcome of such environmental shifts is eutrophication, which frequently triggers the growth of toxin-producing microplankton and leads to Harmful Algal Blooms (HABs). These blooms introduce toxins into the food chain, causing serious health issues in humans. This study focusses on three locations around Karachi coastal waters and the Indus River Estuarine (IRE) ecosystems. Seventy-six diatoms, twenty-six dinoflagellates and thirty-four dinocyst species were recorded, out them seven species were potential toxin. Dinoflagellates were dominant. However, two species *Alexandrium tamarense* and *Alexandrium ostenfeldii* were most dominant with 84 percent and 75 percent and only six species of diatoms *Asteromphalus flabellatus, Navicula cancellata, Pleurosigmamor photype, Surirella fastuosa, Pseudo-nitzschia seriata* sp. and *Thalassionema* were recorded at all locations. While, dinocyst assemblage is generally dominated by *Protoperidinium* spp. *Protoperidinium avellanum Lingulodinium polyedrum, Protoperidinium conicum* and *Protoperidinium minutum Fragilidium mexicanum* at all three locations along Karachi coast.

Sixteen diatom and six dinoflagellate species were encountered in a detailed study of Indus River Estuary that was carried out. Among dinoflagellates *Protoperidinium* spp. was dominant with 42.5% cell abundance. It was observed that phytoplankton species abundance is more likely controlled by the abiotic factor rather than biotic mechanism and their distribution triggered by the temperature and salinity. Additionally, this study will include an overview of the HAB events that have occurred in Pakistan over past three decades.

**Keywords:** Microplankton diversity, HAB events, Karachi-Sindh coast

**Financing:** NA

**Acknowledgments:** HEC-Pakistan is greatly acknowledged.

Parallel Session 18: Modelling, Early Warning and Forecasting

O-092

# Distribution patterns of phytoplanktonic assemblages associated with harmful dinoflagellates in the Chilean fjord system based on a 16-year time series

**Gemita Pizarro Nova[1],** Rodrigo Martínez[3], Pamela Carbonell[3], Leonardo Guzmán[3], Pablo Salgado[1], César Alarcón[1], Carolina Toro[1], Marta Godoy[1], Verónica Muñoz[2], Luis Iriarte[2], Loreto López[3], Karen Correa[3], Bianca Zubicueta[3], Carolina Soto[3]

(1) Instituto de Fomento Pesquero (IFOP), Centro de Estudios de Algas Nocivas (CREAN), Enrique Abello 0552, Punta Arenas, Chile
(2) Instituto de Fomento Pesquero (IFOP), Centro de Estudios de Algas Nocivas (CREAN), A. Barrios 472, Puerto Aysén, Chile
(3) Instituto de Fomento Pesquero (IFOP), Centro de Estudios de Algas Nocivas (CREAN), Padre Harter 574, Puerto Montt, Chile

A 16-year quasi-monthly time series (2007–2023) of quantitative phytoplankton monitored in surface waters (0–10 m) of the Chilean Fjord System (ChFS, 41°–54°S) was analyzed. A characterization of phytoplanktonic assemblages is presented based on the composition and density of microalgae that coexist with harmful dinoflagellates (HD) during the warmer austral seasons of the year (spring, summer and autumn). Using PRIMER-v7 for the cluster analysis of the monitoring sites, the density of 192 species distributed across 146 sites were considered. The toxin-producing dinoflagellates *Alexandrium catenella* (Ac), *A. ostenfeldii* (Ao), *Protoceratium reticulatum* (Pr), *Dinophysis acuta* (Dac) and *D. acuminata* (Da) were used as indicator species for those sites or clusters whose assemblages contained at least one of these HD, called HD-sites (HDS) clusters. The results show significant latitudinal differences between the HDS clusters. These differences are consistent with natural geographical barriers, such as extensive gulfs and channels connected to the Pacific Ocean. The number of HDS clusters was highest in the fjords central area (Aysén region: 43°50'–45°) characterized by the indicator species Ac (n=32), Da (n=26), Pr (n=18) and Dac (n=3), followed by the southernmost area (Magallanes region: 48°30'–54°) characterized by Ac (n=12) and Da (n=1). The lowest number of HDS clusters was in the fjords northern area (Los Lagos region: 41°30'–43°S), characterized by Pr (n=5) and Da (n=3). The relationships between surface temperature and salinity in the HDS cluster are analyzed, as well as the relationships between the Ac-HDS clusters and the historical levels of paralytic shellfish toxicity in the ChFS.

Keywords: Harmful dinoflagellates, phytoplanktonic assemblages, Chilean Fjord System.

Financing: Monitoring and Research Program for Harmful Microalgae and Marine Toxins (red tide) in the Fjords of Chile.

Acknowledgments: We thank the Undersecretariat of Economy and Small Enterprises and the Undersecretariat for Fisheries and Aquaculture, Ministry of Economy, Government of Chile.

Parallel Session 18: Modelling, Early Warning and Forecasting

O-093

# Pollution dynamics and sustainable management of toxic elements associated with harmful algal blooms in coastal Bangladesh

**Dr. M. Safiur Rahman**[1]

(1) Bangladesh Atomic Energy Commission, Chemistry Division, Physical Sciences, 4 -Kazi Nazrul Islam Avenue, Shahbag, Dhaka 1000, Bangladesh

Harmful algal blooms (HABs) are increasingly recognized as a major environmental and public health concern, particularly in coastal and estuarine ecosystems. In Bangladesh, the frequency and severity of HABs are rising, posing significant threats to aquatic biodiversity, fisheries, aquaculture, and human health. Common HAB-forming phytoplankton in Bangladeshi waters include Tripos spp., Dinophysis spp., *Protoperidinium* spp., *Chaetoceros* spp., and *Pseudo-nitzschia* spp. However, there has been no prior research in the country to identify or quantify HAB-associated biotoxins such as microcystins, saxitoxins, and domoic acid. This study aims to fill that gap through future biotoxin analyses supported by the IAEA project (INT7022).

To assess the ecological and toxicological implications of HABs, plankton samples were collected from the Karnaphuli River estuary using nets of two mesh sizes (20–50 µm and 50–200 µm), along with water and fish samples. Results revealed significant bioaccumulation of trace metals—especially Pb, Cd, Mn, Zn, and Fe—in HAB-associated phytoplankton, with higher concentrations in larger size fractions. Elevated bioaccumulation factors (BAFs) for Fe and Pb were of particular concern. Metal concentrations increased with plankton size, suggesting potential biomagnification risks for fish species that rely on plankton as primary food sources. Pelagic and benthic fishes also showed varied levels of trace metals, with benthic species exhibiting higher metal pollution indices.

This study highlights the urgent need for monitoring HABs and their associated toxins and contaminants in Bangladesh's coastal waters to safeguard ecological health and mitigate risks to fisheries and public health.

**Keywords:** Phytoplankton, Fish, Toxic Elements

**Financing**: INT7022 Project of International Atomic Energy Agency (IAEA), Vienna, Austria

**Acknowledgments:** Ms Marie-Yasmine, DECHRAOUI BOTTEIN, FRANCE; Mr Carlos Manuel ALONSO HERNANDEZ, IAEA and Mr Kristof MOELLER, IAEA

Parallel Session 18: Modelling, Early Warning and Forecasting

O-094

# Changing microalgal communities: Approaches for holistic monitoring of harmful algal blooms

**Kirsty Smith[1],** Raewyn Bennett[2], Kaneihana Marsh[2], Hollie Kereopa[3], Kiara Duke-Love[4], Janine Kamke[5], Kate Schimanski[6], Ash Rabel[7], Nessie Kuka[8], Jason Murray[8], Laura Biessy[1], Sam Murray[1], John Pearman[1], Lesley Rhodes[1], Peter Bell[9], Anne Rolton[1]

(1) Cawthron Institute, Nelson, Aotearoa New Zealand
(2) Te Arawa ki Tai Trust, Maketū, Aotearoa New Zealand
(3) Patuharakeke Te Iwi Trust, Whangārei, Aotearoa New Zealand
(4) Te Ātiawa o te Waka-a-Māui Trust, Waikawa, Aotearoa New Zealand
(5) Auckland Council, Auckland, Aotearoa New Zealand
(6) Environment Canterbury Regional Council, Christchurch, Aotearoa New Zealand
(7) Environment Southland Regional Council, Invercargill, Aotearoa New Zealand
(8) Ngā Hapū o Ngā Moutere e toru - Matakana Island, Aotearoa New Zealand
(9) Plant and Food Research, Nelson, Aotearoa New Zealand

Marine microalgal communities are changing. Primary productivity has increased in some regions and decreased in others, and reports of harmful algal blooms (HABs) are on the rise, with climate and other anthropogenic factors implicated. Current monitoring approaches are spatially and temporally constrained, typically focus only on known problem species and reporting is limited. This prevents us from understanding complex HAB dynamics and detecting long-term trends in microalgal communities, limiting our ability to prepare for, or manage impacts.

Focusing on a series of case study sites, our team of iwi/hapū kaitiaki and scientists are using time integrated samplers (passive and artificial substrate samplers), coupled with environmental DNA metabarcoding and secondary metabolite (toxin) characterization to monitor microalgal communities. These samplers are being compared alongside traditional HAB monitoring methods. The aim of this approach is to provide a comprehensive picture of the entire microalgal community by capturing the commonly monitored pelagic taxa, as well as critically important benthic species. We are sampling across key locations spanning the length of Aotearoa New Zealand, representing a range of latitudes, habitat diversity, water quality, HAB occurrence and economic development, and will provide the most comprehensive picture of microalgal communities in Aotearoa New Zealand to date. Iwi/hapū kaitiaki are broadening this picture by combining conventional water quality with cultural indicators and building indigenous capacity in environmental monitoring. The use of these holistic techniques underpins our planned future research to identify the drivers of HAB community dynamics and pinpoint targets for risk assessments and mitigation efforts.

**Keywords:** Monitoring tools, Climate change, Planktonic and benthic HABs

**Financing:** “Safe New Zealand Seafood Research Platform (CAWX1801)” and “From Reactive to Resilient: Effectively managing our changing microalgal communities (CAW2438)”.

Parallel Session 19: Cyanobacteria & Freshwater HABs
O-095

# Transforming cyanobacteria biomass into sustainable biofertiliser: A review

**Jabulani Gumbo**[1], J Masaka[2], E Kuvawoga[2]

(1) Research & Innovation Department
(2) Faculty of Agriculture and Environmental Sciences, P/Bag 1020, Bindura, Zimbabwe

Cyanobacteria are photosynthetic microorganisms that frequently proliferate in nutrient-rich freshwater bodies, leading to harmful algal blooms (HABs). These blooms pose serious ecological and public health risks due to the release of cyanotoxins and their contribution to aquatic oxygen depletion. However, cyanobacterial biomass also contains valuable nutrients—particularly nitrogen and phosphorus—which makes it a potential resource for sustainable agriculture. This review explores two innovative approaches for converting cyanobacterial biomass into eco-friendly biofertilizer while addressing the challenges posed by toxin contamination. The first approach involves harvesting cyanobacterial cells using environmentally benign flocculants. The harvested biomass undergoes cell lysis to release intracellular nutrients, including proteins and micronutrients. Cyanotoxins released during this process are then degraded using microbial consortia, particularly those derived from cattle manure and sawdust, which have shown effective biodegradation capabilities. The second approach employs nanotechnology for nutrient recovery. Nanomaterials—such as functionalized biochar, metal oxides, or zeolites—are used to adsorb nitrates and phosphates from the water column or from lysed biomass solutions through mechanisms such as physisorption and chemisorption. These nutrient-laden nanomaterials can be applied directly to soils as slow-release fertilizers or further processed into granulated biofertilizer products. By converting environmental pollutants into valuable agricultural inputs, these approaches offer a circular bioeconomy solution that supports both water quality improvement and sustainable crop production. This review highlights the scientific principles, benefits, and potential challenges of each method and suggests future research directions for large-scale implementation.

**Keywords:** eutrophic water, biofertilizer, nanomaterial adsorption

Parallel Session 19: Cyanobacteria & Freshwater HABs

O-096

# Cyanobacterial community responses to nutrient reduction and warming: Insights from 45 years of monitoring

**Jordan Facey**[1], Jan Köhler[1]

(1) Leibniz-Institute of Freshwater Ecology and Inland Fisheries, Community and Ecosystem Ecology

The shallow, polymictic Lake Müggelsee, Germany has been routinely monitored for over 45 years. There has been an 87% and 79% reduction in annual mean TN and TP loads, respectively, coinciding with a consistent warming trend in summer. Cyanobacterial biomass has reduced significantly, however there has been a noticeable shift in the cyanobacterial community as *Dolichospermum* has increased in dominance. We aim to understand long-term changes in cyanobacterial biomass and community composition in response to changing nutrient dynamics and warming. In recent decades, sediment nutrient releases occur frequently with intermittent periods of thermal stratification and rapid deoxygenation of hypolimnial waters. These nutrient pulses are of increased importance to cyanobacteria, given low external inputs, and we show through high temporal resolution phycocyanin profiles that cyanobacteria migrate into nutrient-rich bottom waters during both diurnal and persistent stratification events. The N:P ratio of sediment nutrient releases is generally below the Redfield Ratio, contributing to frequent nitrogen limitation in summer. Nitrogen limitation with a pulsed supply regime appears to incur a growth penalty for N2-fixing cyanobacteria, however *Dolichospermum* spp. appear better adapted to dynamic nitrogen availability. *Dolichospermum* biomass is associated with greater thermal stratification and hypolimnial hypoxia, indicating they are accessing and utilizing nutrient-rich hypolimnial water. Dolichospermum also appears to more tightly regulate heterocyte production, which minimizes the growth penalties of heterocyte production in dynamic N environments. However, the total biomass of *Dolichospermum* blooms remains well-below those of previous decades, highlighting the efficacy of external nutrient loading reductions for cyanobacterial management.

**Keywords:** Warming, nitrogen limitation, nutrient reductions

**Financing:** This work was funded by the Deutsche Forschungsgemeinschaft (DFG), project number KO 2165 / 4-1.

**Acknowledgments:** The authors acknowledge all those involved in the sampling, sample processing and chemical analysis of the long-term ecological program at Lake Müggelsee

Parallel Session 19: Cyanobacteria & Freshwater HABs

O-097

# Three-dimensional analysis of *Microcystis* colonies: What controls size during blooms in North American lakes?

**Ronojoy Hem**[1], Christopher Gobler[1]

(1) Stony Brook University, School of Marine and Atmospheric Sciences, 100 Nicolls Road, Stony Brook, United States

The cosmopolitan cyanobacteria *Microcystis* has formed blooms in over 100 countries across six continents. These single-celled cyanobacteria often aggregate into colonies that promote the formation of blooms. *Microcystis* blooms, which are becoming more frequent and intense, are influenced by factors such as temperature, nutrient levels, and grazer densities. These factors can also alter the colony size distributions within blooms as larger colonies may offer benefits such as enhanced nutrient recycling, chemical resistance, and protection against grazers. Given this, understanding how environmental factors affect colony size can provide insight into the ability of *Microcystis* blooms to form, persist, and decline. Quantifying *Microcystis* colony sizes, however, poses a series of challenges as they are irregularly shaped and can vary significantly in multiple dimensions within ecosystem samples. As a result, biovolume estimations based on low-resolution two-dimensional data may be unreliable. In this study, we employed a novel automated three-dimensional imaging technique to quantify the biovolume of *Microcystis* colonies during blooms across three North American lakes. We observed significant variability in colony size distributions over both space and time. We also explored the potential impact of variable nutrient levels, temperatures, and grazer exposure on *Microcystis* colony size distributions. We observed that the addition of nutrients favored increases in the abundance of smaller colonies. We also observed that the cladoceran grazer, *Daphnia*, can effectively graze on smaller but not larger colonies. Three-dimensional data are key to uncovering how *Microcystis* blooms respond to shifting environmental conditions.

**Keywords:** 3D imaging, *Microcystis*, Bloom Dynamics

Parallel Session 19: Cyanobacteria & Freshwater HABs
O-098

# The fate of toxic cyanobacteria in soil and impacts on food safety: Application of drinking water treatment residuals in CyanoHAB-impacted regions in US

Yuehan Ai[2], Nicholas Basta[1], **Jiyoung Lee[2]**

(1) Ohio State University, School of Environment & Natural Resources
(2) Ohio State University, Environmental Health Sciences

Proper management of the enormous amount of drinking water treatment residuals (WTRs) is of significant importance. Land application of WTR is one of the popular approaches. However, when the source water is affected by harmful algal blooms (HABs), concerns need to be addressed regarding the impact of HAB-affected WTR on soil and crop. This study explores the fate of freshwater cyanobacteria and cyanotoxins introduced into agricultural soil through WTR application.

Two WTRs from HAB-affected source waters were applied to greenhouse soil (5% dry weight) for soybean cultivation. Half of the WTR underwent freeze-thaw (F&T) treatment to inactivate viable cyanobacteria. WTR microbiomes, cyanotoxins, and physicochemical properties were characterized, revealing the presence of microcystin (MC), saxitoxin, and β-Methylamino-L-alanine (BMAA). Both WTRs contained MC-producing Planktothrix and Microcystis, though their core cyanobacterial genera differed.

MC-producing cyanobacteria dynamics in WTR-amended soil were assessed via quantification of MC synthesis genes in soil DNA and RNA. Results indicated that Planktothrix adapted better to agricultural soil than Microcystis, continuously releasing MC and increasing soil toxin concentrations in WTR (no F&T)-amended groups. While no food safety risks were identified from soybean consumption, WTR (high-MC, no F&T group) reduced soybean productivity.

This study highlights the need for systematic evaluation of HAB-affected WTR application rates to mitigate the long-term impacts of toxic cyanobacteria and other WTR biochemical attributes on food security and environmental health.

**Keywords:** microcystin; Soybean: water treatment residuals

Parallel Session 19: Cyanobacteria & Freshwater HABs

O-099

# Is it time to integrate molecular cyanobacterial assays into water monitoring programs?

**Mark Van Asten**[1,2]

(1) University of New South Wales, School of Biotechnology & Biomolecular Science, Science, Sydney, Asutralia
(2) Phytoxigene, Inc., Suite 45 7 Narabang Way, Belrose, Australia

Research has been integral in our understanding of the biosynthetic pathways responsible for biotoxin production. By 2000 the biosynthetic pathway for microcystin was identified and subsequently research groups from around the world begun to investigate the application of this knowledge in developing methods that could enhance and improve on the more traditional cyanobacteria monitoring strategies. Identification of the Nodularin, cylindrospermopsin and saxitoxin pathways followed, which then facilitated the development of additional PCR assays including the Phytoxigene CyanoDTec assay. The overall aim of this assay was to make available a validated and standardized assay that could be used to test the utility of using toxin pathway genes in cyanobacteria (HAB) monitoring programs.

Over the last 10 years, since the availability of the technology the uptake and reliance of the technology as a screening and monitoring tool has been slow. Utilization between countries as well as between US states has varied. The presentation will summarize the data that has been generated over the last 10 years, along with examples on how different environment departments and water authorities are using the technology to monitor and assess risk of toxin producing cyanobacteria, both in source water for water utilities and recreational water system.

**Keywords:** Monitoring qPCRr cyanobacteria

**Financing:** The speaker is an employee of Phytoxigene, Inc. Products of Phytoxigene will feature in the presentation, but data from other sources will be also cited.

Parallel Session 19: Cyanobacteria & Freshwater HABs

O-100

# Latitudinal expansion of toxin cyanobacterial blooms in continental aquatic ecosystems of Southern Chile: Evidence from recent records

**Claudia Pérez**[1], Viviana Almanza[2], Luis Norambuena[1], Gonzalo Fuenzalida[1], Jorge Mardones[1]

(1) Instituto de Fomento Pesquero, Departamento de Medio Ambiente, División de Acuicultura, Balmaceda 252, Puerto Montt, Chile
(2) WaterIQ Technologies, Concepción, Chile

Cyanobacteria are photosynthetic prokaryotic organisms that inhabit marine, brackish, and freshwater environments. In continental waters, they are the main contributors to harmful algal blooms (HABs), which can release toxic metabolites with adverse effects on human health and aquatic ecosystems. In Chile, cyanobacterial blooms have been reported from the central zone (33.9° S) to the southern region of the country (40.8° S), but they have been scarcely studied. The aim of this study was to characterize cyanobacterial HAB events in Chile by identifying the dominant cyanobacterial species and assessing the presence of cyanotoxins. Bloom events were analyzed in continental aquatic systems, specifically in lakes Vichuquén, Villarrica, Cabrera, Huillinco, Tarahuín, and the Mechai stream. Genetic analyses identified *Dolichospermum lemmermannii* and *Microcystis aeruginosa* as the main bloom-forming species. Toxin analyses confirmed the presence of cyanotoxins, detecting at least six microcystin congeners, a hepatotoxic compound known for its effects on human health. In several of the blooms studied, microcystin concentrations exceeded the limits established by the World Health Organization (WHO) for recreational and drinking water use. These findings confirm a geographic expansion of toxic HABs toward higher latitudes in southern Chile in the recorded data. The results provide valuable information for water management and decision-making, highlighting the urgent need to implement monitoring programs, risk management strategies, and public health communication efforts.

**Keywords:** Cyanobacteria, Cyanotoxins, freshwater

**Financing:** Performance Agreement, Undersecretariat of Economy and Small Enterprises

**Acknowledgments:** Undersecretariat of Economy and Small Enterprises, and Under-Secretariat for Fisheries and Aquaculture

Parallel Session 20: New Methods & Technology

O-101

# Non-target analysis by liquid chromatography-high-resolution mass spectrometry: Application in algal and cyanobacterial toxin measurement

Elliott J Wright[1], Daniel G Beach[1], **Pearse McCarron[1]**

(1) National Research Council of Canada, Metrology Research Centre, 1411 Oxford St., Nova Scotia, Canada

Liquid chromatography–high-resolution mass spectrometry (LC–HRMS) enables non-target analysis (NTA) of algal biotoxins, providing potential for comprehensive class screening and retrospective analysis. LC–HRMS data acquisition methods and processing workflows using metabolomics software were developed to analyze samples for a broad range of marine and freshwater biotoxin classes, including known toxins and related analogues. The approach was utilized to provide novel insights on the profile, homogeneity and stability of biotoxin reference materials, including a mussel matrix for marine biotoxins and a cyanobacterial matrix for cyanotoxins. Producing information on hundreds of toxins, NTA provided significant advantages over conventional targeted analysis. These efforts established and validated processes for analyzing environmental sample sets and the methods were applied to passive samplers deployed in Puget Sound, Washington State (USA), between 2016 and 2018, and to an archived set of passive samplers deployed in Ship Harbour, Nova Scotia (Canada), between 2004 and 2006.

Evaluation of the Puget Sound data set revealed varied trends in toxin profiles, including dinophysistoxins, pectenotoxins, yessotoxins, cyclic imines and goniodomins. Similarly diverse toxin profiles were observed in the samplers from Ship Harbour, including analogues not reported in previous targeted analysis. The NTA experiments provided detailed information on spatial and temporal distribution of toxins on both the Northwestern and Northeastern coasts of North America, which is valuable for future research on harmful algae and toxins in the region. Overall, the work highlights best practices for use of NTA, and demonstrates a modern approach for comprehensive toxin analysis.

Parallel Session 20: New Methods & Technology

O-102

# Mining discarded molecular data for HAB gold

**Martin Pfannkuchen**[1], Ana Baričević[1], Mia Knjaz[1], Daniela Marić Pfannkuchen[1], Mirta Smodlaka Tanković[1], Lana Grižančić[1], Tjaša Kogovšek[1], Ivan Podolšak[1], Ivan Vlašiček[1], Ariana Turković[1]

(1) Ruder Boskovic Institut, Center for Marine Research, G. Palaga 5, Rovinj, Istria

The northern Adriatic Sea is a shallow and dynamic marine ecosystem, characterized by steep spatiotemporal ecological gradients, strong anthropogenic pressures and expressed riverine freshwater influences. It is additionally characterized by the highest density of marine traffic in the Mediterranean. Ballast water related species introduction, in combination with long water body retention times render the area particularly prone to species introductions from all seas and oceans. Here, we present an effort to consolidate a multimethod approach to monitor the area for species introductions. The combination of methods based on morphological analyses with methods based on genetic sequences as well as with methods based on gene transcription analyses demonstrated significant improvements in taxonomic scope and resolution. The normally discarded ribosomal RNA sequences derived from metatranscriptomics studies proved particularly effective in monitoring water samples and net hauls for potentially harmful and/or invasive species across the tree of life. We describe the newly developed methodology for the analysis of molecular traces of so far hidden biodiversity and report a wide spectrum of species new to the Mediterranean and the Adriatic Sea.

**Keywords:** Multi-omics, phytoplankton, Invasive species

**Acknowledgments:** P-limit (UIP-2014-09-6563),ADRILife (UIP-2020-02-7868). DOK-2021-02-5104. JERICO-S3, AdriaClim, Cascade, ALIENA, Marless, BRIGANTINE

Parallel Session 20: New Methods & Technology

O-103

# Assessment of novel molecular tools for the early detection of *Alexandrium minutum* in Italian coastal waters (Mediterranean Sea)

**Giorgia Zoffoli**[1], Francesca Cucchi[2], Nicolè Caputo[2], Luca Mirimin[2], Dave Clarke[3], Laura Pezzolesi[1], Monica Cangini[4], Rossella Pistocchi[1]

(1) University of Bologna, Department of Biological, Geological and Environmental Sciences (BiGeA), Via Sant'Alberto 163, 48123, Ravenna, Italy
(2) Atlantic Technological University of Galway, Marine and Freshwater Research Centre, Dublin Road, H91 T8NW, Galway, Ireland
(3) Marine Institute, Rinville, H91 R673, Oranmore, Ireland
(4) Fondazione Centro Ricerche Marine, Italian National Reference Laboratory for Marine Biotoxins, Viale A. Vespucci 2, 47042, Cesenatico, Italy

The genus *Alexandrium* comprises cosmopolitan dinoflagellates capable of producing Paralytic Shellfish Toxins (PSTs), namely saxitoxins (STXs), which pose significant risks to human health through the consumption of contaminated shellfish. In Italy, PSTs have been detected in molluscs from both the Adriatic and Tyrrhenian Seas, generally below the EU regulatory limit (800 µg STXs eq./kg). However, higher concentrations have been reported in recent years in Sardinia, where *A. minutum*, and occasionally *A. pacificum*, have been identified as major producers. The official monitoring program for harmful algal species in the Sardinia region currently relies on Utermöhl-based microscopy of water samples. The present study evaluated the applicability of two DNA-based techniques, real-time quantitative PCR (qPCR) and digital PCR (dPCR), as complementary tools for the early detection of *A. minutum*. Seawater samples were collected during two winter monitoring campaigns (2022–2024) from key mussel farming sites in the Gulf of Oristano, the study area. DNA was extracted and analyzed using a previously published probe-based assay targeting *A. minutum* SSU rDNA, that was initially applied via qPCR and then successfully adapted to dPCR. Both methods demonstrated a strong correlation with microscopy ($\rho > 0.7$) and greater sensitivity, generally yielding higher abundance estimates and enabling earlier bloom detection. In some samples, however, the target concentration was underestimated; a genus-specific assay revealed the presence of other *Alexandrium* species potentially including *A. pacificum* or unidentified species not routinely detected by microscopy. These findings support the use of molecular methods as valuable complements to existing surveillance frameworks, enabling more timely detection.

**Keywords:** *Alexandrium minutum*, real-time quantitative PCR (qPCR), digital PCR (dPCR)

**Financing:** This research was funded under a Ph.D. program of Italy's NRRP (D.M. 351/2022), supported by the European Union – NextGenerationEU (Reg. (EU) 2021/241).

**Acknowledgments:** We gratefully acknowledge the Cooperativa Pescatori Arborea for providing the samples and supporting research within their mussel farms in the Gulf of Oristano (Sardinia, Italy).

Parallel Session 20: New Methods & Technology

O-104

# A rapid molecular assay for discrimination of potentially toxic *Pseudo-nitzschia* spp. using recombinase polymerase amplification and nanopore sequencing

**Robert Hatfield**[1], María García Portela[4], Nishimura Tomohiro[3], Kirsty Smith[2]

(1) Centre for Environment Fisheries and Aquaculture Science, Food Safety, Harmful Algal Blooms, Cefas, Barrack Road,, Dorset, United Kingdom
(2) Cawthron Institute, New Zealand
(3) Japan Fisheries Research and Education Agency, Japan
(4) Centro Nacional Instituto Español de Oceanografía (IEO-CSIC), Spain

The genus *Pseudo-nitzschia* includes numerous species capable of producing domoic acid, a neurotoxin responsible for amnesic shellfish poisoning. Accurate and timely species-level identification is critical for effective monitoring and risk assessment. We present the development and validation of a novel molecular assay that combines recombinase polymerase amplification (RPA) with nanopore sequencing to enable rapid discrimination of *Pseudo-nitzschia* species. The assay was validated against approximately ten known *Pseudo-nitzschia* species, achieving high specificity and adequate sensitivity. Application to environmental samples from Scottish coastal waters revealed unexpected diversity, including taxa not previously recorded in the region. A subsequent field study in New Zealand demonstrated similarly high diversity, with results showing near-perfect concordance with a comprehensive isolate-based survey previously conducted across Aotearoa. To enhance throughput, the RPA assay was further adapted into a lateral flow format, offering a potential tool for routine monitoring programs. This integrated approach provides a scalable, rapid, and cost-effective solution for the detection and surveillance of potentially toxic *Pseudo-nitzschia* species in diverse marine environments.

**Keywords:** Nanopore Sequencing, *Pseudo-nitzschia*, Domoic Acid

**Financing:** Cefas Seedcorn

**Acknowledgments:** Cefas Seedcorn, Food Standards Scotland, Cawthron Institute, Plancton Andino and University of Copenhagen.

Parallel Session 20: New Methods & Technology

O-105

# Ammonium concentrations limiting HAB species growth cannot be accurately determined using the traditional indolphenol blue colorimetric method – the fluorometric ortho-phthaldialdehyde method is recommended instead

William G. Sunda[1], Nathan S. Hall[2], D. Ransom Hardison[3], **R. Wayne Litaker[4]**

(1) University of North Carolina at Chapel Hill, Department of Earth Marine and Environmental Sciences, Research Professor, Mitchell Hall, 104 South Rd. 27514, Morehead City, North Carolina, United States of America
(2) University of North Carolina at Chapel Hill, Department of Earth Marine and Environmental Sciences, Institute of Marine Sciences, Research Assistant Professor, 3431 Arendell Street, Morehead City, NC 28557, United States of America
(3) National Oceanic and Atmospheric Administration, National Ocean Service, National Centers for Coastal Ocean Science, Beaufort Laboratory, Research Scientist, 101 Pivers Island Rd., Beaufort NC 27517, United states of America
(4) CSS Corporation under contract with National Oceanic and Atmospheric Administration, National Ocean Service, National Centers for Coastal Ocean Science, Beaufort Laboratory, Research Scientist, 101 Pivers Island Rd., Beaufort, North Carolina 27517, United States of America

Modeling harmful algal bloom (HAB) dynamics requires determining whether nutrients or other factors limit growth. In systems where ammonium ($NH_4^+$) is the limiting nutrient this can be challenging. $NH_4^+$ concentrations measured in field samples, where ammonium uptake, nutrient addition experiments, and gene expression suggest limitation, are often much higher than those shown by laboratory experiments to limit phytoplankton growth rates. One possible reason for this discrepancy is an overestimation of $NH_4^+$ concentrations by the standard colorimetric methods commonly used for $NH_4^+$ analysis. In this study, we compared the $NH_4^+$ concentrations measured in estuarine water samples using the standard autoanalyzer-indolphenol blue (IPB) colorimetric method with those determined in the field in unfiltered samples using the fluorescent ortho-phthaldialdehyde (OPA) method calibrated by standard additions. Results showed that $NH_4^+$ concentrations measured by the OPA method were lower than those in duplicate samples determined by the IPB method. The largest differences were observed in samples with OPA $NH_4^+$ measurements < 1 µM. A major reason for this discrepancy is the lower detection limit of the OPA method (0.014 µM) compared to the IPB method (~0.3 µM). Many $NH_4^+$ concentrations measured with the OPA method fell within $NH_4^+$ levels that limit phytoplankton growth rates (< 0.1 µM), indicating N-limitation is more prevalent in productive estuarine waters than previously thought. The situation is analogous to accurately measuring iron in iron-limited ocean water samples where extremely low, growth-limiting ambient concentrations could only be accurately measured once the analytical methodology was sufficiently refined for such low measurements.

**Keywords:** Ammonium, measurement, growth-limitation

**Financing:** NOAA. National Centers for Coastal Ocean Science, Centers for Coastal Ocean Science research funding.

Parallel Session 21: Ecology, Biology and Biogeography

O-106

# Recurrent co-occurrence of *Pseudo-nitzschia australis* and *Eucampia zodiacus* in Baja California coastal waters: Evidence of emerging harmful phytoplankton assemblages

**Mary Carmen Ruiz de la Torre[1],** Victor Mathos[2], Linda Zumaya-Basurto[3], Mauro Santiago-García[4]

(1) Universidad Autónoma de Baja California, Facultad de Ciencias Marinas, Ensenada, Carretera Ensenada-Tijuana No.3917, Ensenada, Mexico
(2) Universidad Autónoma de Baja California, Facultad de Ciencias Marinas, Carretera Ensenada-Tijuana No.3917, Ensenada, Mexico
(3) Universidad Autónoma de Baja California, Facultad de Ciencias Marinas, Carretera Ensenada-Tijuana No.3917, Ensenda, Mexico
(4) Universidad Autónoma de Baja California, Facultad de Ciencias Marinas, Carretera Ensenada-Tijuana No.3917, Ensenada, Mexico

Phytoplankton dynamics in coastal upwelling systems are highly sensitive to oceanographic variability. Between 2020 and 2024, we conducted seasonal field surveys in Bahía de Todos Santos and other coastal sites along the Baja California Peninsula. Our data consistently revealed the recurrent co-occurrence of *Pseudo-nitzschia australis*, a domoic acid-producing diatom, and *Eucampia zodiacus*, a species increasingly recognized as harmful due to its bloom-forming capacity and ecological impact. This diatom assemblage was most frequently observed during spring and autumn ([insert specific months]), under conditions characterized by surface stratification, moderate salinity (33.5–34.8), and reduced upwelling intensity (12–14 °C). Over multiple years and sampling stations, cell counts and CTD profiles confirmed the persistence of this association (5 of 7 campaigns, across 10 stations). While P. australis has been widely monitored due to its toxicity, *E. zodiacus* has received limited attention in the region, despite its reported impacts on aquaculture elsewhere, including gill clogging in fish and food web alterations. The repeated co-occurrence of these taxa suggests the emergence of a potentially harmful phytoplankton assemblage driven by environmental change. Our findings contribute to a better understanding of regional HAB dynamics and underscore the importance of incorporating non-toxic but ecologically disruptive species into monitoring frameworks. The presence of *P. australis* and *E. zodiacus* at bloom-forming densities raises concerns about nutrient depletion, hypoxia, and trophic disruptions in aquaculture zones. Furthermore, the potential for domoic acid bioaccumulation through filter feeders poses indirect risks to food safety and ecosystem health.

**Keywords:** Baja California, *Pseudo-nitzschia australis*, *Eucampia zodiacus*

**Financing:** CONAHCYT-CB [CB-2016-283790], CONAHCYT-PRONACE and Marine Navy network for Harmful Algal monitoring.

Parallel Session 21: Ecology, Biology and Biogeography

O-107

# *Gymnodinium catenatum* in the shellfish production areas of the north-eastern Atlantic

**Yolanda Pazos[1],** Aldo Barreiro[2], Alexandra D. Silva[2,3], André Sobrinho-Gonçalves[3], Bárbara Frazão[3], Catarina Churro[3], Benlahcen Rijal Leblad[4], Niama Maamour[4], Mina Dellal[5], Asmae Bennouna[6], Faid El Madani[7], Mohamed Staiti[8], Moulaye Mohamed Wagne[9], Ousmane Ndiaye[10], Raúl Fernández[11], Luz Mamán[11]

(1) INTECMAR, Xunta de Galicia, Instituto Tecnológico para el Control del Medio Marino de Galicia, Peirao de Vilaxoán, 36611, Vilagarcía de Arousa. Pontevedra, Spain
(2) CIIMAR/CIMAR LA, Interdisciplinary Centre of Marine and Environmental Research, Universidade do Porto, Terminal de Cruzeiros do Porto de Leixões, 4450-208, Matosinhos, Portugal
(3) IPMA, I.P. Portuguese Institute for the Sea and Atmosphere, Departamento do Mar e dos Recursos Marinhos, Divisão de Oceanografia e Ambiente Aquático, Av. Doutor Alfredo Magalhães Ramalho 6, 1495-165, Algés, Portugal
(4) INRH. Institut National de Recherche Halieutique, Surveillance et Suivi du Milieu Marin de l'INRH à Tanger, Centre Regional de l'INRH à Tanger, Tanger Km 7, Route Ksar Sghir, Malabata. B.P. 5268. Dradeb, Tanger, Marocco
(5) INRH. Institut National de Recherche Halieutique, Surveillance et Suivi du Milieu Marin de l'INRH à Dakhla, Centre Regional de l'INRH à Dakhla, Dakhla Km 7, Route Boujdour, B.P. 127 Bis, Dakhla, Marocco
(6) INRH. Institut National de Recherche Halieutique, Surveillance et Suivi du Milieu Marin de l'INRH à Agadir, Surveillance et Suivi du Milieu Marin de l'INRH à Agadir, Centre Regional de l'INRH à Agadir, P.K. 07, route d'Essaouira, Anza 80000, Agadir, Marocco
(7) INRH. Institut National de Recherche Halieutique, Surveillance et Suivi du Milieu Marin de l'INRH à Nador, 13, Bd Zerktouni,, Nador, Marocco
(8) INRH. Institut National de Recherche Halieutique, Surveillance et Suivi du Milieu Marin de l'INRH à Laâyoune, BP 3039 Laâyoune EL AMAL 70003 INRH BP 75 Laâyoune port 70000, Laâyoune, Morocco
(9) IMROP, Maruritanian Institute of Oceanographic Research and Fisheries, Marine and Coastal Environment Research, BP:22, Nouadhibou, Mauritania
(10) Université de Nouakchott, Faculté des Sciences et Techniques, UR-Biodiversité et Valorisation des Ressources Végétale, BP 880, Nouakchott, Mauritania
(11) CACCRP, Centro Andaluz de Control y Calidad de los Recursos Pesqueros. Agencia de Gestión Agraria y Pesquera de Andalucía, Consejería de Agricultura, Pesca, Ganadería y Desarrollo Sostenible, Junta de Andalucía, Carretera de El Rompido a Nuevo Portil Km 4, CP 21459 Nuevo Portil-Cartaya, Huelva, Spain

Following severe Paralytic Shellfish Toxins (PSTs) outbreaks in Europe during the 1970s, monitoring efforts, particularly for biotoxins, have intensified significantly. *Gymnodinium catenatum*, a toxic chain-forming dinoflagellate associated with PSTs is now regularly monitored in the water column in shellfish production areas along the Canary Current Upwelling System. In parallel, sediment studies reveal a widespread distribution of cysts across the region, including northern Europe, where blooms do not occur. These regional upwelling systems facilitate cyst resuspension and germination, transporting cells to the continental shelf, while upwelling relaxation promotes cell accumulation and growth. Downwelling events concentrate biomass nearshore, often triggering blooms that impact both suspended and benthic aquaculture. The species also persists in retention areas such as coastal lagoons.

Although *G. catenatum* is a strong swimmer capable of enduring turbulence, its vegetative cells are limited by low temperatures. Due to its consistent association with PSTs, any detection of this species in routine monitoring triggers an immediate alert. A comprehensive approach is employed, encompassing phytoplankton community analysis, vertical profiling, satellite imagery, physical oceanographic models, flow cytometry, molecular tools, and even the examination of *Noctiluca* vacuoles for the presence of *G. catenatum*. This work aims to integrate decadal time-series data from microscopy-based observations across multiple monitoring sites to better understand the biogeographic connectivity of bloom events in the north-western Atlantic. Given the species' rarity, high toxicity, and the unpredictable context of climate change, coordinated international efforts are urgently needed to improve predictive capacity and risk mitigation strategies for both ecosystems and public health.

**Keywords**: *Gymnodinium catenatum*, Time series, HABs monitoring

**Financing:** Xunta de Galicia, IPMA, Universidade do Porto, Institut National de Recherche Halieutique Marocco, IMROP Mauritania, Université de Nouakchott, Junta de Andalucía

Parallel Session 21: Ecology, Biology and Biogeography

O-108

# Long term salinity adaptation in *Nodularia spumigena* supports northwards expansion potential in the Baltic Sea

**Carolin Peter**[1], Mireia Bertos-Fortis[1], Elin Lindehoff[1], Hanna Mazur-Marzec[2], Catherine Legrand[1,3]

(1) Linnaeus University, Department of Biology and Environmental Science, Faculty of Health and Life Sciences, Universitetsplatsen 1, 39231 Kalmar, Sweden
(2) University of Gdansk, Institute of Oceanography, Division of Marine Biotechnology, Marszalka Pilsudskiego 46, 81-378 Gdynia, Poland
(3) University Jönköping, Gjuterigatan 5, 55318 Jönköping, Sweden

In the Baltic Sea, the filamentous cyanobacterium Nodularia spumigena, a known producer of the hepatotoxin nodularin, frequently forms extensive summer blooms in the central basins. While the northern basins are characterized by lower temperatures and salinities that limit bloom formation, ongoing climate change may facilitate a northward expansion – provided N. spumigena can adapt to low salinities.

This 12-year study investigated the long-term adaptive capacity of two *N. spumigena* strains, KAC11 (from the central Baltic Proper) and KAC66 (from the northern Baltic Proper), to reduced salinities (3 and 5 psu) compared to a control (7 psu). Growth rates, nodularin content (per biomass), toxin profiles, and buoyancy behavior were assessed. KAC66 maintained stable growth rates and morphology at lower salinity. but demonstrated a threefold increase in toxicity at long-term exposure to 3 psu. KAC11 initially showed a 62% reduction in growth rate at 3 psu but fully recovered after 12 years of adaptation. At 3 psu, KAC11 filaments were 78% smaller in volume but toxicity remained comparable to 7 psu; while at 5 psu, toxicity was reduced by 50%. Buoyancy assays revealed that both strains formed the typical surface scum only at 7 psu. At lower salinities, KAC66 remained suspended in the water column, whereas KAC11 tended to sink. These different responses highlight the ecological plasticity of N. *spumigena*.

The observed recovery of growth rates and sustained or greatly increased toxicity at low salinities suggest a potential risk to the Bothnian sea ecosystems, especially benthic communities, should a northward expansion occur.

**Keywords:** cyanobacteria, nodularin, salinity adaptation

**Financing:** Research council FORMAS strong research environment EcoChange.

Parallel Session 21: Ecology, Biology and Biogeography

O-109

# First record of a *Trichodesmium sp.* bloom in waters of the Argentine Continental Shelf and its possible relationship with the outbreak of *Alexandrium* spp.

**María Guillermina Ruiz**[1], Lucrecia Allega[2], Leilén Luciana Gracia Villalobos[1,3], María Belén Mattera Coy[1], Harold Fenco Chavesta[4], Reinaldo Agustín Maenza[4], Raúl Reta[4]

(1) National Institute of Fisheries Research and Development (INIDEP), Marine Chemistry and Red Tide Program, Paseo Victoria Ocampo 1, Mar del Plata, Argentina
(2) National Institute of Fisheries Research and Development (INIDEP), Remote Sensing Program, Paseo Victoria Ocampo 1, Mar del Plata, Argentina
(3) Center for the Study of Marine Systems (CESIMAR- CONICET), Bv. Almte Brown 2915, Puerto Madryn, Argentina
(4) Institute of Fisheries Research and Development (INIDEP), Physical Oceanography Office, Paseo Victoria Ocampo 1, Mar del Plata, Argentina

We describe a bloom of the subtropical cyanobacterium *Trichodesmium* sp. in waters north of the Argentine Continental Shelf, which constitutes the southernmost known record of this genus in the Southwestern Atlantic Ocean (36°54.263' S, 55°55.150' W). The bloom coincided with persistent positive sea surface temperature anomalies in the area and also preceded an unusual bioluminescent outbreak of *Alexandrium* species off the Mar del Plata coast. Based on these observations, the objectives of this study were: 1) to taxonomically identify the organisms responsible for both blooms using optical microscopy, pigment composition, and toxin presence; 2) to characterize spatiotemporal distribution of the *Trichodesmium* sp. bloom using a satellite-based algorithm specific to this genus; and 3) to analyze the oceanographic and meteorological conditions associated with these blooms (temperature, salinity, currents and winds). The *Trichodesmium* sp. bloom changed the sea surface color to orange, persisted for at least 10 days and extended in a SW-NE direction for more than 150 km, close to the 50 m isobath associated with a SW surface current influenced by mean winds from the NE sector. *Alexandrium* bloom was composed of several species, including *A. catenella* and A. affine, in agreement with absolute maxima sea surface temperature on the Mar del Plata coast. Toxins were detected in the second bloom, but not in the first. Given that *Trichodesmium* sp. produces ammonium, we discussed the possible interrelationship between both blooms based on the observed environmental conditions, and the implications of these potentially toxic blooms within areas of fishing interest.

**Keywords:** *Trichodesmium* sp., *Alexandrium* spp., sea surface temperature anomalies

**Financing**: National Institute of Fisheries Research and Development (INIDEP) & Center for the Study of Marine Systems (CESIMAR- CONICET), Argentina.

Parallel Session 21: Ecology, Biology and Biogeography

O-110

# Intensification and spread of inshore *Alexandrium catenella* blooms in Cape Cod, Massachusetts

**Michael Brosnahan[1],** Sylvain Gaillard[1], Nate Spada[1], David Beaudoin[1], Michael Staiger[1], Mrunmayee Pathare[1], Kali Horn[1], Anushka Rajagopalan[3], Hayden Kinkade[1], Renee Gagnee[5], Nathan Sears[4], Chrissy Petitpas[6], Terry O'Neil[6], Brianne Shanks[6], Alyson Mello[6], Florence Cenci[7], Serena Sung-Clarke[1], Mindy Richlen[1], Donald Anderson[1], Dennis McGillicuddy[2], David Ralston[2]

(1) Woods Hole Oceanographic Institution, Biology, 266 Woods Hole Rd., Woods Hole, MA, USA
(2) Woods Hole Oceanographic Institution, Applied Ocean Physics and Engineering, 266 Woods Hole Rd., Woods Hole, MA, USA
(3) University of Edinburgh, School of Geosciences, Drummond St., Edinburgh, UK
(4) Town of Orleans, Natural Resources Department, 19 School St., Orleans, MA, USA
(5) Town of Chatham, Natural Resources Division, 261 George Ryder Rd., Chatham, MA, USA
(6) Commonwealth of Massachusetts, Division of Marine Fisheries, 836 S Rodney French Blvd, New Bedford, MA, USA
(7) Commonwealth of Massachusetts, Division of Marine Fisheries, 30 Emerson Ave, Gloucester, MA, USA

A long-term trend toward more intense Alexandrium catenella blooms in Nauset Marsh (Cape Cod, MA USA) accelerated sharply in late 2022, when a bloom developed four months earlier and persisted three times longer than historical norms. The following April, *Alexandrium* cells and paralytic shellfish toxins (PSTs) were detected within embayments up to 100 km south and west of the bloom's epicenter. Event response surveys documented massive new cyst production that drove even earlier bloom development in Nauset and its neighboring systems in late 2023 and 2024. The early initiation of these events coincided with unusually warm winters, providing a near optimal temperature regime for this organism. Wintertime water temperatures were sufficiently cold to break cyst dormancy but not cold enough to suppress cyst germination or vegetative cell growth. Because springtime temperatures have warmed less, Nauset cyst beds remain active late into April and May, driving repeated cycles of bloom development, new cyst production, and renewal through continued cyst germination. A parallel population genetics study has demonstrated strong linkage of newly established, localized blooms to the 2022 Nauset population. Thus, expansion of PSP on Cape Cod traces specifically to spread from Nauset rather than stimulation of cryptic cyst deposits. Still, *Alexandrium* are frequently recorded in plankton samples from across the region, suggesting that cryptic, self-seeding cyst deposits may already be widespread and responsive to altered seasonal temperatures. If recent climate conditions persist, the number and size of these populations is likely to grow, requiring expanded PSP monitoring within inshore systems.

**Keywords**: Cyst physiology, Population genetics, Response to environmental change

**Financing:** Woods Hole Center for Oceans and Human Health (NSF: #OCE-2418297 and NIEHS: #2P01ES028938), NOAA NCCOS (#NA19NOS4780186), and the IOOS NHABON initiative.

Parallel Session 21: Ecology, Biology and Biogeography

O-111

# Spatiotemporal dynamics of the 2018 *Alexandrium catenella* bloom in Aysén, Southern Chile

**David Cassis**[1], Sylvana Galaz[1], Diego Caro[2], Fabio Labra[3], Marcos Godoy[2]

(1) AquaBC Chile, Rapid Testing, Imperial 202, Puerto Varas, Chile
(2) Centro de Investigaciones Biológicas Aplicadas (CIBA), Fitoplancton, Lago Panguipulli 1390, Puerto Montt, Chile
(3) Centro de Investigación e Innovación para el Cambio Climático, Facultad de Ciencias, Av. Ejército Libertador 146, Santiago, Chile

In the early summer of 2018, a widespread bloom of the dinoflagellate *Alexandrium catenella* occurred in the Aysén Region of southern Chile, resulting in the mortality of approximately 3,250 tonnes of farmed salmon across 115 aquaculture sites. We analyzed oceanographic and biological data from 20 monitoring stations across the Chonos Archipelago and the Puyuhuapi and Yacaf Channels between December 2017 and March 2018. The bloom was most intense along the Moraleda Channel during January–February, extending southward through the Pérez Channel with limited penetration into adjacent fjords. Peak *A. catenella* concentrations were detected earlier in the Puyuhuapi–Yacaf channel system than in neighbouring stations at Magdalena Sound. Satellite chlorophyll data and particle transport modelling suggest a modest initial inflow from the Moraleda Channel into the Puyuhuapi Channel was enhanced by local circulation patterns, particularly by outflow from Magdalena Sound, which strengthened northward flow towards Yacaf Chanel.

*Alexandrium* abundance peaked in subsurface layers with oceanic signatures (Temperature 12–14°C; Salinity 29–35 PSU), while lower concentrations were associated with more estuarine waters (Temperature ≈10°C; Salinity 22–25 PSU). These patterns highlight the important role of fjord circulation and hydrographic structure in modulating harmful algal bloom dynamics in southern Chile.

**Keywords:** *Alexandrium catenella*, Harmful algal bloom, Phytoplankton dynamics

**Financing**: Private funding.

Parallel Session 22: HABs in a Changing World & Emerging Issues

O-112

# Dynamics of the massive cyst beds of the toxic dinoflagellate *Alexandrium catenella* in the rapidly warming Pacific Arctic

**Donald Anderson**[1], Evangeline Fachon[1], Kali Horn[1], Robert Pickart[2], Loreley Lago[2], Kathi Lefebvre[3], Gay Sheffield[4], Emma Pate[5], Jacqueline Grebmeier[6]

(1) Woods Hole Oceanographic Institution, Biology Department, MS # 32, WHOI, Woods Hole MA, US
(2) Woods Hole Oceanographic Institution, Physical Oceanography Department, MS 32, Woods Hole Oceanographic Institution, Woods Hole MA, US
(3) Northwest Fisheries Science Center, Environmental and Fisheries Science Division, Seattle WA, USA
(4) University of Alaska Fairbanks, Sea Grant Program, Nome AK, USA
(5) Nome Eskimo Community, Nome AK, USA
(6) University of Maryland, Chesapeake Biological Laboratory, Solomons MD, USA

The Bering, Chukchi, and Beaufort seas are warming rapidly, leading to an elevated risk of blooms of the saxitoxin-producing dinoflagellate *Alexandrium catenella*. This species is a recognized concern in southeastern Alaska, but its distribution and impacts in northern waters are poorly understood. This talk synthesizes eight years (2018-2025) of observations, focusing on the dynamics of the extraordinarily large and dense A. catenella cyst beds recently documented in the US waters of the Chukchi and Bering Seas. Collectively, these comprise the largest and densest *A. catenella* cyst accumulation globally, with area and cyst concentration 15-20X higher than similar features elsewhere. The size of the Chukchi cyst bed reflects repeated encystment inputs from blooms transported through Bering Strait from the south, with minimal germination losses in cold years. This dynamic was documented in 2022 when a huge *A. catenella* bloom was transported northward through Bering Strait, culminating in a mass encystment event. Throughout that time, cold temperatures suppressed germination from the northern cyst beds. In warmer years, it is thought that locally initiating blooms in northern waters lead to additional cyst deposition. Observations in 2022 suggest that the origin of the northern Bering Sea bloom was from unidentified cyst beds in the Gulf of Anadyr. Bloom inputs are also hydrographically feasible from the southeastern Bering Sea, where another large cyst bed has recently been documented. The unprecedented Pacific Arctic cyst beds represent a significant threat to Alaskan Arctic ecosystems and the human communities that depend on those resources for food and survival.

**Keywords:** *Alexandrium*, Arctic, cysts

**Financing:** NSF Office of Polar Programs, NOAA's Arctic Research program; NOAA ECOHAB Program, National Science Foundation Graduate Research Fellowship, North Pacific Research Board Graduate Student Award.

Parallel Session 22: HABs in a Changing World & Emerging Issues

O-113

# Summertime heat waves in the lower Chesapeake Bay and their effects on blooms of the harmful algae *Margalefidinium polykrikoides*

**Margaret Mulholland**[1], Sophie Clayton[2], Michael Echevarria[3], Peter Bernhardt[1], Eduardo Perez-Vega[1], Yifan Zhu[4], Alfonso Macias-Tapia[1], Michelle Tomlinson[5], Eileen Hofmann[1]

(1) Old Dominion University, Department of Ocean and Earth Sciences, 4600 Elkhorn Avenue, Norfolk, United States
(2) The National Oceanography Centre, Southampton, United Kingdom
(3) Hampton Roads Sanitation District, Virginia Beach, United States
(4) University of Connecticut, Avery Point, United States
(5) NOAA, National Centers for Coastal Ocean Science, Silver Spring, United States

Estuarine heat waves are projected to exert profound impacts on marine communities. Many of these impacts are thought to be negative. From 2019-2024, estuarine heat waves in the lower Chesapeake Bay impacted the initiation, magnitude and duration of summertime blooms of *Margalefidinium polykrikoides*. We observed that the timing of heat waves with respect to the biological processes involved in bloom initiation could both positively and negatively affect the magnitude and duration of blooms in the lower Chesapeake Bay. For example, in 2019, 2023, and 2024 estuarine heat waves occurred in June during the period when M. polykrikoides blooms routinely initiate in shallow sub-tributaries of the lower Chesapeake Bay. This resulted in a failure of the bloom to initiate. In contrast, in 2020, 2021, and 2022, heat waves occurred in July, after blooms of *M. polykrikoides* had initiated and been transported to the lower James River and Chesapeake Bay. During these years, *M. polykrikoides* populations continued to thrive outside of the super-heated shallow estuaries where blooms had initiated. This suggests that excystment and bloom development processes are temperature sensitive, and that summertime warming of shallow waters where blooms of this organism initiate could actually reduce bloom formation or create conditions conducive for the emergence of new phytoplankton populations.

**Keywords:** *Margalefidinium polykrokoides*, estuarine heat waves

**Financing:** NOAA MERHAB, NOAA ECOHAB and the Hampton Roads Sanitation District.

Parallel Session 22: HABs in a Changing World & Emerging Issues

O-114

# Combined effects of warming and nitrogen availability on harmful algal blooms in the Dutch coastal North Sea

**Andrea Budiša**[1], Arnaud P. Louchart[1], Dedmer B. Van de Waal[1]

(1) NIOO-KNAW, AqE, Droevendaalstesteeg 10, Wageningen, Netherlands

Eutrophication generally stimulates the proliferation of phytoplankton, which is expected to be further promoted by climate change. These global change factors act at the same time, and it is therefore pivotal to explore how their combination affects the foundations of the marine food web. In the North Sea, blooms were shown to start earlier and last longer, largely due to rising temperatures and changes in nutrient availability. Monitoring data show that temperature increases and decreases in nutrient concentrations have promoted harmful algae in the area, notably including *Phaeocystis globosa*, which accounts for most of the phytoplankton spring biomass. A microcosm experiment with a North Sea spring phytoplankton community was performed to assess how the combination of ongoing warming and shifts in nutrient supply may impact *P. globosa* blooms. We exposed the sampled community to mid- and end-century temperature scenarios under the no-policy baseline scenario 8.5 (i.e., +2.4 and +4.8 °C), combined with nitrate enrichment simulating a sudden river discharge. The results show a strong temperature effect, which enhanced net phytoplankton community growth rates. Moreover, we observed temperature-dependent changes in the growth characteristics (functional traits) of various size classes, including nanoeukaryotes such as *P. globosa*. Specifically, they showed enhanced chlorophyll-a contents while morphological traits, such as cell size and complexity, were not impacted. Overall, our findings show that global warming in the Dutch North Sea may promote P. globosa, impacting the structure, functioning, and services of these coastal ecosystems.

**Keywords:** Global warming, Nanoeukaryotes, Eutrophication

**Financing:** Funded by Horizon Europe Project Advancing Understanding of Cumulative Impacts on European Marine Biodiversity, Ecosystem Functions, and Services for Human Wellbeing – ACTNOW (No 101060072).

Parallel Session 22: HABs in a Changing World & Emerging Issues

O-115

# The role of harmful dinoflagellate blooms in controlling the temporal and spatial dynamics of hypoxia and acidification in Northwest Atlantic estuaries

**Ryan Wallace**[1], Andrew Lundstrom[2], Christopher Gobler[2]

(1) Adelphi University, Department of Environmental Studies and Sciences, 1 South Ave, Garden City, United States
(2) Stony Brook University, School of Marine and Atmospheric Sciences, 39 Tuckahoe Rd, Southampton, NY, United States

As a consequence of climate change, hypoxia and acidification are becoming more common in marine ecosystems. In parallel, the impacts of harmful algal blooms (HABs) on coastal zones have increased. Although the fields of HABs and ocean acidification (OA) are well-established individually, the precise, coupled temporal and spatial dynamics of these conditions are poorly described. Here, continuous measurements of water column pH, the partial pressure of carbon dioxide ($pCO_2$), carbonate chemistry, dissolved oxygen (DO) concentrations, and cell enumeration of three HAB species (*Alexandrium catenella, Dinophysis acuminata, Margalefidinium polykrikoides*) were made during the onset, peak, and demise of each bloom across three temperate Northeast US estuaries. Temporal and vertical dynamics were resolved using multiparameter/multi-depth telemetered sampling arrays, whereas spatial mapping was achieved using a high-throughput underway sampling system. During this study, *A. catenella* blooms (>$10^6$ cells $L^{-1}$) co-occurred with normoxic and normocapnic conditions, while D. acuminata blooms co-occurred with high algal biomass (chlorophyll a > 100 µg $L^{-1}$), hypoxia, acidification (pH < 7.2), and hypercapnia ($pCO_2$ > 3,000 µatm). Ephemeral M. polykrikoides blooms caused brief periods of basification, hypocapnia ($pCO_2$ < 250 µatm), and supersaturation of DO at the surface that were succeeded by longer periods of acidification and hypoxia at depth. Diurnal vertical profiles demonstrated that oxic surface waters saturated with respect to calcium carbonate and DO during the day transitioned to unsaturated and hypoxic at night. Collectively, this study demonstrates the dynamic nature of HABs, hypoxia, and acidification in estuaries, therefore these co-stressors must be considered in management scenarios.

**Keywords:** Acidification, Hypoxia, Dinoflagellates

**Financing:** National Oceanic and Atmospheric Administration (NOAA)

**Acknowledgments:** We are appreciative of the field and laboratory assistance from Craig Schenone, Mairead Farrell, and Christopher Gioia.

Parallel Session 22: HABs in a Changing World & Emerging Issues

O-116

# The impact of environmental change on long-term trends in harmful algal blooms in a southeastern Australian estuary

**Dora Vig**[1], Penelope A. Ajani[1], Steve Brett[2], Javier Pérez-Burillo[3], Hazel Farrell[4], Shauna A. Murray[1]

(1) University of Technology Sydney, School of Life Sciences, Faculty of Science, 4/15 Broadway, 2007, Sydney, Australia
(2) Microalgal Services, 308 Tucker Rd, 3204, Ormond, Australia
(3) University of New South Wales, School of Biotechnology and Biomolecular Sciences, Faculty of Science, Gate 11, Botany Street, 2052, Sydney, Australia
(4) NSW Food Authority, NSW Department of Primary Industries, PO Box 232, 2430, Taree, Australia

Aquaculture is the fastest-growing food industry globally, driven by the demand for sustainable seafood. However, harmful algal blooms (HABs) increasingly threaten marine stocks, including in Australia, where long-term data remain scarce. Botany Bay, a key site for Sydney Rock Oyster farming since the 1870s, has experienced major setbacks, including QX disease in the 1990s and recurrent HABs. These events have led to severe economic and ecological impacts, raising concerns over the role of long-term environmental changes. Here, we leverage a long-term eDNA time series from Botany Bay (2016–2023) to study phytoplankton temporal dynamics at the community, species, and intraspecific levels. Focusing on toxic diatom and dinoflagellate species (including the *Pseudo-nitzschia* species complex, *Alexandrium* spp., and *Prorocentrum* spp.), we assigned taxonomy to 69 amplicon sequence variants (ASVs) via phylogenetic placement and applied Hierarchical Modelling of Species Communities (HMSC) to evaluate environmental drivers of temporal occurrence. Beta diversity analyses revealed clear seasonal turnover in community composition for both diatoms and dinoflagellates. Variance partitioning confirmed strong recurring seasonal patterns in the presence–absence of most *Pseudo-nitzschia* species, while much of their relative abundance was explained by gradients in temperature, salinity, and phosphate. While seasonality was a key driver of presence–absence patterns, especially for *Alexandrium* spp., dinoflagellates showed higher sensitivity to environmental conditions overall. At the ASV level, strain-specific responses to environmental variables were evident in both diatoms and dinoflagellates. These findings underscore the value of integrating high-resolution molecular data with ecological modelling to understand phytoplankton dynamics and anticipate harmful bloom conditions.

**Keywords**: Harmful algal blooms, eDNA

**Financing:** Fisheries Research and Development Corporation / Oysters Australia Scholarship

Parallel Session 23: New Method & Technology

O-117

# Non-targeted mass spectrometry-based metabolomics for comprehensive annotation of cyanobacterial metabolites in Greek Lakes

**Sevasti-Kiriaki Zervou[1],** Triantafyllos Kaloudis[1,2], Spyros Gkelis[3], Theodoros Triantis[1], Anastasia Hiskia[1]

(1) Institute of Nanoscience and Nanotechnology (INN), NCSR Demokritos, Athens, Greece
(2) AquOmixLab, Athens Water Supply and Sewerage Company (EYDAP SA), Greece
(3) School of Biology, Aristotle University of Thessaloniki, Thessaloniki, Greece

Cyanobacterial harmful algal blooms (HABs) in freshwater ecosystems pose significant ecological and public health threats due to the diverse array of bioactive metabolites they produce. Untargeted metabolomics, employing high-resolution mass spectrometry, offers a powerful approach to comprehensively characterize this molecular diversity. However, the annotation of these often-novel compounds remains a major bottleneck, limiting a full understanding of bloom toxicity and their ecological impact. This study presents a comprehensive workflow for the annotation of cyanobacterial metabolites from cyanobacteria bloom samples collected from several Greek lakes. Untargeted analysis was performed using liquid-chromatography coupled with high resolution mass spectrometry (LC-HRMS). Data processing utilized an integrated computational workflow, including MZmine for feature detection and alignment along with CyanoMetDB mass list search, GNPS2 for feature-based molecular networking and spectral annotation, and SIRIUS for enhanced structural elucidation. The presence of a wide variety of bioactive cyanobacterial peptides belonging to the classes of microcystins (cyanotoxins), anabaenopeptins, cyanopeptolins, aeruginosins and microginins, was revealed. The findings emphasize the complex chemical ecology of freshwater cyanobacterial HABs. Robust annotation of such diverse metabolites is essential for understanding bloom dynamics, predicting toxicity, and developing effective mitigation strategies.

**Keywords**: cyanobacterial metabolites, non-targeted analysis, computational metabolomics

**Acknowledgments:** We are grateful to the developers of the MS computational platforms and tools (MZmine, GNPS/GNPS2, Sirius, Cytoscape), which are freely offered to the research community.

Parallel Session 23: New Method & Technology

O-118

# Metabolomic insights in the basal metabolism of *Amphidinium* and *Coolia* species associated with biofilms

**Nadia Valeria Herrera Herrera**[1], Elvia Becerra Martínez[2], Claudia Judith Hernández Guerrero[3], Christine Johanna Band Schmidt[1]

(1) Centro Interdisciplinario de Ciencias Marinas (IPN-CICIMAR), Plankton and Marine Ecology, Av. Instituto Politécnico Nacional s/n, Col. Playa Palo de Santa Rita, La Paz, Baja California Sur, Mexico
(2) Centro de Nanociencias y Micro y Nanotecnologías (IPN-CNMN), Av. Luis Enrique Erro s/n, Unidad Profesional Adolfo López Mateos, Zacatenco, Mexico city, Mexico
(3) Centro Interdisciplinario de Ciencias Marinas (IPN-CICIMAR), Technology Development, Av. Instituto Politécnico Nacional s/n, Col. Playa Palo de Santa Rita, La Paz, Baja California Sur, Mexico

The genera *Amphidinium* and Coolia commonly co-occur in marine benthic ecosystems and produce a variety of metabolites and toxins within mucilage-rich biofilm. Despite their ecological relevance, the metabolic pathways associated with their primary (basal) metabolism remain poorly understood. This study aimed to determinate the basal metabolism of *Amphidinium carterae*, *A. operculatum*, *A. thermaeum*, and *Coolia malayensis* under culture conditions. Nuclear Magnetic Resonance (NMR) spectroscopy combined with multivariate data analysis enabled untargeted metabolic profiling of these dinoflagellates. Cultures were grown in modified GSe medium at 24 ± 1°C, salinity 34, under a 12:12 h light-dark cycle at 150 µmol photons $m^{-2} s^{-1}$. Cells were harvested during exponential growth for all bioassays. In parallel, biofilm formation was assessed by ultrastructural analysis and quantification of Transparent Exopolymer Particles (TEPs). The NMR data revealed the presence of 34 metabolites (16 amino acids, 2 sugars, 9 organic acids, 4 nitrogenous bases and 3 miscellaneous metabolites). The metabolomic profiles of each species showed differences in the active basal metabolism related to cellular protection and energy production. Notably, TEPs played a key role in early-stage biofilm development. Among the species analyzed, *A. thermaeum* and *A. operculatum* exhibited higher levels of extracellular TEPs aggregates compared to *A. carterae* and *C. malayensis*, suggesting species-specific differences in extracellular mucilage production. These findings contribute to a higher understanding of the physiological and ecological functions of benthic dinoflagellates and highlight the relevance of basal metabolites and TEPs in their biofilm dynamics.

**Keywords:** benthic dinoflagellate, metabolite, mucilage

**Financing:** The project was funded by two sources: institutional projects (SIP 2025-1372) and a student fellowship from SECIHTI (CVU 747731).

**Acknowledgments:** We are grateful to Dr. Mary Carme Ruiz de la Torre and MSc Linda Zumaya for their laboratory support in TEPs analysis.

Parallel Session 23: New Method & Technology

O-119

# Strengthening marine toxin surveillance: Implementing isotopic techniques on ciguatoxin quantitation in the Philippines

**Ma. Llorina Mestizo[1],** Tammara Grace Angeles[1], Marc Lawrence Romero[2], Alvin Awatin[2], Rhett Simon Tabbada[1]

(1) Philippine Nuclear Research Institute, Department of Science and Technology (DOST-PNRI), Chemistry Research Section, Atomic Energy Division, Commonwealth Avenue, Diliman, Quezon City, Philippines
(2) Bureau of Fisheries and Aquatic Resources, Department of Agriculture (DA – BFAR), Aquatic Toxicology Laboratory, National Fisheries Laboratory Division, Arcadia Building, Quezon Avenue, Quezon City, Philippines

Philippines had been utilizing radioligand receptor binding assay or rRBA on an expansive application on quantifying notable harmful algal toxins. The national mandate to mitigate such occurrence is referred from prevalent reports on saxitoxin-producing species in the region. The method, furthermore, expands its application to other HAB toxins such as brevetoxins (BTX) and ciguatoxins (CTX). It is effective in saxitoxin quantification, therefore, enabling the national regulatory body to utilize such a method is forthcoming. The rRBA for quantifying CTX is designed using the AOAC guidelines for national acceptance and subsequent accreditation. The statistical evaluation of the method provided satisfying results for both BTX-3 and CTX3C standards demonstrating low inter-experimental variability with relative standard deviation of <20%, with an acceptable average Hill slope values of -0.8290 to -1.193. The method is robust as observed for assays conducted by different analysts on independent days, conducted using different batches of reagents prepared (df = 14, p value > 0.999). The EC50 values in this work for BTX-3 (n=12) and P-CTX3C (n=6) are 3.567 nM± 0.697 and 1.644 nM±0.207, respectively. Based on these findings, a toxin equivalency factor of 2.170 is proposed for implementation in routine monitoring and future interlaboratory comparisons. Together with the scientific information at hand, incorporating the quantitation method with related algal bloom data can be used to identify protection goals towards public policy and societal and economic values. This is an ongoing effort towards an effective analytical testing laboratory and its valuable implementation of seafood safety monitoring program.

**Keywords:** radioligand receptor binding assay, ciguatoxins, seafood safety monitoring program

**Financing:** Philippine Council for Agriculture, Aquatic and Natural Resources Research and Development, Department of Science and Technology (DOST-PCAARRD).

**Acknowledgments:** Philippine Council for Agriculture, Aquatic and Natural Resources Research and Development, Department of Science and Technology (DOST-PCAARRD) International Atomic Energy Agency (IAEA).

Parallel Session 23: New Method & Technology

O-120

# Optimization of the extraction protocol for Pacific ciguatoxins from marine products prior to analysis using the neuroblastoma cell-based assay

**Mélanie Roué**[1], Thomas Yon[2], Philippe Cruchet[2], Jérôme Viallon[2], J. Sam Murray[3], Emilie Passfield[3], Mireille Chinain[2], Hélène Taiana Darius[2]

(1) French National Research Institute for Sustainable Development (IRD), UMR SECOPOL, P.O. Box 6570, 98702 Faa'a, French Polynesia
(2) Institut Louis Malardé (ILM), UMR SECOPOL, Laboratory of Marine Biotoxins, P.O. Box 30, 98713 Papeete, French Polynesia
(3) Cawthron Institute, 98 Halifax St East, PB 2, The Wood, Nelson 7010, New Zealand

Ciguatera poisoning (CP) is a foodborne illness caused by the consumption of marine products contaminated with ciguatoxins (CTXs), a group of potent neurotoxins produced by *Gambierdiscus* dinoflagellates. While numerous methods have been developed to extract and purify trace levels of CTXs from complex biological matrices, their effectiveness for nonpolar CTX congeners remains poorly characterized. This represents a critical gap, as these nonpolar toxins significantly contribute to the CP risk and must be accurately detected to support robust food safety monitoring programs.

First, six published extraction/purification protocols were evaluated using fish flesh previously spiked with CTX3C then analyzed by the neuroblastoma cell-based assay (CBA-N2a). Recovery rates ranged from 6% to 45%, highlighting the need for improved methodologies. Subsequently, an optimized three-day protocol, suitable for high-throughput processing, was developed achieving recovery rates of 73% and 70%, for CTX1B and CTX3C respectively, which also eluted in a single fraction.

Further tests on naturally contaminated fish samples demonstrated a significant reduction in matrix-related interferences in CBA-N2a, thereby increasing sensitivity and enabling CTX detection at levels complying with the US-FDA guidance level. However, signal suppression observed in LC-MS/MS confirmatory analyses remains an area for future improvement.

This optimized protocol represents significant progress towards the technological development and harmonization of CTX extraction in marine organisms, regardless of their trophic status. Its use in combination with CBA-N2a enables better quantification of CTXs in marine products, enhancing/improving food safety measures and risk assessment strategies for CP in regions where populations are highly dependent on lagoon resources.

**Keywords:** ciguatoxins, extraction protocol, CBA-N2a

**Financing:** OPEX-CTX program funded by the Government of French Polynesia (4402/MED/REC) and from France (AFD CPF 1554 01 n ◦ 2113).

Parallel Session 23: New Method & Technology

O-121

# An electrochemical immunosensor for tetrodotoxin and saxitoxin detection: A step towards integrated seafood toxin monitoring

**Jaume Reverté[1],** Andrew D. Turner[2], Mirjam Klijnstra[3], Arjen Gerssen[3], Manolis Mandalakis[4], Panagiota Peristeraki[5], Maria Rambla-Alegre[1], Jorge Diogène[1], Mònica Campàs[1]

(1) IRTA, Marine and Continental Waters (AMiC), 43540, La Ràpita, Spain
(2) Centre for Environment Fisheries and Aquaculture Science (CEFAS), Barrack Road, Weymouth DT4 8UB, United Kingdom
(3) Wageningen Food Safety Research, Wageningen University & Research, Akkermaalsbos 2, 6708 WB Wageningen, The Netherlands
(4) Hellenic Centre for Marine Research (HCMR), Institute of Marine Biology, Biotechnology and Aquaculture, 71003 Heraklion, Greece
(5) Hellenic Centre for Marine Research (HCMR), Institute of Marine Biological Resources and Inland Waters, 71003 Heraklion, Greece

The presence of toxins such as tetrodotoxin (TTX) and saxitoxin (STX) in fish and shellfish poses a significant threat for food safety and public health due to their potent neurotoxic effects, which can lead to severe poisoning cases and fatalities. Traditional detection methods typically target a single toxin family, rendering them ineffective when several toxins are present simultaneously. In light of recent findings regarding the co-occurrence of TTX and STX in seafood, there is clearly a demand for advanced platforms able to detect several toxin families in a single analysis. In this work, a novel multiplexed electrochemical immunosensor for the dual detection of TTX and STX is proposed. The device includes an array of four electrodes: two test electrodes for detecting the presence of TTX and/or STX in seafood samples, and two control electrodes as reference thresholds according to the current regulatory safety limits for each toxin family. The combined information provided by the dual biosensor enables not only the identification of the specific toxins present in a sample, but also an assessment of whether toxin levels exceed safety limits, offering a rapid, effective and easy-to-interpret screening method with potential to be applied in toxin monitoring. This dual-detection approach could pave the way towards integrated monitoring systems capable of identifying multiple marine toxins in a single test, thereby improving seafood safety and public health protection.

**Keywords:** Biosensor, Antibody, Food Safety

**Financing:** This work was funded by the Ministerio de Ciencia e Innovación (MICIN) and the Agencia Estatal de Investigación (AEI) (Spain) through the BiOCEANsing (PID2023-149899OB-21) project.

**Acknowledgments:** The authors acknowledge support from the shellfish monitoring program of Catalonia (Direcció General de Política Marítima I Pesca Sostenible, Generalitat de Catalunya).

Parallel Session 24: New Method & Technology

O-122

# Reversal of nondepolarizing nicotinic acetylcholine receptor block induced by 6- or 7-membered cyclic imine toxins using 3,4-diaminopyridine in isolated mouse diaphragm preparations

**Jordi Molgo[1],** Nicolas Lamassiaude[1], Rómulo Aráoz[1], Evelyne Benoit[1], Muriel Delepierre[2], Armen Zakarian[3], Denis Servent[1]

(1) Université Paris-Saclay, CEA,, Département Médicaments et Technologies pour la Santé, Service d'Ingénierie Moléculaire pour la Santé (SIMoS), EMR9004 CNRS. F-91191 Gif sur Yvette, France.
(2) Institut Pasteur, Department of Structural Biology and Chemistry CNRS, UMR3528, Paris France.
(3) University of California Santa Barbara, Department of Chemistry and Biochemistry, Santa Barbara, CA 93106, USA

Cyclic imine toxins (CiTXs) are a family of marine macrocyclic phycotoxins worldwide-distributed, comprising the gymnodimines (GYMs), spirolides (SPXs), pinnatoxins (PnTXs), pteriatoxins (PteTXs), portimines, prorocentrolides and spiroprorocentrimine. CiTXs and acyl derivative products of shellfish metabolism contaminate and bioaccumulate in filter-feeding bivalves, edible mollusks and marine invertebrates and represent a menace for wildlife conservation and a risk for shellfish consumers. CiTXs interact and block with various affinities muscle-type nicotinic acetylcholine (ACh) receptors (nAChRs) expressed in skeletal muscles.

3,4-diaminopyridine (3,4-DAP) is a $K^+$-channel blocker that prolongs the action potential and indirectly enhances $Ca^{2+}$ entry into motor nerve terminals increasing quantal ACh release in skeletal muscles. 3,4-DAP has been used efficiently to treat muscular weakness in humans with myasthenic syndromes. The aim of this work was to determine whether 3,4-DAP by increasing evoked ACh release would be able to reverse the action of CiTXs on nAChRs. We used isolated mouse phrenic-nerve hemi-diaphragm muscle preparations, and monitored nerve-evoked isometric muscle contractions in the presence of GYM-A, PnTX-A, PnTX-G and PteTX-A and afterwards the action of 3,4-DAP, in the continuous presence of the respective CiTXs. Our results show that 3,4-DAP improves neuromuscular transmission in a time- and concentration-dependent manner, and completely reverses the block caused by the CiTX studied, supporting the view that GYM-A, PnTX-A, PnTX-G and PteTX-A are competitive inhibitors of the muscle-type nAChRs. The ability of 3,4-DAP to antagonize the action of CiTXs is related to the increased ACh release that is able to displace CiTXs from their putative nAChR binding sites.

**Keywords:** Cyclic imine toxins, nicotinic acetylcholine receptors, 34-diaminopyridin

Parallel Session 24: New Method & Technology

O-123

# Disclosing the functions of nuclear receptors NR1J1 in bivalves and toxin metabolism. New insights from in vitro and in vivo studies

Juliana Rodrigues[1], Cristina Plata-Calzado[2], Maria Paula Gómez-Román[1,3], Concepción Medrano-Padial[2], Antonio Casas-Rodríguez[2], Ana M. Camean[2], Elza Fonseca[1], **Alexandre Campos[1]**

(1) Centro Interdisciplinar de Investigação Marinha e Ambiental (CIIMAR/CIMAR), University of Porto, Terminal de Cruzeiros do Porto de Leixões, Av. General Norton de Matos, s/n, Matosinhos, Portugal
(2) Universidad de Sevilla, Area of Toxicology, Faculty of Pharmacy, Profesor García González n ◦ 2, Seville, Spain
(3) School of Medicine and Biomedical Sciences, Instituto de Ciências Biomédicas Abel Salazar, University of Porto, Rua de Jorge Viterbo Ferreira, Porto, Portugal

The nuclear receptor (NR) NR1J genes identified in marine invertebrates share high sequence homology with VDR/PXR/CAR NR family commonly found in vertebrates. The NR pregnane X receptor (PXR), for instance, is known to regulate a wide number of genes involved in xenobiotic metabolism, including those from phase I (CYP3A family members), phase II (including glutathione S-transferases, sulfotransferases, UDP-glucuronosyltransferases, and carboxylesterases) and phase III (hepatic transporters such as OATP2, MRP2, and MDR1). Despite this similarity, the mode of action and biological roles of the NR1J gene family in invertebrates remain largely overlooked. To gain insight into the molecular functions of these genes and their potential involvement in biotoxin metabolism, our group conducted a series of in vitro and in vivo assays to the NR1J1 from marine mussel Mytilus galloprovincialis. A dual-luciferase reporter gene assay with COS-1 cells demonstrated that NR1J1 proteins can be activated by various putative agonists, including multiple marine and freshwater toxins. Notably, the NR1J1 paralogs exhibited differential sensitivity to these toxins, with activation being concentration-dependent in some cases. These in vitro studies also revealed that M. galloprovincialis NR1J1 proteins are activated by several other natural compounds. In addition, we observed co-transcriptional activation of several NR1J1 paralogs, as well as CYP and ABCB1 genes, in adult mussels exposed to different toxic and non-toxic algal extracts. These findings strongly support the hypothesis that the NR1J gene family in invertebrates may perform functions analogous to vertebrate PXR, and may play a critical role in the detoxification of biotoxins in bivalves.

**Keywords:** Algal toxins, xenobiotic metabolism, Bivalves

**Financing:** Funded by Nanoplanet (2022.02340.PTDC) and BlueShellfish projects (grant no. 101086234, doi 10.3030/101086234)

**Acknowledgments:** C.P.-C. thanks Junta de Andalucía (PREDOC_00447) and A.C-R. the Spanish MICINN (PRE2020-094412) for their predoctoral grants awarded.

Parallel Session 24: New Method & Technology

O-124

# Cytotoxic and membrane-disruptive properties of *Prymnesium parvum* extracts

Zsuzsanna Neer[1,2], Hélène-Christine Prause[3,4], Endre Kiss[5], Tamás Felföldi[2], Balázs Vajna[2], János Matkó[6], Allen Place[7], **Elisabeth Varga[1]**

(1) University of Veterinary Medicine Vienna, Clinical Department for Farm Animals and Food System Science, Centre for Food Science and Veterinary Public Health, Veterinärplatz 1, Vienna, Austria
(2) Eötvös Loránd University, Department of Microbiology, Faculty of Science, Pázmány Péter sétány 1/C, Budapest, Hungary
(3) University of Vienna, Department of Food Chemistry and Toxicology, Faculty of Chemistry, Währinger Str. 38-40, Vienna, Austria
(4) University of Vienna, Vienna Doctoral School in Chemistry, Faculty of Chemistry, Währinger Str. 40, Vienna, Austria
(5) Max Perutz Labs, BioOptics FACS Facility, Dr.-Bohr-Gasse 9, Vienna, Austria
(6) Eötvös Loránd University, Department of Immunology, Faculty of Science, Pázmány Péter sétány 1/C, Budapest, Hungary
(7) University of Maryland, Institute of Marine and Environmental Technology, Center for Environmental Science, 701 E. Pratt St., Baltimore, United States of America

The ichthyotoxic microalga *Prymnesium parvum* is known to produce a group of complex polyether compounds, called prymnesins. These toxins are known to affect biological membranes, leading to the disruption of membrane integrity in e.g. fish gill tissues. Due to the lack of purified compounds, methanolic extracts of P. parvum (PRM) were applied at varying toxin levels to gain further insights into their cytotoxicity.

Molecular studies indicated that PRM can interact with membrane phospholipids and sterols, destabilizing the bilayer structure and leading to uncontrolled ion fluxes and cell lysis. To study the underlying features of the cell membrane's susceptibility to PRM, a set of fluorescence microscopic assays was set up in the rainbow trout-derived gill epithelial cell line, RTgill-W1. Cytotoxicity/loss of membrane integrity was quantified based on the cellular uptake of propidium iodide, Hoechst33342 staining for nuclear morphology and apoptotic cells were detected with AnnexinV staining.

Our results demonstrated a concentration-dependent shift in the dominant mode of cell death, where lower toxin levels predominantly triggered apoptosis, characterized by nuclear morphological changes, a decrease in mitochondrial mass, and Annexin V staining. The pH backslide of the lysosomal vesicles might serve as an amplifier of the process. Whereas higher toxin concentrations trigger necrosis, marked by rapid membrane rupture and loss of cellular integrity. These findings highlight the dual nature of toxin-mediated cytotoxicity and underscore the importance of concentrations in determining cellular outcomes. The modifications in membrane integrity and permeability significantly impact both the functional and structural viability of cells, thereby influencing fish survival.

**Keywords:** cytotoxicity, prymnesins, RTgill-W1

**Financing:** This research was funded in part by the Austrian Science Fund (FWF) [grant DOI:10.55776/I5707] .

**Acknowledgments:** This research was supported using resources of the VetCore Facility (VetImaging) of the University of Veterinary Medicine Vienna.

Parallel Session 24: New Method & Technology

O-125

# Combined toxicity of co-occurring harmful algal bloom species: Cellular and molecular effects on gametes of the Pacific oyster (*Crassostrea gigas*)

**Rima Beesoo**[1], Madre Mathilde[2], Malwenn Lassudrie[2], Véronique Séchet[3], Liliane Carpentier[3], Yohan Didier Louis[4,5], Caroline Fabioux[1], Hélène Hegaret[1]

(1) Univ Brest, CNRS, IRD, IFREMER, LEMAR, F-29280, Plouzané, France
(2) IFREMER, LITTORAL/LER-BO, F-29900, Concarneau, France
(3) IFREMER, DYNECO, Laboratoire Phycotoxines, F-44000 Nantes, France
(4) Earth and Environmental Science Department, University of Milan Bicocca, MI 20126, Italy
(5) MaRHE Center (Marine Research and High Education Center), Magoodhoo Island, Faafu Atoll, Maldives

Harmful algal blooms (HABs) often coincide with the spawning season of the Pacific oyster *Crassostrea gigas*, threatening reproductive success and aquaculture. The co-occurrence of multi-species HAB may further amplify the negative effects of toxic blooms on bivalve reproduction, posing risks to population stability. While individual HAB impacts are documented, combined toxicity and molecular effects remain unclear. This study assessed the in vitro toxicity of co-occurring HAB species on oyster gametes.

Co-occurrence of toxic dinoflagellates from the genera *Dinophysis* and *Alexandrium* along the French coast was identified using data from the French phytoplankton monitoring network. Gamete toxicity and reactive oxygen species (ROS) production were assessed through flow cytometry following exposure to individual and combined HAB mixtures at sub-lethal, equitoxic concentrations. Gene expression was analyzed using RNA-seq, with analysis limited to oocytes due to their higher RNA yield. Results showed that spermatozoa were more sensitive than oocytes to HAB exposure. Co-exposure to Alexandrium minutum and Dinophysis acuta resulted in synergistic toxicity in both gametes. Sperms exhibited higher toxicity and ROS levels compared to single-species exposures. Oocytes showed a lower response, with a moderate increase in toxicity but higher ROS levels following co-exposure. Differential gene expression analysis revealed that co-exposure induced more genes associated with toxicity pathways in oocytes. Upregulated genes were involved in oxidative stress, apoptosis and membrane integrity.

These findings highlight the amplified risk multi-species HAB events pose to oyster reproduction and the need to integrate co-occurring species effects into risk assessments and aquaculture management to better safeguard oyster populations.

**Keywords**: Harmful algal blooms; *Crassostrea gigas*; Gamete toxicity

**Financing:** French National Research Agency (ANR) under the project HABISISblue Postdoctoral Fellowship

**Acknowledgments:** The authors gratefully acknowledge all the colleagues who provided valuable help during the experiment, Nelly Le Goïc, Amélie Derrien, Massimo Milan and Marianna Pauletto.

Parallel Session 24: New Method & Technology

O-126

# Toxicity of *Karenia* species on Greenshell mussel reproduction: Insights into the potential bloom impact on aquaculture in New Zealand

**Mathilde Madre**[1], Malwenn Lassudrie[1], Damien Réveillon[3], Julien Vignier[2], Anne Rolton[2]

(1) Ifremer, COAST, LER-BO,Concarneau, F-29900, France, France
(2) Cawthron Institute, 98 Halifax Street East, Nelson 7010, New Zealand
(3) Ifremer, PHYTOX, Metalg, Nantes, F-44000, France

*Karenia* is a genus of dinoflagellates that includes species capable of inducing harmful algal blooms (HABs). Blooms of *Karenia* species occur on all continents, particularly *Karenia mikimotoi*, which can reach concentrations up to $10^8$ cells·$L^{-1}$. These blooms can cause mass mortalities of marine fauna, including in aquaculture.

In New Zealand, *Karenia* spp. can bloom during summer, coinciding with the reproductive period of the Greenshell™ mussel (*Perna canaliculus*). Species such as *K. mikimotoi, K. brevisculcata, K. papilionacea, K. selliformis*, and *K. longicanalis* are now routinely monitored by the Cawthron Institute due to their bloom-forming potential. However, their effects on the early life stages of Greenshell™ mussels, a species of major economic importance in New Zealand, remain poorly characterized.
This study aimed to assess how New Zealand Karenia species can affect the reproduction of *P. canaliculus*. Embryo-larval development tests, sperm viability assays, and ROS (reactive oxygen species) production measurements were used to evaluate the toxicity of the five aforementioned species at bloom-level concentrations. Additionally, three strains of *K. mikimotoi* were tested to assess intraspecific variability.

*K. selliformis* and one *K. mikimotoi* strain impaired embryo-larval development, possibly due to gymnodimines and gymnocin-C production, respectively. *K. papilionacea* also had significant effects on D-larvae viability, though the responsible toxins remain unidentified. *K. brevisulcata* produces toxins, yet causes no significant effects.

These findings suggest that, at environmental bloom levels ($10^6$–$10^7$ cells·$L^{-1}$), *K. mikimotoi, K. selliformis,* and *K. papilionacea* may significantly impair the early development of Greenshell™ mussels and thus pose a risk to aquaculture.

**Keywords:** Reprotoxicity, Bivalve, Dinoflagellate

**Financing**: Funded by ISblue and Ifremer (mobility), Région Bretagne and ANR HABIS (PhD), and New Zealand's MBIE via Shellfish Aquaculture and CMC Programmes.

**Acknowledgments:** My sincere thanks to the Cawthron Institute and its research team for their warm welcome and support during my visit.

Parallel Session 25: HABs in a Changing World & Emerging Issues

O-127

# Effects of temperature and light on the growth and domoic acid production of the diatom *Pseudo-nitzschia multiseries* from the California Current System

**William P. Cochlan**[1,2], Christopher E. Ikeda[1,3], Brian D. Bill[4], Vera L. Trainer[5], David Senn[6], Charles G. Trick[7]

(1) San Francisco State University, Estuary and Ocean Science Center, 3150 Paradise Drive, Tiburon, CA 94920, USA
(2) Northwest Indian College, Salish Sea Research Center, 2522 Kwina Road, Bellingham, WA 98225, USA
(3) National Oceanic and Atmospheric Administration, Pacific Marine Environmental Laboratory, 7600 Sand Point Way NE, Seattle, WA 98115, USA
(4) National Oceanic and Atmospheric Administration, Environmental and Fisheries Science Division, Northwest Fisheries Science Center, 2725 Montlake Blvd. E., Seattle, WA 98112, USA
(5) University of Washington, Olympic Natural Resources Center, 1455 S. Forks Avenue, Forks, WA 98331, USA
(6) San Francisco Estuary Institute, 4911 Central Avenue, Richmond, CA 94804, USA
(7) University of Toronto, Department of Physical and Environmental Sciences, 1265 Military Trail,, Toronto, Ontario M1C 1A4, Canada

Toxic blooms of the diatom genus *Pseudo-nitzschia* are common in the coastal waters of eastern boundary upwelling systems, including those of the California Current System (CCS) off the west coast of the United States, where ocean warming due to climate change has already been observed. However, the relationship between toxic blooms of elevated domoic acid (DA) and regions of increased water temperature remains uncertain. It has not been examined in conjunction with alterations in light and macronutrient availability. This study used unialgal cultures of acclimated *P. multiseries* – a toxigenic species isolated from Monterey Bay, a well-known DA hotspot, to examine these relationships in multi-factorial experiments to determine which light and temperature conditions promote the greatest cellular growth and/or DA production under both macronutrient-sufficient and -deficient conditions expected in episodic upwelling regions such as the CCS where silicate limitation of diatom growth is frequently found. The specific growth rate of this diatom increases with higher temperatures and greater irradiance, however the cellular concentrations of domoic acid and the rates at which DA is produced only significantly increases with elevated temperature and silicate deficiency. There is no consistent relationship between light levels and DA production rates. At higher temperatures, cells reduce their affinity for silicate by raising the threshold concentrations required for silicate uptake, resulting in only minimal declines in their growth rate. Our results demonstrate that a multi-factorial approach to examine toxigenicity can effectively determine which oceanic conditions are the most valuable predictors of potential DA exposure in coastal ecosystems.

**Keywords**: *Pseudo-nitzschia*, domoic acid, temperature/light

**Financing:** Funding: California Ocean Protection Council (OPC; Prop. 84), California State University Council on Ocean Affairs, Science & Technology (COAST), and San Francisco Estuary Institute (SFEI).

**Acknowledgments:** We thank Ms. Lindsey Metz for her assistance in conducting the experiments presented here.

Parallel Session 25: HABs in a Changing World & Emerging Issues

O-128

# Evaluating 37 years of harmful algal blooms in Southern Chile

**Alejandro Clement[1],** Nicole Correa[1], Stephanie Saez[1], Francisca Muñoz[1], Carmen Gloria Brito[1], Carlos Flores[1], Laura Latorre-Melín[1], Maria J. Calderón[1], Carla Palma[1], Andrea Colilef[1], Alvaro Jorquera[1], Carmen Tellez[1], Gustavo Contreras[1]

(1) Plancton Andino SpA, Terraplen 869, Puerto Varas, Chile

This study provides an overview of a long-term Phytoplankton Monitoring Program, with an emphasis on HABs in southern Chile over the past 37 years. The analysis of this dataset reveals variations in bloom frequency and monitoring intensity. Notably, the significant events involving *Pseudochattonella* cf. *verruculosa* and *Alexandrium catenella* in 2016 resulted in a substantial increase in sampling frequency. This introduction generates biases that complicate direct comparisons between datasets pre- and post-2015. We calculated the $HAB_f$ INDEX to analyze trends from 2015 to 2025. The results show no significant overall increase in HAB events in marine inlets. However, A. catenella occurrences have decreased, while *Prorocentrum micans*, *Heterosigma akashiwo*, and *P.* cf. *verruculosa* have become more common. These population dynamics suggests that they are linked to climate anomalies such as reduced rainfall and freshwater flux, and potential shifts in nutrient stoichiometry within fjords and estuaries. Large-scale phenomena like El Niño create conditions favorable for HAB development, though outcomes vary. Looking ahead, we emphasize the need to integrate automated digital bio-imaging with predictive numerical and machine learning models. These innovations offer promising tools to enhance the resolution, timeliness, and accuracy of HAB monitoring, ultimately supporting efforts to mitigate the social, environmental, and economic impacts of future blooms.

**Keywords:** Phytoplankton Monitoring, HABf INDEX, Time-Series

**Financing:** Plancton Andino SpA

**Acknowledgments:** The entire Plankton Andino team, Sonia Eller, my family and co-workers.

Parallel Session 25: HABs in a Changing World & Emerging Issues

O-129

# The emerging risks of toxic benthic dinoflagellates in the Magellan Subantarctic ecoregion under climate change scenarios: Is migration to the south an option?

Francisco Bahamonde Mihovilovich[2,3,4,5], **Máximo Jorge Frangopulos Rivera[1,2,3,4]**, Luiz L. Mafra Jr.[6], Luciano Fernandes[7], Aldo Barreiro[8], José Luis Iriarte Machuca[9,10], Andrés Mansilla[2,3]

(1) Centro de Investigación Gaia-Antártica (CIGA), Universidad de Magallanes, Avenida Bulnes 01855, Punta Arenas, Chile
(2) Laboratorio de Ecosistemas Marinos Antárticos y Subantárticos (LEMAS), Universidad de Magallanes, Avenida Bulnes 01890, Punta Arenas, Chile
(3) Centro Internacional Cabo de Hornos (CHIC), Universidad de Magallanes, Ohiggins 310, Puerto Wiliams, Chile
(4) Instituto Milenio Biodiversidad de Ecosistemas Antárticos y Subantárticos (BASE), Universidad de Chile, las Palmeras 3425, Santiago, Chile
(5) Programa de Doctorado en Ciencias Antárticas y Subantárticas, Universidad de Magallanes, Avenida Bulnes 01855, Punta Arenas, Chile
(6) Centro de Estudos do Mar, Universidade Federal do Paraná, Pontal do Paraná, Brazil
(7) Universidade Federal do Paraná, Setor de Ciências Biológicas, Departamento de Botânica, Curitiba, Brazil
(8) Centro Interdisciplinar de Investigação Marinha e Ambiental (CIIMAR), Terminal de Cruzeiros do Porto de Leixões, Porto, Portugal
(9) Centro de Investigación Dinámica de Ecosistemas Marinos de Altas Latitudes (IDEAL), Universidad Austral de Chile, Punta Arenas, Chile
(10) Instituto de Acuicultura y Medio Ambiente, Universidad Austral de Chile, Puerto Montt, Chile

Under projected sea surface temperatures increases of 0.4 to 1.4 °C by mid-21st century, climate change is expected to drive the distribution of resilient marine species. Among them, toxic benthic dinoflagellates are expanding poleward from tropical regions, intensifying threats to coastal ecosystem and public health. The Magellan Subantarctic ecoregion (MSE), a biogeographic unique and understudied area, offers a natural laboratory to investigate this phenomenon. This study presents the first integrated characterization of toxin-producing benthic dinoflagellates across multiple coastal sites in the ESM. Morphological identification was combined with targeted LC-MS/MS analysis of lipophilic phycotoxins to assess species presence and toxin profiles. Species from the genera *Amphidinium*, *Prorocentrum* and *Vulcanodinium*, known contributors to benthic harmful algal blooms (BHABs), were identified. In macroalgal samples, *Prorocentrum lima* and *Vulcanodinium rugosum* were associated with the detection of Dinophysistoxin-1 (DTX-1) and Pinnatoxin-G (PnTx-G), respectively. Okadaic acid (AO) and Dinophysistoxin-2 (DTX-2) were not detected. Additionally, *Amphidinium carterae* and *A. operculatum*, likely producers of Amphidinols/Amphidinolides, were found in sediment samples, and further analysis is required to confirm toxin production. These results provide the presence of BHAB - forming species and their associated phycotoxins (DTX-1 and PnTx-G) in the MSE, suggesting a subantarctic expansion of toxigenic benthic dinoflagellates. Our findings underscore the urgent need to implement continuous monitoring BHABs programs and risk assessment strategies in the subantarctic coastal ecosystem vulnerable to climate change-driven biogeographic shifts.

**Keywords**: Magellan Subantarctic Ecoregion, Marine Toxins, Benthic Harmful Algal Blooms (BHABs)

**Financing:** PROGRAMA DE BECAS DOCTORADO NACIONAL CHILE (ANID)

## Parallel Session 25: HABs in a Changing World & Emerging Issues

### O-129

**Acknowledgments:** FONDECYT Regular 1241697; CONICYT-PIA AUB2300001; ANID BASAL FB210018; FOVI 220095; ANID MILENIO ICN2021_002.

Parallel Session 25: HABs in a Changing World & Emerging Issues

O-130

# Increasing presence of harmful algal bloom toxins in Arctic food webs linked to ocean warming

**Kathi Lefebvre[7],** Raphaela Stimmelmayr[2], Gay Sheffield[4], Emily Bowers[8], Donald Anderson[1], Evie Fachon[1], Patrick Charapata[6], Steve Kibler[5], Rance Hardison[5], Emma Pate[3]

(1) WHOI, Biology, Woods Hole, United States
(2) North Slope Borough, Utiagvik, United States
(3) Nome Eskimo Community, Nome, United States
(4) University of Alaska Fairbanks, Nome, United States
(5) National Ocean Service, Beaufort, United States
(6) Georgia Aquarium, Atlanta, United States
(7) Ocean and Earth Environmental Services, United States
(8) Ocean Associates, Seattle, United States

Climate change-related ocean warming and reduction in sea ice extent, duration, and thickness increase the risks from harmful algal blooms (HABs) in the Alaskan Arctic. Two toxigenic species of concern include the dinoflagellate *Alexandrium catenella* and some diatoms in the genus *Pseudo-nitzschia*. These harmful algae produce the potent neurotoxins, saxitoxin and domoic acid, that impact marine wildlife health and cause the human illnesses known as paralytic shellfish poisoning (PSP) and amnesic shellfish poisoning (ASP), respectively, when ingested in varying amounts. Domoic acid also affects animals through domoic acid poisoning (DAP). This talk presents data on algal toxin concentrations quantified in Arctic food web samples of phytoplankton, zooplankton, benthic clams, benthic worms, and pelagic fish collected during the summer months over five years (2019 – 2023) from the Beaufort, Chukchi, and Northern Bering seas. Both neurotoxins were present in all years and in all species tested, but with variable concentrations between years. Additionally, toxin concentrations differed between vector species revealing the pathways of highest exposure risk to top predators such as bowhead whales (*Balaena mysticetus*) and Pacific walruses (*Odobenus rosmarus*). Bowhead whales and walruses, as well as the marine vector species that they feed on, are critically important for Tribal communities that rely heavily on marine resources for nutritional, cultural, and economic well-being. This uniquely Arctic relationship, emphasizes the need to understand HAB toxin uptake and depuration dynamics in species used for subsistence purposes throughout the coastline of the Beaufort, Chukchi, and Northern Bering seas.

**Keywords:** climate change, warming oceans, food web

**Financing:** National Centers for Coastal Ocean Science (NCCOS) Competitive Research Program (CRP) Ecology and Oceanography of Harmful Algal Blooms (ECOHAB) under award NA20NOS4780195

**Acknowledgments:** National Centers for Coastal Ocean Science (NCCOS) Competitive Research Program (CRP) Ecology and Oceanography of Harmful Algal Blooms (ECOHAB) under award NA20NOS4780195

Parallel Session 25: HABs in a Changing World & Emerging Issues

O-131

# The IOC Harmful Algal Information System – The value of the global long time series database HAEDAT

**Dave Clarke**[1], Maarten De Rijcke[2], Eileen Bresnan[3], Adriana Zingone[4], Gustaaf Hallegraeff[5], Yun Sun[6], Henrik Enevoldsen[6]

(1) Marine Institute, Marine Environment and Food Safety, Shellfish Safety, Rinville, Oranmore, Galway, Ireland
(2) Flanders Marine Institute (VLIZ), InnovOcean Campus, Jacobsenstraat 1, 8400 Oostende, Belgium
(3) Marine Directorate of the Scottish Government, Marine Laboratory, Plankton, 375 Victoria Road, Aberdeen, Scotland
(4) Stazione Zoologica Anton Dohrn, Villa Comunale, 80121 Napoli, Italy
(5) University of Tasmania, Institute for Marine and Antarctic Studies, IMAS Directorate, 217E IMAS, Hobart, Austrailia
(6) Intergovernmental Oceanographic Commission of UNESCO, 7, Place de Fontenoy, 75352 Paris Cedex 07 SP, France

The UNESCO-IOC Harmful Algal Information System (HAIS) is built within the International Oceanographic Data and Information Exchange (IODE), in cooperation with WoRMS, ICES, PICES, IAEA and ISSHA. It consists of three components; the Taxonomic Reference List of Harmful Micro Algae, the database on the geographic distribution of toxin-producing microalgae (OBIS/HABMAP), and the Harmful Algae Event database (HAEDAT). Since 1985, HAEDAT collects global records of events caused by microalgae that have involved a management action or negative economic/ecological/social impacts.

Information from HAEDAT and OBIS/HABMAP has been the foundation for the first Global HAB Status Report (2021) and is increasingly used by the scientific and policy communities in peer regional or global publications on various topics, e.g., desalination, remote sensing, coastal HABs and the impacts of climate change drivers on observed and predicted changes in the harmful microalgae distribution and their multiple impacts.

To ensure HAEDAT and OBIS/HABMAP continue to be up to date and relevant resources for regional and global HAB assessments, the IOC-FAO Intergovernmental Panel on Harmful Algal Blooms has established a Task Team whose terms of reference include: advising and encouraging regional groups and editors on data compilation, quality control and submission of HAB data to OBIS/HABMAP and HAEDAT, and production of associated metadata documents. These HAB databases also require improvements to stay aligned with changing platform and application technologies and comply with data access and the requirements of multiple audiences. To this aim, updates to improve data input, event recording, and the overall functionality of HAEDAT are currently under development.

**Keywords:** HABs, HAEDAT, database

Parallel Session 26: HABs and Social Dimensions

O-132

# HABs and human affairs: Lessons from our interactions with bacterial and viral pathogens

**Gustaaf Hallegraeff**[1]

(1) University of Tasmania, Institute for Marine and Antarctic Studies, College of Science and Engineering, Private Bag 129, Hobart, Australia

Historically, humans have tended to live in fear of HABs, e.g. the Biblical River Nile red tides, Captain Vancouver's PSP fatalities, and Hitchcock's crazed DA birds. Imagine having to cope with the 2019 COVID pandemic at a time when microscopic life was unknown. Starting in the late 1980s, HAB science has now matured to the point that we can readily identify who they are, where they come from, and what they are doing in our waters. However, with our usual human narcissism, HAB research has primarily focused on their impact on humans while the natural function of most aquatic toxins and the reasons for HAB blooming behaviour remain largely unknown. Less than 4% of known microalgal taxa cause adverse effects for human society. Darwin never knew about the microbial world, and classical ecological laws of competitive exclusion and trait selection do not readily apply to microbial roulette. We should learn to better live with HABs and educate the public on their amazing life stories (e.g. the UN Plankton Manifesto), and what we can learn from them, rather than focus on their negative impacts. Trust in the media is under pressure; we should celebrate our successes but not overreact as we did with COVID.

Parallel Session 26: HABs and Social Dimensions

O-133

# Harmful Algal Bloom perceptions among school students in Southern Chile: Insights into a preventive education and communication approach

**Pamela Carbonell**[1], Andrés Marin[2], Mauricio Hernández[3], Leonardo Guzmán[1]

(1) Instituto de Fomento Pesquero, Padre Harter 574, Puerto Montt, Chile
(2) Universidad de Los Lagos, Ciencias Sociales, Osorno, Chile
(3) Centro de Estudios del Desarrollo Regional y Políticas Públicas (CEDER), Universidad de Los Lagos, Osorno, Chile

Moving towards more preventive and participatory education and communication approaches on Harmful Algal Blooms (HAB) demands a better understanding of individuals' perceptions about this natural phenomenon. Accurate and complete perceptions about associated risks and impacts is the basis for peoples' behavioral change, plus objective knowledge on the subject. Recent studies have explored and described HAB perceptions from different stakeholder groups, such as adults, entrepreneurs and ordinary citizens. However, there is limited knowledge about the conditions driving different perceptions about HABs, and particularly among school students of areas affected by these events. Here, we present the results from a survey applied to 837 primary and secondary students in varied geographical contexts from the northern area of the Chilean fjords (Los Lagos region), a highly vulnerable zone that has been sporadically affected by severe HAB events (e.g. Alexandrium catenella blooms, 2002, 2006, 2009, 2016, 2018). We use a Qualitative Comparative Analysis (QCA) approach to identify the conditions that help explain students' more or less clear perceptions about HABs, both in coastal and inland settings. Results show that proximity to the coast, rurality, years of schooling and family history have a strong impact on a clearer perception of HABs. Moreover, 84% have heard of HABs, but 47% are aware about the intoxication symptoms, and only 19% associate them with respiratory paralysis. A better conditions understanding for clear and accurate perceptions about HAB can lead to more effective education and communication approaches, and to achieve the expected behavioral changes.

**Keywords**: Harmful Algae Bloom, Education-Perception, Disaster Risk Reduction

Parallel Session 26: HABs and Social Dimensions

O-134

# Investigating the association between Harmful Algal Blooms and asthma incidence in coastal Madagascar: A multi-year remote sensing analysis

**Kira Hülsdünker**[1], Giacomo De Nicola[1], Christopher D. Golden[1], Marissa Childs[1], A. K. Symphonia Razafinimanana[2], Paubert T. Mahatante[3]

(1) Harvard T. H. Chan School of Public Health, Nutrition, Public Health
(2) Ministère de la santé publique Madagascar
(3) SANSAFA/SADC - Southern African Non-State Actors platform in Fisheries and Aquaculture

Background: Harmful algal blooms (HABs) are increasingly prevalent phenomena, not only impacting ecosystems but also Public Health. While studies have demonstrated links between HAB exposure and respiratory symptoms, comprehensive population-level analyses in developing regions remain scarce. Madagascar, with its extensive 4,828 km coastline and significant asthma burden, provides a unique setting to examine these relationships. This study aims to investigate the association between harmful algal blooms and asthma incidence in coastal communities around the coast of Madagascar.
Methods: We analyzed satellite-derived chlorophyll-a concentration data from the Copernicus Marine Service (4x4 kilometer resolution) from 2012 to 2022, together with monthly asthma counts provided by 372 coastal healthcare facilities. Environmental variables, including temperature and precipitation, were incorporated alongside socioeconomic factors and healthcare facility characteristics. Statistical analysis employed a Big Generalized Additive Model (BAM) with random effects for individual clinics.
Findings: The analysis revealed a significant nonlinear relationship between maximum chlorophyll-a concentration and asthma incidence ($p = 0.035$). Notable heterogeneity between clinics was observed through clinic-level random effects ($p < 0.001$). The proximity of clinic catchment areas to the coast showed a significant association with asthma cases ($p < 0.001$), while population density exhibited a negative correlation. Spatial autocorrelation analysis was further conducted which showed clustering patterns of high chlorophyll-a concentrations (Moran's I statistic), indicating region-specific bloom behavior.

Interpretation: Our findings suggest a complex relationship between HABs and asthma incidence in coastal Madagascar. The observed associations highlight the importance of HAB-monitoring in coastal regions which are vulnerable to climate change impacts.

**Keywords**: Public Health, asthma, aerosolization

**Financing**: This research received no specific grant from any funding agency.

Parallel Session 26: HABs and Social Dimensions

O-135

# A preliminary study on valuation method of economic loss on marine ecosystem caused by HABs: Based on impacts of hypoxic environment on ecosystem

**Yingze Xu**[1], Zhiming Yu[1], Yongquan Yuan[1], Xiuxian Song[1]

(1) Institute of Oceanology, Chinese Academy of Sciences, Qingdao 266071, China

Abstract: HAB induced- or exacerbated-hypoxic environment has damaged marine ecosystems significantly. However, traditional methods of economic loss valuation mostly focus on direct market losses resulting from it, making it difficult to quantify indirect and intergenerational ecological costs. This paper proposes a comprehensive valuation framework that integrates the population dynamic model and the shadow price method, aiming to evaluate the long-term cumulative effects and cascading losses of HAB-induced hypoxia quantitatively. By constructing a dynamic model to quantify the impact of hypoxic events on biomass (such as population migration, recruitment disruption, and food chain disruption), and combining the shadow price method to internalize external costs of ecological damages (like fishery reduction and water quality deterioration), and introducing the social discount rate to reflect future losses, which demonstrates the time value and intergenerational equity comprehensively. Through the analysis of real cases, this method can value the economic losses comprehensively caused by HAB-induced hypoxia, supplementing the non-market values, which are ignored by traditional methods like market-pricing, and providing quantitative basis for ecological compensation mechanism of HABs, sustainable fishery management and decision-making from prevention and mitigation of HABs. It owns theoretical significance and practical reference for improving the valuation of ecological products and ecosystem impacts on HABs.

**Keywords**: HABs; Hypoxic environment; Population dynamic model; Shadow price method; Economic loss valuation

**Financing**: This work was financially supported by Laoshan Laboratory (LSKJ202203700), the National Key Research and Development Program of China (2024YFF0506902).

**Acknowledgments**: Thanks for all members of the research team of mitigation and control of HABs from Institute of Oceanology, Chinese Academy of Sciences.

Parallel Session 26: HABs and Social Dimensions

O-136

# Assessment of national policies on Harmful Algal Blooms in the Latin American and Caribbean (LAC): Challenges for policy makers towards 2030 Agenda for Sustainable Development

**Leon Vergara[1],** Mercy Borbor-Cordova[1], Rosalba Alonso-Rodriguez[2], Veronica Davila[3], João Paulo Felizardo[6], Natalia Jiménez Conejo[8], Daniel Carrasco-Palma[4], Maria Fernanda Barrera[4], Sonia Sánchez Ramírez[5], Nelly Jacobo Huavil[5], Roberto Meigikos dos Anjos[6], Ana Martínez Goicoechea[7], Álvaro Morales Ramírez[8], Julian Franco[9], Soraya J. Silva[10], Angel Moreira[11], Ana Salinas[12], Oscar Amaya[12], Jennifer Guerra[12], Krissia Portillo[12]

(1) Escuela Superior Politécnica del Litoral ESPOL, Facultad de Ingeniería Marítima y Ciencias del Mar FIMCM, Campus Gustavo Galindo Km. 30.5 Vía Perimetral P.O. Box 09-01-5863, Guayaquil, Ecuador
(2) Universidad Nacional Autónoma de México (UNAM), Instituto de Ciencias del Mar y Limnología (ICMyL), Unidad Académica Mazatlán, Cap. Joel Montes Camarena s/n, Cerro del Vigía, 82047, Mazatlán, México
(3) Universidad Autónoma de Occidente (UAdeO), Unidad Regional Culiacán, Cd Universitaria, 80040 C, Culiacán, México
(4) Universidad de Chile, Laboratorio de Toxinas Marinas, Facultad de Medicina, Av. Independencia 1027, Segundo piso, Pabellón G. Comuna de Independencia, Santiago, Chile
(5) Instituto del Mar del Perú (IMARPE), Dirección General de investigaciones en Oceanografía y Cambio Climático, Av. Panamericana N 3524, 24540, Callao, Perú
(6) Universidade Federal Fluminense (UFF), Geochemistry Department, Laboratory of Radioecology and Environmental Changes, Outeiro São João Baptista s/n, Centro, Niterói, Río de Janeiro, Brasil
(7) Dirección Nacional de Recursos Acuáticos (DINARA), Biología Pesquera, Unidad de Gestión Pesquera Atlántica (UGEPA), Av del Puerto s/n, La Paloma, Uruguay
(8) Universidad de Costa Rica, Centro de Investigación en Ciencias del Mar y Limnología, Ciudad de la investigación, San Pedro, Montes de Oca, San José, Costa Rica
(9) Instituto de investigaciones Marinas y Costeras "José Benito Vives de Andréis" - INVEMAR., Programa de Calidad Ambiental Marina, Calle 25 # 2-35 Playa Salguero, Santa Marta, Colombia
(10) Instituto Venezolano de Investigaciones Científicas, Centro de Oceanología y Estudios Antárticos, Km 11, Carretera Panamericana, Altos de Pipe, Estado de Miranda, Venezuela
(11) Centro de Estudios Ambientales de Cienfuegos. (CEAC), Carretera a Castillo de Jagua Km 1 y 1/2, Apartado Postal 5, Ciudad Nuclear, CP 59350, Cienfuegos, Cuba
(12) Universidad de El Salvador, Laboratorio de toxinas marinas, Facultad de ciencias y matemáticas, Final Av. 25 Norte, San Salvador, El Salvador

Harmful algal blooms pose multifaceted threats in Latin America and the Caribbean, impacting public health, marine ecosystems, and key economic sectors (fisheries, aquaculture, tourism). These impacts are exacerbated by anthropogenic nutrient pollution and climate change, underscoring the need for robust and coordinated policy responses. This study, conducted in collaboration with the International Atomic Energy Agency (IAEA) and the regional REMARCO network, critically examines the current state of national public policies addressing HABs in eleven LAC countries: Brazil, Chile, Colombia, Costa Rica, Cuba, Ecuador, El Salvador, Mexico, Peru, Uruguay and Venezuela.

Framed within the context of the United Nations 2030 Agenda for Sustainable Development, the assessment acknowledges that HAB management intersects with multiple Sustainable Development Goals (SDGs 2, 3, 6, 12, 13, and 14), but places particular emphasis on SDG 17 (Partnerships for the Goals) as effective HAB mitigation demands strong regional cooperation and governance.

Methodologically, this research combines a comprehensive bibliographic review with a quantitative and qualitative survey of national experts, researchers, and stakeholders. A SWOT analysis was applied to evaluate each country's HAB monitoring programs, management strategies, early warning systems, and institutional frameworks. This critical appraisal reveals regional institutional and policy challenges such as gaps in interagency coordination and uneven monitoring capacities, while identifying opportunities for collaboration and policy convergence to mitigate HAB impacts. Ultimately, the study aims to provide a regional reference document to guide and strengthen national HAB policy development, offering insights to enhance monitoring, early warning, and governance through improved partnerships across the LAC region.

**Keywords**: Public policies, 2030 agenda, HAB management

**Financing**: This is a contribution to the Marine-Coastal Research Stressors Network for Latin America and the Caribbean (REMARCO). Within IAEA-RLA/7025, 7028 and 7022 projects.

**Acknowledgments**: This is a contribution to the Marine-Coastal Research Stressors Network for Latin America and the Caribbean (REMARCO). Within IAEA-RLA/7025, 7028 and 7022 projects.

Parallel Session 26: HABs and Social Dimensions

O-137

# What does an average recreator know about harmful algal blooms? Communication takeaways from a Utah, USA public perception survey

**Hannah Bonner**[1], Karen Valcarce[2]

(1) Utah Department of Environmental Quality, Division of Water Quality, 195 N 1950 W, Salt Lake City, UT, USA

(2) Utah Department of Health and Human Services, 288 N 1460 W, Salt Lake City, UT, USA

Recreator knowledge and confidence in identifying harmful algal blooms (HABs) are critical for protecting public health and shaping recreationalist risk perception. Our research used a structured, close-ended questionnaire to gather information on recreators' perceptions of HABs in the Western United States (n=200). Our results indicate that the majority (86%) of recreators are familiar with HABs and most (61%) are at least moderately concerned about them. Participants had a 62% accuracy at identifying harmful water conditions for themselves and a 63% accuracy at identifying harmful water conditions for their dog. Respondents learned about HABs from news reports (75%) and/or seeing signs at a waterbody (54%). Recreators who are non-White race and/or 65+ years old are at elevated risk for inadvertent HAB exposure. This work identified baseline recreator HAB literacy in the intermountain region of Utah, USA and provides recommendations for public entities developing future education campaigns.

**Keywords**: perception, communication, survey

Parallel Session 27: Toxicity

O-138

# Histological damage and mortality rates in juveniles of the oyster *Magallana gigas* due to exposure to cells and cell lysates of *Alexandrium* spp.

**MSc. Ismavy de la Caridad Castillo Quintana**[1], Dr. Ignacio Leyva Valencia[1], Dr. Christine J. Band Schmidt[1], Dr. Pedro Cruz Hernández[2], Dr. María del Carmen Rodríguez Jaramillo[2], MSc. José Luis Ramírez Arce[2]

(1) Interdisciplinary Center of Marine Sciences – National Polytechnic Institute, Department of Plankton and Marine Ecology, Av. Instituto Politécnico Nacional s/n, Playa Palo de Santa Rita neighborhood, ZIP code 23096, La Paz, Baja California Sur, Mexico, La Paz, Mexico
(2) Northwest Biological Research Center, Av. Instituto Politécnico Nacional 195, Playa Palo de Santa Rita Sur, La Paz, Baja California Sur, Mexico; ZIP code 23096., La Paz, Mexico

Harmful Algal Blooms (HABs) can lead to the accumulation of toxins and/or bioactive extracellular compounds (BECs) in the tissues of bivalve mollusks, often leading to their death. This study assessed histological damage and survival in juvenile *Magallana gigas* exposed to cells and cell lysates of *Alexandrium affine* and *Alexandrium pseudogonyaulax*. Results showed that juveniles exposed to *A. affine* cells displayed inactivity in response to physical stimuli within the first 8 hours, followed by mortality of up to 85%, with an LC50 of 6,300 cells/mL after 20 hours of exposure. In contrast, exposure to *A. affine* cell lysates did not affect juvenile survival. When juveniles were exposed to *A. pseudogonyaulax* cells, mucus production was evident, and the organisms became inactive, but no lethal effects were observed. In contrast, exposure to cell lysates caused mortality after 20 hours, with an LC50 of 2,500 cells/mL. Histological lesions in juveniles exposed to *A. affine* cells and *A. pseudogonyaulax* lysates included structural loss in gill tissue, mantle erosion, digestive tubule atrophy, and a high presence of hemocytes in damaged tissues. These results suggest that harmful metabolites from these dinoflagellates can reduce the filtering activity of *M. gigas* juveniles, affecting their feeding and survival.

**Keywords**: phycotoxins, bivalve mollusks, mortality

**Financing**: Interdisciplinary Center for Marine Sciences – National Polytechnic Institute, La Paz, Mexico Northwest Biological Research Center,S.C., La Paz, Mexico

Parallel Session 27: Toxicity

O-139

# Pathological fingerprint of harmful algal blooms in farmed salmon from Southern Chile

**Diego Caro[1],** Rudy Suarez[4], Maria Fernanda Sotomayor[1], Karina Kusch[1], David Cassis[3], Marcos Godoy[2]

(1) Centro de Investigaciones Biologicas Aplicadas (CIBA), Lago Panguipulli #1390, Puerto Montt, Chile
(2) Laboratorio Institucional, Universidad San Sebastián, Sede de la Patagonia, Facultad de Ciencias de la Naturaleza, Lago Panguipulli #1390, Puerto Montt, Chile
(3) AquaBC, Puerto Varas, Chile
(4) Centro Acuicola y Pescquero de Investigacion Aplicada (CAPIA), Universidad Santo Tomás, Facultad de recursos naturales y Medicina Veterinaria, Buena Vecindad 91, Puerto Montt, Chile

Harmful algae blooms (HABs) have been identified as the cause of large-scale mortalities of salmonids throughout the world. The harmful effects vary by species and may combine hypoxia, mechanical abrasion of branchial tissues, and oxidative injury driven by reactive oxygen species (ROS) and lipid peroxidation.

This study analyzes and compares the effects of harmful algal blooms on Pacific salmon (*Oncorhynchus kisutch*) and Atlantic salmon (*Salmo salar*) during the growing phase in southern Chile (Regions X and XI) between 2009 and 2024. Systematic necropsy and histopathological analysis of different tissues were conducted during each event. Causative blooms were dominated by *Alexandrium catenella* (1-350 cells mL, 2009), *Pseudochattonella* cf. *verruculosa* (7.000–20.000 cells mL, 2016; 45–300 cells mL, 2024), *Thalassiosira pseudonana* (60.000 cells mL, 2023) and *Heterosigma akashiwo* (48–474 cells mL, 2024)

In all cases, the gill constituted the primary lesion site. These ranged from acute to chronic, and were characterized by necrotic, vascular disturbances such as lamellar thrombosis, congestion and oedema; adaptative responses including epithelial hyperplasia, synechiae and goblet cell proliferation and, in chronic cases, reparative fibrosis. The type and severity of lesions were modulated by algal species, cell density and duration of exposure.

These results highlight the impacts of HABs on salmonids and align with experimental data, confirming ROS-mediated oxidative stress as the central driver of branchial pathology. Continuous phytoplankton surveillance, standardized gill scoring and timely cage relocation are therefore critical for safeguarding animal welfare and mitigating economic losses in Chilean salmon farming.

**Keywords**: Gill disease, Harmful algae blooms, Fish Pathology

**Financing**: Centro de Investigaciones Biológicas Aplicadas (CIBA), Lago Panguipulli 1390, Puerto Montt, Chile.

Parallel Session 27: Toxicity

O-140

# Effects of the antibiotic azithromycin on *Daphnia*-cyanobacteria interaction: Revealing the impacts of environmentally relevant concentrations

**Michael Celano[1],** Júlia de Pinho[2], Tainá Silva[1], Mariana Marques[1], Julia Silberman[1], Mauro Vilar[1], Sandra Azevedo[1]

(1) Federal University of Rio de Janeiro, Carlos Chagas Filho Institute of Biophysics, Carlos Chagas Filho Institute of Biophysics, Avenida Carlos Chagas Filho, 372 - Bloco G - Sala G0-057 Cidade Universitária, Rio de Janeiro, Brasil
(2) Oswaldo Cruz Foundation - FIOCRUZ, National Institute of Quality Control in Health, National Institute of Quality Control in Health, Av. Brasil 4365, Rio de Janeiro, RJ, 21040-900, Rio de Janeiro, Brasil

Artificial eutrophication has degraded water bodies globally, promoting CyanoHABs. In addition to nutrient input, these environments also suffer from continuous contamination by emerging contaminants, such as antibiotics, further reducing water quality and increasing impacts on aquatic biota. During the COVID-19 pandemic, the global consumption of the macrolide antibiotic azithromycin increased significantly, with a 96% rise in Brazil, resulting in concentrations of approximately 3 $\mu g.L^{-1}$ in surface waters. Considering its possible impacts in plankton communities, consequently affecting aquatic food webs, we evaluated the effects of environmentally relevant concentrations of AZT (0.3, 0.6 and 3.0 $\mu g.L^{-1}$) on the zooplankter *Daphnia similis* submitted to diets with different proportions of the edible green microalgae and the microcystin-producing cyanobacterium *Microcystis aeruginosa*. *Daphnia* responses were examined through feeding behavior, survival, somatic growth and population parameters (15-days). Although AZT did not affect D. similis, the cyanobacterium negatively impacted all parameters evaluated in the microcrustacean. In general, the cyanobacterium inhibited *Daphnia* feeding rate. However, in the presence of the antibiotic, zooplankton increased its feeding rate and therefore consumed more toxic cells. Furthermore, AZT intensified the toxic effects of the cyanobacterium on Daphnia, resulting in remarkable reduction in survival, fecundity and population growth, besides delayed sexual maturation. Our results suggest that environmental concentrations of AZT may potentiate the impacts of toxic cyanobacteria on zooplankton, which may disrupt aquatic food webs by impairing energy transfer to higher trophic levels. This reinforces the need for stricter regulations on antibiotic pollution and more research on the effects of antibiotics on non-target organisms.

**Keywords**: Cyanotoxins, microcystin, zooplankton

**Financing**: This research received no external funding.

**Acknowledgments**: The authors are thankful to CAPES, Brazil, for its financial support through a master's scholarship granted to M.R.C.

Parallel Session 27: Toxicity

O-141

# Combined biotoxin exposure in the smalltooth sawfish, *Pristis pectinata*: Clues to an unusual mortality event throughout the Florida Keys, United States

**Alison Robertson**[1,2], Ross Boucek[3], Adam Brame[4], Theresa Cody[5], Ashley Dawdy[7], Sarah Dietrick[1,2], Dean Grubbs[7], Elizabeth Murphy[1,2], Michael Parsons[8], Gregg Poulakis[5], John Roman[1,2], Andy Selwood[6]

(1) University of South Alabama, Stokes School of Marine & Environmental Sciences, 600 Clinic Drive, Mobile, United States
(2) Dauphin Island Sea Lab, 101 Bienville Blvd, Dauphin Island, United States
(3) Bonefish Tarpon Trust, 2937 SW 27th Avenue, Miami, United States
(4) National Oceanic and Atmospheric Administration, Southeast Regional Office, NOAA Fisheries, 263 13th Avenue South, St. Petersburg, United States
(5) Florida Fish and Wildlife Commission, 100 8th Avenue Southeast, St. Petersburg, United States
(6) The Cawthron Institute, 98 Halifax Street, Nelson, New Zealand
(7) Florida State University, 3618 Coastal Highway 98, St. Teresa, United States
(8) Florida Gulf Coast University, The Water School, 10501 FGCU Blvd., Fort Myers, United States

The Florida Keys host a diverse ecosystem vital for subsistence, recreational, and commercial fisheries, contributing significantly to the local economy. However, climate-driven and human-induced disturbances have impacted these resources in the last few decades. Adding to these impacts, in Fall 2023, a myriad of behavioral abnormalities were documented in over 50 fish species crossing many trophic and migratory guilds, initiating a response effort to determine the cause. During these events, significant mortalities of the critically endangered elasmobranch, *Pristis pectinata*, were observed, raising concerns about the long-term impacts of this species. Subsequent environmental sampling revealed elevated levels of *Gambierdiscus* and a complex suite of marine neurotoxins in the water. Fish necropsy results showed no macroscopic effects in fish, however, subsequent toxin testing by in vitro assay, targeted liquid chromatography-tandem mass spectrometry (LC-MS/MS), and untargeted LC-high resolution mass spectrometry (LC-HRMS) revealed the bioactivity and presence of a variety of benthic algal toxins in whole water, epiphytic microalgae (20-200 µm), and in tissues of symptomatic sawfish. Subsequent chemical partitioning, assay-guided fractionation, and LC-HRMS analyses aided in toxin profiling in sawfish tissues and significant differences were observed between blood, gill, liver, brain, and muscle, highlighting a complex combined waterborne toxin exposure. Archived tissues from sawfish recovered from prior years in the absence of behavioral abnormalities have served as important field controls, while algae and sediments collected from sawfish foraging habitat have further aided in uncovering possible causes to this unprecedented event.

**Keywords**: Ecological Risk Assessment, Mixture Toxicology, Ecotoxicology

**Financing**: National Oceanic and Atmospheric Administration Event Response, Havenworth Coastal Conservation Foundation, Bonefish Tarpon Trust, Florida Fish & Wildlife Commission, National Institute of Environmental Health Sciences.

Parallel Session 27: Toxicity

O-142

# Saxitoxin linked to deaths of northern fur seals in the Southeast Bering Sea

Kathi Lefebvre[1], **Chelsea Campbell[2,3],** Lauren Divine[2], Hanna Hellen[2], Paul Melovidov[2], Kathy Burek Huntington[4], Emily Bowers[1,5], Natalie Rouse[4], Evangeline Fachon[6,7], Thomas Farrugia[8], Robert Pickart[6], Peigen Lin[9], Lorely Lago[6], Frank Bahr[6], Emmanuelle Furst[10], Colleen Duncan[11], Patrick Charapata[12], Donald Anderson[6], Gulce Kurtay[13,14]

(1) Environmental and Fisheries Science Division, Northwest Fisheries Science Center, National Marine Fisheries Service, NOAA, Seattle, WA, USA
(2) Ecosystem Conservation Office, Aleut Community of St. Paul Island, AK, USA
(3) College of Fisheries and Ocean Science, University of Alaska Fairbanks, Fairbanks, AK, USA
(4) Alaska Veterinary and Pathology Services, Eagle River, AK, USA
(5) Ocean Associates, Inc, Arlington, VA, USA
(6) Woods Hole Oceanographic Institution, Woods Hole, MA, USA
(7) Massachusetts Institute of Technology (MIT)-WHOI Joint Program in Oceanography/Applied Ocean Science & Engineering, Woods Hole, MA, USA
(8) Alaska Ocean Observing System, Anchorage, AK, USA
((9) School of Oceanography, Shanghai Jiao Tong University, Shanghai, China
(10) Alaska SeaLife Center, Seward, AK, USA
(11) College of Veterinary Medicine and Biomedical Sciences, Colorado State University, Fort Collins, CO, USA
(12) Georgia Aquarium, Center for Species Survival, Atlanta, GA, USA
(13) University of Washington, Cooperative Institute for Climate, Ocean, and Ecosystem Studies, Seattle, WA, USA
(14) Pacific Marine Environmental Laboratory, NOAA, Seattle, WA, USA

In August 2024, a northern fur seal mortality event was observed on St. Paul Island, AK in the southeast (SE) Bering Sea. Ten seals in good body condition were found dead along with piles of dead fish on Benson Beach located on St. Paul Island. Full necropsies of the five available adult seals, one pup and several fish did not reveal any overt causes of death. Testing of tissues for the algal neurotoxins domoic acid (DA) and saxitoxin (STX), confirmed the presence of STX in multiple tissues and physiological exposure in all five adult NFS and the two fish available for testing. DA was not detected in any samples. Complimentary samples of the SE Bering Sea ecosystem during the same time frame and location as the die off revealed bloom densities of *Alexandrium catenella* (the dinoflagellate that produces STX), large *A. catenella* cyst beds, and high prevalences of STX in fish (100%, n = 22), zooplankton (93%, n = 28), clams (100%, n = 10) and worms (93% n = 15) in the foraging area of NFS. High STX concentrations were observed in fish, clams, worms, and NFS urine providing compelling evidence for a STX poisoning event.

**Keywords**: northern fur seals, saxitoxin, Bering Sea

**Financing**: Ecology and Oceanography of Harmful Algal Blooms (ECOHAB)

**Acknowledgments**: Aleut Community of St. Paul Island, ECOHAB Network and Partners, John L Prescott Grant Program, and others!

Parallel Session 28: HABs in a Changing World & Emerging Issues

O-143

# Extreme flood event triggers a massive toxic bloom of *Dinophysis* cf. *acuminata* in Southern Brazil

**Luiz Mafra Jr.**[1], Carlos E. J. de Azevedo Tibiriçá[2], Karoline Magalhães Lubiana[1], Regiane Valejo Maciel[1], Fabiola Kaviatkovski[1], Pedro Almeida Rodrigo[1], Rafaela Cristine Zem[1], Mathias Alberto Schramm[3], Thiago Pereira Alves[3], Rodrigo Barcellos Hoff[4], Maurício Almeida Noernberg[1]

(1) Universidade Federal do Paraná - UFPR, Centro de Estudos do Mar, Av. Anibal Khury, 2033, Pontal do Paraná, PR, Brazil
(2) Instituto do Meio Ambiente de Santa Catarina - IMA, R. Modesto Fernandes Viêira, 1, Itajaí, SC, Brazil
(3) Instituto Federal de Santa Catarina, Campus Itajaí, Av. Ver. Abrahão João Francisco, 3899, Itajaí, SC, Brazil
(4) Ministério de Agricultura e Pecuária - MAPA, Laboratórios Federais de Defesa Agropecuária, Seção Laboratorial Avançada de Santa Catarina (SLAV/SC), Rua João Grumiché, 117, São José, SC, Brazil

Dinoflagellates of the *Dinophysis acuminata* complex are the primary producers of diarrhetic shellfish toxins (DSTs) in southern Brazil, regularly causing harvesting bans in coastal aquaculture areas. Although typically present at low densities, massive blooms occasionally occur under specific meteorological conditions, leading to extensive ecological and socio-economic impacts. In early May 2024, a persistent high-pressure system blocked cold fronts, resulting in record rainfall (~1/3 of annual precipitation in one week) over Rio Grande do Sul (RS) State. The ensuing flood affected over 85% of RS municipalities and increased freshwater discharge ~8-fold to ~20,000 $m^3$ $s^{-1}$ in the Patos Lagoon estuary. This freshwater plume spread >1500 km along the southern Brazilian coast, reducing surface salinity by 6–7 psu below historical norms. Dinoflagellates dominated the phytoplankton assemblage, with okadaic acid-producing *D.* cf. *acuminata* reaching $6.8\times10^4$ cells $L^{-1}$ by mid-July. The bloom lasted ~2 months, during which 61% of mussel and 43% of oyster samples exceeded DST regulatory limits (max: 4140 and 820 µg DST $kg^{-1}$, respectively). *Dinophysis caudata* (PTX-2 producer) and *D. tripos* were also detected, including in offshore waters over the continental shelf and slope, with potential implications for fisheries and migratory marine megafauna. Observations of abundant heterotrophic grazers, *Noctiluca scintillans*, ingesting *Dinophysis* cells suggest a role in bloom decline and toxin transfer to higher trophic levels. This extreme event – fueled by global warming and the El Niño phenomenon – highlights the vulnerability of coastal systems to climate-driven hydrological disturbances and their potential to trigger widespread harmful algal blooms.

**Keywords**: large-scale bloom, El Niño Southern Oscillation, extreme events

**Financing**: CNPq - INCT Biodiversidade da Amazônia Azul; NANO-DOAP - POGO Ocean

**Acknowledgments**: Nelson Silveira (Atlântico Sul Oysters), for sharing salinity data from Baía Sul, Florianópolis.

Parallel Session 28: HABs in a Changing World & Emerging Issues

O-144

# Turbulence, temperature and termination: Another role for climate change in *Karenia brevis* blooms

**Cynthia Heil**[1], Devin Burris[1], William Scott[1], Sarah Klass[1], Patricia Glibert[2]

(1) Mote Marine Laboratory, Red Tide Institute, 1600 Ken Thompson Parky, Sarasota, Florida, United States
(2) University of Maryland Center for Environmental Science, 2020 Horns Point Rd, Cambridge, Maryland, United States

Blooms of the toxic dinoflagellate *Karenia brevis* are annual events in the eastern Gulf of Mexico dating back at least to the colonial era, and are subject to changing environmental influences including both coastal eutrophication to global warming. Changing nutrient inputs and weather patterns related to climate change may potentially influence both bloom duration and termination. We investigated the interacting influences of turbulence and temperature on the potential termination of blooms via both analyses of historical bloom events and by laboratory experimentation. Several examples of historical bloom termination coincide with the rapid passage of multiple, intensive winter cold fronts, while the passage of smaller, single front events generally had little longer-term influence on blooms. Laboratory experiments suggest that exposure to sudden large (>4°C) temperature reductions had a greater influence on cell concentrations and viability (as percent abnormal cells) than turbulence when turbulence was held at low to moderate levels. With higher turbulence exposure, over 50% of the population displayed abnormal cell morphology within 30 minutes of exposure, suggesting that physical stress was acting more rapidly on cells than temperature shock. These data suggest that changes in the frequency and magnitude of cold front passage in the Gulf of Mexico associated with climate change may potentially bloom termination patterns.

**Keywords**: *Karenia*, Temperature, Turbulence

**Financing**: Funding for this research was provided by NOAA ECOHAB Grant #NA19NOS4780183 with additional support provided by the Barancik and Economos Foundations.

Parallel Session 28: HABs in a Changing World & Emerging Issues

O-145

# Global occurrence of mixed blooms of harmful algae: Toxicity and impacts on marine resources

**Leila Basti**[1]

(1) CGIAR

Harmful algal blooms (HABs) have increased over the past decades and their impacts on public health and coastal socio-economic activities (e.i. aquaculture, fisheries, tourism, and recreation) have been on the rise. The intensification of these HAB and associated impacts has been linked to several anthropogenic activities as well as climate change. A large number of studies have been published on their physiology, ecology, toxicity and impacts on aquatic organisms. Almost all studies, however, have focused on the most recurrent events of HAB caused by single species. Mixed blooms of several species of HAB do often occur and cause mass mortalities of organisms or other effects on coastal ecosystems. Little is known about the impact of these HAB, as well as the ecological interactions between the species occurring in mixture, and the role that climate change plays in the occurrence and toxicity types of blooms, notably warming and ocean acidification. We present the results of meta-analyses of the spatiotemporal global occurrence of Mixed HAB and associated fish kills and the correlation with global warming and ocean acidification driven from global databases (e.g. OBIS, HEADAT, WOS, OCADS). We also present experimental results on the impacts of several mixed blooms of the most recurrent fish-killing dinophytes and raphidophytes of human and animal health concerns on the life cycle of a model shellfish organism. The results of this study are aimed at making recommendation for best practices in fisheries and aquaculture for ecosystem-based management of HAB.

**Keywords**: HAB, Mixed Bloom

**Financing**: Partially funded by MEXT, JSPS, and Presidential Discretionary Fund (TUMSAT).

Parallel Session 28: HABs in a Changing World & Emerging Issues

O-146

# Baseline dataset of harmful algal blooms (2024-2025) for Saudi Arabian Red Sea coast

Hassan Kateb[1], Abdulwahab Al Hossami[1], Silvia Arossa[1], Abdulnasser Alqutob[1], Haifa Alassaf[1], **Afrah Al Othman[1]**, Eman Sabbagh[1], Lotfi Rabaoui[1], Mohammad Qurban[1]

(1) National Center for Wildlife, Riyadh, Saudi Arabia

This study presents the first consolidated dataset of Harmful Algal Blooms (HABs) along the Saudi Arabian Red Sea coast, compiled by the National Center for Wildlife (NCW, Saudi Arabia). Covering the period from April 2024 to April 2025, the dataset documents seven distinct HAB events. Six of these events were recorded between April and May 2024, while a single event was observed in April 2025. Data collection was enabled through a multi-source reporting network, incorporating verified observations from NCW field staff, the Saudi Coast Guard, local fishing communities and other national stakeholders.

Spatial analysis reveals a significant geographic concentration, with all recorded HABs (seven events) occurring in the central Red Sea region. Temporally, most blooms were transient, typically dissipating within several days without intervention. Importantly, no widespread fish kills, or mass mortality events were directly attributed to these blooms during the reporting period.

This dataset provides a critical baseline to understand HAB occurrence patterns in Saudi Red Sea waters. Its significance lies in guiding the design and implementation of a national HAB early detection and monitoring system, to be overseen by NCW. The forthcoming system will prioritize surveillance of sensitive marine ecosystems, including Marine Protected Areas (MPAs), coral reefs, seagrass meadows, aquaculture zones, and key tourism areas. By enabling proactive monitoring and rapid response, the initiative aims to minimize ecological and economic impacts, thereby supporting marine habitat conservation and biodiversity protection across the region.

**Keywords**: HABs, Red Sea, Saudi Arabia

**Financing**: National Center for Wildlife (NCW, Saudi Arabia)

Parallel Session 29: In Situ Monitoring and Remote Observing Systems

O-147

# Aqusens: A field-deployable holographic imaging system for HAB cell detection

**Holly Bowers**[1], Maxim Batalin[2], Kendra Negrey[3], Raphael Kudela[3], Alexis Pasulka[4], Nicholas Soares[4], Clarissa Anderson[5], Henry Ruhl[6]

(1) Moss Landing Marine Labs, 8272 Moss Landing Road, Moss Landing, California, USA
(2) Lucendi, Inc., 11040 Santa Monica Blvd., Suite 220, Loss Angeles, California, USA
(3) University of California, Santa Cruz, 1156 High Street, Santa Cruz, California, USA
(4) California Polytechnic State University, 1 Grand Avenue, San Luis Obispo, California, USA
(5) Southern California Coastal Ocean Observing System, 9500 Gilman Drive, Mail Code 0208, La Jolla, California, USA
(6) Central & Northern California Ocean Observing System, 7700 Sandholdt Road, Moss Landing, California, USA

The Aqusens is a robust, portable imaging flow cytometry (IFC) platform based on holographic imaging coupled with machine learning. Unlike traditional IFCs (FlowCam, Imaging Flow CytoBot [IFCB]) that utilize lenses, the Aqusens is imaging patterns created by light passing through the sample and diffracting around every object. These light patterns are then processed by proprietary algorithms to reconstruct intensity and phase images associated with all objects (3 micron to several millimeters). The platform does not contain expensive and complex optical or mechanical components, and substantial end-user training for operation and maintenance is not required. Bespoke software controls operations and analyzes data in real-time, and can be customized to perform automated processing of samples, identify organisms of specific types, and apply adaptive sampling based on remote viewing of reports and images.

The platform has been deployed under several scenarios, including installations at two monitoring stations in Monterey Bay (California, USA): one for alerting an abalone company about trends in HAB species, and the other for comparison to data being collected by an IFCB. These stations, along with efforts to deploy an Aqusens at the Cal Poly Pier, present unique infrastructure challenges, and are part of the coastal California HAB monitoring program (CalHABMAP). Other deployments include high throughput image generation for MBARI's Synchro test-bed program, underway operations in San Francisco Bay (USGS cruises), and support of local citizen science (The Pacific Plankton Program). A pathway will be developed for data integration into public portals (CalOOS/HABDAC).

**Keywords**: imaging, holography, machine-learning

**Financing**: This work is supported by NOAA/IOOS/Ocean Technology Transition award NA23NOS0120246 to H. Bowers, M. Batalin and R. Kudela.

Parallel Session 29: In Situ Monitoring and Remote Observing Systems

O-148

# Real-time monitoring of harmful algae: SAMS validation against optical microscopy and FlowCam technologies

**Nicole Correa**[1], Alejandro Clement[1], Pablo Campos[2], Jose Rozas[2]

(1) Plancton Andino SpA, Terraplen 869, Puerto Varas, Chile
(2) Retina Lab, Decher 869 of. 1, Puerto Varas, Chile

Automation in plankton monitoring has emerged as a key strategy to overcome the operational and temporal limitations of traditional methods. This study evaluated the performance of the automated SAMS (Self-driven Algae Monitoring System), developed by Retina-Lab, for the detection and quantification of *Alexandrium catenella*, comparing its results with traditional optical microscopy and FlowCam. Diluted cultures in filtered seawater were used to generate three reference concentrations (low: 1–5 cell/mL; medium: 20–50 cell/mL; high: >200 cell/mL), with 10 replicates per level. Results were analyzed using linear regression and two-way ANOVA. SAMS showed strong agreement with conventional methods, with coefficients of determination ($R^2$) ≥ 0.89 and no statistically significant differences ($p > 0.05$), validating its accuracy for quantifying harmful species. SAMS is currently operational at 20 aquaculture sites in Chile and is expanding to Mexico, Canada, and Norway. Its capacity to analyze in situ plankton samples has enabled the observation of specific cellular structures and features often missed in preserved samples, such as dividing cells, nuclei, diverse athecate forms, several amoebae, and distinct pigmentation of cells. During the austral summer of 2025, SAMS remotely detected natural *A. catenella* cells in the Chonos Archipelago, Chile, peaking at 28 cell/mL. It also documented a bloom of *Akashiwo* sanguinea in Ensenada, Mexico, in April with concentrations exceeding 1,500 cell/mL. The integration of automated technologies like SAMS, FlowCam and others represents a major advancement in marine science and environmental management, reinforcing the role of technological innovation in early warning systems for HABs detection.

**Keywords**: Automated monitoring, Technology validation, HABs

**Financing**: Planton AndinoRetina-Lab

**Acknowledgments**: Plancton AndinoRetina-Lab, Dr. Daniel Varela (Universidad de Los Lagos).

Parallel Session 29: In Situ Monitoring and remote Observing Systems

O-149

# Developing an AI-assisted model to differentiate *Pseudo-nitzschia* morphotypes from warm tropical waters using IFCB-generated images

**Gian Carlo Gaetos**[1], Jhunas Paul Viernes[2], Paul Samuel Ignacio[2], Deo Florence Onda[1]

(1) Microbial Oceanography Laboratory, The Marine Science Institute, College of Science, University of the Philippines Diliman, Quezon City Metro Manila 1101, Philippines
(2) Department of Mathematics and Computer Science, University of the Philippines Baguio, Gov. Pack Road, Baguio City 2600, Philippines

The marine diatom *Pseudo-nitzschia* includes about 60 recognized species, half of which are known to produce domoic acid (DA) – a potent neurotoxin that causes amnesic shellfish poisoning (ASP). However, morphological landmarks when using light microscopy remain limited in differentiating many of the species from each other, in addition to it being time-consuming and necessitates highly specialized taxonomic expertise. The accurate identification of different *Pseudo-nitzschia* is important for assessing bloom toxicity, as DA production varies within the genus, and thus, also in data-driven decision making to mitigate and manage its effects. This has significant implications since in many developing countries, image-based identification remains the usual approach in monitoring. In this work, a CNN-based Artificial Intelligence (AI) model was trained and optimized to accurately detect and classify phytoplankton images collected using an Imaging Flow CytoBot (IFCB) from select bays in the Philippines. Results showed a high number of morphotypes of Pseudo-nitzschia using the features identified by the model. We then looked at the temporal variability and succession of these morphotypes, and verified the identity of some of them using molecular methods as *P. brasiliana*, *P. cuspidata, P. micropora,* and *P. pseudodelicatissima*. When combined with environmental data, this high throughput data will enable rich insights into the bloom dynamics and ecology of HABs, leading to enhanced monitoring and mitigation approaches in the region
.

**Keywords**: *Pseudo-nitzschia*, Imaging Flow Cytobot (IFCB), Artificial Intelligence (AI)

**Financing**: DOST-ASTHRDP; UPD OIL; ISSHA

**Acknowledgments**: DOST-ASTHRDP; UPD OIL; ISSHA; MOLab-UPMSI, The HABs Watch.

Parallel Session 29: In Situ Monitoring and remote Observing Systems

O-150

# Developing an Imaging FlowCytobot monitoring program to detect harmful algal blooms in Alaska

**Thomas Farrugia**[1]

(1) Alaska Ocean Observing System, Alaska Harmful Algal Bloom Network, 1007 W. 3rd Ave, Suite 100, Anchorage, Alaska, United States

Marine living resources are a primary source of food throughout the state, and harmful algal blooms (HABs) are a growing but unpredictable risk to many ocean users and communities. Subsistence and recreational shellfish harvesting, commercial aquaculture operations, and wildlife are all potentially impacted by the toxins produced by HABs. As climate change continues to impact the physical characteristics of Alaska's coastal waters, harmful algal species are responding in unpredictable ways and there is a growing need to better monitor for HABs and understand the factors that lead to HAB events. However, the length and remoteness of Alaska's coastline makes HAB monitoring and research difficult.

One approach to facilitate the detection of HABs is the use of Imaging FlowCytobots (IFCBs). During the summers of 2024 and 2025, multiple IFCBs were deployed aboard research vessels to monitor for HABs in the Gulf of Alaska, Aleutian Islands, and Bering, Chukchi and Beaufort Seas. Several HAB species were detected at low levels by these IFCBs with at least one bloom of *Alexandrium catenella*. As part of a communication plan established before the initiation of the cruise, an advisory of this finding was sent to coastal communities in the region to alert them of this potential threat to their food security. This work constitutes the beginning of an Alaska IFCB program that will grow in the coming years and fit within a larger HAB monitoring and research framework being developed by members of the Alaska Harmful Algal Bloom Network.

**Keywords**: Arctic, Imaging FlowCytoBot, Warming oceans

**Financing**: This work was funded through the National HAB Observing Network of the Integrated Ocean Observing System.

**Acknowledgments**: Thank you to all the members of the Alaska Harmful Algal Bloom Network.

Parallel Session 29: In Situ Monitoring and remote Observing Systems

O-151

# From pixels to patterns: Automated in situ imaging reveals diel vertical migration among phytoplankton

**Karin Garefelt**[1], Bengt Karlson[2], Michael L. Brosnahan[3], Kaisa Kraft[4], Anders Torstensson[5], Jukka Seppälä[4], Allan Cembella[6], Anders Andersson[1]

(1) KTH Royal Institute of Technology, Department of Gene Technology, Science for Life Laboratory, Stockholm, Sweden
(2) Swedish Meteorological and Hydrological Institute, Research and Development, Oceanography, Västra Frölunda, Sweden
(3) Woods Hole Oceanographic Institution, Woods Hole, United States
(4) Finnish Environment Institute, Research Infrastructure Unit, Helsinki, Finland
(5) Swedish Meteorological and Hydrological Institute, Community Planning Services, Oceanography, Västra Frölunda, Sweden
(6) Alfred Wegener Institute, Helmholtz Centre for Polar and Marine Research, Bremerhaven, Germany

Every day, phytoplankton embark on a remarkable journey—migrating vertically through the water column to optimize light, nutrient access, and predator avoidance. Yet, the diel vertical migration (DVM) patterns of most phytoplankton taxa remain underexplored, as traditional microscopy is too labour-intensive to comprehensively study many taxa. In this study, we apply in situ imaging flow to map DVM at an unprecedented scale and resolution at a station in the Skagerrak (North East Atlantic) and in the central Baltic Sea. At the Skagerrak site, an Imaging FlowCytobot continuously captured vertical profiles across the water column, revealing variation in phytoplankton depth distributions over the diel cycle for a period of c. 10 weeks. Some taxa, including many cyanobacteria, ciliates, and dinoflagellates, shifted 2–10 meters between night and day; others remained at stable depths. Notably, 49% of phytoplankton biomass in the size range <10 – 150 µm in the Skagerrak and 72% in the Baltic Sea belonged to migratory taxa—highlighting the ecological importance of DVM. Most populations peaked near the surface at midday, but other patterns were also observed. Many shared taxa showed consistent behavior across both regions, while others diverged, likely reflecting differences in species traits or local conditions. Migration signals varied between seasons. This study shows that DVM is widespread in phytoplankton communities and demonstrates the value of automated, high-throughput tools in studying marine plankton dynamics. As we uncover these underwater rhythms, new questions arise about what drives phytoplankton migration and how it shapes marine ecosystems.

**Keywords**: Imaging flow cytometry, Diel vertical migration

**Financing**: Supported by FORMAS (2022-01515), EU Horizon 2020 JERICO-NEXT (No 654410), and VR (2021-05563).

**Acknowledgments**: We thank M. Molin, W. Eikrem, S. Wengberg, and A. Granhed for their contributions to sampling, annotation, study design, and access to the Tångesund site.

Parallel Session 30: HABs in a Changing World & Emerging Issues

O-152

# Aerosol particles in the Western Philippines increase the growth of *Alexandrium minutum* in batch cultures

**Richard Redil**[1,2], Irene Rodriguez[2]

(1) Bolinao Marine Laboratory, Marine Science Institute, Luciente 1.0, Bolinao, Philippines
(2) Marine Science Institute, College of Science, University of the Philippines Diliman, P. Velasquez Street, Quezon City, Philippines

Atmospheric aerosols released from anthropogenic sources have increased in the last few decades due to rapid industrialization, carrying with them environmentally relevant nutrients which are deposited into our oceans. These often-overlooked nutrient sources are often understudied, especially regarding their effects on harmful algal blooms (HABs). The prevention and mitigation of HABs are critical priorities in the Philippines, given its dependence on aquaculture and fish catches as key food sources. As the country is experiencing increased industrialization, there is a need to study aerosol composition and its possible effects on HABs.

From May to October 2023, aerosol particles in the Western Philippines were collected and analyzed for their inorganic nutrient ($PO_4$, $NO_3$+$NO_2$, and $NH_3$) and trace metal content. Throughout the sampling period, the macronutrient $NH_3$ was found to be the main component of aerosols, while the micronutrient Fe was the most abundant among trace metal concentrations. Exposure of the HAB-forming dinoflagellate *Alexandrium minutum* to aerosol leachates increased their maximum cell density ($p = 0.00981$) and improved overall growth (Area Under the Curve; $p = 0.000153$), exemplifying the possible contributions of aerosols for HAB growth. Interestingly, treatments enriched with only N and P similar to aerosols, did not differ in growth from those exposed to only seawater, alluding that the enhanced growth on aerosol-enriched treatments might be due to micronutrients (i.e., Fe) present in the aerosol. The observed complex relationship between aerosols and HAB growth implies the need for further studies, especially in a rapidly changing world.

**Keywords**: *Alexandrium minutum*, nutrients, aerosols

**Financing**: The experiment was funded by the Philippine Department of Science and Technology through the Philippine Council for Agriculture, Aquatic and Natural Resources Research and Development.

**Acknowledgments**: Special thanks to the GREAT Scholarship program of DOST-PCAARRD, the Marine Science Institute, and the Bolinao Marine Laboratory for their help with this project.

Parallel Session 30: HABs in a Changing World & Emerging Issues

O-153

# Harmful Algal Blooms in South-Central Chile: Impacts, challenges, and research perspectives

**Oscar Espinoza-González**[1], Javier Paredes-Mella[1], Luis Norambuena-Subiabre[1], Pablo Salgado[2], Leonardo Guzmán[1], Jorge I. Mardones[1], Héctor Tardón[3], Jonnathan Vilugrón[1], Julia Cáceres-Chamizo[1], Matias Volke[4], Cristina Hernández[5]

(1) Instituto de Fomento Pesquero, Departamento de Medio Ambiente, Centro de Estudios de Algas Nocivas, Padre Harter 574, Puerto Montt, Chile
(2) Instituto de Fomento Pesquero, Departamento de Medio Ambiente, Centro de Estudios de Algas Nocivas, Enrique Abello 680, Punta Arenas, Chile
(3) Instituto de Fomento Pesquero, Departamento de Medio Ambiente, Colón 3656, Talcahuano, Chile
(4) Instituto de Fomento Pesquero, Departamento de Medio Ambiente, Camino Ten Ten s/n, Castro, Chile
(5) Secretaria Ministerial Regional de Salud de la Región de Los Lagos, Laboratorio de Salud Pública, Avenida Crucero, Puerto Montt, Chile

Harmful algal blooms have significant impacts on public health, the economy, and the social environment. The 2016 *Alexandrium catenella* bloom in the coastal waters of south-central Chile (39°–44°S) marked a major shift in the understanding of this microalga's distribution. In response to the lack of data for informed decision-making and the potential risks posed by similar blooms driven by climate variability and/or climate change, the Pacific HAB Monitoring Program (36°–44°S) was launched in 2018. This study evaluated the phytoplankton community, occurrence of HAB species and toxins, presenting several key findings: a paralytic shellfish poisoning (PSP) outbreak caused by *A. catenella*; the persistent presence of *Alexandrium ostenfeldii*, a producer of saxitoxins and gymnodimines; the accumulation of cysts in sediments as a potential factor in bloom recurrence; an amnesic shellfish poisoning (ASP) event linked to *Pseudo-nitzschia seriata* and *P. delicatissima* groups; mass mortality of marine organisms associated with Kareniaceae species; and a brown tide event caused by *Scrippsiella* cf. *precaria*. These findings are discussed in relation to atmospheric, oceanographic conditions and hydrographic events (e.g., upwelling, river discharges, and currents) occurring during alternating phases of the El Niño–Southern Oscillation (ENSO) and the Southern Annular Mode (SAM). Future research directions include remote in situ detection, the application of artificial intelligence, and big data analysis to develop HAB forecasting platforms. Integrating these technologies into monitoring programs is essential to improve the timeliness and quality of data, enhance early warning capabilities, support mitigation efforts, and ultimately enable the development of reliable forecasting systems.

**Keywords**: HABs, South-Central Chile, Monitoring Program

**Financing**: SUBPESCA. Performance Agreement IFOP-MINECON and EMT 2018-2025.

**Acknowledgments**: We thank colleagues from the CREAN group at IFOP for their collaboration in laboratory and field work.

Parallel Session 30: HABs in a Changing World & Emerging Issues

O-154

# Mussels under stress: Okadaic acid accumulation from toxin-coated microplastics and its molecular and histological consequences

**Estela Pires**[1], Mario Jorge Araújo[2], Maria Carolina Slota Kutz[1] , Francisco Jose Lagreze Squella[1] , Simone Sühnel[3], Alexandre Campos[2] , Luiz Mafra Jr.[1]

(1) Federal University of Paraná, Center for Marine Studies, 83255-000, Pontal do Paraná, Brazil
(2) University of Porto, Interdisciplinary Center of Marine and Environmental Research, Cruise Terminal of the Port of Leixões, Matosinhos, Portugal
(3) Federal University of Santa Catarina, Center for Agricultural Sciences, 88040-900, Florianopolis, Brazil

Microplastics (MPs) provide a substantial surface for the colonization of harmful microalgae and the adsorption of their phycotoxins in marine environments, potentially facilitating toxin transfer along the food web. However, the combined effects of MPs and associated phycotoxins on marine organisms remain poorly understood. This study investigated whether okadaic acid (OA), a diarrhetic shellfish toxin from the dinoflagellate Prorocentrum lima, can be transferred to and accumulated in the tissues of the mussel Perna perna exposed to OA-coated 5 µm polystyrene microspheres. The study also assessed the possible negative effects this toxic combination would induce. Mussels were exposed to dissolved OA, to MPs, or to OA-coated MPs under laboratory conditions for 14 days, and effects on the digestive glands (DG) were assessed through histological and proteomic analyses. OA accumulation occurred rapidly, reaching $1.81 \pm 0.21$ ng $g^{-1}$ after 2 days and increasing to $12.84 \pm 4.50$ ng $g^{-1}$ by day 14. The prolonged presence of OA in tissues of animals exposed to OA-coated MPs suggests limited detoxification or elimination in the presence of MPs, highlighting their role as unintentional vectors of phycotoxins. Exposure led to pronounced cellular stress, significantly changing the expressions of proteins indicating tissue inflammation, morphological alterations in the digestive diverticula, and disruption of critical molecular pathways, such as those involving phosphatases. These responses indicate potential immune impairment and reduced resilience to disease. In light of increasing concerns about plastic pollution and marine biotoxins, these findings underscore the urgent need for interdisciplinary strategies integrating different ecotoxicological biomarkers and environmental policy to assess ecological risks and inform mitigation efforts.

**Keywords**: Harmful Algae, Plastic Pollution, Diarrhetic Shellfish Poisoning

**Financing**: International Atomic Energy Agency (RC#23548); Coordination of Superior Level Staff Improvement (CAPES, Brazil); Program H2020/Horizon Europe Blueshellfish (ID: 101086234)

Parallel Session 30: HABs in a Changing World & Emerging Issues

O-155

# HABs Watch: Developing and implementing an integrated in situ observation network for HAB monitoring under disaster risk reduction (DRR) framework

**Deo Florence L. Onda**[1], Hazel Alvarez[1], Paul Samuel Ignacio[2], Jay Robert Ramos[1], Lance Licnachan[1,2]

(1) The Marine Science Institute, College of Science, University of the Philippines - Diliman, velasquez st, up diliman,, QUEZON CITY, Philippines
(2) University of the Philippines - Baguio, Department of Mathematics and Computer Science, College of Science, Gov Pack Rd., Baguio City, Philippines

HABs occurrences remain a significant threat to many coastal areas in the Philippines, which are predicted to further expand and increase in frequency in the coming years due to confounding effects of coastal pollution and climate change, making it an eminent disaster risk. To ensure public safety and secure livelihood and food supply, more proactive and early warning systems for monitoring and prediction are necessary. However, current government policies are still largely reactive and still utilize conventional methods dependent on manual collection, toxin testing, and microscopy-based approaches limited to paralytic shellfish toxins (PSTs). Here, we established the Philippine's HABs Watch, a model network of monitoring stations utilizing Imaging Flow Cytobots (IFCB) coupled with an AI-based classification model integrated into a near real-time notification system targeting relevant stakeholders and managers. Such information is made publicly available and easily accessible using apps and websites, incorporating these into a decentralized but integrated communication framework for science-informed decision-making by local managers. However, full utilization of such systems necessitates stakeholders' buy in and policy alignment. Thus, we further developed science communication materials, consultative processes, and emergency response frameworks to align actions at different governance levels. We further discuss local experiences and insights that are shaping HABs communication within the framework of Disaster Risk Reduction (DRR), bringing the issue at the forefront of disaster response.

Parallel Session 31: In Situ Monitoring and Remote Observing Systems

O-156

# Improved strategies for tracking *Karenia brevis* across bloom stages

**Katherine Hubbard**[1], Julie Koester[1], Eric Muhlbach[1], Yida Gao[1], Matthew Garrett[1], Alicia Hoeglund[1], Charles Tilney[2], Cary Lopez[1], Michelle Gaither[4], Yonggang Liu[3], Sebin John[3]

(1) Florida Fish and Wlidlife Conservation Commission-Fish and Wildlife Research Institute (FWC-FWRI), Harmful Algal Blooms, 100 8th Ave SE, Saint Petersburg, United States
(2) Fisheries and Oceans Canada, Remouski, Canada
(3) University of South Florida-College of Marine Science, Physical Oceanography, Saint Petersburg, Florida, United States
(4) University of Central Florida, Biology, Orlando, Florida, United States

Harmful algal blooms (HABs) caused by *Karenia brevis* occur nearly annually along Florida's Gulf Coast and negatively impact human and wildlife health, economies, and water quality. Bloom severity varies from short, localized events to regional ones that can endure for years, and localized onset and termination can occur multiple times during a single bloom event. Novel observations of *K. brevis* within a broad monitoring and event response network are helping to improve our understanding of bloom dynamics and severity. The integration of Imaging Flow Cytobots (IFCBs) into >40 vessel-based surveys and for >400 dockside monitoring days allowed real-time bloom tracking and assessment of the highly plastic morphology of *K. brevis*. High frequency IFCB sampling guided by complementary culture studies resolved diel patterns in cellular biovolume linked to asexual division. Field observations with IFCBs revealed that while *K. brevis* cell division rates can vary considerably throughout a bloom, average growth tends to be slow (<0.35 divisions per day). Extensive morphological variability within *K. brevis* populations also occurred across a bloom, including periods with high proportions of vegetative versus rounded cells. Genetic techniques (e.g., quantitative and digital PCR) augmented in situ sampling to provide confirmation of *K. brevis* from seawater and sediment samples. Collectively these tools and observations are helping parameterize newly coupled ocean circulation and ecosystem models within the Finite Volume Coastal Ocean Model to more accurately simulate complex *K. brevis* dynamics and identify key biological, chemical, geological, and physical drivers at relevant scales.

**Keywords**: *Karenia brevis*, Imaging FlowCytobot

Parallel Session 31: In Situ Monitoring and Remote Observing Systems

O-157

# An early warning system for detecting harmful algal blooms in the English Channel

**Gavin Tilstone[1],** Andrey Kurekin[1], Stephanie Allen[1], Silvia Pardo[1], Ben O'Driscoll[1], Claire Widdicombe[1], Peter Miller[1], Francis Gohin[2], Anouska Panton[5], Duncan Purdie[5], Tania Hernandez-Farina[4], Alain Lefebvre[3], Juliane Wihsgott[1], Matthew Palmer[1]

(1) Plymouth Marine Laboratory, EOSA, West Hoe, Plymouth, United Kingdom
(2) Institut Français de Recherche pour l'Exploitation de la Mer (Ifremer) – Brest, Département Océanographie et Dynamique des Ecosystèmes, Centre de Bretagne, CS 10070, 29280, Plouzané, France
(3) Institut Français de Recherche pour l'Exploitation de la Mer (Ifremer) Boulogne., Océanographie et Dynamique des Ecosystèmes, Centre Manche Mer du Nord - 150,, Quai Gambetta - 62200, Boulogne, France
(4) Institut Français de Recherche pour l'Exploitation de la Mer (Ifremer) Port-en-Bessin., Avenue du Général de Gaulle BP 32, 14 520, Port-en-Bessin, France
(5) University of Southampton, Ocean and Earth Science, National Oceanography Centre Southampton, Waterfront Camps, European Way, SO14 3ZH, Southampton, United Kingdom

A web alert system for the detection of HAB events in the French-English Channel was developed. The system provides near real time risk indicator maps of four HAB species (Karenia mikimotoi, Phaeocystis globosa, Pseudo-nitzschia spp., Dinophysis spp.) and a suite of other environmental parameters using data from the Copernicus European satellites. Each of the products can be viewed as daily maps, and specific points or areas on the maps can be viewed as time series. Boat tracks and observations from autonomous systems such as gliders, can be overlaid on the HAB risk indicator and water quality maps to track changes over depth and oxygen concentration in the water column. Multiple satellite, autonomous instrument and in situ sample data are used to track the development, magnitude and spread of HABs in near real time and over the past ten years. Multiple satellite data are also combined to develop proxies for HAB species that occur at very low cell density.

**Keywords**: Ocean colour, Karenia mikimotoi, Dinophysis spp.

**Financing**: European Regional Development Fund through the INTERREG France-Channel-England for S3-EUROHAB (Grant No. 106)

**Acknowledgments**: We thank the skipper and crews of the ships used to collect the in situ data and to NEODAAS for satellite data.

Parallel Session 31: In Situ Monitoring and Remote Observing Systems

O-158

# Development of an early detection, warning and prediction system for cyanobacteria in the Baltic Sea

**Bengt Karlson[6],** Lars Arneborg[6], Dimitrios Antivachis[2], Lars Axell[7], Maria Karlberg[4], Inga Kozsalka[2], Jonas Nilsson[1], Anders Torstensson[4], Malin Olofsson[3], Aida Zuberovic Muratovic[5]

(1) Region Gotland, Visby, Sweden
(2) Stockholm University, Department of Meteorology, Stockholm, Sweden
(3) Swedish University of Agricultural Sciences, Department of Aquatic Sciences and Assessment, Uppsala, Sweden
(4) Swedish Meteorological and Hydrological Institute, Community Planning Services, Oceanography, Västra Frölunda, Sweden
(5) Swedish Food Agency, Uppsala, Sweden
(6) Swedish Meteorological and Hydrological Institute, Oceanographic Research, Västra Frölunda, Sweden
(7) Swedish Meteorological and Hydrological Institute, Oceanographic Research, Norrköping, Sweden

Blooms of filamentous and diazotrophic cyanobacteria are recurrent phenomena in the brackish waters of the Baltic Sea. These blooms negatively affect the aquatic ecosystem, tourism and may also affect desalination plants on the coast that uses brackish water for drinking water production. Some cyanobacteria produce toxins that pose a threat to human health, while others cause problems by, for example, accumulating on beaches and clogging of water-production filters. To mitigate negative societal impacts, an early detection, warning, and prediction system is currently under development. Here, we combine satellite remote sensing, automated in situ observations and other monitoring methods during 2023-2025 to evaluate the best practice for early warning. Firstly, analyses of time series data, including microscopy, qPCR and LC-MS/MS quantification of toxin concentrations, provides insights into periods of heightened risk. Secondly satellite remote sensing of ocean color, provides information on the distribution of near-surface blooms with broad geographic coverage under cloud-free conditions. Sentinel 3 (OLCI-sensor) and PACE (OCI-sensor) were compared. Thirdly, bio-optical sensors such as phycocyanin-fluorometers, mounted on research and merchant vessels and on an oceanographic glider, complements satellite observation by offering additional information about the distribution of cyanobacteria. Fourthly, the Imaging FlowCytobot, operated on a research vessel, provide high resolution data on plankton abundance and diversity. Analyses of cyanotoxins using LC-MS and ELISA result in information on the actual toxicity levels. Finally, the regional ocean model NEMO-Nordic, combined with a Lagrangian drift model, facilitate the prediction of advection of the blooms.

**Keywords**: Cyanobacteria, Cyanotoxins, Warning

**Financing**: Swedish research council Formas grant number 2021-01565European Union Maritime, Fisheries and Aquaculture Programme (EMFAF) 2021-2027.

Parallel Session 31: In Situ Monitoring and Remote Observing Systems

O-159

# Monitoring of potentially harmful microalgae in the coastal area of the Magdalena Department, Colombian Caribbean coast

**Julian Franco Angulo**[1], Edgar Arteaga[1], Luisa Espinosa[1]

(1) Instituto de Investigaciones Marinas y Costeras de Colombia - INVEMAR, Programa de Calidad Ambiental Marina, Santa Marta, Colombia

In the last years, the increase of harmful algal blooms - HABs in the coastal areas of the world has been observed, causing great economic losses and increasing public health problems. In Colombia, there are reports of HABs, however, an early warning system and related legislatin is absent in the country. For this reason, the Institute of Marine and Coastal Research – INVEMAR, in cooperation with the International Atomic Energy Agency, has strengthened national capacities for the monitoring and management of HABs in Colombia through 6 regional projects (RLA7014 - RLA7028). In order to establish a long-term early warning system, the presence of potentially harmful microalgae was evaluated in two strategic areas of the department of Magdalena. Between 2014 and 2023, samples of benthic dinoflagellates associated with seagrasses were collected in the Tayrona National Natural Park, and samples of cyanobacteria were collected in the Ciénaga Grande de Santa Marta. Potentially harmful species of *Gambierdiscus, Prorocentrum* and *Ostreopsis* were morphologically identified, and the first record of *Gambierdiscus caribaeus* and *Prorocentrum borbonicum* in the Colombian Caribbean was made by molecular identification. Moreover, the permanent presence of at least 15 potentially harmful genera of cyanobacteria was observed, and low concentrations of microcystins were detected. These results are fundamental for the formulation and implementation of a national contingency plan and the prevention and reduction of risk due to the presence of harmful species.

**Keywords**: Dinoflagellates, Cyanobacteria, Toxins

**Financing**: This research was funded by INVEMAR, the International Atomic Energy Agency and the Ministry of Environment and Sustainable Development of Colombia.

**Acknowledgments**: Special Acknowledgements to INVEMAR, International Atomic Energy Agency and Ministry of Environment and Sustainable Development of Colombia for the logistical, technical and economic support.

Parallel Session 31: In Situ Monitoring and Remote Observing Systems

O-160

# Harmful algal bloom detection in small, inland water bodies using machine learning and satellite imagery

**Emily Dorne**[1]

(1) DrivenData, United States

Harmful algal blooms (HABs) pose significant threats to human health, aquatic ecosystems, and local economies. While HABs are traditionally monitored through manual water sampling, the visibility of blooms from space has led to increased interest in remote sensing techniques. Remote sensing approaches offer cost-effective, scalable, and near real-time detection capabilities over large geographic areas.

Current satellite-based monitoring tools predominantly rely on chlorophyll estimates from the Ocean and Land Colour Instrument on Sentinel-3, which has a 300m spatial resolution. While suitable for oceans and coastal regions, this resolution is too coarse for detecting HABs in smaller water bodies like lakes, rivers, and reservoirs. Sentinel-2 provides higher resolution imagery but has a narrower range of spectral bands.

We present CyFi (Cyanobacteria Finder), an open-source Python package that utilizes machine learning on 10-30m resolution Sentinel-2 satellite imagery to detect cyanobacteria levels in small, inland water bodies. CyFi uses a gradient boosted decision tree machine learning model that was trained on a dataset of nearly 13,000 in situ cyanobacteria measurements from across the continental U.S. CyFi effectively identifies high and low cyanobacteria levels, empowering more timely and targeted public health action. Our findings indicate that CyFi performs at least as well as a leading Sentinel-3 based method, but offers significantly broader coverage of U.S. water bodies due to the higher resolution of Sentinel-2 data. This dramatically expands the applicability of remote sensing-based estimates as a tool for HABs management.

**Financing**: This project was supported by funding from NASA Mission Directorate's Earth Science, Applied Sciences, Health and Air Quality, and NASA Prizes, Challenges, and Crowdsourcing Programs.

# Poster Communications

## (Including posters presented as Ignite Talks)



Poster Session 01: Taxonomy

P-001

# Phylogeny and ultrastructure of a novel marine *Gymnodinium* species (Gymnodiniales, Dinophyceae) isolated from Hokkaido, Japan

**Koyo Kuwata**[1], Mitsunori Iwataki[1]

(1) University of Tokyo, Graduate School of Agricultural and Life Sciences, 1-1-1 Yayoi, Bunkyo, Japan

The unarmored dinoflagellate *Gymnodinium* is one of the largest genera with over 200 described species and presents challenges in light microscopic species identification due to its limited morphological differences. This study investigated the phylogeny and ultrastructure of two *Gymnodinium* cultures isolated from Hakodate Bay, Hokkaido, Japan, in June 2024. Cell morphology was examined by using LM, SEM, and TEM, and the phylogenetic position was inferred from LSU rDNA sequences. Two strains had an identical LSU rDNA sequence, which was placed in the clade of *Gymnodinium* sensu stricto but not accommodated within any known species. This species was closely related to an undescribed *Gymnodinium* species reported from the French Mediterranean and then sister to the clade of five microreticulate cyst-forming *Gymnodinium* species, such as *G. catenatum*. Motile cells were ellipsoidal, measured 15.7–25.6 µm long and 12.4–19.1 µm wide, and swam solitary or in two-cell chains. The hypocone was slightly wider than the epicone. The nucleus was located in the epicone with an extension downward into the hypocone. Brownish chloroplasts were distributed parietally, with two spherical pyrenoids located laterally in the hypocone. A sulcal extension reached the horseshoe-shaped apical groove, resembling those of other *Gymnodinium* species. Morphologically, it could be distinguished from known *Gymnodinium* species based on cell size, nucleus shape, and the position of the two pyrenoids. TEM revealed that the pyrenoids were separated by chloroplast membranes, and the partial structure of the flagellar apparatus contained nuclear fibrous connective, a diagnostic feature of the genus *Gymnodinium*.

**Keywords:** Pyrenoid, SEM, TEM

Poster Session 01: Taxonomy
P-002

# Identification of *Pseudo-nitzschia* species using rRNA (Nanopore technology) in Southern Chile

**Laura Latorre-Melín[1],** Robert Hatfield[2], Nicole Correa[1], Stephanie Sáez[1], Carlos Flores[1], Carla Palma[1], Álvaro Jorquera[1], Alejandro Clément[1]

(1) Plancton Andino SpA, Terraplén 869, Puerto Varas, Chile
(2) Centre of Environment Fisheries and Aquaculture Science (CEFAS), Barrack Road, Weymouth, Dorset, United Kingdom

Species of the genus *Pseudo-nitzschia* have historically been difficult to identify using light microscopy. Therefore, Chilean monitoring authorities has grouped them into two broad taxonomic categories (*P. seriata* and *P. delicatissima* complexes), based on the transapical length of the valve. To further our understanding of the *Pseudo-nitzschia* species present in southern Chile, we undertook a novel survey combining data generated from conventional light microscopy, imaging flow cytometry and nanopore sequencing. The data generated identified the presence of twelve species of *Pseudo-nitzschia*, of which *P. australis, P. delicatissima*, and *P. fraudulenta* were the most abundant. The other species identified were *P. bucculenta, P. turgidula P. seriata, P. plurisecta, P. subpacifica, P. pungens, P. hasleana, P. granii* and *P. americana*. This unique study provides a detailed characterization of *Pseudo-nitzschia* species dynamics in southern Chile, highlighting previously hidden diversity and contributing to the better understanding of the functional groups currently used in monitoring to ensure public safety and support the mussel farming industry in Chile.

**Keywords:** *Pseudo-nitzschia*, Molecular Biology, Nanopores

**Financing:** Plancton Andino (Chile) and CEFAS (UK).

**Acknowledgments:** We would like to thank to the Center for Environment Fisheries and Aquaculture Science (CEFAS, UK) for the opportunity to develop this research together.

Poster Session 01: Taxonomy
P-003

# Catalog of planktonic dinoflagellates from the Guatemalan Pacific: New records and paralytic shellfish poisoning events

**Karla Paz**[1], Yuri Okolodkov[2], Fernando Cobo[3]

(1) Universidad de San Carlos de Guatemala USAC, Instituto de Investigaciones Hidrobiológicas IIH CEMA USAC, Centro de Estudios del Mar y Acuicultura CEMA, Edificio T-14 ciudad universitaria zona 12, Guatemala, Guatemala
(2) Universidad Veracruzana, Laboratorio de Botánica Marina y Planctología, Instituto de Ciencias Marinas y Pesquerías, Calle Hidalgo No. 617, Col. Rio Jamapa, Boca del Rio Veracruz, C.P. 94290,, Veracruz, México
(3) Universidad de Santiago de Compostela, Departamento de Zoología, Genética y Antropología física, Facultad de Biología, 15782 Santiago de Compostela,, Santiago de Compostela, España

This poster presents a catalog of planktonic dinoflagellates from the Pacific coast of Guatemala, based on samples collected between 2019 and 2022 across ten sites. A total of 42 species were identified, belonging to 14 genera and 6 orders, with morphological descriptions, diagnostic features, and geographic records. A literature review contextualizes the presence of each species in the regional marine ecosystem, accompanied by diagrams or photographs to aid identification. Ecological and toxicological aspects are also addressed, emphasizing their relevance for monitoring harmful algal blooms (HABs).

A notable case occurred in April 2022 in Tiquisate (Escuintla), where 11 cases of paralytic shellfish poisoning (PSP) were reported after consuming bivalves of the genus Tagelus, resulting in four deaths. Analysis of the bivalves' stomach contents revealed *Pyrodinium* cells and frequent *Noctiluca scintillans*. Toxicological tests by the Ministry of Public Health and Social Assistance (MSPAS) showed up to 7,069.4 mouse units (MU)/100 g of clam tissue in Madre Vieja, equivalent to 1,413 µg STX eq./g—over 18 times the FAO's permissible limit of 400 MU/100 g.

This HAB event, between April and May 2022, is likely linked to nutrient enrichment and oceanographic changes at the onset of the rainy season. The most affected areas were Madre Vieja, El Semillero, and Playa de la Isla, where the highest toxicity levels were recorded.

**Keywords:** Dinoflagellates, Saxitoxins, HAB´S

**Financing**: The Catalog of Planktonic Dinoflagellates from the Guatemalan Pacific was published thanks to the support of the Directorate General for Research of USAC.

**Acknowledgments**: We sincerely thank ISSHA for the grant supporting our attendance, and CEMA-USAC for their valuable assistance throughout this research and participation in the event.

Poster Session 01: Taxonomy
P-004

# Harmful algae: 17 years of research in Buenos Aires coastal waters (Argentina)

**Inés Sunesen**[1], Jonás Tardivo Kubis[1], Delfina Aguiar Juárez[1], Eugenia Sar[1]

(1) Universidad de San Carlos de Guatemala USAC, Instituto de Investigaciones Hidrobiológicas IIH CEMA USAC, Centro de Estudios del Mar y Acuicultura CEMA, Edificio T-14 ciudad universitaria zona 12, Guatemala, Guatemala
(2) Universidad Veracruzana, Laboratorio de Botánica Marina y Planctología, Instituto de Ciencias Marinas y Pesquerías, Calle Hidalgo No. 617, Col. Rio Jamapa, Boca del Rio Veracruz, C.P. 94290,, Veracruz, México
(3) Universidad de Santiago de Compostela, Departamento de Zoología, Genética y Antropología física, Facultad de Biología, 15782 Santiago de Compostela,, Santiago de Compostela, España

This poster presents a catalog of planktonic dinoflagellates from the Pacific coast of Guatemala, based on samples collected between 2019 and 2022 across ten sites. A total of 42 species were identified, belonging to 14 genera and 6 orders, with morphological descriptions, diagnostic features, and geographic records. A literature review contextualizes the presence of each species in the regional marine ecosystem, accompanied by diagrams or photographs to aid identification. Ecological and toxicological aspects are also addressed, emphasizing their relevance for monitoring harmful algal blooms (HABs).

A notable case occurred in April 2022 in Tiquisate (Escuintla), where 11 cases of paralytic shellfish poisoning (PSP) were reported after consuming bivalves of the genus Tagelus, resulting in four deaths. Analysis of the bivalves' stomach contents revealed Pyrodinium cells and frequent Noctiluca scintillans. Toxicological tests by the Ministry of Public Health and Social Assistance (MSPAS) showed up to 7,069.4 mouse units (MU)/100 g of clam tissue in Madre Vieja, equivalent to 1,413 µg STX eq./g—over 18 times the FAO's permissible limit of 400 MU/100 g.

This HAB event, between April and May 2022, is likely linked to nutrient enrichment and oceanographic changes at the onset of the rainy season. The most affected areas were Madre Vieja, El Semillero, and Playa de la Isla, where the highest toxicity levels were recorded.

Keywords: Dinoflagellates, Saxitoxins, HAB´S

Financing: The Catalog of Planktonic Dinoflagellates from the Guatemalan Pacific was published thanks to the support of the Directorate General for Research of USAC.

Acknowledgments: We sincerely thank ISSHA for the grant supporting our attendance, and CEMA-USAC for their valuable assistance throughout this research and participation in the event.

Poster Session 01: Ecology, Biology, and Biogeography
P-005

# Trophic transfer of paralytic shellfish toxin: Impact on biochemical composition and reproduction of the carnivorous snail *Chorus giganteus*

**Paola Andrade**[1], Ángel Urzúa[1], Jorge Navarro[2]

(1) Universidad Católica de la Santísima Concepción, Ecology, Science, Alonso de Rivera 2850, Concepción, Chile
(2) Universidad Austral de Chile, Institute of Marine and Limnological Sciences, Science, Las Encinas 220, Isla Teja, Valdivia, Chile

*Alexandrium catenella*, producer of paralytic shellfish toxin (PST), is one of the main generators of HABs across the coast of Chile and can affect multiple organisms throughout the trophic chain. The objective of this work is to identify the effect of indirect consumption of PST, on reproductive and biochemical aspects of *Chorus giganteus*, an edible gastropod present across the coasts of Chile. One group of snails was exposed to a 'toxic diet', feeding on bivalves previously fed with A. *catenella*, while another group was fed a 'non-toxic diet', consisting of uncontaminated bivalves. Both groups were maintained for 63 days. The results indicate that toxic snails have a higher total protein content than the non-toxic group, however the total lipid content did not differ. Regarding the fatty acid profile, a higher content of essential polyunsaturated acids (DHA and EPA) was observed in toxic snails. A higher egg-mass production was observed in toxic snails, where only 62% showed embryonic development with 57% of hatching success. An inverse relationship between egg-mass production and the PST level of the snails could also be identified. There was no egg-mass production in the aquarium with the snails showing the highest average PST level (120 ± 80 µg STX.2HCL eq. 100 $g^{-1}$). It is possible that *C. giganteus* activate their reproductive process as a response to toxin stress, however when toxin levels are high, reproduction could be inhibited. Indirect consumption of PST could generate modifications in the biochemical composition of *C. giganteus*, also impacting on their fecundity.

**Keywords**: paralytic shellfish toxin, gastropod, reproduction and biochemical composition

**Financing**: Agencia Nacional de Investigación y Desarrollo (ANID-CHILE), with a research grant to P. Andrade (FONDECYT-Postdoctorado-3180316, FONDECYT-Initiation-11250835), Á. Urzúa (ANID-BMBF-180034), JM Navarro (ANID-Center FONDAP IDEAL-15150003).

**Acknowledgments**: Agencia Nacional de Investigación y Desarrollo (ANID-CHILE)

Poster Session 01: Ecology, Biology, and Biogeography
P-006

# Diversity of benthic dinoflagellates in the Magellan Subantarctic ecoregion: Morphological characterization in intertidal habitats with special emphasis on toxic species

**Francisco Bahamonde Mihovilovich**[1,2,3,4], Máximo Frangopulos[1,3,4,5], Luiz L. Mafra Jr.[6], Luciano F. Fernandes[7], Juan Pablo Rodríguez[1,2,3], Fabio Méndez[1,2,3,4], Johanna Marambio[1,3], Andrés Mansilla[1,3]

(1) Laboratorio de Ecosistemas Marinos Antárticos y Subantárticos, Universidad de Magallanes, Punta Arenas, Chile.
(2) Programa de Doctorado en Ciencias Antárticas y Subantárticas, Universidad de Magallanes, Punta Arenas, Chile.
(3) Centro Internacional Cabo de Hornos (CHIC), Universidad de Magallanes, Puerto Williams, Chile.
(4) Instituto Milenio Biodiversidad de Ecosistemas Antárticos y Subantárticos (BASE), Universidad de Chile, Santiago, Chile.
(5) Centro de Investigación Gaia-Antártica (CIGA), Universidad de Magallanes, Punta Arenas, Chile.
(6) Centro de Estudos do Mar, Universidade Federal do Paraná, Pontal do Paraná, PR, Brasil
(7) Universidade Federal do Paraná, Setor de Ciências Biológicas, Departamento de Botânica, Curitiba, PR, Brasil.

Benthic Harmful Algal Blooms (BHAB) represent and emerging global issue especially in the context of global climate change. However, knowledge about BHABs in South America remains limited, particularly in cold waters ecosystems. The Magellan Subantarctic ecoregion (MSE) constitutes a unique biogeographic setting to explore the diversity and distribution of benthic dinoflagellates in high-latitude coastal environments, where the presence and impacts of toxigenic species are still poorly documented. This study provides the first morphological characterization of benthic dinoflagellates in two intertidal sub-habitats -macroalgae and sediments- from multiple coastal study sites within the MSE during austral summer 2025. Live samples were analyzed using optical and inverted microscopy to assess species richness and spatial patterns. Preliminary results revealed high taxonomic diversity, with 36 dinoflagellates species identified, corresponding to 22 genera. Amphidiniales and Gymnodiniales were the most species rich orders (9 species each) followed by Peridiniales (6 species). Most taxa (28 spp.) were restricted to sandy sediments, while only 7 spp. occurred across both sub-habitats. Clear spatial variability among sites suggest that local environmental factors may influence species distribution. Notably, several taxa from toxin-producing genera such as Amphidinium and Prorocentrum, underscoring the need for further integrative studies linking taxonomy, toxin profiles, and environmental drives to better assess the risks associated with BHABs in sub-antarctic regions.

**Keywords**: Benthic Dinoflagellates, Biodiversity, Magellan Sub-antarctic Ecoregion

**Financing**: FONDECYT Project Number 1241697; ANID BASAL FB210018; FOVI 220095; ANID MILENIO ICN2021_002; ANID GRANT/NATIONAL DOCTORATE PROGRAM, CHILE, FOLIO #21240092 (FB).

Poster Session 01: Ecology, Biology, and Biogeography
P-007 (Ignite Talk)

# Dead or alive? Assessing viability and recovery of rounded *Karenia brevis* cells induced by putrescine and temperature stress

**Devin Burris**[1,2], Michael Parsons[1], Vince Lovko[2], Cindy Heil[2]

(1) Florida Gulf Coast University, 10501 FGCU Blvd. S., Fort Myers, United States
(2) Mote Marine Laboratory, Red Tide Institute, 1600 KEN THOMPSON PKWY, SARASOTA, United States

Monitoring of *Karenia brevis* blooms heavily relies on the enumeration and identification of cells for accurate and timely reports. *Karenia brevis* morphology however, can vary greatly depending on life stage and environmental conditions, making accurate identification and confirmation increasingly difficult. Spherical *K. brevis* cells, believed to form under stressful conditions, have been documented in previous studies and observed in multiple laboratories. Rounded cells have been associated with factors such as low salinity, reduced light, temperature fluctuations, and nitrogen limitation. Similar morphological changes have been seen in cells exposed to algicidal compounds such as the amine putrescine and curcumin. LC-MS analysis revealed that samples containing 99% of rounded cells had an average of approximately 3pg/cell of brevetoxin. Although low, this percentage is within previously reported concentrations for normal morphological cells. While many dinoflagellates produce cysts in response to adverse conditions, it remains unclear whether *K. brevis* forms cysts or whether these rounded cells remain viable. This study assessed the viability of rounded *K. brevis* cells induced by putrescine and temperature stress by analyzing brevetoxin production, cell division, and potential morphological recovery. In addition to broadening criteria for *K. brevis* cell identification, this research also provides insight into the possibility of cells recovering from natural and artificial stressors, including those used in bloom mitigation efforts.

**Keywords**: *Karenia brevis*, Putrescine, Spherical cells

Poster Session 01: Ecology, Biology, and Biogeography
P-008

# *Alexandrium catenella* in Chilean fjords: Characteristics of its genome and effect of temperature on core genes (sxtA4 and sxtG) of the synthesis cluster

**Pamela Carbonell[1,2],** Shauna Murray[3], Pablo Salgado[4], Luis Norambuena[1], Leonardo Guzmán[1], Gemita Pizarro[4], Marcela Astorga[5], Gonzalo Fuenzalida[6]

(1) Instituto de Fomento Pesquero, Padre Harter 574, Puerto Montt, Chile
(2) Universidad Austral de Chile, Escuela de Graduados, Programa de Doctorado en Ciencias de la Acuicultura, Puerto Montt, Chile
(3) 3University of Technology Sydney, Climate Change Cluster, School of Life Sciences, NSW, 2007, Sydney, Australia
(4) Instituto de Fomento Pesquero, Enrique Abello 0552, Punta Arenas, Chile
(5) Universidad Austral de Chile, Los Pinos S/N, Puerto Montt, Chile
(6) Universidad Santo Tomás, Ciencias Básicas, Valdivia, Chile

*Alexandrium catenella* is the main producer of paralytic toxins (PSTs) in the fjords of Chile. To determine the PST general characteristics (specific profile and toxicity), 15 strains of this species were studied, isolated from the Chilean fjords (41° - 55°S) and cultivated under temperature, salinity, light intensity, nutrients and photoperiods, standard conditions. The toxins were analyzed by Ultra High-Performance-LC (UHPLC) – tandem MS (MS/MS). Gonyautoxins (GTX1-4, GTX2-3) were the dominant analogues, followed by Carbamoyl (C1 and C2), Neosaxitoxin (Neo-SXT) and Saxitoxin (SXT).

The genes copies number quantification associated with PST synthesis can help to understand the toxin biosynthesis regulation. In this study, the number of sxtA4 gene copies (qPCR), which is a precursor gene of the PST synthesis cluster, showed an average of 126 ± 31 (±SD) copies. On the other hand, the genome size (flow cytometry) was estimated at 78.36 ± 9.76 pg. The correlation between the sxtA4 copies number and the PST concentration per cell was relatively low (Spearman = 0.39; $p<0.0001$), while the relationship between the gene copies number and the genome size was more robust (Spearman = 0.81; $p<0.0001$).

A decrease in sxtA4 expression was observed with increasing temperature (12° - 15° - 17°C), which may indicate that this variable influences the cluster and subsequent PST synthesis. The sxtA4 genes copies number and toxin content low correlation can be attributed to the expression of other genes in the cluster. These results were also obtained for this species in other parts of the world.

**Keywords**: *Alexandrium catenella*, PSP, Genoma

Poster Session 01: Ecology, Biology, and Biogeography
P-009 (Ignite Talk)

# Ecosystem service trade-offs driven by eutrophication and socioeconomic pressures in reservoir cascade

**Sheila Cardoso**[1,2], Paulo Alves de Lima Ferreira[3], Diego de Souza Sardinha[1], Rubens C.L. Figueira[3], Marcelo Pompêo[4], Eduardo Vicente[5], Viviane Moschini-Carlos[2]

(1) Federal University of Alfenas (UNIFAL), Environmental Sciences Program, Institute of Science and Technology, Rodovia José Aurélio Vilela,BR 267, Km 533 11999 - Cidade Universitária, 37715-400, Poços de Caldas, MG, Brazil
(2) State University of São Paulo (UNESP), Environmental Sciences Program, Institute of Science and Technology, Av. Três de Março, 511 - Alto da Boa Vista, 18087-180, Sorocaba - SP, Brazil
(3) University of São Paulo (USP), Oceanographic Institute, Praça Oceanográfico, 191 - Vila Universitaria, 05508-120, São Paulo - SP, Brazil
(4) University of São Paulo (USP), Ecology Department, Biosciences Institute, Rua do Matão, trav. 14, nº 321, Cidade Universitária, 05508-090, São Paulo - SP, Brazil
(5) Valencia University, Microbiology and Ecology Department, Burjassot, 46100, Valencia, Spain

Paleolimnological analyses offer essential long-term insights into environmental transformations, supporting the evaluation of ecosystem services (ES) and the understanding of aquatic systems' responses to anthropogenic and natural pressures. This study employs an integrated framework that combines paleolimnological data, environmental monitoring, and socioeconomic indicators to assess changes in two hydrologically connected reservoirs. Geochemical proxies associated with eutrophication and metal accumulation, along with monitoring records and governmental statistics, were used to identify key factors influencing ecosystem stability (ES) dynamics. Stratigraphically constrained cluster analysis delineated major paleoenvironmental phases, and standardized ES indicators were aggregated. Redundancy Analysis explored relationships between external drivers—such as population and economic trends—and observed ES shifts. Sediment profiles indicated pronounced eutrophication, evidenced by elevated nutrient inputs, increased phytoplankton biomass (Chlorophyll-a and Pheophytin), and prevalence of pigments from Chlorophyceae and Cyanobacteria. This process intensified from the mid-1990s to early 2000s, with marked impacts on support and regulation services by 2022. Although metals did not show toxic effects on biota, their spatial distribution signaled growing human influence. Provisioning services declined due to reduced water availability, compounded by drought and demographic pressure. Effects were more pronounced in the Jaguari reservoir, linked to distinct land-use practices. Mitigation strategies include land-use regulation, wetland rehabilitation, reforestation, and riparian zone restoration to enhance water resilience.

**Keywords:** Phtosynthetic pigments, myxoxantophyll, eutrophication.

**Financing:** FAPESP (Fundação de Amparo a Pesquisa do Estado de São Paulo, grants 2019/10845-4; 21/11283-0 and 21/10637-2) and the UNESP Post-Doctoral Program (PROPe 13/2022).

**Acknowledgments:** To ICT-UNESP, University of Valencia's Microbiology and Ecology Department, and the Biosciences and Oceanographic Institutes of the University of São Paulo.

Poster Session 01: Ecology, Biology, and Biogeography
P-010

# Morphological landmarks in *Prorocentrum koreanum* showed consistency in varying salinity conditions as revealed by Imaging Flow CytoBot coupled with machine learning

**Gerard Paul Chan[1],** Kristian Boado[1], Joshua Allen Canlas[1], Samantha Mari Peniano[1], James Suello[1], Jay Robert Ramos[1], Paul Samuel Ignacio[2], Bryan Miguel Tul-ao[2], Deo Florence Onda[1]

(1) University of the Philippines - Diliman, The Marine Science Institute, P. Velasquez Street, University of the Philippines - Diliman, Quezon City, Philippines
(2) University of the Philippines - Baguio, Department of Mathematics and Computer Science, Gov. Pack Road, University of the Philippines - Baguio, Baguio City, Philippines

Conventional methods for HABs monitoring employ morphological landmarks and light microscopy but with limited resolution and throughput. However, some features are insufficient to distinguish species and can be conflated by potential morphological plasticity in response to varying environmental conditions (i.e., salinity), resulting in inaccurate identification of target species such as in the case of *Prorocentrum koreanum*. High-throughput imaging systems like Imaging Flow CytoBot (IFCB) coupled with machine learning present an opportunity to understand consistency in morphology. Here, *P. koreanum* from Manila Bay was exposed to varying salinity regimes (15, 33, 38 PSU) representing natural conditions where cells can be transported, and monitored for 30 days with periodic sampling. Results showed growth rates were significantly higher in 33 (0.26 cells day$^{-1}$) and 38 (0.29 cells day$^{-1}$) than 15 PSU (0.11 cells day$^{-1}$), indicating euryhaline tolerance. Extraction of 234 features using machine learning revealed that only nine showed >60% change between 0 and 30 days. Post-hoc Tukey Test showed that while significant differences were detected across salinities and time points, trends were consistent in direction (i.e., increasing) regardless of salinity treatment. Additionally, non-significantly different pairs within the same growth phase suggest changes were associated more with growth phase than salinity. This includes features associated with cell size and asymmetry, suggesting cells grew larger in later phases where competition was lower. Although many features remain unmapped relative to cell functions, they remain useful in training models to improve species delineation using IFCB images for more efficient monitoring.

**Keywords**: Morphological Plasticity, Machine Learning, Imaging Flow Cytobot

Poster Session 01: Ecology, Biology, and Biogeography
P-011

# First report of the marine dinoflagellate *Tripos furca* bloom in a warm temperate bay (South Africa)

**Phumlile Cotiyane-Pondo**[1,2,3], Mfundo Bizani[1,2], Shaun H.P Deyzel[1,2], Thomas G. Bornman[1,2]

(1) South African Environmental Observation Network (SAEON), Elwandle Coastal Node, Gqeberha, South Africa
(2) Institute for Coastal and Marine Research (CMR), Nelson Mandela University, Gqeberha, South Africa
(3) University of the Western Cape, Department of Biodiversity and Conservation Biology, Cape Town, South Africa

Harmful algal blooms (HABs) are a known and well-recorded phenomenon along the west coast of southern Africa. The occurrence of HABs along the east coast was rare; however, bloom events caused by dinoflagellate species have become persistent in Algoa Bay (South Africa), starting with the observation of the non-toxin producing *Noctiluca scintillans*. This was followed by the presence of the non-indigenous and toxin-producing *Lingulodinium polyedra*, observed for the first time in December 2013 along the south and southwest coasts of South Africa. Most recently, a high-density bay-scale bloom of *Tripos furca* was observed in Algoa Bay, characterized by water discoloration in April 2025. Historically, the phytoplankton community composition of Algoa Bay was diatom-dominated; however, dinoflagellate abundances have increasingly contributed to the overall compositional changes. This study investigated the influence of environmental drivers on the phytoplankton community and the successive community shift from multi-species to a monospecific bloom of *Tripos furca*. Initial observation indicates that anomalous warming and sporadic cooling events during the upwelling season resulted in the occurrence of *Tripos furca*, followed by low levels of dissolved oxygen concentrations in the water column. Although the bloom was short-lived, our findings suggest that under global climate change, the frequencies and intensities with which these blooms occur are likely to increase, as upwelling and warming events intensify in the region, with implications for higher trophic levels and socio-economic impacts. Continuous environmental observations as part of the long-term ecological research (LTER) initiative will provide insights into bloom dynamics in Algoa Bay.

**Keywords**: Phytoplankton, *Tripos furca*, Africa

**Financing**: South African Environmental Observation Network (SAEON)Shallow Marine and Coastal Research Infrastructure (SMCRI).

**Acknowledgments**: South African Environmental Observation Network (SAEON) Shallow Marine and Coastal Research Infrastructure (SMCRI).

Poster Session 01: Ecology, Biology, and Biogeography
P-012 (Ignite Talk)

# Toxicity and bioluminescence in *Pyrodinium bahamense* blooms: The luminous lies of cheats

**Kathleen Cusick**[1], Sydney Hall[2], Nicole Brown[1], Gregory L. Boyer[2], Edith Widder[3]

(1) UMBC, Biological Sciences, 1000 Hilltop Circle, Baltimore, United States
(2) State University of New York, College of Environmental Science and Forestry, Syracuse, United States
(3) Ocean Research and Conservation Association, Vero Beach, United States

Dinoflagellates that form some of the most recurring toxic blooms are also bioluminescent, yet the two traits are rarely linked when examining bloom development and persistence. *Pyrodinium bahamense* is a saxitoxin (STX)-producing bioluminescent dinoflagellate that blooms in Florida, Puerto Rico, and the Indo-Pacific. STX is a potent neurotoxin that binds with high affinity to the voltage-gated sodium channel in humans and causes Paralytic Shellfish Poisoning. Its role in the ecology of *P. bahamense* remains unknown. Our field data from multiple sites in Florida showed a consistent, statistically significant negative correlation between toxicity and cell abundance. However, a strong, statistically significant negative correlation between nutrients (N, P) and cell abundance was found indicating the decrease in toxicity was not due to a lack of nutrients. The underlying mechanism for toxin decrease with increased cell abundance remains unknown. SxtA4 is a core biosynthetic gene that is essential for toxin synthesis. Single-cell genotyping revealed that within populations, a small proportion lacked sxtA4. However, a strong, statistically significant negative correlation was found between stxA4 transcripts and the sxtA4/rbcL ratio, suggesting cells make fewer sxtA4 transcripts as a bloom progresses. Our collective results have led us to hypothesize that as blooms develop, “cheaters” emerge: these cells/strains “lose” their toxicity yet retain their bioluminescence. Both toxicity and bioluminescence are energetically costly. However, the underlying mechanism for population decrease in toxicity remains to be determined: whether it occurs at the genetic level, due to the sxtA4-genotype emerging; or the transcriptional level, via sxtA4 repression.

**Keywords**: saxitoxin; bioluminescence; *Pyrodinium bahamense*

**Financing**: Internal funding (UMBC START award) to KC.

Poster Session 01: Ecology, Biology, and Biogeography
P-013 (Ignite Talk)

# Mixotrophic strategies and habitat Influences on dinoflagellate blooms in the coastal Baltic Sea

**Johanna Exner**[1], Hanna Farnelid[1], Catherine Legrand[2], Elin Lindehoff[1]

(1) Department of Biology and Environmental Science, Centre of Ecology and Evolution and Microbial Model Systems, Linnaeus University, 392 31 Kalmar, Sweden
(2) School of Health and Welfare, Jönköping University, Gjuterigatan 5, 55111 Jönköping, Sweden

Dinoflagellate red tides often result in ecological challenges with negative economic consequences (fish and shellfish kills, aquaculture and tourism losses). These harmful algal blooms (HABs) are frequently mixotrophic, meaning they can both perform photosynthesis (autotrophy) and consume dissolved organic matter (DOM) for energy (heterotrophy). This metabolic flexibility may provide a competitive advantage in supporting bloom formation and maintenance. This study investigates how different sources of DOM from freshwater inflow and aquatic vegetation affect bloom dynamics and mixotrophic activity of dinoflagellates in the coastal Baltic Sea. Field campaigns were conducted during late summer (June-September) of 2024 in a coastal region of southeast Sweden. Two bays, with distinct vegetation cover and freshwater inflow, were sampled. Nutrient uptake was measured using in-situ incubations combined with stable isotope analysis. Freshwater inflow was tracked via changes in salinity, colored dissolved organic matter (cDOM), and concentrations in dissolved inorganic nitrogen (DIN). The study area exhibited salinity levels between 0.3 and 6.7 PSU and background chlorophyll a concentrations ranging from 1.36 and 5.02 µg $L^{-1}$. Preliminary results indicate that during a notable red tide event (chlorophyll a concentration of 89.3 µg $L^{-1}$), *Prorocentrum micans* was the dominant species in areas rich in aquatic macrophyte diversity. This study contributes to our understanding of dinoflagellate bloom dynamics in coastal ecosystems characterized by high diverse aquatic vegetation and provides insights into how specific habitat characteristics influence bloom initiation and development.

Poster Session 01: Ecology, Biology, and Biogeography
P-014

# Bloom of *Heterocapsa circularisquama* in Mar del Plata Harbor, Southwest Atlantic Ocean: Description of two strains with lytic activity against other plankton components

**Elena Fabro[1],** Gastón Almandoz[1], Martina Mascioni[1], Belén Matera[2], Bernd Krock[3], Urban Tillmann[3]

(1) conicet, phycology, fcnym UNLP, paseo del bosque s/n, la plata, Argentina
2) inidep, inidep, escollera norte, mar del plata, Argentina
(3) AWI, ecological chemistry, Bremerhaven, Germany

*Heterocapsa circularisquama* is a thecate dinoflagellate originally described from a bloom in Japan, where it caused mortality in pearl oysters. Since then, multiple episodes of shellfish mass mortality associated with this species have been reported in coastal regions of Japan, and later in China and Kuwait. In April 2021, a reddish-brown discoloration of the water was observed in Mar del Plata Harbor due to an algal bloom. For two consecutive days, water samples were collected for plankton analysis and cell cultures. Microscopic counts confirmed the occurrence of an exceptional bloom ($7.7 \times 10^6$ and $1.4 \times 10^6$ cells $L^{-1}$) of a small dinoflagellate accounting for 87.8% and 65.7% of the total protistan cells on the two sampling days, respectively. Morphological and molecular analyses identified both strains as *H. circularisquama*, representing the first confirmed record of this species in the Argentine Sea. Bioassays using whole-cell suspensions, culture supernatants, and methanol cell extracts revealed lytic activity against other planktonic organisms. Considering its confirmed lethality to bivalves, it is crucial to monitor for potential future blooms of this species in other regions of the South Atlantic Ocean.

**Keywords**: bloom, *Heterocapsa circularisquama*, lytic activity

**Financing**: EU project CoastCarb, Horizon 2020 Programme of the EU. Consejo Nacional de Investigaciones Científicas y Técnicas (Conicet, Argentina).

Poster Session 01: Ecology, Biology, and Biogeography
P-015 (Ignite Talk)

# Linking organic matter sources to diarrhetic shellfish toxin accumulation in coastal mussels during a harmful algal bloom

**João Paulo Felizardo**[1], Alana Guimarães[1], Ricardo Coutinho[4], Luiz Mafra Jr[3], Silvia Nascimento[2], Roberto Dos Anjos[1]

(1) Universidade Federal Fluminense Laboratory of Radioecology and Environmental Changes, Departamento de Geoquímica, Rua Passo da Pátria, 156 - Universidade Federal Fluminense Campus da Praia Vermelha (LARA) - São Domingos, Niterói. CEP. 24210-346, Niterói, Brasil
(2) Federal University of the State of Rio de Janeiro UNIRIO Marine Microalgae Laboratory (MiMar), Biology, Av. Pasteur 296, Rio de Janeiro, RJ, 22290-250, Rio de Janeiro, Brasil
(3) Universidade Federal do Paraná, Oceanografia e Engenharia de Aquicultura, Avenida Beira-Mar, s/n, Pontal do Sul, Pontal do Paraná, PR, Pontal do Paraná, Brasil
(4) Instituto de Estudos do Mar Almirante Paulo Moreira (IEAPM), Departamento de Biotecnologia Marinha, Rua Kioto, nº 253, Praia dos Anjos, CEP: 28930-000, Rio de Janeiro/RJ. Marinha do Brasil +2, Arraial do Cabo, Brasil

We investigated the relationship between isotopic trophic markers and the accumulation of okadaic acid (OA) in *Perna perna* mussels collected from Arraial do Cabo, southeastern Brazil, following a massive harmful algal bloom (HAB) recorded in December 2021 to March 2022. The bloom, dominated by *Scrippsiella*, *Tetraselmis*, and unidentified dinoflagellates likely from the family Kareniaceae, extended along >150 km of coastline and resulted in widespread discoloration of coastal waters.
Stable isotope analysis ($\delta^{13}C$ and $\delta^{15}N$) revealed a narrow dietary range centered on phytoplankton/particulate organic matter (POM), with minor contributions from detrital and sewage-derived sources. Okadaic acid concentrations in mussel tissues ranged from 3.59 to 89.5 ng/g dry weight (mean = 19.3 ng/g), below the Brazilian legal limit for human consumption (160 ng/g wet weight).

A significant positive correlation was observed between OA levels and $\delta^{15}N$ values ($R^2 = 0.61$, $p < 0.001$), suggesting that individuals occupying higher trophic positions accumulated greater amounts of OA. No significant correlations were found between OA and biometric parameters such as shell length or tissue mass. These findings highlight that not only HAB occurrence but also organic matter origin and assimilation pathways strongly influence the accumulation of diarrhetic shellfish toxins in filter-feeding bivalves. Our study underscores the value of ecological tracers in understanding toxin dynamics in coastal ecosystems, offering insights into the trophic mechanisms underlying OA bioaccumulation following algal bloom events.

**Keywords**: Okadaic acid; Stable isotopes; Trophic transfer

**Financing**: International Atomic Energy Agency (IAEA) through the BRA7012 project and the Fundação de Amparo à Pesquisa do Estado do Rio de Janeiro (FAPERJ).

**Acknowledgments**: This work was supported by IAEA (BRA7012), with logistical support from IEAPM and a postdoctoral fellowship granted by FAPERJ.

Poster Session 01: Ecology, Biology, and Biogeography
P-016 (Ignite Talk)

# Succession of *Ostreopsis* blooms: Community structure of zoosporic parasites associated with dinoflagellates on the Basque coast

**Alan Denis Fernández Valero[1],** Yago Laurenns Balparda[1,2], Pablo Aramendi[1], Jone Bilbao[1,2], Laia Moreno[1], Marina Salido[1,2], Estibalitz Txurruka[1], Sergio Seoane[1,2]

(1) University of the Basque Country - UPV/EHU, Plant Biology and Ecology, Science and Technology (ZTF-FCT), Barrio Sarriena. Postal 48940, Leioa, Bizkaia, Spain
(2) Research Centre for Experimental Marine Biology and Biotechnology (Plentzia Marine Station, PiE-UPV/EHU), Areatza Hiribidea, 47, Postal 48620, Plentzia, Bizkaia, Spain

The climate emergency is causing an increase in the frequency and intensity of toxic dinoflagellate blooms in regions where these events had not previously been registered. Such is the case of the annual *Ostreopsis* blooms on the Bay of Biscay, which in 2020 and 2021, caused health problems during the summer months. To better understand the dynamics of these blooms, this study focused on analyzing the biological factors that could influence the development of *Ostreopsis*, specifically parasite and saprophyte relationships. Zoosporic parasite diversity was assessed using a methodological combination that included metabarcoding techniques, microscopic observation and culture of isolated strains.
The results revealed a diversity of parasites associated with *Ostreopsis* blooms, where three main groups are highlighted: Syndiniales (Dino-Group-II), Perkinsid (Perkinsidae) and Chytrids (Chytridiomycota). The community structure of these zoosporic parasites was observed to vary seasonally, depending on the diversity of available hosts. Chytridiomycota dominated in spring and summer, while Perkinsids - in particular the ASV1388 and ASV1135 sequences - were predominant in summer. On the other hand, Syndiniales showed the highest relative abundance values during summer and autumn. Parasitic interaction between *Ostreopsis* and the groups Perkinsids and Chytridiomycota were confirmed through the isolation, culture and identification of strains collected during spring and summer months. These insights suggest a dynamic and seasonal relationship between zoosporic parasites and *Ostreopsis* proliferation, which could have key implications for future monitoring and management of these events.

**Keywords**: *Ostreopsis*, Zoosporic parasite, Perkinsidae

**Financing**: – Ostreobila Project. Programa INTERREG VI-A España-Francia-Andorra (POCTEFA 2021-2027).– Diputación foral de Guipúzcoa, Ayuntamiento de San Sebastián.– ParAqua – COST Action CA20125

Poster Session 01: Ecology, Biology, and Biogeography
P-017

# Southernmost detection of Pectenotoxins-2 in Antarctic waters using SPATT

**Máximo Jorge Frangopulos Rivera**[1,2,3], Gemita Pizarro[4], Claudia Zamora[4], Vanessa Monge[2,3], Luis Norambuena[5], Erling Johnson[1], Francisco Bahamonde[2,3,6,7], Pablo Guerrero[2,8,9]

(1) Universidad de Magallanes, Centro de Investigación GAIA Antartica (CIGA), Instituto de la Patagonia, Avenida Bulnes 01855, Punta Arenas, Chile
(2) Instituto Milenio Biodiversidad de Ecosistemas Antárticos y Subantárticos (BASE), Las Palmeras 3425, Santiago, Chile
(3) Universidad de Magallanes, Centro Internacional Cabo de Hornos (CHIC), O'higgins 310, Puerto Williams, Chile
(4) Centro de Estudios de Algas Nocivas (CREAN), Instituto de Fomento Pesquero (IFOP), Enrique Abello 0552, Punta Arenas, Chile
(5) Centro de Estudios de Algas Nocivas (CREAN), Instituto de Fomento Pesquero (IFOP), Puerto Montt 5501679, Chile
(6) 6Laboratorio de Ecosistemas Marinos Antárticos y Subantárticos, Universidad de Magallanes, Avenida Bulnes 01890, Punta Arenas, Chile
(7) Programa de Doctorado en Ciencias Antárticas y Subantárticas, Universidad de Magallanes, Avenida Bulnes 01890, Punta Arenas, Chile
(8) Universidad de Concepción, Departamento de Botánica, Facultad de Ciencias Naturales y Oceanográficas, Concepción, Chile
(9) Instituto de Ecología y Biodiversidad (IEB), Santiago, Chile

In recent years, reports of Harmful Algal Blooms (HABs) in the Southern Ocean around Antarctica have emerged, posing a potential threat to marine ecosystems. This study focuses on a new record of the lipophilic toxin Pectenotoxin-2 (PTX-2), which is primarily produced by dinoflagellates of the genus Dinophysis. During a research survey undertaken west of the Antarctic continent en route from New Zealand to Ushuaia, aboard the Commandant Charcot, samples of dissolved toxins in seawater were collected using the SPATT (Solid Phase Adsorption Toxin Tracking) method. SPATT samplers were deployed at the water intake of the vessel's wet laboratory and pumped slowly at a constant flow rate of around 1 L per minute. Toxin monitoring using the SPATT method was conducted between 7 February and 2 March 2024. During the survey, the SPATT sampler was replaced with a fresh one every five days and a total of seven transects were tracked. In the laboratory extracts of the dissolved lipophilic toxins were analyzed using HPLC/MS. Analysis of the samples over the course of one month showed that three of the seven SPATT samplers tested (SPATT samplers 4, 5 and 7) had positive PTX-2 results, with respective values of 2.3, 1.5 and 1.4 ng/vial. SPATTs 4 and 5 represent the southernmost detection of these lipophilic toxins to date (77°S). We discuss the implications of an expansion of marine toxin-producing microalgae towards the Antarctic continent and the risk of HABs emerging on the southern continent in scenarios involving global warming and human activity.

**Keywords**: Marine toxins, Antarctic, Spatt

**Financing**: Ponant Expeditions

**Acknowledgments**: ANID MILENIO ICN2021_002; BASAL FB210018; Ponant Expeditions.

Poster Session 01: Ecology, Biology, and Biogeography
P-018

# Spatial distribution of harmful algal blooms in Nuevo Gulf and their likely negative effects on the environment during spring 2022

**Leilén Gracia Villalobos**[1], Guillermina Ruiz[1], Gabriela Williams[1]

The study of the distribution and abundance of harmful algal bloom (HAB)-forming species is highly relevant in Argentine Patagonia due to their negative effects on public health and bivalve mollusk fisheries. In this work, we studied the spatial distribution of harmful phytoplankton species and their associated toxins in Nuevo Gulf. Sampling was carried out in coastal waters west of Nuevo Gulf at different depths (0, 15, and 30 m). Phytoplankton community characterization was performed using optical microscopy and chemotaxonomy. The phytoplankton community was dominated by diatoms in the coastal zone (at 0 m) and by dinoflagellates in the zone furthest from the coast (at 15 and 30 m). *Alexandrium catenella* was the predominant species in all samples, with the highest concentrations observed at 15 and 30 m, being $5 \times 10^4$ and $3.6 \times 10^4$ cells $L^{-1}$, respectively. However, the highest levels of toxins per cell (527.16 fmol $cells^{-1}$), produced by this species were recorded at coastal zone. Densities of other toxigenic species were $8.8 \times 10^3$ cells $L^{-1}$ for *Azadinium* spp., $4.5 \times 10^2$ cells $L^{-1}$ for *Dinophysis acuminata*, and $2.5 \times 10^3$ cells $L^{-1}$ for *Pseudo-nitzschia* spp. High cell abundances and toxicity of *A. catenella* recorded are in spatiotemporal agreement with reported deaths of several Southern Right whales and other marine organisms in Nuevo Gulf. These results demonstrate that HAB events can vary considerably in intensity and duration, as well as their harmful effects on biota.

**Keywords**: *Alexandrium*, Phytoplankton, Nuevo Gulf

Poster Session 01: Ecology, Biology, and Biogeography
P-019

# Genetic diversity and vertical distribution of amphidomatacean dinoflagellates off the coast of Hokkaido, Japan, detected by metabarcoding and quantitative PCR analyses

**Koyo Kuwata**[1], Kazuma Nakano[1], Taketoshi Kodama[1], Kazutaka Takahashi[1], Mitsunori Iwataki[1]

(1) University of Tokyo, Graduate School of Agricultural and Life Sciences, 1-1-1 Yayoi, Bunkyo, Japan

The small thecate dinoflagellates of *Azadinium* and *Amphidoma*, belonging to the family Amphidomataceae, include species producing the marine toxin azaspiracids (AZAs). In the Northwest Pacific, 12 amphidomatacean species have been observed mainly from coastal areas. In Japan, AZAs have been detected in *Azadinium spinosum* and *A. poporum*. This study aimed to explore the species composition of amphidomatacean dinoflagellates, especially toxigenic species distributing off the Japanese coast. Seawater samples were collected at 12 depths (0–200 m) across five stations in the Kuroshio-Oyashio transition zone off the coast of Hokkaido, Japan, during an R/V Shinsei-Maru cruise in September 2024. Environmental DNA sequences of ITS2 related to the Amphidomataceae were analyzed using metabarcoding, and the two toxigenic species were quantified using LSU rDNA-based species-specific qPCR assays. Metabarcoding revealed the presence of 12 species, including six species previously unreported from Japan (*A. concinnum, A. obesum, A. perforatum, A. polongum, A. languida,* and *A. parvula*). qPCR showed that high cell densities (17–57 cells $L^{-1}$) of *Az. spinosum* were at seawater depths of 0–60 m, but z. poporum was below the detection limits (<1 cell $L^{-1}$). Moreover, metabarcoding distinguished three intraspecific ribotypes (A–C) in A. spinosum: ribotype A dominated in the warmer Kuroshio-influenced waters, ribotype C in the cooler Oyashio-influenced waters, and ribotype B occurred in both. These results suggest that A. spinosum is more widespread offshore than previously known, with the ribotypes adapted in distinct ecological niches.

**Keywords**: *Amphidoma*, *Azadinium*, shellfish poisoning

Poster Session 01: Ecology, Biology, and Biogeography
P-020

# Harmful algal blooms in Latin America and Caribbean

**Ana Martínez Goicoechea**[1,12], Karla Paz[2,12], Rosalba Alonso-Rodríguez[3,12], Angel Moreira[4,12], Marcelo Hernando[5,7,12], Gastón Almandoz[6], Irene Schloss[7], Andreana Cadaillon[7], Tomasa Cuellar Martínez[3,12], Daniel Carrasco[8,12], Joao Paulo de Sá Felizardo[9,12], Leon Antonio Vergara[10,12], Ana María Salinas[11,12], Krissia Portillo[11,12]

(1) Dirección Nacional de Recursos Acuáticos (DINARA), Unidad de Gestión Pesquera Atlántica (UGEPA), Av del Puerto s/n, La Paloma, Uruguay
(2) Centro de Estudios del Mar y Acuicultura de la Universidad de San Carlos de Guatemala, Guatemala
(3) Instituto de Ciencias del Mar y Limnología, Universidad Nacional Autónoma de México, Mazatlán, Sinaloa, México
(4) Centro de Estudios Ambientales de Cienfuegos (CEAC), Carretera a Castillo de Juagua Km 1 y 1/2, Ciudad Nuclear, Cienfuegos, Cuba
(5) Comisión Nacional de Energía Atómica, Centro Atómico Constituyentes, Departamento de Radiomicrobiología, Buenos Aires, Argentina
(6) Facultad de Ciencias Naturales y Museo, División Ficología, Universidad Nacional de La Plata, La Plata, Argentina
(7) Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET), Argentina
(8) Universidad de Chile, Laboratorio de Toxinas Marinas, Facultad de Medicina, Castro, Chile
(9) Universidad Federal do Rio do Janeiro (UFRJ), Departamento de Biología Marinha, Rio do Janeiro, Brasil
(10) Escuela Superior Politénica del LItoral ESPOL, Facultad de Ingeniería Marítima y Ciencias del Mar, Guayaquil, Ecuador
(11) Universidad de El Salvador, Laboratorio de Toxinas Marinas, El Salvador
(12) Red de investigación de Estresores Marinos Costeros en Latinoamerica y el Caribe (REMARCO)

Since 2009, Latin America and the Caribbean have begun a process of harmonization of methods for monitoring algal blooms using European standards to implement monitoring programs in the member countries of IAEA ARCAL, projects RLA 7014 to 7028. The objective of this work is to present a list of species linked to harmful algal blooms (HABs) in the region, including their biogeography, toxicology, and background studies.
The region hosts several harmful taxa and toxins, such as saxitoxins (STX), ciguatoxins (CTX), okadaic acid (OA), dinophysistoxins (DTX), yessotoxins (YTX), domoic acid (DA), and emerging toxins. Paralytic Shellfish Poisoning (PSP) is a major concern in some countries, mostly associated with *Alexandrium catenella* in the south (Argentina and Chile), and with *Pyrodinium bahamense* and *Gymnodinium catenatum* at lower latitudes (e.g., Mexico, Guatemala, El Salvador, Cuba). In Argentina and Chile due to *Alexandrium catenella*, and in lower latitudes (e.g., Mexico, Guatemala, El Salvador, Cuba) due to *Pyrodinium bahamense* and *Gymnodinium catenatum*. Frequent blooms of *Margalefidinium polykrikoides* in tropical areas impact aquaculture, fisheries, and tourism. Mid-latitude countries like Argentina, Uruguay, and Brazil face Diarrhetic Shellfish Poisoning (DSP), mainly caused by the Dinophysis acuminata complex. Ciguatera Poisoning (CP), caused by *Gambierdiscus* spp. and other benthic species, affects the Caribbean and tropical Atlantic. The South Atlantic, especially off Uruguay and Argentina, sees recurrent blooms of Azadinium spp. Pseudonitzschia spp. are widespread, but Amnesic Shellfish Poisoning (ASP) remains a minor issue. Most countries report at least one harmful event per year, underscoring the need for ongoing monitoring and mitigation.

## Poster Session 01: Ecology, Biology, and Biogeography

### P-020

**Keywords**: HAB, Dinoflagellates, Biotoxins

**Financing**: This work was promoted and partially funded by the International Atomic Energy Agency (IAEA).

**Acknowledgments**: We would like to acknowledge to REMARCO and IAEA for making this work possible.

Poster Session 01: Ecology, Biology, and Biogeography
P-021

# Amphidomataceae blooms in the Río de la Plata continental shelf, Southwest Atlantic

**Ana Martínez Goicoechea**[1], Ricardo Silva[2], Elena Fabro[3]

(1) Dirección Nacional de Recursos Acuáticos (DINARA), Biología Pesquera, La Paloma, Rocha, Uruguay
(2) Instituto Nacional de Investigación y Desarrollo Pesquero (INIDEP), Mar del Plata, Argentina
(3) Museo La Plata, Facultad de Ciencias Naturales y Museo, La Plata, Argentina

The continental shelf at the mouth of the Río de la Plata in the Southwest Atlantic is characterized by remarkable oceanographic conditions resulting from the convergence of the warm, saline Brazil Current and the colder, fresher Malvinas Current, in addition to the freshwater discharge from the Río de la Plata. This unique combination fosters high productivity, recognized globally, and may contribute to the area being a potential hotspot for harmful algal blooms (HABs).
The marine dinophyte family Amphidomataceae produces lipophilic toxins known as azaspiracids (AZAs), which can cause azaspiracid shellfish poisoning (AZP) in humans following the consumption of contaminated seafood. Blooms of Amphidomataceae have previously been recorded during spring in the northern waters of the Argentine continental shelf.
In this study, we observed a large bloom of Amphidomataceae in the mid-continental shelf at the mouth of the Río de la Plata during spring (3.08 X $10^5$ cells $L^{-1}$), along with a smaller bloom in autumn (3.27 x $10^4$ cells $L^{-1}$). These findings suggest that such blooms are recurrent throughout the year and not restricted to a specific season.
At least four *Azadinium* species were involved in the blooms: *A. spinosum, A. dexteroporum, A. luciferelloides* and *A. asperum*, occurring alongside other small dinoflagellates such as *Oxytoxum laticeps*, *O. gracile*, and potentially toxic genera including *Karenia* and *Karlodinium*. This indicates that the mid-continental shelf region off Uruguay and Argentina provides favorable conditions for the proliferation of these small dinoflagellates, with possible implications for fisheries and seafood safety.

**Keywords**: Dinoflagellates, Amphidomataceae, Southwestern Atlantic

**Financing**: The results of this work were founded partially by the CTMFM (Comisión Técnico Mixta del Frente Marítimo).

**Acknowledgments**: We want to thanks the CTMFM for making this work possible.

Poster Session 01: Ecology, Biology, and Biogeography
P-022

# Seasonal and spatial distribution of three dominant diatom genera: *Chaetoceros*, *Skeletonema*, and *Pseudo-nitzschia* in Singapore waters

**Aye Aye Mon**[1]

(1) Tropical Marine Science Institute, National University of Singapore, 18 Kent Ridge Road, S (119227), Singapore

This study examines the spatial distribution and seasonality of three dominant diatom genera: *Chaetoceros*, *Skeletonema*, and *Pseudo-nitzschia* in Singapore's waters over five years (January 2020 to December 2024). Phytoplankton abundance was quantified monthly, alongside environmental parameters including temperature, salinity, and nutrient concentrations across the Singapore Strait, the Southern Islands, and the West Johor Strait. Among the sampling areas, the West Johor Strait was typically characterized by lower salinity and higher nutrient levels, and it generally recorded overall higher densities of diatoms compared to the East Singapore Strait and Southern Islands. During the study period, *Chaetoceros* spp. and *Skeletonema* spp. were detected year-round and were the dominant diatoms across all study areas. *Chaetoceros* spp. was the more dominant genus in the West Johor Strait, whereas *Skeletonema* spp. dominated in the Southern Islands. *Pseudo-nitzschia* spp. was detected less frequently, usually at low densities, and was more often absent from the West Johor Strait. Seasonal patterns were more apparent at the East Singapore Strait. Mean concentrations of *Chaetoceros* peaked during the northeast monsoon (January-March), *Skeletonema* peaked during both monsoons (January and September), and *Pseudo-nitzschia* peaked from the end of the southwest to the early northeast monsoon (September-November). Results of a Canonical Correspondence Analysis indicated that *Pseudo-nitzschia* spp. preferred more saline waters; *Chaetoceros* abundance was associated with higher nutrients (especially NO2-N) and lower salinity; and *Skeletonema* favored lower water temperature. These findings highlight the seasonal variability and spatial differences in the abundance of dominant diatom genera in Singapore's waters.

**Keywords**: Diatoms, Distribution, Singapore

**Financing**: This work was funded by the Public Utilities Board of Singapore under the project "Ecological, Water and Sediment Quality: Monitoring and Interpretation".

**Acknowledgments**: I thank the Coastal Marine Cluster staff for their contributions to fieldwork and the Public Utilities Board of Singapore for funding support for this project.

Poster Session 01: Ecology, Biology, and Biogeography
P-023

# Comparison of growth and toxin production of *Vulcanodinium rugosum* strains grown under two different conditions: Batch and agitated cultures

**Angel Ramón Moreira González**[1], Pedro Reis Costa[2], Catarina Churro[2], Lisbet Díaz Asencio[1], Donaida Consorcia Chamero Lago[1]

(1) Centro de Estudios Ambientales (CEAC), AP 5, CP 59350, Ciudad Nuclear, Cienfuegos, Cuba
(2) IPMA-Português do Mar e Atmosfera, Avenida Alfredo Magalhães Ramalho 6, 1449-006, Lisboa, Portugal

*Vulcanodinium rugosum*, a benthic-planktic dinoflagellate, is known to produce marine emergent neurotoxins: Pinnatoxins and Portimines. Blooms of *Vulcanodinium rugosum* were associated to acute dermatitis cases in recreational beaches in Cienfuegos Bay, Cuba. The aim of this study was to compare the growth and toxin production of two *Vulcanodinium rugosum* strains isolated from Cuba and cultured under two different conditions: batch and agitated cultures. Strains were grown in F2 media and incubated at 26 °C. Two different stages were also tested: static and agitated stages, this last using rotating equipment. The highest cell densities were recorded for VR5 strain at the end of stationary phase in the agitated stage. Toxins analysis of the cultures showed the presence of Portimine A and B; and Pinnatoxins D, E and F. Portimine-A and Pinnatoxin-F were the predominant toxins in this order, and the sum of them exceeded more than 90% of the total toxins. The highest toxin concentrations were recorded for VR12 strain at the end of stationary phase in the static stage. This is an important result for the surveillance program of toxic microalgae species in Cienfuegos Bay.

**Keywords**: *Vulcanodinium rugosum*, Portimine-A, Pinnatoxin-F

**Financing**: Blueshelfish Project Horizon 2020IAEA

**Acknowledgments**: AENTA, CITMA (Cuba)

Poster Session 01: Ecology, Biology, and Biogeography
P-024

# A spatio-temporal analysis of the occurrence of harmful algal blooms in Chile: A review between 1956 and 2021

**Doris Oliva**[1], Camila Barria[2], Pablo Conejeros[1], Pablo Herrera[1], Benjamín Suárez-Isla[3], Leonardo Guzmán[4], L. René Durán[5]

(1) Universidad de Valparaíso, Instituto de Biología, Centro de Investigación y Gestión de Recursos Naturales (CIGREN), Ciencias, Gran Bretaña 1111, Valparaiso, Chile
(2) Universidad Austral de Chile, Programa de Doctorado en Ciencias de la Acuicultura, Puerto Montt, Chile
(3) Universidad de Chile, Laboratorio de Toxinas Marinas, Medicina, Santiago, Chile
(4) Instituto de Fomento Pesquero, División de Investigación en Acuicultura, Puerto Montt, Chile
5) Copulhue Spa, Conchas Blancas, Isla de Quinchao, Chiloé, Chile

Harmful Algal Blooms (HABs) are a global problem and have apparently increased in frequency, intensity and geographical distribution at different latitudes. This review describes the occurrence of toxic and ichthyotoxic HAB events in Chile. Fourty-one species and/or genera, mostly dinoflagellates (52%), diatoms (33%) and silicoflagellates (10%) caused HABs. A total of 501 harmful events have been recorded between 1956 and 2021, being 240 (47.9%), 238 (47.5%), 14 (2.7%), 8 (1.5%) and 1 (0.2%) event caused by diatoms, dinoflagellates, silicoflagellates, rafidophytes and haptophytes, respectively. The main harmful species recorded are *Alexandrium catenella*, *Dinophysis* spp, *Protoceratium reticulatun* and *Pseudo-nitzschia* spp. The apparent increment in frequency of HAB events was observed with a maximum of 25 events per year in period 2006 - 2016 and 46 events during the years 2017 and 2021 The number of events per region was 201, 147, 101, 14, 12, 10 and 2 events in Aysén (41%), Los Lagos (30%), Magallanes (21%), Atacama (2.8%), Coquimbo (2.4%), Antofagasta (2%) and Arica-Parinacota (0.4%), respectively. The ichthyotoxic blooms are produced by silicoflagellates, rafidophytes and haptophytes (23 events), and 10 events caused salmon mortalities. These ichthyotoxic events are much less frequent, but they hold high economic impacts. The first event recorded in 1988 in northern Patagonia was caused by *Heterosigma akashiwo*. Over the years, the number of HAB-related species and the apparent expansion of their geographic distribution occurred from south to north. The explanation of this pattern is analyzed, considering changes in monitoring effort, aquaculture production and climate.

**Keywords**: HABs, ichthyotoxic blooms, geographical distribution

**Financing**: Fondo de Investigación Pesquera y de Acuicultura, Project 2020-15. and Agencia Nacional de Investigación y Desarrollo (ANID) / Programa de Becas / Doctorado Becas Chile/21210109,

**Acknowledgments**: We acknowledge Jeanette Santana from Universidad de Valparaíso for providing library support and Instituto de Metereología for assisting in climate analysis.

Poster Session 01: Ecology, Biology, and Biogeography
P-025

# Experimental exposure of harmful microalgae *Alexandrium catenella*, *Prorocentrum lima* and *Heterosigma akashiwo* on the Chilean mussel *Mytilus chilensis*

**Doris Oliva[1],** Camila Barria[2], Catalina Lizama[1], Piera Vásquez-Calderón[1], Pablo Herrera[1], Pablo Conejeros[1], Karin Lohrmann[3], L. René Durán[4]

(1) Universidad de Valparaíso, Instituto de Biología, Centro de Investigación y Gestión de Recursos Naturales (CIGREN), Ciencias, Gran Bretaña 1111, Playa Ancha, Valparaiso, Chile
(2) Universidad Austral de Chile, Programa de Doctorado en Ciencias de la Acuicultura, Puerto Montt, Chile
(3) Universidad Católica del Norte, Biología Marina, Ciencias del Mar, Coquimbo, Chile
4) Copulhue Spa, Conchas Blancas, Isla de Quinchao, Chiloé, Chile

HABs cause damage to human health, aquaculture and fishery resources, with an impact on the economies of countries that depend on the extraction/cultivation of marine organisms and tourism. *Mytilus chilensis* is a relevant species for Chilean aquaculture, therefore the aim of this work is to analyze the effect of three harmful microalgae reared in the laboratory: *Alexandrium catenella*, *Prorocentrum lima* and *Heterosigma akashiwo* on the Chilean mussel. Adult mussels were obtained from aquaculture center in Chiloé Archipelago and exposed for 5 days to triplicate treatments of harmful microalgae (1) *A. catenella* (AC 879), (2) *H. akashiwo*, (3) *P. lima* (K0075), plus a control treatment without microalgae. 500 cells/ml of A. catenella, 10,000 cells/ml of H. akashiwo and 3,200 cells/ml of P. lima were added for each treatment with water changes every 24 hours. After 5 days of exposure to harmful microalgae, mussels were fed for 5 days with a mix of microalgae (*Isochrysis lutea*, *Chaetoceros muelleri*, *Pavlova luteri*). Samples were taken at 1, 5 and 10 days after the experiment, for toxin (*A. catenella*) and histology analysis. An increase in the concentration of toxin to 50.97 µg Eq STX/100g was observed on the fifth day of exposure to A. catenella, which did not imply obvious tissue damage due to hemocytic infiltrations. For *H. akahiwo* and *P. lima*, no clear changes in tissue infiltrations were observed. Despite the relatively low incidences, the presence of infiltrations in the gonad, gills and plicate membrane could generate a decrease in reproductive success.

**Keywords**: histology, exposure experiments, toxins

**Financing**: Fondo de Investigación Pesquera y de Acuicultura, Project 2020-15 and Agencia Nacional de Investigación y Desarrollo (ANID) / Programa de Becas / Doctorado Becas Chile/21210109.

Poster Session 01: Ecology, Biology, and Biogeography
P-026 (Ignite Talk)

# Biogeography and toxin diversity of *Alexandrium* along Chilean Pacific coast

**Javier Paredes-Mella[1],** Oscar Espinoza-González[1], Ana Flores-Leñero[2], Luis Norambuena-Subiabre[1], Jorge Mardones[1], Julia Cáceres-Chamizo[1], Bianca Zubicueta-Olivares[1], Cristina Hernández[3], Gonzalo Fuenzalida[1], Leonardo Guzmán[1]

(1) Centro de Estudios de Algas Nocivas (CREAN), Instituto de Fomento Pesquero (IFOP), Puerto Montt, Chile
(2) Scottish Association for Marine Science (SAMS-UHI), Oban, UK
(3) Laboratorio de Salud Pública, Secretaría Regional Ministerial de Salud, región de Los Lagos, Puerto Montt, Chile

The genus *Alexandrium* includes some of the most harmful algal bloom (HAB) species worldwide. In Chile, *A. catenella* has been extensively studied due to recurrent and severe blooms reported since 1972 in the Patagonian channels and fjords. In 2016, an exceptional bloom extended for the first time along the Pacific coast. Its northernmost detection to date is off the Bío-Bío Region (36°S). To investigate the distribution and toxins diversity of *Alexandrium* genus along central (43°–36°S) and northern (30°–18°S) Chile, two monitoring databases were analyzed, incorporating species abundance and toxin profiles, alongside the characterization of isolated strains. In central Chile, *A. ostenfeldii* was consistently detected, while *A. catenella* appeared only sporadically. Accordingly, paralytic shellfish toxins (PSTs) were detected at low concentrations and infrequently, whereas gymnodimine was consistently present but remained below the detection limit (<DL). In northern Chile, *A. catenella* was absent; however, a morphotype identified as *Alexandrium* cf. *catenella*, along with *A. ostenfeldii*, was recorded. High PST concentrations were observed, while gymnodimine again remained below the detection limit. Strain isolation in central Chile confirmed the presence of *A. catenella* and, notably, led to the first record of *Alexandrium tropicale* in the region. In the north, toxin analysis of an *A. ostenfeldii* strain revealed the production of both saxitoxin and gymnodimine. These findings highlight the complex biogeography of *Alexandrium* species and their associated toxins along the Chilean coast, emphasizing the need for expanded and regionally tailored monitoring efforts in both historically studied and understudied areas.

**Keywords**: *Alexandrium tropicale*, gymnodimine, biogeography.

**Financing**: FIPA 2023-17. Evaluación de biotoxinas en la zona norte de Chile. SUBPESCA. Convenio desempeño IFOP-MINECON y EMT 2018-2024.

Poster Session 01: Ecology, Biology, and Biogeography
P-027

# Phytoplankton assemblages associated with a bloom of *Pseudo-nitzschia pseudodelicatissima* complex and *Phaeocystis* spp. in subantarctic fjords of southern Chile during the austral spring 2021

**Gemita Pizarro Nova**[1], Francisco Bahamonde[2,3,4,5], César Alarcón[1], Carolina Toro[1], Pablo Salgado[1], Luis Norambuena[6], Erling Johnson[7], Andrés Mansilla[2], José Luis Iriarte[8,9], Máximo Frangopulos[4,5]

(1) Centro de Estudios de Algas Nocivas (CREAN), Instituto de Fomento Pesquero (IFOP), Medio Ambiente, Enrique Abello 0552, Punta Arenas 6200000, Chile
(2) Laboratorio de Ecosistemas Marinos Antárticos y Subantárticos, Universidad de Magallanes, Punta Arenas, Chile
(3) Programa de Doctorado en Ciencias Antárticas y Subantárticas, Universidad de Magallanes, Punta Arenas, Chile
(4) Instituto Milenio Biodiversidad de Ecosistemas Antárticos y Subantárticos (BASE), Universidad de Chile, Santiago, Chile
(5) Centro Internacional Cabo de Hornos (CHIC), Universidad de Magallanes, Puerto Williams, Chile
(6) Centro de Estudios de Algas Nocivas (CREAN), Instituto de Fomento Pesquero (IFOP), Puerto Montt 5501679, Chile
(7) Centro de Investigación Gaia-Antártica (CIGA), Universidad de Magallanes, Punta Arenas, Chile
(8) Centro de Investigación Dinámica de Ecosistemas Marinos de Altas Latitudes (IDEAL), Universidad Austral de Chile, Punta Arenas, Chile
(9) Instituto de Acuicultura y Medio Ambiente, Universidad Austral de Chile, Puerto Montt, Chile

The fjords and channels of southern Chile are a highly sensitive region to harmful algal blooms (HABs), with areas becoming increasingly exposed to these events. As part of the Spring 2021 EXOFAN oceanographic survey, phytoplanktonic assemblages were studied in the area between the Strait of Magellan and the Beagle Channel (53°–56°S), within the Magellan Subantarctic Ecoregion (MSE), in Chile. Qualitative and quantitative samples were collected at depths of 0, 5, 10 and 25 meters, alongside vertical profiles of physicochemical variables (temperature, salinity, chlorophyll, and nutrients, among others). Univariate and multivariate analyses were performed using R (v4.2.0) and PRIMER (v7.0.24). A total of 115 taxa were identified and distributed across six phyla and eight classes, with Bacillariophyta and Dinophyta being the most prevalent. Significant spatial variability (taxonomic composition and cell density) was observed among phytoplanktonic assemblages along the MSE. While some taxa were restricted to specific locations, most were widely distributed in terms of cell density. Several toxin-producing species were recorded, including lipophilic and hydrophilic types, High densities of the *Pseudo-nitzschia pseudodelicatissima* complex (up to 20,000 cells/ml) were observed in the Strait of Magellan and high densities of the Haptophyta *Phaeocystis* spp. (up to 13,000 cells/ml) were observed in the Beagle Channel; The latter was associated with a dark green coloration observed in surface waters (5 m). The distribution of phytoplanktonic assemblages during the southern spring in the MSE, as well as its relationship with the toxic species and environmental gradients, is discussed.

**Keywords**: Keyword: Southern Chile, *Pseudo-nitzschia*, *Phaeocystis*

## Poster Session 01: Ecology, Biology, and Biogeography

### P-027

**Financing**: FONDECYT Regular 1241697; CONICYT-PIA AUB2000006; ANID BASAL FB210018; ANID MILENIO ICN2021_002; AGENCIA NACIONAL DE INVESTIGACIÓN Y DESARROLLO (ANID)/ PROGRAMA DE BECAS/ DOCTORADO NACIONAL CHILE

**Acknowledgments**: FONDECYT Regular 1241697; CONICYT-PIA AUB2000006; ANID BASAL FB210018; ANID MILENIO ICN2021_002; ANID/ PROGRAMA DE BECAS/ DOCTORADO NACIONAL CHILE, FOLIO #21240092 (FB)

Poster Session 01: Ecology, Biology, and Biogeography
P-028 (Ignite Talk)

# Assessment of potentially toxigenic benthic dinoflagellates in two Cuban coral reefs: Abundance patterns across sites and substrates

**Gabriel Livan Rojas Abrahantes**[1,2], Lisbet Díaz Asencio[1], Victor Alfonso Cervantes Urieta[4], Allan D. Cembella[2,5], Catarina Churro[6,7], Pedro Reis Costa[6,8], Lorena María Durán Riveroll[2,3]

(1) Centro de Estudios Ambientales de Cienfuegos, Departamento de Estudios de la Contaminación Ambiental, Carretera Castillo de Jagua Km 1.5, Cienfuegos, Cuba
(2) Centro de Investigación Científica y de Educación Superior de Ensenada, Departamento de Biotecnología Marina, Carretera Ensenada-Tijuana 3918, Zona Playitas, C.P. 22860, Baja California., Ensenada, México
(3) Secretaría de Ciencia, Humanidades, Tecnología e Innovación, México
(4) Universidad Autónoma de Guerrero, Facultad de Ecología Marina, Av. Javier Méndez Aponte 1, Fracc. Servidor Agrario, CP 39070, Acapulco, México
(5) Alfred-Wegener-Institut, Department of Ecological Chemistry, Helmholtz-Zentrum für Polar-und Meeresforschung, 27570, Bremerhaven, Germany
(6) Portuguese Institute for the Sea and Atmosphere - IPMA, I.P, Morada, Av. Alfredo Magalhães Ramalho, 6, 1495-165, Lisboa, Portugal
(7) Interdisciplinary Centre of Marine and Environmental Research - CIIMAR, erminal de Cruzeiros do Porto de Leixões, 4450-208, Matosinhos, Portugal
(8) Centre of Marine Sciences – CCMAR/CIMAR LA, University of Algarve, Campus de Gambelas 8005-139 Faro, Portugal

Ciguatera poisoning (CP), the most widespread non-bacterial seafood poisoning worldwide, is caused by ingestion of ciguatoxins produced by benthic dinoflagellates from the genera Gambierdiscus and Fukuyoa. Despite historical knowledge of Cuba as CP hotspot, ecological and toxicological data on benthic toxigenic dinoflagellates remain scarce. This study provides a preliminary assessment of abundance and substrate associations of potentially toxigenic benthic dinoflagellates from two Cuban coral reef systems: Rancho Luna (RL) and Guanahacabibes Peninsula (GCB). Epiphytic dinoflagellates were detached from dominant macroalgae collected from six sites, preserved with Lugol's iodine, and quantified using optical microscopy. In addition, fresh samples were also collected for strain isolation and culturing. Five genera were identified: *Gambierdiscus*, *Prorocentrum*, *Amphidinium*, *Coolia*, and *Ostreopsis*, with cell densities ranging from 31 to 1229 cells $g^{-1}$ wet weight. Statistical analysis of cell density by Kruskal-Wallis and PERMANOVA tests revealed significant ($P<0.05$) spatial variability and substrate preferences among taxa. *Gambierdiscus* and *Ostreopsis* showed the highest spatial heterogeneity, with peak densities found at Laberinto (RL) and Paraíso Perdido (GCB), respectively. The phaeophyte *Dictyota* spp. hosted the greatest dinoflagellate abundance across all genera, but *Gambierdiscus* was also abundant on the rhodophyte *Dichotomaria* sp.; in contrast, the chlorophyte *Halimeda* sp. consistently supported only the lowest cells density ranges. From the eighty strains isolated, 45 were identified so far as *G. carolinianus*(2), *G. caribaeus*(14), and *G. carpenteri*(29) using the LSUrDNA (D8-D10). These preliminary findings highlight significant ecological variability in benthic dinoflagellate communities between Cuban reefs systems and provide a crucial baseline for future ciguatera risk assessments.

**Keywords**: Marine microalgae; Ciguatera poisoning; HAB monitoring

## Poster Session 01: Ecology, Biology, and Biogeography
### P-028 (Ignite Talk)

**Financing**: Funded by SECihti, IAEA project RLA7025, Cuban national project CiguaTox, coordinated by AENTA, and by EU through the BlueShellfish project Grant number 101086234 - HORIZON-MSCA-2021-SE-01

**Acknowledgments**: The authors thank CEAC, Cuba for field support and CICESE for academic guidance throughout the study.

Poster Session 01: Ecology, Biology, and Biogeography
P-029

# Spatial distribution of harmful algal bloom in Nuevo Gulf and its effects on a coastal ecosystem with anthropogenic impact

**Leilén Luciana Gracia Villalobos[1,2],** María Guillermina Ruiz[2], Nora Gladys Montoya[2], Gabriela Noemí Williams[1]

(1) CESIMAR Center for the Study of Marine Systems (CESIMAR-CONICET), Boulevard Brown 2975, Puerto Madryn, Argentina
(2) National Institute of Fisheries Research and Development, Marine Chemistry and Red Tide Program, Paseo Victoria Ocampo 1, Mar del Plata, Argentina

The study of the distribution and abundance of harmful algal bloom (HAB)-forming species is highly relevant in Argentine Patagonia due to their negative effects on public health and bivalve mollusk fisheries. In this work, we studied the spatial distribution of harmful phytoplankton species and their associated toxins in Nuevo Gulf, in the coast of Puerto Madryn city. Sampling was carried out in coastal waters west of Nuevo Gulf at different depths (0, 15, and 30 m) during spring 2022. Phytoplankton community characterization was performed using optical microscopy and chemotaxonomy. The phytoplankton community was dominated by diatoms in the coastal zone (at 0 m) and by dinoflagellates in the zone furthest from the coast (at 15 and 30 m). *Alexandrium catenella* was the predominant species in all samples, with the highest concentrations observed at 15 and 30 m, being 5 x $10^4$ and 3.6 x $10^4$ cells $L^{-1}$, respectively. However, the highest levels of toxins per cell (527.16 fmol $cells^{-1}$), produced by this species were recorded at coastal zone. Densities of other toxigenic species were 8.8 x $10^3$ cells $L^{-1}$ for *Azadinium* spp., 4.5 x $10^2$ cells $L^{-1}$ for *Dinophysis acuminata*, and 2.5 x $10^3$ cells $L^{-1}$ for *Pseudo-nitzschia* spp. The high cell abundances and toxicity of *A. catenella* recorded were in spatiotemporal agreement with reported deaths of several Southern Right whales and other marine organisms in Nuevo Gulf. These results demonstrate that HAB events can vary considerably in intensity and duration, as well as their harmful effects on biota
.

**Keywords**: Harmful microalgae, *Alexandrium catenella*, Nuevo Gulf

**Financing**: PICT 2019-00454 & National Institute of Fisheries Research and Development

Poster Session 01: Ecology, Biology, and Biogeography
P-030

# Harmful microalgae (motile cells and cysts) and marine toxins on the Southern Chilean continental shelf between the Chacao Channel (41°S) and Cape Horn (56.2°S)

**Pablo Salgado[1],** Gemita Pizarro[1], César Alarcón[1], Roberto Raimapo[1], Carolina Toro[1], Marta Godoy[1], Claudia Zamora[1], Luis Norambuena[2], Gonzalo Fuenzalida[3], Carolina Zuñiga[1], Pamela Carbonell[2], Leonardo Guzmán[2]

(1) Centro de Estudios de Algas Nocivas (CREAN), Instituto de Fomento Pesquero (IFOP), Enrique Abello 0552, Punta Arenas, Chile
(2) Centro de Estudios de Algas Nocivas (CREAN), Instituto de Fomento Pesquero (IFOP), Padre Harter 574, Puerto Montt, Chile
(3) Facultad de Ciencias, Universidad Santo Tomás, Av. Ramón Picarte 1160, Valdivia, Chile

Harmful algal bloom (HAB)-producing microalgae were recently studied at 27 oceanic stations off Chilean Patagonia (Los Lagos, Aysén, and Magallanes regions) during the CIMAR-29 oceanographic survey. Phytoplankton from net trawl and Niskin bottle samples, respectively, and phytobenthos (dinoflagellate resting cysts) from surface sediment samples were analyzed qualitatively and quantitatively. Trawl phytoplankton from 12 stations were molecularly analyzed (qPCR) for harmful dinoflagellates; and size-fractionated plankton samples (20–100, 100–200, >200 µm) were screened for paralytic, amnesic, and lipophilic toxins by HPLC-Fl and HPLC-MS/MS. A total of 145 phytoplanktonic taxa were identified by light microscopy, including the toxin-producing dinoflagellates *Alexandrium catenella*, *Alexandrium ostenfeldii*, *Protoceratium reticulatum*, *Dinophysis acuta*, *Dinophysis acuminata*, and diatoms of the *Pseudo-nitzschia seriata* and *Pseudo*-nitzschia *delicatissima* groups. *Alexandrium* cf. *fragae* was identified for the first time in Chilean waters. Fifty-six cyst morphotypes were recorded in sediments, including *A. catenella, A. ostenfeldii,* and *P. reticulatum*, all with low densities and restricted geographical distributions. qPCR detected *A. catenella* at 9 stations (75%), A. ostenfeldii at 7 (58%), and *P. reticulatum* at all 12 stations (100%) analyzed. The paralytic toxins gonyautoxin (GTX)-2/3, N-sulfocarbamoilgonyautoxina-2 (C1), N-sulfocarbamoilgonyautoxina-3 (C2), the amnesic toxin domoic acid (DA), and the lipophilic toxins pectenotoxin (PTX)-2, gymnodinime (GYM)-A, and the spirolide 13-desmethyl-spirolide C (SPX1) were detected at several stations, at low concentrations, and mainly in the microphyto- and zooplanktonic fractions (<200 µm). No toxins were detected at only two stations. This study increases our knowledge of HAB species on the continental shelf off Chilean Patagonia.

**Keywords**: harmful microalgae, dinoflagellate resting cysts, marine toxins

**Financing**: National Oceanographic Committee (CONA) funded the CIMAR-29 cruise.

**Acknowledgments**: Thanks to CONA for funding the project, the Commander, Officers, and Crew of the AGS “Cabo de Hornos” of the Chilean Navy, and the SHOA staff.

Poster Session 01: Ecology, Biology, and Biogeography
P-031

# Spatial and temporal variability of dinoflagellate assemblages in relation to water quality parameters in Singapore waters

**Shereen S. P. Yim**[1]

(1) National University of Singapore, Tropical Marine Science Institute, S2S, 18 Kent Ridge Road, 119227, Singapore, Singapore

This research aimed to explore the spatial and temporal variability of phytoplankton communities and key water quality parameters that shape the environment of Singapore waters through a comprehensive monitoring. Water samplings were conducted monthly for five years (2020–2024). Strong spatial and temporal variability were observed among the water parameters and phytoplankton communities. Estuarine ecosystem is typically characterized by elevated nutrient concentrations and lower salinity, whereas coastal ecosystems exhibit comparatively lower nutrient levels and higher salinity. During the southwest monsoon, higher temperatures and phosphate concentrations were recorded across all sampling sites. In contrast, higher salinity levels were observed during the northeast monsoon period, indicating distinct seasonal influences. About 40 dinoflagellates were identified from the study area but only 12 targeted dominant genera will be discussed. *Protoperidinium* was the most dominant genus at all the sampling sites. Higher abundance of *Alexandrium, Cochlodinium, Dinophysis, Gymnodinium, Heterocapsa, Noctiluca, Scrippsiella* and *Tripos* were observed at East Singapore Strait (coastal). Prorocentrum was the highest at Southern Islands (coastal), whereas *Gyrodinium* was the highest at West Johor Strait (estuarine). Canonical correlation analysis (CCA) revealed that most dinoflagellate taxa exhibited positive correlations with salinity, but negative correlations with nitrate, nitrite and dissolved oxygen. In contrast, *Gyrodinium* showed a positive correlation with ammonia. These relationships were reflected in the phytoplankton distribution, with higher dinoflagellate concentrations observed in the coastal ecosystem compared to the estuarine environment. Although *Protoperidinium* showed the highest concentrations across all sites, the CCA indicated weak correlations between this genus and the measured water quality parameters.

**Keywords**: dinoflagellates, water quality, spatial and temporal variability

**Acknowledgments**: I wish to thank Coastal Marine Cluster (TMSI) for assisting with field work. This work was supported by Public Utilities Board to TMSI.

Poster Session 01: Microbiomes, Biological & Chemical Interactions
P-032

# Zooplankton community responses to harmful algal blooms induced by non-indigenous and indigenous dinoflagellates *Lingulodinium polyedra* and *Tripos furca*

**Mfundo Bizani**[1,2], Phumlile Cotiyane-Pondo[1,2], Thomas G. Bornman[1,2], Shaun H.P. Deyzel[1,2]

(1) South African Environmental Observation Network, Elwandle Coastal Node, Ocean Sciences Campus, Nelson Mandela University, 4 Gomery Avenue, Summerstrand, Gqeberha, South Africa
(2) Institute for Coastal and Marine Research, Nelson Mandela Metropolitan University, Ocean Sciences Campus, Nelson Mandela University, 4 Gomery Avenue, Summerstrand, Gqeberha, South Africa

Our understanding of zooplankton responses to HABs remains limited, particularly in ecosystems where they have been anthropogenically introduced. HABs rarely occur along southeast coast of South Africa, and are usually associated with non-toxin producing *Noctiluca scintillans*. However, in December 2013 the region experienced an extensive HAB, which persisted for months and affected > 500 km of coastline. This event was caused by a non-indigenous toxin-producing *Lingulodinium polyedra* and its impact on the coastal seas was widespread and severe, with instances of low dissolved O2 levels and fish kills being reported in the region. Recently a similar bloom (April 2025) caused by indigenous *Tripos furca* was recorded in the same region, although there were no records of severe fish kills during this recent bloom, the HAB persisted for weeks and reduced dissolved O2 levels in the water column. This study investigated the impact of the *L. polyedra* bloom on the mesozooplankton of Algoa Bay and reports successive changes in zooplankton composition during the bloom of *L. polyedra*, and compared it to that of the *T. furca*. Results show that the non-indigenous dinoflagellate had an impact on zooplankton community, with a shift in dominance from a large copepod dominated community to one dominated by microzooplankton. Whereas, the bloom of indigenous dinoflagellate did not impact the population of large calanoid copepods. The results of the study suggest that non-indigenous HAB had a negative impact on zooplankton communities compared to native species, with implications for the higher trophic levels of the coastal pelagic ecosystem.

**Keywords**: Microzooplankton, Upwelling, Tintinnids

**Financing**: The authors would like to thank the South African Environmental Observation Network and SMCRI for funding this study.

Poster Session 01: Microbiomes, Biological & Chemical Interactions
P-033

# Identification of potential luxR homologs related to the quorum-sensing system in *Microcystis aeruginosa*

**Ana Paula Blanco Ortiz**[1,2]

(1) Universidad Nacional Agraria La Molina, Facultad de Ciencias, Av. La Molina s/n - La Molina, Lima, Perú
(2) Instituto Peruano de Energía Nuclear, Laboratorio de Biología Molecular, Av. José Saco Km. 13 - Carabayllo, Lima, Perú

A less-studied causal factor for the occurrence of Cyanobacterial Harmful Algal Blooms (CyanoHABs) are the complex biological interactions mediated by Quorum-Sensing (QS), a cell-to-cell communication system based on the release of chemical signals, known to drive a range of physiological responses like cellular proliferation, biofilm formation and toxin synthesis in cyanobacteria. Thus, the study of the molecular mechanisms of QS has been proposed as a novel approach for the development of CyanoHAB prevention and mitigation strategies. The QS system is controlled by two gene families: luxI and luxR, coding for the signal molecule synthetase and its receptor protein respectively. In cyanobacterial genomes, luxR genes are significantly more numerous, disclosing their ability to recognize a wide variety of signal molecules, even produced by other bacteria. Therefore, the aim of this study was to identify potential luxR genes throughout the genome of *Microcystis aeruginosa*, the most global-wide reported CyanoHAB forming species. A pool of canonical LuxR proteins was selected from UniProt and aligned with an *M. aeruginosa* genome extracted from the NCBI database to identify potential luxR loci. The matches were then searched for ORFs and their translated sequences for conserved domains and functional motifs compatible with the LuxR family. Six potential luxR genes were identified in silico and a set of luxR specific primers were designed. Additionally, a microcystin-producing *Microcystis* strain was cultured on BG11 medium under laboratory conditions and confirmed by microscopic and molecular analyses. Finally, the luxR primers were tested by PCR amplification assays on the cultured strain's DNA.

**Keywords**: luxR, *Microcystis*, Quorum Sensing

**Financing**: This work was funded by the XVII Undergraduate Thesis Grant Competition of the Vice-Rectorate for Research at Universidad Nacional Agraria La Molina.

**Acknowledgments**: This research would not have been possible without the support of the Molecular Biology Laboratory at the Peruvian Institute of Nuclear Energy.

Poster Session 01: Microbiomes, Biological & Chemical Interactions
P-034

# Genomic signatures of HAB phytoplankton growth-promoting microbiome bacteria

**Christopher Bolch**[1], Andrew Bridle[1], David Green[3], Frederick De Boever[3], Shauna Murray[4], Shady Amin[5], Gustaaf Hallegraeff[1], Shikder S Islam[1,2]

(1) University of Tasmania, Institute for Marine and Antarctic Studies, Private Bag 129, Hobart, Australia
(2) Khulna University, Fisheries and Marine Resource Technology Discipline, Khulna, Bangladesh
(3) Scottish Association for Marine Science, Oban, Argyll, PA37 1QA, Scotland, United Kingdom
(4) University of Technology Sydney, School of Life Sciences, PO Box 123, Broadway, Sydney, Australia
(5) New York University, PO Box 129188, Saadiyat Island, Abu Dhabi, United Arab Emirates

Growth and health of HAB phytoplankton is reliant on, or enhanced by, unique microbiomes that inhabit the phycosphere, a narrow fluid layer around the algal “host” where DOC and microbial metabolites are exchanged. These microbiome bacteria (algal-associates) differ in functional and metabolic capacities from close relatives from other marine environments by production of growth promoters, growth inhibitors, vitamins and a wide range of cell-signalling molecules that can be crucial for maintaining phytoplankton growth. Using comparative genomics, we documented a range of metabolic pathways enriched in algal-associate genomes compared to related non-algal associate genomes. Enriched pathways included uptake of algal DOC (long chain fatty acids, amino acids, biopolymers), iron metabolism/transport (iron uptake, iron siderophore cross-membrane transport), several pathways linked to the management of oxidative stress (glutathione-S, taurine metabolism) and B-group vitamins (B12, B6), and extracellular transcription factors (ECF Sigma) associated with response to environmental stress. Enrichment of many of these pathways are evident across other genera of algal-associates, indicating they may be common adaptations to phycosphere micro-environments that, in-turn, support and enhance HAB phytoplankton growth in the ocean.

**Keywords**: microbiome, genomics, HABs

**Financing**: This work was supported by Australian Research Council Discovery Grants DP210102493 (CJB, GMH, DHG & SA), and DP18010001 (SAM & CJB).

**Acknowledgments**: The authors thank Arjun Verma (UTS) for DNA sequencing support, and Sam Murray (Cawthron) for dinoflagellate field collections.

Poster Session 01: Microbiomes, Biological & Chemical Interactions

P-035

# Do toxic dinoflagellates host distinctive bacteria in their phycospheres?

**Yunyan Deng**[1]

(1) CAS Key Laboratory of Marine Ecology and Environmental Sciences, Institute of Oceanology, Chinese Academy of Sciences, Qingdao, 266071, China

Dinoflagellates encompass highly abundant and diverse toxin-producing species among marine phytoplankton. Toxic dinoflagellate blooms draw great attention due to their widespread impacts on human health, aquaculture, fishery, and coastal ecosystems. Among all the documented dinoflagellate toxins, only a few have been fully identified, while many fish-killing toxins are still as-yet-unidentified. Previous works suggested that some bacterial taxa may affect the production of toxins in dinoflagellates to some extent, however the vast majority of the foregoing insights were derived from lineages with their toxins having been well-identified. Moreover, little is currently known about impact of dinoflagellate-derived toxins on the co-existing bacterial flora. These precedent investigations have exasperated the necessity for more comprehensive studies on the interactions between toxic dinoflagellates and bacteria. Here we characterized the bacterial communities associated with 22 clonal cultures of dinoflagellates using DNA metabarcoding method, including 11 confirmed toxic species and 11 species that have not been reported to be toxic. Beta diversity analysis revealed that all the 11 species in toxic group were clustered together and distinctly separated from non-toxic group, strongly suggesting the bacterial community composition was largely influenced by toxic dinoflagellate hosts. The toxic group was found to include higher relative abundance of non-carbohydrate utilizers and xenobiotic-degrading taxa and showed inhibitory effects on algicidal bacteria. These findings suggested that toxic dinoflagellates host bacterial communities distinctive from non-toxic species in multiple ways in their phycospheres.

**Keywords**: algicidal bacteria; oxidative stress resistance; toxic dinoflagellates;

**Financing**: The National Science Foundation of China (Grant No. 42176207).

**Acknowledgments**: We sincerely thank Dr. Fengting Li for her help with part of the experiments.

Poster Session 01: Microbiomes, Biological & Chemical Interactions
P-036

# Exploring the 16S rRNA- and 18S rRNA-based microbial communities in coastal seawater during harmful algal blooms along Chilean coasts

Jingming Hu[1], Yanrong Zhou[1], Joaquín Rilling[2], Marco Campos[2], Tay Ruiz-Gil[2], Cristobal González[2], Javiera Manquian[2], Karen Vergara[2], Mariela Gonzalez[3], Andrés Ávila[3], Leonardo Guzmán[4], Oscar Espinoza-González[4], Gonzalo Fuenzalida[4], Pamela Carbonell[4], Gonzalo Gajardo[5], Carlos Riquelme[6], Henry Camerón[6], Shoko Ueki[7], Satoshi Nagai[8], Fumito Maruyama[9], So Fujiyoshi[9], Kyoko Yarimizu[9], Ishara Uhanie Perera[9], Jacquelinne Acuña[2], Qian Zhang[1], **Milko Jorquera[2]**

(1) Xiamen University, College of the Environment and Ecology, Xiamen, China
(2) Universidad de La Frontera, Laboratorio de Ecología Microbiana Aplicada, Departamento de Ciencias Químicas y Recursos Naturales, Temuco, Chile
(3) Universidad de La Frontera, Departamento de Ingeniería Matemática, Centro de Modelación y Computación Científica, Temuco, Chile
(4) Instituto de Fomento Pesquero (IFOP), Centro de Estudios de Algas Nocivas (CREAN), Puerto Montt, Chile
(5) Universidad de Los Lagos, Laboratorio de Genética, Acuicultura & Biodiversidad, Departamento de Ciencias Biológicas y Biodiversidad, Osorno, Chile
(6) Universidad de Antofagasta, Centro de Bioinnovacion, Facultad de Ciencias del Mar y Recursos Biológicos, Antofagasta, Chile
(7) Okayama University, Institute of Plant Science and Resources, Okayama, Japan
(8) Japan Fisheries Research and Education Agency, Bioinformatics and Biosciences Division, Genome Structure Analysis Group, Yokohama, Japan
(9) Hiroshima University, The IDEC Institute, Hiroshima, Japan

Harmful algal blooms (HABs) are relevant for public health, the economy, the ecosystem and biodiversity along Chilean coasts, where they occur regularly. Currently, the HAB holobiont (HAB species and their microbiome) is recognized as a crucial player for HAB occurrence, with certain associated bacteria being potential predictors of algal bloom dynamics. By using DNA metabarcoding sequencing, we explored the composition of microbial communities in coastal seawater samples (1 and 0.2 µm fractions) from diverse HABs occurred in northern (Akashiwo sanguinea in 2019 and 2020) and southern (Heterosgima akashiwo in 2021 and Alexandrium catenella in 2022) Chile. During A. sanguinea (AS) bloom, associated bacterial diversity was greater before blooms than during AS blooms. Microbial communities before and during AS blooms were clearly differentiated. The bacterial community was dominated by Pseudomonadota and Bacteroidota during AS blooms, where positive relationships within microbial communities were revealed. Members of Pseudomonadota and Bacteroidota were also suggested as keystone taxa in AS blooms. During H. akashiwo (HA) and A. catenella (AC) blooms, differentiated microbial communities between both blooms were observed. Proteobacteria, Bacteroidota and Cyanobacteria were dominant bacterial taxa in both HA and AC blooms, and a differentiated interaction in microbial communities in both blooms was also observed. Blastopirellula and Dino-Group-I-Clade-1 were suggested as keystone taxa in AC bloom, but keystone taxa were not suggested in HA bloom. In general, our results showed a high and differentiated

## Poster Session 01: Microbiomes, Biological & Chemical Interactions

### P-036

interaction between 16S rRNA– and18S rRNA–based microbial communities in different stages and seawater fractions during HABs occurred along Chilean coasts.

**Keywords**: Bacterioplankton, DNA metabarcoding, Holobiont

**Financing**: SATREPS-Japan, code JPMJSA1705

Poster Session 01: Microbiomes, Biological & Chemical Interactions
P-037

# Functional shifts in aquatic plant-associated bacterial communities during *Microcystis* suppression

**Hayoung Lee**[1,2], Seonah Jeong[1], Chi-Yong Ahn[1,2]

(1) Korea Research Institute of Bioscience and Biotechnology (KRIBB), Cell Factory Research Center, 125, Gwahak-ro, Yuseong-gu, Daejeon, Republic of Korea
(2) Korea University of Science and Technology (UST), KRIBB School of Biotechnology, Department of Environmental Biotechnology, 217, Gajeong-ro, Yuseong-gu, Daejeon, Republic of Korea

Harmful algal blooms (HABs) caused by *Microcystis*, a genus of cyanobacteria, negatively affect aquatic ecosystem health due to the production of hepatotoxins known as microcystin. One biological approach to suppressing *Microcystis* involves the use of allelochemicals released by aquatic plants. Aquatic plants secrete allelochemicals that inhibit the growth of cyanobacteria, while also providing habitats for bacterial communities that either possess algicidal potential or interact closely with cyanobacteria. In this study, four aquatic plants (*Hydrilla verticillata, Myriophyllum spicatum, Najas marina,* and *Potamogeton maackianus*) were collected from an urban stream during summer, when both HABs and aquatic plant growth are most active, and co-cultivated with *Microcystis* for 7 days. The inhibition of *Microcystis* growth was monitored, and the bacterial communities were analyzed using 16S rRNA gene sequencing through NGS (Next-Generation Sequencing). Additionally, the predicted functions of bacterial communities significantly correlated with *Microcystis* were investigated using PICRUSt2. The predicted functions of the bacterial community changed in a common pattern during the suppression of *Microcystis*, regardless of plant species. Interestingly, although the composition of the bacterial community varied across aquatic plant species, the functional differences were similar. When *Microcystis* was co-cultured with the plants, functions related to competition and defense were predominant in the bacterial communities. After *Microcystis* was suppressed, various nutrient uptake pathways became more prominent, and the bacterial communities tended to return to the functional state typically observed in their original environment. These findings suggest that aquatic plant-associated bacterial communities may contribute to the suppression of *Microcystis* through compositional and functional shifts.

**Keywords**: Bacterial community, *Microcystis* inhibition, Predicted function

Poster Session 01: Microbiomes, Biological & Chemical Interactions
P-038 (Ignite Talk)

# Complex viral and bacterial interactions revealed for the harmful bloom forming dinoflagellate *Karenia brevis*

**Joaquín Martínez Martínez**[1], Anne E. Booker[1], Cong Fei[2], Shady Amin[2], Cynthia Heil[3], Patricia Glibert[1]

(1) University of Maryland Center for Environmental Science, Horn Point Laboratory, Cambridge, MD 21613, United States
(2) New York University Abu Dhabi, Abu Dhabi 129188, United Arab Emirates
(3) Mote Marine Laboratory and Aquarium, Sarasota, FL 34236, United States

Almost every year, *Karenia brevis* (Dinoflagellate) forms dense blooms along the west coast of Florida, producing lethal concentrations of neurotoxic brevetoxins. *K. brevis* blooms' devastating ecological and economic consequences make them a target of extensive research and monitoring efforts aimed at mitigating their impacts. There is no single known causative factor behind the initiation, maintenance, and termination phases of *K. brevis* blooms. Instead, it appears that the right combination of physical currents and nutrient supply contributes to their dynamics. Biological drivers of *K. brevis* dynamics, including mixotrophy and bacterial interactions (beneficial and detrimental), have also been investigated. Notably, despite well-documented examples of viral interactions contributing to the demise of phytoplankton blooms, data on viral infection of *K. brevis,* specifically, are scant. We designed an experiment where we incubated a *K. brevis* strain culture with size-fractionated seawater from a coastal bloom event to assess how environmental microbes (both bacteria and viruses) may influence bloom dynamics. We uncovered evidence of complex interactions between *K. brevis* and diverse bacterial and viral taxa, both with potential beneficial or algicidal effects on *K. brevis'* physiology. Further evidence suggests that environmental factors may tip the balance toward either beneficial or detrimental microbial players.

**Keywords**: *Karenia brevis*, Viruses, Bloom dynamics

**Financing**: This work was supported by the NOAA ECOHAB Program grant number NA19NOS4780183.

Poster Session 01: Microbiomes, Biological & Chemical Interactions
P-039

# Do extracellular vesicles play a role in the allelopathic interaction of saxitoxin-producing *Raphidiopsis raciborskii* with other phytoplankton?

**Cezar Nascimento**[1,2], Mauro Vilar[2], Paulo Bisch[1], Ana Beatriz Pacheco[1]

(1) Federal University of Rio de Janeiro, Laboratory of Biological Physics (LAFISBIO), Carlos Chagas Filho Institute of Biophysics, Health Sciences Center, Block G, Room G1-043 – Carlos Chagas Filho Avenue, 373 – University City, Rio de Janeiro, Brazil
(2) Federal University of Rio de Janeiro, Laboratory of Ecophysiology and Toxicology of Cyanobacteria, Carlos Chagas Filho Institute of Biophysics, Health Sciences Center, Block G, Room G0-057 – Carlos Chagas Filho Avenue, 373 – University City, Rio de Janeiro, Brazil

*Raphidiopsis raciborskii* is a filamentous, nitrogen-fixing cyanobacterium widely distributed in tropical and temperate regions. Toxin-producing strains from Latin America synthesize saxitoxins (STXs), neurotoxins that block voltage-gated ion channels. This cyanobacterium also exerts allelopathic effects on other phytoplankton via secretion of substances that impair target-cell physiology. Extracellular vesicles (EVs), secreted by both prokaryotes and eukaryotes, can transport bioactive molecules in a protected and targeted manner, but their role in cyanobacteria remains poorly understood. This study aimed to characterize EVs from two toxic Brazilian strains of *R. raciborskii* and assess their role in allelopathy. EVs were isolated and characterized by particle tracking analysis and transmission electron microscopy. STX content in extracellular fractions, with or without EVs, was quantified by ELISA, and cellular STX content by HPLC-RfD. Allelopathic effects were tested on the green alga *Monoraphidium capricornutum*, evaluating growth and photosynthesis after exposure to cyanobacterial exudates with or without EVs. *R. raciborskii* EVs ranged from 100–300 nm and contained STX (mean 0.5 ng $mm^{-3}$), though at much lower concentrations than cells (mean 20 ng $mm^{-3}$). The STX analogue profile also varied between EVs and cells. Exposure of M. capricornutum to purified, concentrated EVs had no effect. However, cyanobacterial exudates, regardless of EV presence, inhibited algal growth and photosynthesis. These findings suggest that EVs do not contribute to *R. raciborskii* allelopathy, opening new avenues for exploring other EV functions in toxic cyanobacteria.

**Keywords**: Cyanobacteria, Extracellular Vesicles, Toxin

**Financing**: This work was supported by CNPq and the Carlos Chagas Filho Foundation for Research Support of Rio de Janeiro State (FAPERJ).

Poster Session 01: Microbiomes, Biological & Chemical Interactions
P-040

# Assessment of the allelopathic potential of *Ulva* sp. and *Macrocystis pyrifera* against the toxic microalga *Alexandrium catenella*

**Yugreisy Polanco**[2,3], Alejandra Llanos-Rivera[1], Allisson Astuya-Villalón[1,2]

(1) Universidad de Concepción, Departamento de Oceanografía, Facultad de Ciencias Naturales y Oceanográficas, Concepción, Chile
(2) Universidad de Concepción, Laboratorio de Biotoxinas y Centro de Investigación Oceanográfica COPAS COASTAL, Concepción, Chile
(3) Universidad de Concepción, Doctorado en Ciencias con Mención en Manejo de Recursos Acuáticos Renovables, Facultad de Ciencias Naturales y Oceanográficas, Concepción, Chile

In this study, the allelopathic effect of fresh thalli of *Ulva* sp. and *Macrocystis pyrifera* on the bloom-forming microalga *Alexandrium catenella* was evaluated through co-culture experiments. Additionally, the effect of the filtered culture medium of Ulva sp. was assessed. The thalli were carefully washed and grown under aseptic conditions. Cell density, photosynthetic efficiency (Fv/Fm), pH, and nutrient concentration were measured in the culture of a Chilean strain of *A. catenella* over a six-day period. Both the fresh thallus and the filtered medium of Ulva sp. significantly inhibited the growth of A. *catenella*, with reductions in cell density of up to 93%, along with observable cell lysis. In comparison, the fresh thallus of *M. pyrifera* resulted in a lower growth inhibition, showing a 47.5% decrease from day three. In both cases, a dose-dependent effect was observed between macroalgal biomass and growth inhibition. The photosynthetic efficiency of *A. catenella* was more strongly affected by Ulva sp. than by *M. pyrifera*, decreasing from 0.6 to 0 at the highest concentrations. Although the culture pH increased as a function of macroalgal biomass, growth inhibition occurred even within pH ranges considered suitable for A. catenella. Nutrient concentrations declined over time but remained at levels insufficient to explain the observed effects. The results suggest that the growth inhibition of *A. catenella* could be associated with the production of species-specific allelopathic compounds by the macroalgae, while nutrient competition, pH variation, and bacterial activity were ruled out as determining factors.

**Keywords**: allelopathy, Growth inhibition, allelopathic compounds

**Financing**: The project is funded by the Toxins laboratory at University of Concepción and COPAS COASTAL.

Poster Session 01: Microbiomes, Biological & Chemical Interactions

P-041

# HALOBISE. Platform to understand the effects of the harmful algal bloom holobiont in a changing environment to predict their impact on aquatic ecosystem services

**Jesús Romalde**[1], Yolanda Pazos[2], Jean Armengaud[3], Aldo Barreiro[4], Susana Cristóbal[5]

(1) Cross-disciplinary Research Center in Environmental Technologies (CRETUS), Department of Microbiology and Parasitology, CIBUS-Faculty of Biology, Universidade de Santiago de Compostela, 15782, Santiago de Compostela, Spain
(2) INTECMAR, Xunta de Galicia, Instituto Tecnolóxico para o Control do Medio Mariño de Galicia, Peirao de Vilaxoán, 36600, Vilagarcía de Arousa, Spain
(3) CEA, Commissariat à l'Energie Atomique et aux Energies Alternatives, UMR0496 - DRF/Joliot/DMTS/SPI/Li2D, CEA Marcoule, D765 CEA Marcoule, D765, CEA Marcoule, D765 CEA Marcoule, D765. BP17171. 30200, Bagnols-sur-Cèze, France
(4) CIIMAR, Centro Interdisciplinar de Investigação Marinha e Ambiental, Blue Biotechnology and Ecotoxicology, Avenida General Norton de Matos Avenida General Norton de Matos 4450-208, Matosinhos, Portugal
(5) Linköping University, Medical Faculty, Floor 13, Medical Faculty, Linköping University Floor 13 SE-581 85, Linköping, Sweden

HALOBISE project will holistically study the Harmful Algal Bloom (HAB) holobiont, to understand the dynamics of the event and to enhance the management of their impact on Ecosystem Services. By understanding the interactions between algae and the surrounding microbiome, we can develop more accurate early warning systems for phycotoxin occurrence, preventing the harvesting of seafood from contaminated production areas and ensuring their compliance with health requirements. The incorporation of knowledge on the HAB holobiont and bioindicators into monitoring programs and dynamic modelling can provide a more comprehensive view of ecosystem diversity and productivity, helping to predict the ending of HABs and avoiding unnecessary closures and disruptions for producers. With objectives in mind, sampling and characterization of holobionts during the development of HAB related to lipophylic episodes in mussel production areas of Galician Rías, as well as sampling of harmful cyanobacteria blooms in transitional waters of Portugal will be analyzed. The associated microbiome and phageoma will be studied by metaproteomic and metagenomic approaches. In addition, laboratory experiments to analyze the effect of global change indicators on the holobiont (coastal and transitional waters) will be performed. All these results will be helpful not only to identify gaps and needs for the assessment of the HAB effects on ecosystem services, but also to develop a prototype platform-instrument for early warning and management of HABs. The engagement with stakeholders will be crucial to translate the results into usable knowledge.

**Keywords**: HABs-holobiont, Deep-metaproteomics, HABs-phageoma

**Financing**: Water4All 2023 Joint Transnational Call for transnational research projects on "Aquatic Ecosystem Services" (Water4All Partnership). Water4All2023-810. Xunta de Galicia.

Poster Session 01: Ciguatera and Benthic HABs
P-042 (Ignite Talk)

# First observation of *Ostreopsis fattorussoi* Accoroni, Romagnoli & Totti in benthic mucilage in the Eastern Mediterranean: A new risk for coastal ecosystems?

**Yelda Aktan**[1]

(1) İstanbul University, Faculty of Aquatic Sciences, Onaltı Mart Şehitleri Str. No:2, Vezneciler, Fatih, İstanbul, Türkiye

The Mediterranean ecosystem has been undergoing rapid changes in recent decades due to climatic and anthropogenic pressures, particularly in coastal areas. These pressures have intensified harmful algal events, including mucilage formation, benthic and planktonic blooms, and water discoloration events. In this study, we report the first observation of the toxic benthic dinoflagellate *Ostreopsis fattorussoi* in mucilage samples from the Eastern Mediterranean coast of Turkey. The species was identified within dense mucilage mats covering rocky substrates and seagrass beds. Given its toxin-producing potential and known ecological impacts, the presence of *O. fattorussoi* may represent an emerging threat to local marine ecosystems. This finding highlights the importance of enhanced monitoring efforts under ongoing climate-driven changes.

**Keywords**: Benthic mucilage, dinoflagellate, Eastern Mediterranean

**Financing**: This work is supported by the Scientific Research Projects Coordination Unit of Istanbul University (Project Number: FBA-2023-39521 and FBA-2023-39425).

**Acknowledgments**: The author thanks Dr. Cecilia Totti for her contributions to the identification of the species and her valuable insights.

Poster Session 01: Ciguatera and Benthic HABs
P-043

# Hotspots and hideouts: Comparative study of the annual cycle of *Ostreopsis* spp. blooms in NW Mediterranean and in El Hierro (Canary islands)

**Elisa Berdalet**[1], Rosa Trobajo[2], Emilio Soler-Onís[3], David Mann[2], Ted T. Packard[3], Magda Vila[1], Marta Estrada[1], May Gómez[3], Josep Lloret[1], Ico Martínez[3], Alba Garriga[2], Sofía I. Homedes[1], Sofía Huelbes[3], Adrian Kryk[2]

(1) Institut de Ciències del Mar (ICM, CSIC), Biologia Marina i Oceanografia, Passeig Marítim de la Barceloneta, 37-49, Barcelona, Catalonia, Spain
(2) IRTA, Marine and Continental Waters, 43540 La Ràpita, Catalonia, Spain
(3) University of Las Palmas de Gran Canaria, Grupo de Ecofisiología Marina (EOMAR), IU-ECOAQUA, Campus Universitario de Tafira, 35017 Las Palmas, Islas Canarias, Spain

The biogeographic expansion of the genus *Ostreopsis* in the 21st century raises questions about the environmental and ecological factors supporting its proliferation. To explore them, we conducted a comprehensive year-round study (starting in February 2024) in three contrasting environments: i) the hot spot of Sant Andreu de Llavaneres, in the NW Mediterranean Sea, where recurrent high biomass blooms occur; ii) La Restinga Harbour (semiconfined and anthropogenically affected harbor) and iii) the Charco Manso (a pristine, wave exposed rocky area), these last two being in the NE subtropical Atlantic Ocean Island of El Hierro.
In El Hierro Island, *Ostreopsis ovata, O. fattorussoi,* and *O. lenticularis* were nearly absent in the pristine site, with well-structured and highly diverse macroalgal communities that exhibited clear spatial organization and strong seasonality.
In contrast, *Ostreopsis* spp bloomed at intervals in La Restinga in June 2024 and from February to April 2025, with maximum concentrations of $3x10^6$ cell $gFW^{-1}$, within the same range attained in the NW Mediterranean site.
Unlike the summer-restricted blooms of *O. ovata* in the Mediterranean, no direct link with temperature was observed in La Restinga. In these two sites, *Ostreopsis* spp. were epiphytes of turf and disrupted macroalgal communities, dominated by a few opportunistic and ephemeral groups.
At microbial community level, we are analyzing the diatom species (by metabarcoding), cyanobacteria and bacteria potentially involved in biofilm formation, as well as the capacity of the whole microbenthos to act as a carbon source or sink by measuring the respiratory activity.

**Keywords**: *Ostreopsis*, bHABs, ecology

**Financing**: PID2022-138753OB-C21, PI E. Berdalet (ICM-CSIC); PID2022-138753OB-C22, PI R. Trobajo (IRTA); MICIU, Spain. Grant CEX2024-001494-S funded by AEI 10.13039/501100011033.

**Acknowledgments**: To the Reserva Marina La Restinga – Mar de Las Calmas, MAPA, the staff at GESTIÓN DEL MEDIO RURAL DE CANARIAS, Gobierno de Canarias.

Poster Session 01: Ciguatera and Benthic HABs
P-044

# *Ostreopsis* spp. and benthic diatom interactions in contrasting sites: NW Mediterranean and El Hierro (Canary Islands)

Rosa Trobajo[1], David G. Mann[1], Emilio Soler-Onis[2], Adrian Kryk[1], Alba Garriga[1], Sofía I. Homedes[3], Ico Martínez[2], Sofía Huelbes[2], May Gómez[2], Ted. T. Packard[2], Magda Vila[3], Marta Estrada[3], **Elisa Berdalet[3]**

(1) IRTA, Marine and Continental Waters, 43540 La Ràpita, Catalonia, Spain
(2) University of Las Palmas de Gran Canaria, Grupo de Ecofisiología Marina (EOMAR), IU-ECOAQUA, Campus Universitario de Tafira, 35017 Las Palmas, Islas Canarias, Spain
(3) Institut de Ciències del Mar (ICM, CSIC), Biologia Marina i Oceanografia, Passeig Marítim de la Barceloneta, 37-49, Barcelona, Catalonia, Spain

*Ostreopsis* becomes noticeable during blooms, when it can produce high levels of toxins and smother the benthos with polysaccharide. Considerable efforts have been made to identify the abiotic factors associated with blooms, to allow prediction of their occurrence. Locally, blooms are often associated with particular temperature regimes and hydrodynamics. However, the sea conditions associated with blooms are not consistent across the geographical range (e.g. Totti et al. 2010, Berdalet et al. 2017). Overall, abiotic factors may be better regarded as permissive 'scene-setters', allowing rapid growth of *Ostreopsis* if other undefined conditions are met. Biotic interactions may be important (e.g. Ternon et al. 2018). However, interactions with other microbenthos have been little studied, partly through lack of practical means of identification. In the ECOS project we take advantage of the new possibilities opened by DNA metabarcoding, combined with established microscopical methods, to determine the influence of microeukaryotes on the yearly cycle of *Ostreopsis* at three contrasting sites: one in the Mediterranean (Llavanares) and two in Canary Islands (El Hierro). Here we present results for the first annual cycle. In each site we have sampled the most abundant substrata (red and brown macroalgae and mixed turfs) at least monthly and characterized the microeukaryotic benthic community by microscopy (diatoms) and DNA metabarcoding using general (V4 18S rDNA) and targeted (rbcL) markers. Preliminary results show an extremely diverse community of photosynthetic microeukaryotes and an interesting, inverse relationship between blooms of *Ostreopsis* and the centric diatom *Actinocyclus*, but different *Actinocyclus* species in the two regions.

**Keywords**: *Ostreopsis*, diatoms, metabarcoding

**Financing**: PID2022-138753OB-C21, PI E. Berdalet (ICM-CSIC); PID2022-138753OB-C22, PI R. Trobajo (IRTA); MICIU, Spain. Grant CEX2024-001494-S funded by AEI 10.13039/501100011033.

**Acknowledgments**: To the Reserva Marina La Restinga – Mar de Las Calmas, MAPA, and the staff at GESTIÓN DEL MEDIO RURAL DE CANARIAS, Gobierno de Canarias.

Poster Session 01: Ciguatera and Benthic HABs
P-045

# Taxonomic and metabolomic diversity of benthic cyanobacterial mats on caribbean coral reefs

**David Berthold**[1], Sofia Iliakopoulou[2], Angelika-Ioanna Gialleli[2], Anastasia Hiskia[3], Triantafyllos Kaloudis[2,3], Petra Visser[4], H. Dail Laughinghouse IV[1]

(1) Fort Lauderdale Research and Education Center-IFAS, University of Florida, Davie, FL, United States of America
(2) Laboratory of Organic Micropollutants, Water Quality Control Department, EYDAP SA, Menidi, Athens, Greece
(3) Institute of Nanoscience and Nanotechnology, NCSR Demokritos, 15341 Ag. Paraskevi, Athens, Greece
(4) Institute for Biodiversity and Ecosystem Dynamics, Department of Freshwater and Marine Ecology, University of Amsterdam, Amsterdam, The Netherlands

Benthic cyanobacterial mats (BCMs) are integral to nutrient cycling and ecosystem functioning in tropical coral reefs, but their excessive proliferation, often linked to eutrophication and climate change, can drive reef degradation. This study examined BCMs from Curaçao and Bonaire using amplicon 16S rRNA barcoding, metagenomes, and untargeted metabolomics to characterize cyanobacterial diversity and their metabolite profiles. Taxonomic analysis using the Cyanoseq database revealed that *Dapis*, an unidentified Desertifilaceae genus, and *Okeania* were the dominant cyanobacterial genera across sites, similarly to Florida dominant taxa such as *Dapis* and *Okeania*, although with different species. Metabolomic profiling identified over 10,000 features, with 2,262 and 571 showing significant differences among taxa and locations, respectively. Notably, several bioactive and ecologically relevant metabolites were found to be taxa-specific: cytotoxic microcolins were abundant in *Okeania*-dominated mats, dolastatins in *Caldora* and *Symploca hydnoides*, and rivulariapeptolides in *Rivularia*. Additionally, known cyanotoxins such as microcystins, anatoxins, and lyngbyatoxins were detected, particularly in Dapis and Okeania, highlighting their potential to disrupt coral health and food webs. These findings emphasize the genetic and chemical diversity of marine cyanobacteria, their ecological significance, and the need for ongoing molecular and chemical monitoring of BCMs on coral reefs.

**Keywords**: Benthic proliferations, Marine cyanobacteria, bioactive compounds

Poster Session 01: Ciguatera and Benthic HABs
P-046

# Working together to address a global challenge: Towards a harmonized standard operating procedure for detecting ciguatoxins using the neuroblastoma cell-based assay

**Rosa María Ceinos**[1,2], Begoña Ben-Gigirey[1], Pablo Sosa[2], Jorge Diogène[3], Sandra Leonardo[3], Christopher Loeffler[4], Sophie Trotereau[5], Fernando Real[6], María José Ramos Sosa[6], Andrés Sanchez Henao[6], Jean Turquet[7], Mirjam Klijnstra[8], H. Taiana Darius[9], Lucía Soliño Alonso[1,2]

(1) Oceanographic Center of Vigo, Spanish Institute of Oceanography (IEO-CSIC), Subida a Radio Faro, 50, 36390, Vigo, Spain
(2) EU Reference Laboratory for Monitoring of Marine Biotoxins (EURLMB)-Spanish Agency for Food Safety and Nutrition (AESAN), CITEXVI, Campus Universitario de Vigo, 36310, Vigo, Spain
(3) Institute of Agrifood Research and Technology, Ctra Poble Nou km 5.5, 43540, Sant Carles de la Ràpita, Spain
(4) German Federal Institute for Risk Assessment (BfR), Department of Safety in the Food Chain, National Reference Laboratory for the Monitoring of Marine Biotoxins,, Max-Dohrn-Str. 8-10, 10589, Berlin, Germany
(5) French Agency for Food, Environmental and Occupational Health and Safety (ANSES), 14 rue Pierre et Marie Curie, 94701, Maisons-Alfort Cedex, France
(6) University Institute of Animal Health and Food Safety (IUSA), Group of Fish Health and for Aquaculture and Wild Species, University of Las Palmas de Gran Canaria,35416 Arucas, Las Palmas, Spain
(7) Technical, Research and Development Center for Aquatic Environments (CITEB/ CYROI), 2 Rue Maxime Rivière, 97490 Sainte Clotilde, La Réunion, France
(8) Wageningen University & Research, Wageningen Food Safety Research, Akkermaalsbos 2, 6708 WB, Wageningen, The Netherlands
(9) Institut Louis Malardé (ILM), Laboratory of Marine Biotoxins, UMR 241-SECOPOL (IFREMER, ILM, IRD,UPF) P.O. Box 30, 98713, Papeete, French Polynesia

Ciguatera poisoning (CP) is a food-borne disease, caused by the consumption of seafood containing ciguatoxins (CTXs). Herbivorous fish and marine invertebrates acquire the toxins while feeding, when ingesting toxigenic microalgae of the genera *Gambierdiscus* and *Fukuyoa*. CTXs may be bioaccumulated and biotransformed up to the food webs by predation or scavenging. Despite being endemic in tropical and subtropical areas, CP outbreaks have occurred outside these typical boundaries, due to imported fish and the spread of CTX-producing microalgae towards temperate regions. This new scenario poses a risk for consumers and food safety issues in CP non-endemic countries. In the European Union, Regulation 853/2004 states that fish containing CTXs must not be placed in the market but no regulatory limits, or specific procedures for the detection of CTXs are specified. Among methods available to detect CTX, the neuroblastoma-2a cell-based assay (CBA-N2a) has been widely employed, with laboratories applying their own protocols. Within this frame, the harmonization and validation of methods for CTX detection are urgently needed. To advance towards an agreed Standard Operating Procedure (SOP) for CTX detection using CBA-N2a, the European Reference Laboratory for Monitoring of Marine Biotoxins (EURLMB) created a working group of experts from nine research institutions worldwide in 2023. In the first stage the working group summarized the main steps of the CBA-N2a protocols used by the participating laboratories. Next steps will envisage establishing a step-by-step protocol followed by inter-laboratory comparisons for CBA validation in parallel with the harmonization of CTX extraction procedure in seafood.

## Poster Session 01: Ciguatera and Benthic HABs

### P-046

**Keywords**: ciguatera, neuroblastoma-2a cell-based assay, seafood safety

**Acknowledgments**: The EURLMB thanks F. Rodríguez for his coordination and participation at the initial stages of this Working Group.

Poster Session 01: Ciguatera and Benthic HABs
P-047

# Presence, diversity, and toxicological characterization of benthic dinoflagellates *Gambierdiscus* spp. in the Mediterranean Sea

**Joan Josep Cervera-Piñana**[1], Lourdes Barreiro-Crespo[1], Andrés Sánchez-Henao[1,2], María García-Altares[1], Sandra Gimeno-Monforte[1], Jaume Reverté[1], Mònica Campàs[1], Francisco Rodríguez[3], Maria García-Portela[3], Rosa Trobajo[1], David G. Mann[1], Cintia Flores[4], Maria Rey[1], Karl Andree[1], Jorge Diogène[1], Maria Rambla-Alegre[1]

(1) Institute of Agri-Food Research and Technology (IRTA), Marine and Continental Waters, Carretera del Poble Nou, km 5,5, La Ràpita, Spain
(2) University Institute of Animal Health and Food Safety (IUSA), Ctra. Transmontaña S/N, Arucas, Spain
(3) Spanish Oceanographic Institute (IEO-CSIC), Subida a Radio Faro, 50-52. Cabo Estai, Vigo, Spain
(4) Institute of Environmental Assessment and Water Research (IDAEA-CSIC), C. Jordi Girona 18-26, Barcelona, Spain

Dinoflagellates of the genera *Gambierdiscus* and *Fukuyoa* produce toxins such as ciguatoxins and maitotoxins, which are linked to ciguatera poisoning (CP). However, their diversity and toxicity remain poorly characterized in recently colonized areas, particularly in the Balearic Islands (BI) and nearby islands along the Mediterranean coast of Spain. The first detections of *Fukuyoa* spp. and *Gambierdiscus* spp. in the BI date back to 2010 and 2016, respectively (Tudó et al., 2020).
As part of the CIGUAADAPT project, a sampling campaign was conducted across eight locations along the Mediterranean coast of Spain (Illes Formigues, Maça d'Oros, Illes Mesines, Illes Medes, Columbretes, Tabarca, Isla Grosa, and Islas Hormigas) to assess the presence of *Gambierdiscus* spp.
In this study, nineteen *G. australes*, two *F. paulensis*, and five *G. carolinianus* strains were isolated from four different islands in the Balearic archipelago (Spain), along with four *G. australes* strains from Columbretes (Castelló, Spain). These strains were obtained during various sampling campaigns by capillary isolation and cultivated in ES media. Species identification was confirmed through molecular biology techniques. Biomass from these strains was then produced for toxicity screening using a Neuro-2a cell-based assay and for toxin profile identification via a combination of low- and high-resolution mass spectrometry.
This study represents the first isolation and characterization of *G. carolinianus* in the BI and the first evidence of G. australes presence in peripheral islands along the east coast of Spain. Our findings highlight the need for continued monitoring and risk assessment as these toxic species expand into new habitats.

**Keywords**: *Gamberidiscus*, ciguatera risk assessment, toxicological characterization.

**Financing**: This work was funded by the Ministerio de Ciencia e Innovación (MICIN) and the Agencia Estatal de Investigación (AEI) (Spain) through the CIGUAADAPT (PID2022-137174OR-C21) project.

**Acknowledgments**: Joan Josep Cervera-Piñana acknowledges PRE2022-000401. Authors acknowledge Fishery departments from Catalonia, Balearic Islands, Generalitat Valencia, Murcia and Ministry of Agriculture, Fisheries and Food.

Poster Session 01: Ciguatera and Benthic HABs
P-048

# Toxicological profile of *Gambierdiscus* strains from different species and origins

Maria Rambla-Alegre[1], **Joan Josep Cervera-Piñana[1],** Sandra Gimeno-Monforte[1], Francisco Rodríguez[2], Isabel Ramilio[2], Andrés Sánchez-Henao[1,3], Jorge Diogène[1], Begoña Ben-Gigirey[2]

(1) Institute of Agri-Food Research and Technology (IRTA), Marine and Continental Waters, Carretera del Poble Nou, km 5,5, La Ràpita, Spain
(2) Spanish Oceanographic Institute (IEO-CESIC), Subida a Radio Faro, 50-52. Cabo Estai, Vigo, Spain
(3) University Institute of Animal Health and Food Safety (IUSA), Ctra. Transmontaña S/N, Arucas, Spain

*Gambierdiscus* spp. are marine benthic dinoglagellates that can produce cyclic polyether neurotoxins such as ciguatoxins (CTXs), maitotoxins (MTXs), gambierones, gambieric acids, gambierol and gambieroxide. These toxins are widely studied in relation to their potential involvement on ciguatera poisoning (CP).
The aim of this study was to conduct a preliminary characterisation of MTXs, gambierones, gambieric acids and CTXs in 13 *Gambierdiscus* strains from the Canary Islands (Spain), Cuba, and Indonesia. These comprised strains from the species: *G. excentricus, G. australes, G. carolineanus, G. balechi* and *G. silvae* isolated from macrophyte samples.
Cultures were grown in K/2 medium at 25 °C and approximately 75 µmol photons m-2 s-1 until abundances of 0.33-1.2×106 cells·L-1 were reached. Cell pellets were resuspended in LC-MS grade MEOH and broken with a Biospec products bead beater. Toxins were analyzed by LC-MS/MS using a XevoTM TQ-XS mass spectrometer coupled to an Acquity UPLC I-plus-Class, (Waters Corporation). LC separation was performed with a Waters BEH phenyl column (2.1 x 50mm, 1.7 µm) using alkaline conditions. Standards used were 44-methylgambierone and gambierone (Cifga), CTX1B, CTX3C/B and CTX4A (Phyconesia Pacific Natural Active Compounds) and MTX1 (FUJIFILM Wako Pure Chemical Corporation).
Mainly, 44-methylgambierone and gambierone were quantified in strains from different genera. MTX5 and gambieric acids C and D were tentatively identified in *G. australes* strains. MTX4, sulfo-gambierone and dihydrosulfo-gambierone were tentatively identified in *G. excentricus* strains. CTX1B, CTX3C/B, CTX4A, and C-CTX1 were not detected in any of the analyzed strains. Additional HRMS studies would be needed to confirm our findings.

**Keywords**: *Gambierdiscus*, ciguatoxin-like compounds, maitotoxins

**Financing**: This work was funded by the Ministerio de Ciencia e Innovación (MICIN) and the Agencia Estatal de Investigación (AEI) (Spain) through the CIGUAADAPT (PID2022-137174OR-C21) project.

**Acknowledgments**: Joan Josep Cervera acknowledges MICIN and AEI for the phD funding PRE2022-000401. The authors also acknowledge CERCA/Generalitat de Catalunya program.

Poster Session 01: Ciguatera and Benthic HABs
P-049

# Diversity, toxicity and toxin profile of *Gambierdiscus* in Cuba

**Lisbet Díaz Asencio**[1], Joan Josep Cervera-Piñana[2], María Rey[2], Sandra Leonardo[2], Gabriel L. Rojas-Abrahantes[1,3], Donaida Chamero-Lago[1], Karl B. Andree[4], María Rambla-Alegre[2], María García-Altares[2], Jorge Diogène[2], Mònica Campàs[2]

(1) Environmental Studies Center of Cienfuegos (CEAC), Ciudad Nuclear, Cienfuegos, Cuba
(2) Institute of Agrifood Research and Technology (IRTA), Marine and Continental Waters Program, 43540 La Ràpita, Catalonia, Spain
(3) Centro de Investigación Científica y de Educación Superior de Ensenada, Baja California, México
(4) Institute of Agrifood Research and Technology (IRTA), Aquaculture Program, 43540 La Ràpita, Catalonia, Spain

In Cuba, ciguatera is the most significant non-bacterial seafood-borne illness, both in frequency and public health impact. Aiming to contribute to ciguatera risk assessment, this study explored the diversity, toxicity and toxin profile of *Gambierdicus* species by culturing monoclonal strains from macroalgae samples gathered at several Cuban coastal locations. 152 cultures were successfully established and 32 have been identified so far by sequencing the D1-D3 region of the 28S ribosomal large subunit gene and confirming identification by phylogenetic analysis. The toxicity of the extracts was assessed by Neuro-2a cell based-assay, and the toxin profile was analyzed by liquid chromatography coupled to tandem mass spectrometry (LC-MS/MS) and LC-High Resolution MS. *Gambierdiscus caribaeus* was the most frequent species (25 strains), followed by *G. carpenteri* (6) and *G. belizeanus* (1). Phylogenetic analyses showed no significant differences among G. caribaeus and G. carpenteri strains collected from different locations. No clear evidence of ciguatoxin-like toxicity was observed. Nevertheless, some of the *Gambierdiscus* extracts were toxic to the Neuro-2a cells. No ciguatoxin was confirmed in any of the strains tested by instrumental analysis methods. Most strains were confirmed to produce gambierone and maitotoxin-3. Some strains of *G. caribaeus* and *G. carpenteri* may produce unknown polyether or polyol compounds with molecular weights similar to ciguatoxins, according to HRMS data-dependent experiments that are currently under investigation. This study presents the first preliminary findings on the diversity, toxicity, and toxin profiles of *Gambierdiscus* species in Cuba, contributing to the broader understanding of these harmful algae in the Caribbean region.

**Keywords**: Molecular ID, Toxin production, dinoflagellates

**Financing**: European Project BLUESHELLFISH: Solutions to prevent and mitigate the impacts of HABs in Aquaculture and Fisheries, in the context of global warming (HORIZON-MSCA-101086234).

Poster Session 01: Ciguatera and Benthic HABs
P-050

# Integrated monitoring of toxic benthic dinoflagellates on the Spanish Levantine coast

Olga Carnicer[1], María García Altares[2], Chiara Incani[2], María Rambla Alegre[2], Joan Josep Cervera Piñana[2], Bartolomé Morote Sánchez[1], Javier Gilabert Cervera[1], Jose Manuel Moreno Angosto[1], **Jorge Diogène Fadini[2]**, Margarita Fernández Tejedor[2]

(1) Universidad Politécnica de Cartagena (UPCT), Department of Chemical and Environmental Engineering, Naval and Ocean Engineering, Cartagena, Spain
(2) Institute of Agrifood Research and Technology (IRTA), Marine and Continental Waters, Carretera del Poblenou km 5,5, la Ràpita, Spain

The proliferation of benthic harmful algal blooms (BHABs) in temperate coastal waters has become an increasing concern due to their ecological and public health impacts. In this study, we investigated the occurrence and seasonal dynamics of potentially toxic benthic dinoflagellates associated with macroalgal substrates, from the genera Jania and Corallina, at 15 Mediterranean beaches in southeastern Spain. Monthly sampling campaigns (2024-2025) were conducted to quantify dinoflagellate species abundance and characterize toxin production. *Ostreopsis* spp. were detected at all sites, with a seasonal presence from May to January and peak abundance reaching 7.1 × $10^6$ cells·$g^{-1}$ fresh weight of macroalgae (fw) in October. *Gambierdiscus* spp. were found at four beaches, with maximum abundance of 38 cells·$g^{-1}$ fw in October and November 2024. Field samples and laboratory-cultured strains were analyzed by liquid chromatography-tandem mass spectrometry (LC-MS/MS) and high-resolution mass spectrometry (HRMS) to detect and quantify toxin content. *Ostreopsis* cf. *ovata* produced approximately 1 pg. cell of ovatoxins (a–e, g). Additionally, three *Coolia* and two *Fukuyoa* strains revealed the presence of gambierone and other possible CTX-compounds that are being evaluated. These findings expand the known toxic potential of benthic dinoflagellate assemblages in the Mediterranean. The detection of diverse toxins from multiple genera underlines the importance of integrative monitoring approaches, combining cell counts with toxin profiling, to better assess BHABs-related risks to human and ecosystem health.

**Keywords**: *Gambierdiscus*, *Ostreopsis*, *Coolia*

**Financing**: The project LEVABENTOX is co-financed by the European Union through the European Maritime, Fisheries and Aquaculture Fund.

**Acknowledgments**: This project is developed with the collaboration of the Biodiversity Foundation of the Ministry for Ecological Transition and the Demographic Challenge, through the Pleamar Programme.

Poster Session 01: Ciguatera and Benthic HABs
P-051

# PACIFIC CIGUAWATCH: A regional initiative to improve Ciguatera surveillance and mitigation in the South Pacific

**Clémence Gatti Howell**[1], Hélène Taiana Darius[1], Mireille Chinain[1]

(1) Institut Louis Malardé (ILM), Laboratory of Marine Biotoxins, UMR 241-SECOPOL (IFREMER, ILM, IRD, UPF), P.O. Box 30, 98713 Papeete, Tahiti, French Polynesia

Ciguatera poisoning (CP), caused by the consumption of marine organisms contaminated with ciguatoxins produced by Gambierdiscus spp., remains significantly underreported and poorly understood across many Pacific Island Countries and Territories (PICTs). Despite its considerable health, economic, and cultural impacts, many PICTs currently lack baseline data on CP and need assistance on how to initiate/improve effective surveillance and risk management strategies locally. Building on its longstanding involvement in CP research, the Louis Malardé Institute (ILM) in French Polynesia has developed the Pacific CIGUAWATCH initiative, with the goal of strengthening regional monitoring capabilities in PICTs through remote and on-site trainings in order to standardize data collection methodologies pertaining to the environmental and epidemiological surveillance of CP. Developing tailored surveillance strategies and awareness raising materials, as well as sharing traditional knowledge on CP are also other topics addressed in the frame of this Initiative. This poster highlights the tools available on the open-access digital platform (ciguawatch.ilm.pf), e.g. video tutorials, technical protocols, educational supports, standardized CP case reporting forms, and access to dynamic CP risk maps and CP statistics. By supporting the implementation/reinforcement of CP monitoring and response strategies tailored to each PICT, this initiative aims to promote regional coordination and easier comparison of datasets across the Pacific region. The Pacific CIGUAWATCH initiative represents a scalable and collaborative model for CP risk surveillance and management, with the potential for adaptation in other CP endemic regions.

**Keywords**: Ciguatera surveillance, Pacific Ciguawatch Initiative, PICTs

**Financing**: Délégation à la Recherche de Polynésie françaiseFonds Pacifique - Secrétariat permanent pour le Pacifique (SPP) du Ministère de l'Europe et des affaires étrangères, France.

Poster Session 01: Ciguatera and Benthic HABs
P-052 (Ignite Talk)

# The influence of abiotic and biotic factors on the succession of *Ostreopsis* spp. along the Basque coast (South-East Bay of Biscay)

**Yago Laurenns-Balparda[1,2],** Pablo Aramendi[1], Jone Bilbao[1,2], Alan Denis Fernández-Valero[1], Laia Moreno-Martínez[1], Marina Salido[1,2], Estibalitz Txurruka[1], Sergio Seoane[1,2]

(1) University of the Basque Country (UPV/EHU), Plant Biology and Ecology, Science and Technology, Leioa, Spain
(2) Plentzia Marine Station (PiE - UPV/EHU), Research Centre for Experimental Marine Biology and Biotechnology, Plentzia, Spain

Projections indicate that climate change will lead to an escalation of the geographic ranges, frequency and intensity of benthic HABs in mid-latitude regions. In this sense, *Ostreopsis* is a genus of benthic dinoflagellates that has been associated with toxic outbreaks from mid to late summer in temperate coastal areas, including the Bay of Biscay, where it has become a prevalent and abundant genus during the warmer months. The co-occurrence of both *Ostreopsis* cf. *siamensis* – recently termed *Ostreopsis* sp. 9 – and *Ostreopsis* cf. *ovata* has been confirmed in the south-eastern Bay of Biscay, with the latter linked to multiple health issues reported in the area since 2020.
Consequently, a monitoring programme was developed to analyze the factors that determine the succession of *Ostreopsis* spp. in the south-eastern coast of the Bay of Biscay over three annual cycles. The sampling was conducted at five sites on a monthly basis, with an increase in frequency during summer. The study encompassed the characterization of environmental variables, the microscopic analysis of epiphytic and planktonic samples and molecular analyses.
The epiphytic and planktonic abundances of *Ostreopsis* were minimal or null from November to May and maximal from July to October, particularly in San Sebastian, with maxima of $1.86 \times 10^6$ cells/g and $1.33 \times 10^5$ cells/L. The molecular analyses demonstrated that the eukaryotic groups with the highest relative abundances were Dinoflagellata, Gyrista, Chlorophyta and Apicomplexa, with *Ostreopsis* and, especially, *O.* cf. *ovata*, being the most prevalent photosynthetic organisms during the warmer months in San Sebastian.

**Keywords**: *Ostreopsis* cf. *ovata*, *Ostreopsis* sp. 9 (*Ostreopsis* cf. *siamensis*), Metabarcoding

**Financing**: Basque Government; Ostreobila project funded by the European Union; Provincial Council of Gipuzkoa; Town hall of San Sebastian; Basque Water Agency (URA)

**Acknowledgments**: We thank all the BMCC team for their help during the study.

Poster Session 01: Ciguatera and Benthic HABs
P-053

# Identifying the cause of acute mortality in naïve *Mytilus* sp. from Great Britain, experimentally exposed to the potentially future invasive microalgal species, *Ostreopsis* cf. *ovata*

**Adam Lewis**[1], Ben Maskrey[1], Ryan Alexander[1], Andrew Turner[1], Matthew Green[1], John Bignell[1], Antonella Penna[2], Carmela Dell'Aversano[3,4], Valentina Miele[3], Luciana Tartaglione[3], Michela Varra[3], Silvia Casabianca[2], Samuela Capellacci[2], Chiara Melchiorre[3,4], Linda Percy[5], Jane Lewis[6]

(1) Centre for Environment Fisheries and Aquaculture Science, Barrack Road, Weymouth, United Kingdom
(2) University of Urbino, Department of Biomolecular Sciences, Campus E. Mattei, Via Ca le Suore 2/4, 61029 Urbino (PU), Italy
(3) Università degli Studi di Napoli Federico II, Scuola di Medicina e Chirurgia - Dipartimento di Farmacia, Via D. Montesano 49, 80131, Napoli, Italy
(4) NBFC, National Biodiversity Future Center, Palermo, Italy
(5) University of Westminster, School of Life Sciences, 115 New Cavendish Street, London, United Kingdom.
(6) UHI Shetland, Gremista, Lerwick, Shetland, United Kingdom.

The harmful microalgal species *Ostreopsis* cf. *ovata*, produces effects at multiple trophic levels. The distribution of this species appears to be extending, with detections being recently made in Northern France. An assessment of harmful microalgal species non-native to Great Britain suggested a high possibility of the *Ostreopsis* genus appearing in GB waters under future climate scenarios.
A pre-emptive laboratory study assessed the potential future impacts on GB shellfish from an emergence of *O.* cf. *ovata* in GB waters. GB mussels were exposed under controlled conditions to two strains of *O.* cf. *ovata*, one producing palytoxin analogues and one not. Rapid mortality of mussels was observed in the presence of the palytoxin producing strain.
Exposed mussels were cross-sectioned and placed into cassettes in Davidsons Sea water fixative. Samples were processed to wax block and sectioned at 3µm, and H+E stained. Sections underwent histological assessment, with tissues being graded and scored based upon markers and degradation. Microscopic examination revealed that in some Mussels the gill tissue had started to disintegrate. The worst affected animals were all in the high dose group exposed to the palytoxin producing strain of *O.* cf. *ovata* and were characterized by the more fragile and sensitive gill tissues, becoming damaged, with fine gill structures becoming dissociated from their main architecture. A scoring system was devised to grade the severity of the effects and this correlated with the data.
The study suggests an emergence of *O.* cf. *ovata* could have negative impacts on the survival of GB shellfish.

**Keywords**: climate change, invasive species, ecological damage

**Financing**: Funding was provided by Cefas SeedCorn.

Poster Session 01: Ciguatera and Benthic HABs
P-054

# Changes in benthic dinoflagellates abundance and species composition associated with organic pollution in an oceanic island of the Atlantic Ocean

Geovanna Borsato[1], Alexandra Grigoriyan[1], Raquel Neves[1], Joel DePaula[1], Nilva Brandini[2], **Silvia Nascimento[1]**

(1) Universidade Federal do Estado do Rio de Janeiro, Av Pasteur, 458, Rio de Janeiro, Brasil
(2) Universidade Federal Fluminense, Niterói, Brasil

Nutrient enrichment in coastal areas due to human activities is a threat to biodiversity and may significantly increase harmful algal blooms, that may compromise human health. The Fernando de Noronha Archipelago, in Brazil, comprises two Marine Protected Areas: the National Marine Park (NMP), a no-take zone, and an Environmental Protection Area (EPA), that includes an urban area with 5.000 inhabitants and an estimated tourist flux of 115.000-130.000 persons per year. Benthic dinoflagellates species composition and abundance associated to macroalgal substrates were studied in October 2023 at six sites at the NMP and six at the EPA. Nutrient analyses were conducted in seawater samples. EPA sites were characterized by higher nutrient (DIP, DOP, $NH_4$, $NO_3$, and DON) concentrations compared to those at the NMP. *Ostreopsis* was abundant ($1.4x10^3$ to $2.4x10^5$ cells.$g^{-1}$FWmacroalgae) and represented 84-97% of the total dinoflagellate abundance at five of the six EPA sites. *Ostreopsis* abundance reduced significantly with increasing distance from the sites close to sewage disposal and was lower ($7.0x10^2$ to $9.5x10^3$ cells.$g^{-1}$FWmacroalgae) at the NMP sites, where *Prorocentrum* was the most abundant genus ($1.8x10^3$ to $8.9x10^3$ cells.$g^{-1}$FWmacroalgae). At the NMP, *Ostreopsis* contributed 10-37%, while *Prorocentrum* represented 41-63% of the total dinoflagellate abundance. Species richness at the NMP was 19-27 species, while at the EPA it was 7-10 at five of the six sites. Human activities at the EPA are causing loss of benthic dinoflagellates richness, and are leading to Ostreopsis blooms, particularly of the toxic *O.* cf. *ovata*.

**Keywords**: Benthic harmful algal blooms, *Ostreopsis*, *Prorocentrum*

**Financing**: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) for the financial support to the project PELDILOC to C.E.L. Ferreira (441241/2016-6).

Poster Session 01: Ciguatera and Benthic HABs
P-055

# New molecular and morphological data of *Ostreopsis* species from Brazil

Rodrigo Silvia[1], Fabiano Salgueiro[1], **Silvia Nascimento[1]**

(1) Universidade Federal do Estado do Rio de Janeiro, Rio de Janeiro, Brasil

*Ostreopsis* cf. *ovata* is widely distributed along the Brazilian coast, while *Ostreopsis lenticularis* distribution is restricted to the Fernando de Noronha archipelago. In this study, new *O. cf. ovata* and *O. lenticularis* molecular and morphological data from coastal and oceanic sites located at latitudes between 3°S and 23°S will be presented. *Ostreopsis* strains were isolated from two coastal locations, Natal (5°57'52.4"S) and Arraial do Cabo (22°57'58.0"S, AC), and three oceanic islands, Fernando de Noronha (3°51'25.2"S, FN), Atol das Rocas (3°51'16.4"S, AR), and Trindade (20°30'29.8"S, TR). *Ostreopsis* strains were cultured in F/4 medium, 24°C, 60 µmol $m^{-2}$ $s^{-1}$ photon flux densityand 12h:12h L:D cycles. Cell morphology was observed under light and fluorescence microscopy. Molecular characterization was performed using PCR amplification of the ITS and LSU (D1-D3 and D8-D10) region of the rDNA, followed by sequencing of positive amplicons. Morphological analyses of these *O. cf. ovata* strains revealed variability in cell size and shape, and the shape of the 4'-3' plate suture among cells of the same strain. A total of 18 new ITS sequences were obtained, 14 from *O. cf. ovata* (Natal, FN, TR) and 4 from *O. lenticularis* (FN). Regarding LSU, 24 new D1-D3 sequences from *O. cf. ovata* (Natal, FN, AR, TR) and 2 from *O. lenticularis* (FN) were retrieved, as well as 14 LSU D8-D10 sequences from *O. cf. ovata* (AC, FN, AR). Substantial genetic diversity was observed within *O. cf. ovata* in Brazil, including the presence of multiple subclades within this species complex.

**Keywords**: taxonomy, genetic, species complex

**Financing**: Fundação de Amparo à Pesquisa do Estado do Rio de Janeiro (FAPERJ) and Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq).

Poster Session 01: Ciguatera and Benthic HABs
P-056

# Benthic dinoflagellates from the oceanic Trindade island, South Atlantic Ocean

Giovanna Argollo[1], Geovanna Borsato[1], Joel De Paula[1], Carlos Ferreira[2], **Silvia Nascimento[1]**

(1) Universidade Federal do Estado do Rio de Janeiro, Rio de Janeiro, Brasil
(2) Universidade Federal Fluminense, Niteroi, Brasil

Oceanic islands harbor high marine biodiversity, including various groups of potentially toxic microalgae. To date, few studies have assessed the diversity of benthic dinoflagellates from the South Atlantic Ocean, particularly in insular environments. Benthic dinoflagellate species associated to macroalgae (*Dictyota* spp., *Dictyopteris* spp. and *Canistrocarpus* spp.) were analyzed in samples collected from three sites at Trindade Island in September 2023 (depths 5-7 m) and July 2024 (depths 6-18 m). Species of *Amphidinium, Coolia, Gambierdiscus, Ostreopsis, Plagiodinium, Prorocentrum* and *Sinophysis* were found. Total benthic dinoflagellates abundance varied between $4.7x10^2$ to $2.1x10^3$ cells·g$^{-1}$FW in 2024 and $4.7x10^3$ to $1.9x10^4$ cells·g$^{-1}$FW in 2023 (mean values). *Prorocentrum* abundances reached $1.2x10^4$ cells·g$^{-1}$FW in 2023 and did not surpass $1.2x10^3$ cells·g$^{-1}$FW in 2024. The species *Prorocentrum arenarium, P. borbonicum, P. emarginatum/P. fukuyoi/P. sculptile complex, P. hoffmannianum, P. lima, P. rhathymum* were observed. *Ostreopsis cf. ovata* maximum abundance was $5.2x10^3$ cells·g$^{-1}$FW in 2023 and abundances lower than $1x10^3$ cells·g$^{-1}$FW were found in 2024. *Coolia* abundances ranged between $1x10^3$ to $5.3x10^3$ cells·g$^{-1}$FW in 2023 and were lower than $3x10^2$ cells·g$^{-1}$FW in 2024. *Gambierdiscus* abundances did not reach $1x10^2$ cells·g$^{-1}$FW in both years. *Sinophysis canaliculata* and *S. microcephala* were found in low numbers (< $1x10^2$ cells·g$^{-1}$FW). Overall, *Ostreopsis*, *Prorocentrum* and *Coolia* contributed most to benthic dinoflagellates abundance at Trindade island.

**Keywords**: Benthic harmful algal blooms, abundance, assemblage

**Financing**: Conselho Nacional de Desenvolvimento Científico e Tecnológico (CNPq) for the financial support to the project PELD-ILOC to C.E.L. Ferreira (441241/2016-6).

Poster Session 01: Ciguatera and Benthic HABs
P-057

# Distinct ciguatoxin profiles in fish involved in poisoning events from the Indian Ocean

Joan Josep Cervera-Piñana[1], **Jaume Reverté[1]**, Mònica Campàs[1], Maria García-Altares[1], Sandra Gimeno[1], Jorge Diogène[1], Fanny Maillot[2], Jean Turquet[2], Leon Biscornet[3], Maria Rambla-Alegre[1]

(1) IRTA, Marine and Continental Waters (AMiC), 43540 La Ràpita, Spain
(2) Centre Technique de Recherche et de Valorisation des Milieux Aquatiques (CITEB), C/o CYROI, 2 Rue Maxime Rivière, 97490 Sainte Clotilde, La Réunion
(3) Seychelles Public Health Laboratory, Public Health Authority, Ministry of Health, PO Box 52, Seychelles

Ciguatoxins (CTXs) are highly toxic, lipophilic, cyclic polyethers primarily produced by marine microalgae of the genera Gambierdiscus and Fukuyoa. Metabolization through trophic networks adds complexity to the detection of these compounds, as it generates a high number of analogues. The complementarity of UPLC-MS/MS technique for the detection and quantification of specific CTX analogues with the UPLC-HRMS technique for the confirmation of CTX allows the characterization of CTX profiles.
This methodology has revealed distinct toxin profiles in fish involved in poisoning incidents. Analyses of fish samples from poisoning events in the Indian Ocean, specifically in La Réunion and the Seychelles, report three cases where the analyzed samples showed presence of CTXs but different toxin profiles. In one of the cases, ciguatoxins CTX3B, in one of the three Lutjanus bohar flesh samples, and 2,3-dihydroxy-CTX3C in another, were detected. A second poisoning incident involving Variola louti revealed the presence of CTX1B and its analogues CTX2 and CTX3. A third event revealed the presence of Indian Ocean ciguatoxins (I-CTXs) in a Thyrsitoides marleyi: I-CTX-1, I-CTX-2, and I-CTX-4. The presence of CTX1B congeners and I-CTXs has been confirmed through LC-HRMS. For CTX3B and 2,3-dihydroxy-CTX3C such confirmation has not been possible due to the high limit of detection for CTX3C congeners.
These findings highlight the diversity of ciguatoxin analogues present in fish associated with ciguatera poisoning events in the Indian Ocean and emphasize the importance of advanced analytical techniques such as UPLC-MS/MS for accurate identification and quantification.

**Keywords**: Ciguatoxins, Poisoning events, UPLC-MS/MS

**Financing**: This work was funded by MICIN/AEI (CIGUAADAPT, PID2022-137174OR-C21), Europe and la Région Réunion (CIGUATOXRUN), and European Commission (BLUESHELLFISH, HORIZON-MSCA-101086234).

**Acknowledgments**: Joan Josep Cervera acknowledges MICIN and AEI for the phD funding PRE2022-000401. The authors also acknowledge CERCA/Generalitat de Catalunya program.

Poster Session 01: Ciguatera and Benthic HABs
P-058

# Harmful microalgae on the move: First detection of *Gambierdiscus australes* in Western Continental Mediterranean waters

**Eva S. Fonfría**[1], Emilio Soler Onís[2,3], John Y. Dobson[1], Carolina Pena-Martín[4], Cesar Bordehore[1,5]

(1) Universidad de Alicante, IMEM Ramón Margalef, Ctra San Vicente del Raspeig s/n, San Vicente del Raspeig, Spain
(2) Universidad de Las Palmas de Gran Canaria, Observatorio Canario de Algas Nocivas, Parque Científico Tecnológico Marino de Taliarte, Taliarte, Spain
(3) Universidad de Las Palmas de Gran Canaria, Grupo de Ecofisiología Marina, Campus Universitario de Tafira, Las Palmas de Gran Canaria, Spain
(4) Universidad de Alicante, Departamento de Ciencias Ambientales y Recursos Naturales, Ctra San Vicente del Raspeig s/n, San Vicente del Raspeig, Spain
(5) Universidad de Alicante, Departamento de Ecología, Ctra de San Vicente del Raspeig s/n, San Vicente del Raspeig, Spain

Species of the genus *Gambierdiscus* R. Adachi & Y. Fukuyo (Dinophyceae, Gonyaulacales) are important due to their ability to produce ciguatoxins and maitotoxins, responsible for ciguatera fish poisoning (CFP), the most common non-bacterial food-borne illness globally. Although traditionally restricted to tropical areas, recent records show an expansion into temperate regions, likely driven by climate change and anthropogenic factors. In the Mediterranean Sea, Gambierdiscus species have previously been detected on the insular coasts of Greece, Cyprus, and Spain (Balearic Islands). In this study, *Gambierdiscus australes* Chinain & MA Faust was recorded for the first time along the continental coast of the Iberian Peninsula, specifically in Denia (Alicante, Spain), in March 2023.

To investigate the timing of its introduction, historical samples collected in the same area are being analyzed. Notably, *G. australes* is absent from all samples collected prior to 2012, confirming that its arrival is a recent event. The establishment of this species in Iberian coastal waters suggests a westward expansion from the Eastern Mediterranean, presumably facilitated by rising sea surface temperatures and human-related activities.

Despite current cell densities having low concentrations, these findings highlight the importance of continuous monitoring, given the potential risk of CFP and the ongoing tropicalization of the Mediterranean Sea. Surveillance programs should include both Gambierdiscus species and the broader benthic microalgal communities to assess ecological shifts and mitigate future health risks.

**Keywords**: *Gambierdiscus*, Mediterranean Sea, distribution

**Financing**: This work was supported by the project GVA-THINKINAZUL/2021/043 to CB, supported by the MCIN with the funding from European Union NextGenerationEU (PRTR-C17.I1)

**Acknowledgments**: We also thank the collaboration of Ajuntament de Dénia, el Portet de Dénia and IRTA La Ràpita (Institute of Agrifood Research and Technology).

Poster Session 01: Cyanobacteria & Freshwater HABs
P-059

# Environmentally relevant concentrations of the antibiotic azithromycin stimulate growth and increase microcystin content in *Microcystis aeruginosa*

**Michael Celano**[1], Ana Beatriz Pacheco[1], Tainá Silva[1], Mariana Marques[1], Julia Silberman[1], Mauro Vilar[1], Sandra Azevedo[1]

(1) Federal University of Rio de Janeiro, Carlos Chagas Filho Institute of Biophysics, Carlos Chagas Filho Institute of Biophysics, Avenida Carlos Chagas Filho, 372, Rio de Janeiro, Brazil

Improper discharge of effluents into aquatic environments results in increased nutrient levels and the input of emerging contaminants, such as antibiotics. During the COVID-19 pandemic, a widespread use of the macrolide antibiotic azithromycin has been reported in several countries, resulting in significantly increased concentrations in surface waters (up to 3.0 µg $L^{-1}$). Although subinhibitory, these concentrations can affect non-target organisms, such as algae and cyanobacteria, primary producers in aquatic food webs. This study investigated the effects of environmentally relevant concentrations of azithromycin on the harmful bloom-forming cyanobacterium *Microcystis aeruginosa*. Upon exposure to azithromycin (0.3 and 0.6 µg $L^{-1}$), cell growth, chlorophyll-α content, photosynthetic activity, volumetric and cellular microcystin concentrations were examined. Both antibiotic concentrations significantly stimulated cell growth and reduced chlorophyll-α cell content, without compromising photosynthetic activity. Microcystin concentrations increased in both the intracellular fraction (from the 6th day) and the extracellular fraction (from the 2nd to the 6th day). A four-fold peak increase in the cellular concentration of the toxin was measured following 48h exposure to the highest concentration of the antibiotic. These results suggest that environmentally relevant concentrations of azithromycin may favor the proliferation of toxic cyanobacteria, increasing public and environmental health risks. This underscores the importance of considering antibiotics, alongside nutrients, as key factors driving cyanobacterial proliferation in polluted water bodies, as well as further studies should assess the underlying biochemical and molecular cell responses.

**Keywords**: Eutrophication; Cyanobacteria; Cyanotoxins

**Financing**: This research received no external funding.

**Acknowledgments**: The authors are thankful to CAPES, Brazil, for its financial support through a master's scholarship granted to M.R.C.

Poster Session 01: Cyanobacteria & Freshwater HABs

P-060

# IAEA regional initiative on the assessment and management of saxitoxin-producing freshwater cyanobacteria in Latin America and the Caribbean

**Lisbet Díaz Asencio**[1], Alma L. Aguilar Santos[2], María F. Barrera del Valle[3], Carlos E. García Mansilla[3], Marcelo P. Hernando[4], Arnold Molina Porras[5], Lina G. Ortiz Muñoz[6], Tamara B. Villalobos Oyarce[3], Marie Yasmine Dechraoui Bottein[7], Marianela Mesa Albernas[8], Gabriel L. Rojas Abrahantes[1,9], François Oberhänsli[8], Khalil Sdiri[8], Kristof Moeller[8], Oscar A. Amaya Monterrosa[2], Carlos M. Alonso Hernández[8]

(1) Centro de Estudios Ambientales de Cienfuegos, Ciudad Nuclear, Cienfuegos, Cuba
(2) Laboratorio de Toxinas Marinas, Escuela de Física, Universidad de El Salvador, El Salvador
(3) Laboratorio de Toxinas Marinas, Instituto de Ciencias Biomédicas; Facultad de Medicina; Universidad de Chile, Chile
(4) Centro Atómico Constituyentes, Comisión Nacional de Energía Atómica, Argentina
(5) Centro de Investigación en Ciencias Atómicas Nucleares y Moleculares, Universidad de Costa Rica, Costa Rica
(6) Instituto de Investigaciones Marinas y Costeras, Colombia
(7) Université Côte d'Azur, CNRS, ECOSEAS, France
(8) International Atomic Energy Agency (IAEA) Environment Laboratory, Monaco
(9) Centro de Investigación Científica y de Educación Superior de Ensenada, Baja California, México

The proliferation of toxin-producing cyanobacteria in freshwater and brackish systems is a widespread and growing concern in Latin America and the Caribbean (LAC), though only a few countries in the region have actively studied its impacts. Among the most hazardous cyanotoxins are paralytic shellfish toxins, particularly saxitoxin-group (STX), produced by certain cyanobacterial genera, including *Anabaena, Cylindrospermopsis, Lyngbya, Aphanizomenon, Planktothrix,* and *Raphidiopsis*.
To address critical gaps in the detection and management of STX-producing cyanobacteria, LAC countries, with support from the IAEA, have launched a project to improve STX detection and water safety. A key focus is the implementation of the radioligand-Receptor Binding Assay (r-RBA), a nuclear-derived technique validated for monitoring paralytic shellfish toxins (PSTs) of marine origin and now adapted to detect PSTs from freshwater cyanobacteria. Through IAEA assistance, six LAC countries have strengthened their technical capacities by acquiring essential equipment, reagents, and materials. A regional training course was conducted at the IAEA Environment Laboratories, providing hands-on instruction in toxin extraction methods, r-RBA execution, troubleshooting, quality control, and data analysis using R software. Preliminary results from participants underscored the assay's practical applicability and potential, while also revealing opportunities for improving current regional protocols. Additionally, the results suggest that the RBA is a promising tool for quantifying dissolved STX, if pre-concentration steps are included to lower the limit of detection. This collaborative effort also includes the development of standardized practical guidelines to enhance regional capabilities in monitoring and managing saxitoxin risks, ultimately supporting safer water resources and public health protection across LAC.

**Keywords**: CyanoHABs, Nuclear technique, LATAM

**Financing**: IAEA Technical Cooperation Project 7026 Evaluating Organic and Inorganic Environmental

## Poster Session 01: Cyanobacteria & Freshwater HABs

### P-060

Pollution in Aquatic Environments and Their Impact on the Risk of Cyanotoxin–Producing Cyanobacteria (ARCAL CLXXVIII).

**Acknowledgments**: The International Atomic Energy Agency is grateful to the Government of the Principality of Monaco for the support provided to its Environment Laboratories.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-061

# Plant growth-promoting Rhizobacteria mitigate cyanobacterial microcystin toxicity in *Vicia faba*: Health risk assessment

**Nadia Elidrissi El Yallouli**[1,2,3], elmahdi redouane[1,4], Richard Mugani[1], Lahcen Ouchari[5,6], Mariana Girão[7], Maria F. Carvalho[7,8], Alexandre Campos[7], Vitor Vasconcelos[7,9], Brahim Oudra[1], Majida Lahrouni[1], John Poté[2]

(1) Cadi Ayyad University, Department of Biology, Faculty of Sciences Semlalia, Water, Biodiversity and Climate Change Laboratory, 40000, Marrakech, Morocco
(2) University of Geneva, Geneva, Switzerland, Department F.-A. Forel for Environmental and Aquatic Sciences and Institute for Environmental Sciences, Faculty of Sciences, 1211, Geneva, Switzerland
(3) Istituto Superiore di Sanità, Department of Environment and Health, Istituto Superiore di Sanità, 00161, Rome, Italy
(4) Université de Reims Champagne-Ardenne, Department of Biology, Reims, France
(5) National Center for Scientific and Technical Research (CNRST), Molecular Biology and Functional Genomics Platform, 10000, Rabat, Morocco
(6) Mohammed V University in Rabat, Microbiology and Molecular Biology Team, Plant and Microbial Biotechnology, Biodiversity and Environment Center, Faculty of Sciences, 10000, Rabat, Morocco
(7) University of Porto, CIIMAR - Interdisciplinary Centre of Marine and Environmental Research, 4450-208, Porto, Portugal
(8) University of Porto, ICBAS - Institute of Biomedical Sciences Abel Salazar, 4050-313, Porto, Portugal
(9) University of Porto, Department of Biology, Faculty of Sciences, 4169-007, Porto, Portugal

Cyanobacterial blooms have been increasing in freshwater ecosystems worldwide over the last century, mostly due to eutrophication and climate change (Lakshmikandan et al., 2024). These blooms can produce a wide variety of toxic secondary metabolites, i.e., cyanotoxins, with microcystins (MCs) being the most studied due to their global distribution, ubiquity, and toxicity (Wan et al., 2020). Repeated exposure to these toxins can inhibit crop growth and development, contaminate soil, which raises concerns about health risks and food safety for humans (Weralupitiya et al., 2022). The specificaim of this work was to investigate the potential role of plant growth-promoting rhizobacteria as a bioremediation tool to protect soil-plant systems from MCs and mitigate toxin-related health risks. To this purpose, Vicia faba plants were co-inoculated in sterile soil with MC-resistant rhizobia and rhizobacteria exhibiting growth-promoting traits in a greenhouse pot trial. The plants were exposed to MC-contaminated water at a concentration of 200 µg.$L^{-1}$ of MCs for one month. Results revealed that exposure of non-inoculated plants to these toxins led to decreased growth, impaired photosynthetic efficiency, and reduced nitrogen content in both shoot and root tissues, along with decreased activity of the nitrogen assimilatory enzyme glutamine synthetase in the leaf tissues. Conversely, inoculation with toxin-tolerant bacteria significantly improved these parameters in MC-exposed plants. The estimated daily intake values of MCs for all treatments remained below the recommended tolerable daily intake threshold of 0.04 µg.$kg^{-1}$ of body weightper day, as established by the World Health Organization.

**Keywords**: microcystins, bioremediation, health risk.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-062

# Understanding the drivers of toxic cyanobacterial blooms in the Río de la Plata, Argentina

**Marcelo Hernando**[1,2,3], Paula Dabas[4], Nora Vizioli[4], Gastón Almandoz[5], Natacha Piloni[2]

(1) National Atomic Energy Commission, Radiobiology, San Martin 1650,, San Martín, Argentina
(2) Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET) Godoy Cruz 2290, Godoy Cruz 2290, caba, Argentina
(3) Red de Investigación de Estresores Marinos-Costeros en América Latina y el Caribe (REMARCO), Mar del Plata 7602, Argentina, Mar del Plata (CP 7602), Argentina
(4) Universidad de Buenos Aires, Química Analítica, Facultad de Farmacia y Bioquímica, Junin 954, CABA, Argentina
(5) Universidad Nacional de La Plata, División Ficología, Facultad de Ciencias Naturales y Museo, Paseo del Bosque s/n, 1900, La Plata, Argentina

The Río de la Plata estuary on South America's eastern coast provides essential ecosystem services but receives wastewater. Recurrent toxic cyanobacterial blooms, expected to worsen with climate change and eutrophication, were studied to develop an early warning system for Buenos Aires. Monthly monitoring (2021-2024) at two sites in the estuary's tidal zone (Quilmes and Muelle Pescadores) revealed diverse phytoplankton assemblages, with *Microcystis aeruginosa* and *Dolichospermum* sp. blooms linked to high temperatures and nutrients, showing substantial interannual variability.
During a 2023 bloom in Quilmes (February), *M. aeruginosa* reached 6 million cells $mL^{-1}$, with a lower abundance of *Dolichosphermum* sp. of 800000 cells $mL^{-1}$ with corresponding microcystin (MC) concentrations of 41 and 58 fg $cells^{-1}$ for MC-LR and [D-Leu$^1$], respectively. Such bloom coincided with peak water temperatures of 30°C and high nutrient levels ($NO_3^-$: 10 mg $L^{-1}$; $PO_4^{3-}$: 7.2 mg $L^{-1}$). In mid-January 2025, a bloom of *Merismopedia* sp. (a potential MC producer) reached 62,000 cells $mL^{-1}$ under cooler and less nutrient-rich conditions. Other potentially toxin-producing genera, including *Dolichospermum, Planktothrix, Pseudoanabaena*, and *Aphanizomenon*, were also detected. Additionally, a bloom of the dinoflagellate *Durinskia* sp. was recorded for the first time in the Río de La Plata, reaching 10,000 cells $mL^{-1}$ in Quilmes.
Elevated MC levels and the presence of potentially saxitoxin (STX)/anatoxin-producing genera highlight the urgent need for increased toxin monitoring in water sources and recreational areas. CNEA is developing a radioligand Receptor Binding Assay (RBA) for STX detection. These findings are crucial for national/regional guidelines and risk management.

**Keywords**: Río de la Plata, cyanobacteria, toxicity

**Financing**: International Atomic Energy Agency (IAEA) RLA 7026 project

**Acknowledgments**: IAEA RLA 7026 project and Secretariat General of Environment and Sustainable Development

Poster Session 01: Cyanobacteria & Freshwater HABs
P-063

# The dynamics of a phytoplankton community in microcosms during a *Microcystis aeruginosa* bloom managed with allelopathy

**Marie Jamroszczyk**[1], Ishrat Alam Protyasha[1], Aldo Barreiro Felpeto[1,2], Vítor Vasconcelos[1,2]

(1) CIIMAR, Centro Interdisciplinar de Investigação Marinha e Ambiental, Porto University, Terminal de cruzeiros do porto de Leixões. Av. General Norton de Matos, s/n. 4450-208,, Matosinhos, Portugal
(2) Faculty of Sciences, Department of Biology, Porto University, Rua do Campo Alegre, 4069-007, Porto, Portugal

The toxic cyanobacterium *Microcystis* sp. is responsible for some of the most severe harmful algal blooms (HABs) in freshwater ecosystems worldwide. Its proliferation is favored by prolonged periods of high solar radiation, elevated temperatures, and factors promoting water column stratification. Additionally, eutrophication has been identified as a key contributing factor. Consequently, climate change and anthropogenic eutrophication have intensified the frequency and extent of these HABs.
This study aimed to evaluate a bioremediation approach targeting *Microcystis* sp. blooms using the allelochemical portoamide, produced by the cyanobacterium *Phormidium* sp. Initial assays revealed strong inhibitory effects of portoamides on dense monocultures of various Microcystis aeruginosa strains. To explore this further, we tested the effect of portoamides on a phytoplankton community that developed over 30 days, under two levels of phosphorus eutrophication and with or without inoculation of a dense *M. aeruginosa* population.
Unexpectedly, the *M. aeruginosa* bloom was not suppressed by portoamides but rather appeared to be promoted by allelopathic conditions. Only a few diatom genera persisted alongside the bloom, and at very low abundances. Eutrophication level had no strong qualitative effect on community composition in the presence of *M. aeruginosa*.
These findings suggest that allelopathic bioremediation strategies may yield unintended outcomes when applied to complex, semi-natural communities. Therefore, careful testing and fine-tuning of conditions are essential before such methods can be reliably scaled for ecological applications.

**Keywords**: *Microcystis*, allelopathy, community dynamics

**Financing**: The present work was supported by contract 2024_069_IA_TENURE_1 from FCT (Portugal) to ABF and a fellowship from the program Erasmus Mundus JMD 2022/23 to IAP.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-064

# Algae-on-a-chip: Understanding cyanobacterial bloom toxicity using microfluidic technology

**Chaohong Lin**[1,2], Mathieu Odijk[3], Dedmer B. Van de Waal[1,2]

(1) Department of Aquatic Ecology, Netherlands Institute of Ecology (NIOO-KNAW), Wageningen, the Netherlands
(2) Department of Freshwater and Marine Ecology, Institute for Biodiversity and Ecosystem Dynamics, University of Amsterdam, Amsterdam, the Netherlands
(3) MESA+ Institute for Nanotechnology, University of Twente, Enschede, the Netherlands

Eutrophication is a widespread issue in waterbodies, often triggering harmful cyanobacterial blooms. These blooms can be toxic, depending on whether the dominant species and their genotypes produce toxins. *Microcystis* is a well-known bloom-forming genus capable of producing toxins, yet blooms comprise toxic and non-toxic genotypes. Toxic *Microcystis* blooms occur when toxic genotypes outcompete their non-toxic counterparts through intraspecific competition. The growth and dominance of a genotype are supported by key traits that provide competitive advantages for nutrient acquisition, one of which is growth affinity that is derived from nutrient growth kinetics. Therefore, nutrient growth kinetics provide the mechanisms underlying the competitive dynamics between toxic and non-toxic *Microcystis* genotypes. These dynamics are further complicated by climate change factors including warming and elevated $pCO_2$. Both factors may alter metabolic costs and trigger a reallocation of energy and resources for nutrient acquisition, especially in nutrient-limited conditions. However, to investigate and understand the interplay of nutrients, temperature, and $pCO_2$ on intraspecific competition in *Microcystis* requires extensive tests and precise control across environmental gradients. To address this challenge, we develop microfluidic approaches which create an array of tiny, but tightly and individually controlled bioreactors (x µL) on small microfluidic chips (< 75 × 25 mm), enabling high-throughput tests across environmental gradients. By applying this novel method, we aim to advance our understanding of the physiological and ecological responses of Microcystis to nutrient availability and climate change, providing a fundamental understanding for predicting bloom toxicity.

**Keywords**: Cyanobacterial blooms, Toxins, Microfluidics

**Financing**: European Research Council, BLOOMTOX, project number: 101044452

Poster Session 01: Cyanobacteria & Freshwater HABs
P-065

# Integrating sentinel-2 satellite, in-situ sensor, and nutrient data for enhanced monitoring of cyanobacterial blooms in Lake Mattamuskeet, North Carolina

**Todd Lundell**[1], Dr. Nathan Hall[2], Yair Regev[3], Dr. Jessica Frost[4]

(1) Todd Lundell, BlueGreen Water Technologies, Gainesville, FL
(2) Dr. Nathan Hall, University of North Carolina at Chapel Hill
(3) Yair Regev, BlueGreen Water Technologies, Modi'in-Maccabim-Re'ut, Israel
(4) Dr. Jessica Frost, BlueGreen Water Technologies, Gainesville, FL

Effective monitoring of harmful algal blooms (HABs) in large, shallow freshwater ecosystems like Lake Mattamuskeet (North Carolina, USA) requires a synergistic approach that captures both temporal and spatial variability. This study presents an integrated framework combining high-frequency in-situ sensors, nutrient and pigment sampling, and Sentinel-2 satellite imagery to improve understanding of cyanobacterial bloom dynamics. In-situ sensors deployed across the lake continuously record key physical and biogeochemical parameters, including phycocyanin, chlorophyll-a, turbidity, and temperature. These real-time data are complemented by discrete water sampling for nutrient and pigment analysis. Variables include total and fractionated nitrogen and phosphorus (e.g., $NO_3^-$/$NO_2^-$, $NH_4^+$, $PO_4^{3-}$, TDN, DIN, DON), particulate organic carbon (POC) and nitrogen (PN), silica ($SiO_2$), Secchi depth, and light attenuation (Kd), along with diagnostic pigment biomarkers such as fluorometric chlorophyll-a, phycocyanin, chlorophyll-b, fucoxanthin, peridinin, zeaxanthin, and lutein. Sentinel-2 satellite imagery is used to derive chlorophyll indices and detect surface-level bloom extent. These satellite products are compared with in-situ sensor and nutrient data to evaluate their alignment and sensitivity to environmental drivers. We hypothesize that agreement between in-situ and satellite chlorophyll-a improves under vertically mixed conditions, which promote even biomass distribution. This integrated approach offers a more complete assessment of bloom onset, intensity, and composition. This comprehensive approach enables a more nuanced assessment of bloom onset, composition, and intensity. It emphasizes that while no single method is sufficient alone, the combination of real-time sensors, laboratory-based nutrient diagnostics, and high-resolution satellite imagery offers a robust toolkit for adaptive bloom management in complex freshwater systems.

**Keywords**: Satellite, Insitu-Sensors, Synergy

**Financing**: Private

**Acknowledgments**: Todd Lundell, Dr. Nathan Hall, Yair Regev, and Dr. Jessica FrostBlueGreen Water Technologies, Gainesville, FL.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-066 (Ignite Talk)

# Monitoring microcystin-producing *Microcystis* in the Tobari Bay, Mexico

**Pamela Helué Morales Sandoval**[1], Sergio de los Santos Villalobos[1], Jaquelyn Aguilar Ibarra[1], Ilce Icela González Vázquez[1], Jesus Daniel Moreno Cárdenas[1], Clarissa Isabel Gutiérrez Mendívil[1], Fannie Isela Parra Cota[2]

(1) Instituto Tecnológico de Sonora, Departamento de Ciencias Agronómicas y Veterinarias, 5 de febrero 818 sur, 85000, Ciudad Obregón, México
(2) Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias (INIFAP), Campo Experimental Norman E. Borlaug, Norman E. Borlaug Km. 12, C. P. 85000, Ciudad Obregón, México

Cyanobacterial blooms must be monitored to control toxin-producing strains and address poisoning caused by their toxins. Acute hepatotoxicity, commonly linked to microcystins, is the most frequent form of cyanobacteria-related poisoning. These toxins are produced by species within the genera *Microcystis, Anabaena, Hapalosiphon, Nodularia, Nostoc,* and *Oscillatoria*. Thus, identifying and monitoring potentially toxic cyanobacteria in long-term scenarios, by using integrated approaches, is crucial for designing fast and cost-effective mitigation strategies. This study aimed to identify cyanobacteria and microcystin-producing *Microcystis* during one year in the Tobari Bay, located in Sonora, Mexico, using an integrated approach, such as microscopy, molecular techniques, and satellite imagery to monitor annual greenness and phycocyanin-related parameters. This bay is one of the most impacted coastal ecosystems by agroindustrial activity in Mexico, with runoff from 285,000 hectares of wheat crops (nitrogen loss ~ 70%), which provide 50% of national production, and effluents from livestock, and aquaculture. Key findings revealed a diverse community of cyanobacteria through microscopic monitoring. Molecular analysis using 16S rRNA gene sequencing confirmed the presence of potentially toxic strains, and toxin-related genes were detected, both associated with the nitrogen input in key cropping periods. The expression of mcyA, linked to microcystin production, was quantified using real-time PCR, offering an insight into toxin dynamics. Satellite imagery captured seasonal color changes and identified the most impacted zones in the bay, while whole-genome sequencing of the most abundant cyanobacteria strains provided information on other genes involved in other toxins, which deepened understanding of their genetic background and long-term ecology.

**Keywords**: Cyanobacteria, Molecular analysis, Genetics

**Financing**: Evaluating Organic and Inorganic Environmental Pollution in Aquatic Environments and Their Impact on the Risk of Cyanotoxin–Producing Cyanobacteria (ARCAL CLXXVIII).

**Acknowledgments**: We thank the IAEA, ARCAL, the Government of Mexico, SECHITI, ITSON, and LBRM-Colmena for their support, funding, scholarships, and research infrastructure provided.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-067

# Harmful cyanobacterial blooms associated to the storm Alberto in Cienfuegos Bay, Cuba

**Angel Ramón Moreira González**[1], Augusto Abilio Comas González[1], Aimee Valle Pombrol[1], Dany Domínguez Pérez[2], João M. Silva[2], Cristiana Moreira[2], Alexandre Campos[2], Vitor Vasconcelos[2]

(1) Centro de Estudios Ambientales de Cienfuego, AP. 5, Ciudad Nuclear, CP. 59350 Cienfuegos, Cuba., Cienfuegos, Cuba
(2) CIIMAR Interdisciplinary Center of Marine and Environmental Research, University of Porto, Terminal de Cruzeiros do Porto de Leixões, Avenida General Norton de Matos, S/N, 450-208, Matosinhos, Portugal

In late May and June 2018, large harmful cyanobacteria blooms, associated with dead fishes and foaming in the beaches were observed in Cienfuegos Bay, following the subtropical storm “Alberto”, which triggered one of the largest freshwater inflows ever recorded in Cuban aquatic ecosystems. The aim of this study was to identify harmful cyanobacterial species during the bloom using different approaches such as morphological-based identification and the application of molecular-based methods (taxon specific and cyanotoxin genes). Identification of cyanobacteria was based on observations of morphology using a light compound microscope with phase contrast equipment and digital camera. Molecular methods were used to investigate the presence of particular cyanobacterial groups/taxa genes. A total of 12 potentially toxic cyanobacteria species were identified, belonging to eight genera. Dominant species included *Microcystis panniformis, Sphaerospermopsis torques-reginae* and *Raphidiopsis gangetica*. Molecular analysis confirmed the presence of *Microcistys* spp. in multiple samples, while *Microcystis aeruginosa* was identified in one sample. Successful amplification of the 16S rRNA and phycocyanin operon sequences confirmed cyanobacterial DNA extraction from the environmental samples. For genes involved in cyanotoxin synthesis, genes related to the production of microcystins seem to be present in all samples with at least one positive result for each sample. Apart from the presence of cyrC (PKSM4/PKSM5), involved in the production of cylindrospermopsin, in sample 1, no other genes involved in the production of other cyanotoxins were found. These results are very important in phytoplankton studies, monitoring programs and management of biodiversity in the framework of ongoing national and regional projects.

**Keywords**: harmful cyanobacteria, cyanotoxin genes, estuaries

**Financing**: IAEA.EU’s H2020 R&I program, grant agreement No 823860. Fundação para a Ciência e Tecnologia UIDB/04423/2020 and UIDP/04423/2020.

**Acknowledgments**: AENTA, Ministry of Science, Technology and Environment from Cuba (CITMA).

Poster Session 01: Cyanobacteria & Freshwater HABs
P-068 (Ignite Talk)

# Adaptive role of extracellular vesicles in phosphorus-limited *Microcystis aeruginosa*

**Cezar Nascimento**[1,2], Mauro Vilar[2] , Paulo Bisch[1] , Ana Beatriz Pacheco[1]

(1) Federal University of Rio de Janeiro, Laboratory of Biological Physics (LAFISBIO), Carlos Chagas Filho Institute of Biophysics, Health Sciences Center, Block G, Room G1-043 – Carlos Chagas Filho Avenue, 373 – University City, Rio de Janeiro, Brazil
(2) Federal University of Rio de Janeiro, Laboratory of Ecophysiology and Toxicology of Cyanobacteria, Carlos Chagas Filho Institute of Biophysics, Health Sciences Center, Block G, Room G0-057 – Carlos Chagas Filho Avenue, 373 – University City, Rio de Janeiro, Brazil

*Microcystis aeruginosa* is a widely distributed freshwater cyanobacterium often associated with harmful blooms, posing risks to water quality and public health. Nitrogen and phosphorus (P) inputs are major bloom drivers, while competition for these nutrients among planktonic organisms is intense. Adaptation strategies of *M. aeruginosa* to P limitation involve intracellular polyphosphate storage, high-affinity P transport systems, and secretion of phosphatases that hydrolyze organic P compounds. In this sense, extracellular vesicles (EVs) are structures released by cells, enabling the transport of biologically active molecules in a protected and targeted way. Given the increasing interest in the functional role of EVs in microorganisms, their involvement in cyanobacterial responses to nutrient limitation is still incipient.

This study aimed to characterize EVs from a *M. aeruginosa* strain cultured under contrasting P availabilities (1.0 and 0 mg·L$^{-1}$, referred to as 1P and 0P) during 7 days and to assess whether alkaline phosphatase activity (APA) is associated with EVs. Cultures were monitored during exponential growth for cell density , photosynthetic activity (PHYTO-PAM), and APA (fluorescence-based 4-MUP assay). EVs were isolated from the extracellular fraction of cultures by tangential flow filtration and ultracentrifugation, and quantified by nanoparticle tracking analysis.

No difference was observed in photosynthetic activity between treatments. Under 0P, cell growth was reduced and cellular APA increased by 10-fold. Both EV production and EV-associated APA were higher in 0P. These preliminary results suggest that M. aeruginosa EVs may contribute to phosphate acquisition from organic sources, representing a potential adaptive strategy to nutrient limitation.

**Keywords**: Cyanobacteria, Extracellular vesicles, Nutrient acquisition

**Acknowledgments**: his work was supported by CNPq and the Carlos Chagas Filho Foundation for Research Support of Rio de Janeiro State (FAPERJ).

Poster Session 01: Cyanobacteria & Freshwater HABs
P-069

# Immunoaffinity magnetic beads for microcystins capture and concentration in biological samples

**Stuart Oehrle**[1], Leah Ruth[2]

(1) Northern Kentucky University, Chemistry Dept, Waters Lab 100 Nunn Dr, Highland Heights, USA
(2) Gold Standard Diagnostics Horsham, 795 Horsham Rd., Horsham, USA

Cyanotoxins are a category of toxins produced by cyanobacteria (blue-green algae) that are prevalent in certain bodies of water, where they can reproduce exponentially into harmful algal blooms (HABs), posing a significant health risk. Microcystins are the most commonly found cyanotoxins and have hepatotoxic effects. The US EPA has issued health advisories in drinking and recreational water, but government agencies, public health labs and academic researchers also have an interest in detecting Microcystins in biological samples, primarily urine and blood serum to assess exposure.
Due to the complex nature of urine and blood serum, and possibly low levels of Microcystins, sample clean-up and concentration are needed to prepare samples for downstream detection with sensitive analytical techniques such as LC-MS and ELISA. Immunoaffinity Magnetic Beads (IMB) have emerged as an effective clean-up method. IMB, synthesized by conjugating antibodies onto magnetic nanoparticles, mix with a biological sample whereby the antibody binds the target of interest. The IMB-target complex is separated from the matrix using a strong magnet. The IMB clean-up method possesses high affinity for the target of interest, and by varying the elution volume, can result in a 10-fold concentration of the target to detectable levels.

**Keywords**: HABS, biological matrices

**Acknowledgments**: Boris Polyak, and Fernando RubioGold Standard Diagnostics Horsham.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-070 (Ignite Talk)

# *Didymosphenia geminata* blooms in freshwater ecosystems from Central to Austral Chile (~ 35.4°–54.6° S): Latitudinal distribution and environmental correlates

**David Andrés Opazo Vega**[1], Alejandra Oyanedel[1], Paula Ramírez[1], Mario Ortiz[1], Rodrigo Jaramillo[1]

(1) Instituto de Fomento Pesquero, Departamento de Medio Ambiente, Balmaceda 252, Puerto Montt, Chile

*Didymosphenia geminata* is a benthic, stalk-forming diatom that can produce extensive blooms in freshwater ecosystems, altering their functioning and ecosystem services. In 2010, blooms were first recorded in southern Chile (Futaleufú and Espolón rivers, ~43° S), prompting the continuous monitoring of rivers and lakes from central to southern Chile. To characterize bloom distribution and associated environmental conditions, we analyzed monitoring data collected between 2016 and 2025 from 18 hydrographic basins (~35.4°–54.6° S). Currently, *D. geminata* is present in the benthos of rivers and lakes in 17 of these basins (with >50% of samples testing positive in 8 basins), covering the entire latitudinal gradient studied. However, blooms remain relatively rare, occurring in only 11 basins and in <40% of the samplings. Binomial Generalized Additive Models indicate that the probability of bloom occurrence is highest under low phosphorus concentrations (<0.002 mg/L), supporting the hypothesis that photosynthetic overflow drives stalk elongation during blooms. At phosphorus levels below 0.002 mg/L, the predicted mean bloom probability ranged between 0.3 and 0.8. We explore the relative influence of other abiotic factors on this variability, including variables related to cell and stalk structure, streamflow variability, and light availability.

**Keywords**: *Didymosphenia geminata* blooms, Blooms latitudinal distribution, Blooms environmental correlates

**Financing**: Undersecretariat for Fisheries and Aquaculture - Ministry of Economy, Development and Tourism of Chile.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-071

# First report of the saxitoxin-producing benthic *Microseira* (*Lyngbya*) *wollei* in South America: Emerging concern for cyanobacterial monitoring strategies in the region

**Mauro Cesar Palmeira Vilar**[1], Suema Branco[1], Graciela Maria Dias[2], Ana Beatriz Furlanetto Pacheco[2], Sandra Azevedo[1]

(1) Federal University of Rio de Janeiro, Carlos Chagas Filho Institute of Biophysics, Laboratory of Ecophysiology and Toxicology of Cyanobacteria, Rio de Janeiro, Brazil
(2) Federal University of Rio de Janeiro, Carlos Chagas Filho Institute of Biophysics, Laboratory of Biological Physics, Rio de Janeiro, Brazil

Cyanobacterial blooms caused by planktonic species threaten water supply and recreation worldwide. Recently, some benthic species have raised concern due to their ability to colonize diverse substrates, including water-treatment plants, forming noxious benthic and floating mats. Among these, *Microseira wollei* (formerly *Lyngbya wollei*) is notable for forming mats exceeding 10 kg·m$^{-2}$ F.W. and producing toxic alkaloids such as saxitoxins (STXs). Its distribution includes North America, Southern Europe, Southern and East Asia, and Australia, but no occurrences had been reported in South America until now. This study reports the first occurrence of *M. wollei* and its toxins in Brazilian waters. Specimens were collected from floating mats at the São Sebastião do Alto Dam (Rio de Janeiro, Brazil). Morphological analysis revealed macroscopic tangled filaments (50 µm wide), unbranched, with a conspicuous, colorless mucilage sheath (2.5 µm wide). Cells were dark green, discoid (45 µm width; 2.5–7 µm length), slightly constricted, and lacked aerotopes. Cultures (n=4) of strain LETC-MW-01 were established in ASM-1 medium for biomass production, followed by DNA extraction, amplification, sequencing, and phylogenetic and sxt gene cluster analysis. Freeze-dried biomass was also analyzed for toxins using HPLC-FLD, detecting non-sulfated (STX, neoSTX, dcSTX) and monosulfated (GTXs) analogues. The sxt gene cluster was 38,361 bp; highly similar to previously described clusters. Total saxitoxin content reached 561.50±60.61 ng STXs·mg$^{-1}$ D.W., with gonyautoxins comprising over 75%. The presence of neurotoxic M. *wollei* in South America poses an underestimated risk to environmental health since it can reach high biomasses and impair water supply and wildlife.

**Keywords**: Paralytic Shellfish Toxins, sxt gene, Cyanobacteria

**Financing**: Carlos Chagas Filho Foundation for Research Support of the State of Rio de Janeiro (FAPERJ) Elera Renováveis

**Acknowledgments**: The authors would like to thank the ELERA renováveis for the access to the hydroelectric plant and support in the biomass sample collection.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-072

# Blind spots in toxin monitoring: Freshwater cyanotoxins in marine species of the Salish Sea

**Misty Peacock**[1], Rosa Hunter[1], Megan Schulz[1], Kira Walters[1], Steffan Kinley[1]

(1) Northwest Indian College, Salish Sea Research Center, 2522 Kwina Rd, Bellingham, US

Freshwater cyanotoxins produced by harmful algal blooms (FHABs) are a global threat to coastal ecosystems, with documented impacts on marine shellfish, mammals, and seabirds. Despite these risks, cyanotoxins are rarely monitored in marine environments, raising serious food safety concerns—especially for subsistence harvesters. The Salish Sea, spanning Washington State and British Columbia, is home to seafood that holds deep cultural, economic, and ecological importance. For the Coast Salish Peoples, who have sustainably harvested these resources for millennia, ensuring seafood safety is vital for food security.

While marine toxin monitoring programs are well-established, freshwater cyanotoxins in marine seafood remain largely overlooked, despite clear pathways of exposure. Between 2017 and 2025, we documented more than 200 instances of microcystins, cylindrospermopsin, and anatoxin-a across the marine food web—including in sediment, shellfish, fish, ducks, seabirds, crabs, snails, and feces. These findings highlight bioaccumulation and a critical gap in human health surveillance concerning marine-harvested foods.

Using a One Health framework, our research seeks to better understand the extent of freshwater toxin contamination in the marine environment and its transfer to seafood. By integrating freshwater and marine monitoring, we generate essential data to support tribal policy development, protect marine life, and safeguard the communities who rely on these ecosystems. This work illustrates the importance of a One Health approach in promoting ecosystem, animal, and human health through more resilient and sustainable food systems.

**Keywords**: cyanotoxins, seafood, monitoring

**Financing**: Funding provided by: National Science Foundation award #1840199 and #2332837, and United States Department of Agriculture/National Institute of Food and Agriculture award #017-38424-270979.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-073

# Toxic cyanobacteria in Brazil: New records and geographic distribution

**Taís Poletti**[1], Fernanda Rios Jacinavicius[1], Ernani Pinto[1]

(1) University of São Paulo, Division of Development of Nuclear Analytical Methods and Techniques, Center for Nuclear Energy in Agriculture (CENA), Avenida Centenário, 303 - São Dimas CEP: 13416-000, Piracicaba, Brazil

Toxic cyanobacterial blooms (CyanoHABs) represent a growing challenge to water quality and public health in Brazil. This study compiles data on the occurrence and geographic distribution of cyanotoxins across different regions of the country, based on 421 recorded events between 1993 and 2021. The species *Microcystis aeruginosa* and *Raphidiopsis raciborskii* were most frequently associated with toxin production, with a predominance of records in freshwater reservoirs. The analysis of isolated cyanobacterial strains revealed that a significant proportion exhibited toxicity, and many extracts contained compounds that remain unidentified. Analytical methods such as ELISA, LC-MS/MS, and Artemia salina bioassays were employed to detect and characterize cyanotoxins. The findings highlight important gaps in monitoring and point to the influence of climate change and water supply vulnerability on the intensification of CyanoHABs. This work underscores the urgent need to strengthen monitoring programs and to incorporate cyanotoxin-related risks into environmental management and public health strategies.

**Keywords**: Cyanotoxins, Water quality, Environmental monitoring

**Financing**: This work was funded by project 2023/10220-0 from the Public Policy Research Program (PPPP) of São Paulo Research Foundation (FAPESP) and supported by postdoctoral fellowships.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-074 (Ignite Talk)

# First report of potentially microcystin-producing *Microcystis* in the Dominican Republic

Alfaniris Vargas Fernandez[1], **Patri Isamir Ramirez Ramirez[1]**, Iris García Cruz[2], Claudia Reyes Gutierrez[3], Adrián Gutiérrez Cepeda[1], Alexander Valdez Disla[2], Roel Alejandro Chávez Luzania[4], Sergio de los Santos Villalobos[4], Pedro Leao[5], Vitor Vasconcelos[5,6]

(1) Autonómous University of Santo Domingo (UASD), Research Group on Natural and Marine Products, Faculty of Sciences and Faculty of Health Sciences, Dominican Republic.
(2) Autonomous University of Santo Domingo (UASD), Research Group on Natural and Marine Products, Faculty of Health Sciences, Dominican Republic
(3) Technological University of Santiago (UTESA), Faculty of Health Sciences, Dominican Republic
(4) Instituto Tecnológico de Sonora, 5 de Febrero 818 Sur, Col. Centro,, Ciudad Obregón, Sonora,, México
(5) Interdisciplinary Center for Marine and Environmental Research (CIIMAR), Blue Biotechnology and Ecotoxicology Group, Porto, Portugal
(6) University of Porto, Departament of Biology, Faculty of Sciences, Rua do Campo Alegre, 4169-007, Porto, Portugal

The increase in nutrients in freshwater bodies produces a rapid proliferation of cyanobacteria, increasing the risk of algal blooms and the generation of cyanotoxins in water sources for human consumption, agricultural irrigation, and animal husbandry. Project RLA7026 seeks to harmonize rapid detection methodologies for microcystins in Latin American countries facing similar problems with microalgal and/or cyanobacteria blooms. This study was conducted in the Valdesia reservoir, which supplies drinking water to approximately 4 million people in different locations in the Dominican Republic. The presence of the genus *Microcystis* was identified in this reservoir through morphological observation and the amplification and sequencing of two 16 rRNA
fragments, and a fragment of the mcyA gene associated with microcystin production. This first report highlights the urgent need to implement continuous monitoring of *Microcystis* sp., producer of microcystin in this reservoir, to establish appropriate water management measures and thus avoid harmful effects on public health and the environment.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-075

# Exploring microcystin-LR and its transformation products in waters by a comprehensive LC-HRMS target and suspect screening approach

Vasileios Alampanos[1,2], **Androniki Rapti[3],** Eleni Evgenidou[1,2], Dimitrios Bikiaris[3], Dimitra Lambropoulou[1,2]

(1) 1Laboratory of Environmental Pollution Control,, Chemistry, Aristotle University of Thessaloniki, GR-541 24 Thessaloniki, Greece, Thessaloniki, Greece
(2) Center for Interdisciplinary Research and Innovation (CIRI-AUTH), CIRI, Center for Interdisciplinary Research and Innovation (CIRI-AUTH), Balkan Center, Thessaloniki, GR-57001, Greece, Thessaloniki, Greece
(3) Laboratory of Polymer Chemistry and Technology,, Chemistry, Laboratory of Polymer Chemistry and Technology, Dept. of Chemistry, Aristotle University of Thessaloniki, GR-541 24 Thessaloniki, Greece, THESSALONIKI, Greece

Climate change and increasing eutrophication have led to a global rise in cyanobacterial blooms, which are a major source of toxic secondary metabolites known as cyanotoxins. Among these, microcystins (MCs)—cyclic heptapeptides commonly produced in eutrophic freshwater systems—are the most frequently reported and have been linked to numerous poisoning incidents in humans, livestock, and wildlife. Due to their significant ecological and public health implications, understanding the occurrence and distribution of MCs is critical. In recent years, attention has also expanded beyond the parent compounds to include their transformation products (TPs), which may persist in the environment and contribute further to toxicity and exposure risks. In this context, we offer a customized overview of transformation of microcystin-LR (MC-LR) transformation- one of the most frequently produced and most toxic forms - in aqueous matrices treated by photo-oxidation is provided as proof of concept. Hence, the primary goal of the study was to display an integrated strategy by combining the target (parent-molecule) and suspect screening-(SS) approaches to build an in-house High-Resolution mass spectrometry (HRMS) database able to provide reference information (chromatographic/spectral) for environmental investigations in freshwaters. $MS^2$ spectra were acquired using higher-energy collisional dissociation-(HCD), data-dependent acquisition (DDA), and $[M + 2H]^{2+}$ ions. Data analysis was performed by optimizing a SS workflow. This approach was applied for the tentative identification of more than 10 TPs of MCs. Finally, SS has been successfully applied for screening of MC-LR and its TPs in real samples.

**Keywords**: Microcystins;HRMS; Suspect Screening

**Acknowledgments**: This work is supported by the European Union's Horizon 2020 Research and Innovation Program under Grant Agreement No. 101057285 (SPECTRA Project).

Poster Session 01: Cyanobacteria & Freshwater HABs
P-076 (Ignite Talk)

# Application of non-thermal plasma technologies as an eco-friendly strategy for the treatment of cyanobacteria and health-relevant cyanometabolites

**Luciana Tartaglione[1],** Mara Simonazzi[2], Claudia D'Alterio[1], Franca Guerrini[2], Valentina Miele[1], Mubbshir Saleem[3], Giulia Tomei[3], Martina Varotto[3], Ester Marotta[3], Rossella Pistocchi[2]

(1) University of Naples Federico II, Pharmacy, Via Domenico Montesano, 49, 80131, Naples, Italy
(2) University of Bologna, Biological, Geological and Environmental Sciences, Via S. Alberto 163, 48123, Ravenna, Italy
(3) University of Padova, Chemical Sciences, via F. Marzolo, 1, 35122, Padova, Italy

The rising frequency and severity of cyanobacterial blooms in freshwater systems represent a growing threat to public health and drinking water safety, primarily due to the production of harmful secondary metabolites. To mitigate these risks, water treatment plants often apply chemical oxidants such as chlorine as a pre-treatment step, sometimes mandated by regional or national regulations. However, these traditional methods face limitations in efficacy—particularly regarding cell lysis and cyanotoxin degradation—and may produce harmful disinfection by-products. Non-thermal plasma (NTP) has emerged as a promising and environmentally friendly alternative for water treatment. NTP generates a mix of highly reactive species (e.g., ozone, hydroxyl radicals) upon contact with water, requiring only air and electricity for its production. Previous studies have demonstrated its ability to inactivate microorganisms and degrade persistent organic pollutants, suggesting its potential application in treating cyanobacteria-contaminated waters. This study investigates the feasibility of using NTP for the treatment of toxic cyanobacteria and their metabolites in freshwater. Custom-designed plasma reactors were tested on spiked freshwater samples containing various cyanotoxins and on cultures of the toxin-producing cyanobacterium Microcystis aeruginosa. Treatments were performed in triplicate across increasing exposure times, with untreated samples serving as controls. Key parameters such as cell viability, photosynthetic efficiency, physico-chemical parameters, and cyanometabolite profiles were assessed. Results showed significant impairment of photosynthetic activity and complete degradation of cyanotoxins within minutes of NTP exposure, as confirmed by LC-HRMS. These findings support NTP as a powerful, scalable, and sustainable disinfection method for the treatment of harmful cyanobacterial contaminations in drinking water sources.

**Keywords**: non-thermal plasma, cyanotoxins degradation, culture experiments

**Financing**: European Union–NextGenerationEU - Project Title “Cyanotoxins oxidation by atmospheric plasma, a green technology for water decontamination–PLASMADETOX” - CUP C53D23004460006.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-077

# The technology behind the RBRtridente and how it is ideal for the detection of harmful algal blooms

**Jon Taylor**[1]

(1) RBR, Engineering, 359 Terry Fox Drive, Ottawa, Canada

Accurate, in-situ quantification of photosynthetic pigments is critical for understanding phytoplankton dynamics. A significant challenge in fluorometry is the spectral overlap between key pigments, particularly the phycobilins—phycocyanin (PC) and phycoerythrin (PE)—which complicates their individual measurement and sensitivity to chlorophyll-a. To address this, we developed the RBRtridente, a novel multichannel active fluorometer. The sensor's design incorporates a highly constrained optical geometry to isolate a small measurement volume and utilizes custom narrow bandpass filters to precisely target the excitation and emission spectra of chlorophyll-a (excited at 435 or 470 nm), PC, and PE. This optical architecture is specifically engineered to reject off-axis light and minimize spectral crosstalk between channels. As a result, the RBRtridente achieves an exceptional limit of detection and high measurement specificity, with minimal interference from scattered light or fluorescence from non-target pigments. Coupled with low power consumption for extended deployments, the RBRtridente provides the scientific community with a robust and precise tool for high-resolution studies of phytoplankton community structure and physiology.

**Acknowledgments**: RBR Ltd.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-078

# The development, calibration, and in vivo characterisation of a phycocyanin and phycoerythrin fluorometer

**Jon Taylor**[1]

(1) RBR, Engineering, 359 Terry Fox Drive, Ottawa, Canada

.Accurate discrimination between phycobilin pigments and chlorophyll-a is essential for quantifying cyanobacterial populations in aquatic ecosystems. To address this, we have developed and characterised dedicated fluorometer channels for phycocyanin (PC) and phycoerythrin (PE). The optical design utilises narrow-band excitation and emission filters to precisely target phycobilin spectra while minimising crosstalk from other photosynthetic pigments.

Sensor calibration was performed against purified PC and PE standards, with concentrations verified spectrophotometrically. The channels demonstrated strong linearity and high sensitivity across a range of low pigment concentrations. Performance was further validated using mixed laboratory cultures containing both PC-rich cyanobacteria and chlorophyll-a dominant phytoplankton. Results from these in vivo tests confirm that the design successfully minimises the fluorescence signal from non-target pigments. Notably, the in vivo fluorescence yield per unit of pigment was significantly enhanced compared to the response from purified pigments (in vitro), highlighting the instrument's high sensitivity in live cells.

This robust calibration and demonstrated specificity establish these channels as a reliable tool for in situ monitoring of cyanobacterial communities, providing high-fidelity data even in complex, mixed phytoplankton assemblages.

**Acknowledgments**: RBR Ltd.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-079

# Genetic variability in the microcystin (mcy) operon in both toxin and non-toxin producing *Microcystis* isolates

**Rebecca Tietze**[1], Katelyn McKindles[1,2]

(1) Baylor University, Biology, 1 Bear Place #97388, Waco, United States
(2) Baylor University, Center for Reservoir and Aquatic Systems Research (CRASR), 1 Bear Place #97178, Waco, United States

*Microcystis aeruginosa* is a globally distributed cyanobacterium that causes harmful algal blooms and often produces microcystin, a toxin harmful to humans and animals. Monitoring blooms and toxins is vital for environmental safety; one approach uses PCR primers to detect toxin genes. We tested 10 published primers targeting regions of the microcystin (mcy) operon on DNA extracted from 41 M. aeruginosa strains, including both toxin-producing and non-toxin-producing strains. These primers occasionally failed to show specificity for the toxic strains or against the non-toxic strains tested. To explain this failure, we then cloned and sequenced the mcy operon across both toxin and non-toxin producers. Cloning consisted of amplifying short overlapping regions (2-3 kbp) and long overlapping regions (20-40 kbp) as many of the primers used for short overlapping cloning failed to amplify their mcy operon targets. Primer failure and sequencing suggest significant variation in the operon among *M. aeruginosa* strains, highlighting the challenge of developing primer sets that could successfully test for the presence of toxin genes for many M. aeruginosa strains and account for the variation between them.

**Keywords**: *Microcystis*, Microcystin

**Financing**: This research was supported by the Baylor Undergraduate Research and Scholarly Achievement (URSA) grant.

Poster Session 01: Cyanobacteria & Freshwater HABs
P-080

# Molecular and toxicological characterization of cyanobacteria harmful algal blooms (CyanoHABs) in recreational waters of southern Chilean lakes

**Tamara Villalobos Oyarce**[1], Katerina González[2], Benjamín Suárez-Isla[1], Carlos García[1]

(1) Laboratory of Marin Toxins, Universidad de Chile, Department of Physiology, Faculty of Medicine, Independencia #1027, Santiago, Chile
(2) Physiology Laboratory, Universidad Católica de Temuco, Department of Biological and Chemical Sciences, Faculty of Natural Resources, Manuel Montt #056, Temuco, Chile

Globally, CyanoHABs have increased their prevalence and incidence in different inland water bodies. Chile has not been the exception, and the challenge has arisen to implement techniques for monitoring the identification of blooms that have occurred in the last 5 years. The objective of this study is to characterize the algal blooms that have occurred in 2 lakes in Chile with potential toxic impact. Water samples obtained from algal blooms in lakes Llanquihue (Los Lagos Region) and Villarrica (Araucanía Region) were collected and evaluated morphologically and by PCR quantification (16sRNA; mcyA; sxtA). The presence of cyanotoxins was analyzed by liquid chromatography (LC-pre-ox-FLD). The results obtained indicate that Lake Villarrica has a high prevalence of species of the genus *Dolichospermum*, with toxicities above the WHO reference value for human consumption (STX-group). On the other hand, no cyanobacteria species were detected in Lake Llanquihue; however, in wetlands near the lake, the presence of species of the genus Microcystis was detected. These results show the risk of cyanoHABs in Chile and to public health considering the high tourist activity in the area. The application of this set of techniques could be used in regular monitoring for the prevention and control of cyanoHABs in inland waters intended for human consumption or recreational purposes. In addition, it is pertinent to consider in the future the evaluation of the impact on the trophic chain by monitoring the toxicity of fish, crustaceans and mollusks that may be consumed by the local community.

**Keywords**: Cyanotoxins, Water bodies, Public Health

**Financing**: This research was funded by the International Atomic Energy Agency (IAEA), grant number RLA/7/026 ARCAL CLXXVIII.

**Acknowledgments**: Project RLA-7026 (ARCAL CLXXVIII); Department of Basic-Clinical Oncology and LABTOX U. de Chile; SERNAGEOMIN; Universidad Católica de Temuco; CCHEN.

Poster Session 02: Ichthyotoxic HABs
P-081 (Ignite Talk)

# Why are some blooms of the haptophyte *Prymnesium parvum* harmful but others not?

**Jan Köhler[1],** Paula Torre Zaffaroni[1], Karla Münzner[1], Shambhavi Parmar[1], Sven Würtz[1], Stephanie Spar[1], Tobias Goldhammer[1], Heiner Kuhl[1], Matthias Stöck[1], Elisabeth Varga[2]

(1) Leibniz Institute of Freshwater Ecology and Inland Fisheries, Müggelseedamm 301, Berlin, Germany
(2) University of Veterinary Medicine, Clinical Department for Farm Animals and Food System Science, Unit Food Hygiene and Technology, Centre for Food Science and Veterinary Public Health, Veterinärplatz 1, Vienna, Austria

The lowland River Oder (Poland/Germany) experienced heavy blooms of the haptophyte *Prymnesium parvum* (“golden algae”) in August 2022 and June 2024. During the first bloom, these algae produced B-type prymnesins which killed about 1000 t of fish and most of the mussel populations. The second bloom was genetically almost identical and of similar abundance as the first one but non-toxic. To better understand the drivers of toxin production, we compared environmental conditions and biomass development along the river at these two events. Additionally, we measured growth rates and toxin production of a laboratory culture isolated from the river (ODER1) as a function of salinity and nutrient supply. Both blooms originated from brine storage basins in Upper Silesia and further grew during downstream transport. Along the river, salinity and N:P ratio tended to decline at both events. Despite these longitudinal changes, fish kills were either observed everywhere (2022) or nowhere (2024). In the lower River Oder, salinity was around 1 ppt at both events. In the lab, growth rates of the ODER1 strain declined at salinities below 2 ppt, but toxin production was the highest at 1 ppt. The mean nitrate concentrations and N:P ratios were much higher at the non-toxic event. The most likely trigger of toxin production by this strain was a relative shortage in nitrogen supply. Only a substantial reduction in salt and nutrient loads would prevent future potentially toxic algal blooms.

**Keywords**: *Prymnesium* growth, toxin production, nutrient supply

Poster Session 02: Ichthyotoxic HABs
P-082 (Ignite Talk)

# Autecology and impacts of *Heterosigma akashiwo* in low-inflow estuaries: From research to management

**Daniel Lemley**[1,3], Janine Adams[1,3], Nadine Strydom[2]

(1) Nelson Mandela University, Botany, Science, PO Box 77000, University Way, Summerstrand, Gqeberha, South Africa
(2) Nelson Mandela University, Zoology, Science, PO Box 77000, University Way, Summerstrand, Gqeberha, South Africa
(3) Nelson Mandela University, DSI/NRF Research Chair in Shallow Water Ecosystems and the Institute for Coastal and Marine Research, Science, Gqeberha, South Africa

Harmful algal blooms (HABs) have increased ubiquitously in response to global change pressures. The health of South African estuaries is on a downward trajectory, with more than a third of the country's 290 estuaries being affected by nutrient pollution and freshwater inflow reductions. This degradation of ecosystem health is highlighted by the emergence of the HAB species *Heterosigma akashiwo* (Class Raphidophyceae). Over the last decade, *H. akashiwo* has been recorded in 10 estuaries along the warm temperate south coast, with high-biomass (≥ 60 µg Chl-a $l^{-1}$) accumulations observed in five of these. As such, research efforts have shifted towards focusing on identifying the drivers and impacts of this ichthyotoxic species. From an ecological niche perspective, the species typically occurs in brackish (salinity ~ 17), warm (>20°C), and stratified conditions, where it employs diel vertical migration to access resources and limit advective losses. In terms of harmful impacts, blooms of *H. akashiwo* in South African estuaries have been shown to (1) induce extreme dissolved oxygen conditions (i.e., supersaturated to hypoxic), (2) suppress co-occurring plankton species, (3) inhibit the abundance, development, and biochemical condition of larval fish, (4) influence the abundance, richness, gill morphology, and behaviour of adult fishes, and (5) cause mass fish mortality events. Additionally, estuarine accumulations of *H. akashiwo* potentially act as seed populations for adjacent coastal waters. This talk will demonstrate how the information gathered through these research efforts has been used to inform management interventions and cooperative governance initiatives.

**Keywords**: *Heterosigma akashiwo*, Ichthyotoxic, Eutrophication

**Financing**: Department of Science and Innovation (DSI) / National Research Foundation (NRF) South African Research Chair in Shallow Water Ecosystems (UID: 84375)

**Acknowledgments**: The Nelson Mandela University is thanked for providing research fellowship funding and facilities to lead author Dr. Daniel A Lemley.

Poster Session 02: Ichthyotoxic HABs
P-083

# Intraspecific differences in the effects of salinity on growth and prymnesin production in *Prymnesium parvum*

**Fredrik Ryderheim**[1], Elizabeth M. Mudge[2], Andrea Budisa[4], Kevin J. Flynn[3], Jack Gillies[2], Thomas Ostenfeld Larsen[5], Per Juel Hansen[1]

(1) University Of Copenhagen
(2) National Research Council Canada
(3) Plymouth Marine Laboratory
(4) The Netherlands Institute of Ecology
(5) Technical University of Denmark

*Prymnesium parvum* is a toxin-producing haptophyte known for forming harmful blooms in brackish and inland waters. While salinity has been proposed as a key factor influencing bloom dynamics, the relationship between salinity and toxin production remains poorly understood. We investigated the effect of salinity on prymnesin production across three strains of *P. parvum*. Our results show that while the species can grow across a broad salinity range, prymnesin production is significantly reduced at low salinities—likely due to resource allocation toward coping with hypoosmotic stress. In two strains, elevated toxin quotas under salinity stress were attributed to intracellular accumulation caused by reduced cell division rates, rather than increased synthesis. We also observed substantial intraspecific variation in physiological responses to salinity, yet identified consistent negative correlations between growth rate and cellular prymnesin content. These findings suggest that prymnesin production incurs physiological costs and highlight the importance of strain-specific responses in understanding bloom toxicity and environmental adaptability.

**Keywords**: prymnesins, intraspecific variation, *Prymnesium parvum*

**Financing**: Independent Research Fund Denmark

Poster Session 02: HABs in a Changing World & Emerging Issues
P-084

# Interannual variability of *Alexandrium catenella* in the Sub-Antarctic Magallanes Region: Links to ENSO Events

**César Alarcón**[1], Nicolás Butorovic[2], Gemita Pizarro[1], Carolina Toro[1], Marta Godoy[1]

(1) Instituto de Fomento Pesquero, Medio Ambiente - Centro de Estudio de Algas Nocivas CREAN, División de Acuicultura, Enrique Abello 0552, Punta Arenas, Chile
(2) Universidad de Magallanes, Geociencias y Laboratorio de Climatología, Instituto de la Patagonia, Avenida Bulnes 01890, Punta Arenas, Chile

Between 2006 and 2024, the presence of *Alexandrium catenella* was monitored at multiple stations in the sub-Antarctic region of Magallanes. This dinoflagellate species is responsible for toxic blooms that affect bivalve mollusks, posing risks to human health and causing economic losses in aquaculture. The analysis of 18 years of quantitative data reveals significant interannual fluctuations in cell abundance, with notable peaks in 2009 (90,900 cells/L) and 2010 (41,000 cells/L). These blooms coincided with a moderate-to-strong El Niño event (2009–2010), suggesting a possible influence of anomalous ocean-atmosphere conditions associated with ENSO on the population dynamics of this microalga.
In contrast, La Niña years (such as 2011 and 2022) exhibited lower abundance levels, supporting the hypothesis that warm and stratified conditions favor the proliferation of *A. catenella*. These findings highlight the importance of considering interannual climate variability as a modulator of harmful algal bloom (HAB) events and reinforce the need to maintain continuous monitoring programs—especially under climate change scenarios that may increase the frequency of ENSO events or other extreme climate phenomena in the near future.

**Keywords**: *Alexandrium catenella*, ENSO, Harmful Algal Blooms

**Financing**: Instituto de Fomento Pesquero, Centro de Estudio de Algas Nocivas, Instituto Milenio Biodiversidad de Ecosistemas Antárticos y Subantárticos (BASE), Santiago, Chile

**Acknowledgments**: Instituto de Fomento Pesquero, Centro de Estudio de Algas Nocivas, Instituto Milenio Biodiversidad de Ecosistemas Antárticos y Subantárticos (BASE), Santiago, Chile

Poster Session 02: HABs in a Changing World & Emerging Issues
P-085 (Ignite Talk)

# Flexible feeding in changing fjords: Trophic plasticity of bivalves facing harmful algal blooms and glacial influences in Southern Chile

**Claudia Andrade Diaz**[1], Taryn Sepúlveda[1], Cristian Aldea[1,2,3], Cristóbal Rivera[1], Melissa Ruiz[1,2], Jesús Troncoso[4]

(1) Universidad de Magallanes, Laboratorio de Ecología Funcional, Instituto de la Patagonia, Av. Pdte. Manuel Bulnes 01890, Punta Arenas, Chile
(2) Universidad de Magallanes, Departamento de Ciencias y Recursos Naturales, Facultad de Ciencias, Av. Pdte. Manuel Bulnes 01855, Punta Arenas, Chile
(3) Universidad de Magallanes, Centro de Investigación Gaia-Antártica, Instituto de la Patagonia, Av. Pdte. Manuel Bulnes 01855, Punta Arenas, Chile
(4) Universidade de Vigo, Centro de Investigación Mariña, EcoCost, Edificio Filomena Dato Campus de Vigo 36310, Vigo, España

Bivalves such as *Aulacomya atra* (mussel) and *Austrochlamys natans* (scallop) play ecologically and functionally relevant roles in sub-Antarctic benthic communities and are locally consumed in southern Chile. This study explores their trophic responses to environmental variability in fjord ecosystems influenced by harmful algal blooms (HABs) and glacially shaped conditions. Using stable isotope analysis ($\delta^{13}C$ and $\delta^{15}N$), we examined differences in carbon sources and trophic positioning across Parry Bay, Ballena Sound, and the Kawésqar National Reserve—an area recurrently affected by HABs.

Preliminary results reveal distinct isotopic patterns between species and sites. The scallop *A. natans* exhibited broader $\delta^{13}C$ ranges in Parry Bay (to –20.3 ‰), suggesting access to heterogeneous or allochthonous carbon inputs. In contrast, individuals from Kawésqar showed enriched and consistent $\delta^{13}C$ values (up to –17.1‰), potentially reflecting a more uniform primary production regime, possibly influenced by recurrent blooms. The mussel *A. atra* displayed narrower but site-specific isotopic shifts, indicating some trophic flexibility. Higher $\delta^{15}N$ values in Parry Bay (up to 11.95‰) may reflect trophic enrichment linked to glacial or remineralized nitrogen sources. These findings highlight species-specific trophic plasticity and underscore the utility of bivalves as early indicators of ecological change. Stable isotope signals provide valuable insights into how benthic food webs may reorganize in response to shifting environmental baselines associated with climate change and anthropogenic pressures, including HABs.

**Keywords**: trophic plasticity, stable isotopes, fjord ecosystems

**Financing**: This research was funded by the National Research and Development Agency of Chile – ANID (FONDECYT Initiation No. 11241322, Claudia Andrade).

**Acknowledgments**: The authors would like to thank Leonardo Guzmán, Gemita Pizarro (IFOP, Chile), and CACTI (Vigo, Spain) for their technical and scientific support during this study.

Poster Session 02: HABs in a Changing World & Emerging Issues
P-086

# Harmful algae in Spanish ports: eDNA metabarcoding and microscopy reveal emerging risks in high-traffic maritime hubs associated with ballast waters

**Jone Bilbao**[1,2], Christina Pavloudi[3], Sergio Seoane[1,2]

(1) University of the Basque Country, UPV/EHU, Department of Plant Biology and Ecology, Faculty of Science and Technology, Leioa, Spain
(2) University of the Basque Country, UPV/EHU, Research Centre for Experimental Marine Biology and Biotechnology (Plentzia Marine Station, PiE- UPV/EHU), Plentzia, Spain
(3) European Marine Biological Resource Centre (EMBRC-ERIC), Paris, France

Ports are critical hotspots for biological exchange, where maritime traffic, mainly via ballast water, facilitates the unintentional introduction and spread of harmful aquatic organisms and pathogens (HAOP), including harmful algae. With over 80% of global trade transported by sea, these dynamics pose increasing ecological and economic risks. This study assesses the composition and ecological risk of harmful phytoplankton in three major Spanish ports (Algeciras, Bilbao and Valencia) combining microscopy and eDNA metabarcoding during seasonal campaigns in 2023. It constitutes the first report of harmful algae in Algeciras and Valencia ports, and enabled novel detections in Bilbao. A total of 55 HAB-relevant species (36 toxic, 19 bloom-forming) were identified. Sixteen species appeared in over 80% of samples and were ubiquitous across ports, including toxic *Prorocentrum mexicanum*, *Pseudo-nitzschia seriata* and *Dinophysis acuminata* and bloom-forming *Chaetoceros tenuissimus* and *Gyrodinium jinhaense*, confirming their establishment in Spanish port waters. Port-specific patterns also emerged: Algeciras hosted 45 species and uniquely recorded Noctiluca scintillans, *Chaetoceros debilis* and *Eucampia zodiacus*; Valencia showed the highest richness (46 species) and notable presence of *Dinophysis norvegica* and *Pseudo-nitzschia pseudodelicatissima*; and Bilbao, though hosting fewer species (39), had strong presence of the toxic Chrysochromulina leadbeateri and *Heterosigma akashiwo*. Moreover, EU toxicity thresholds were exceeded by *Alexandrium* spp., *Dinophysis* spp. and *Pseudo-nitzschia* spp. in Bilbao and Valencia ports. Overall, the continuous presence and occasional alert-level concentrations of harmful algae underscore the need for enhanced monitoring and early-warning systems in Spanish ports, to protect coastal ecosystems under intensifying maritime traffic and climate pressure.

**Keywords**: Ports, Ballast water, harmful algae

**Financing**: Partially supported by project IT1471-22 funded by the Department of Education of the Basque Government and project TED2021-130994B-C33 funded by MICCIN.

Poster Session 02: HABs in a Changing World & Emerging Issues

P-087

# Harmful Algal Blooms (HABs) in the Tohoku Region of Japan: A scoping review

**Sang Bobbitt Hanna**[1]

(1) Tohoku University, Graduate School of Agricultural Science, Agriculture, Agricultural Research and Administration Facility,468-1 Aoba-ku, Aramaki Aza-Aoba, Sendai 980-0845, Japan

Harmful algal blooms (HABs) are an escalating threat to Japan's coastal ecosystems, fisheries, and public health, driven by both natural variability and human-induced environmental change. This study combines a comprehensive literature review with a statistical analysis using AI to investigate the correlation between regional HAB occurrences and their ecological and socio-economic impacts, including mass fish mortalities, fisheries revenue loss, and recreational disruptions. Strong positive correlations were found between bloom frequency and these adverse outcomes, reinforcing the need for early detection and response strategies. In addition to analyzing existing data, this study proposes the development of key research tools—such as a large language model for text data analyses, a binomial identification key for dominant bloom species, and region-specific bloom prediction models. These tools are essential for transforming HAB management in Japan from reactive to proactive, and for supporting sustainable marine resource use in the face of increasing environmental pressures.

**Keywords**: Harmful Algal Blooms (HABs), Fisheries Impacts, Large Language Model

**Financing**: Tohoku University's International Marine Sciences Laboratory, Ocean Shot, the World Premier International Research Center Initiative Advanced Institute for Marine Ecosystem Change Institute (WPI-AIMEC).

**Acknowledgments**: Dr. Cheryl Lynn Ames, Tohoku University Graduate School of Agricultural Science International Marine Sciences Laboratory, Sasakawa Peace Foundation Ocean Shot, WPI-AIMEC.

Poster Session 02: HABs in a Changing World & Emerging Issues
P-088 (Ignite Talk)

# Initial assessments of nitrogen-induced 'tipping points' for harmful algal bloom development in New York/Connecticut (USA) estuaries

**Dianne Greenfield**[1,2], Mariapaola Ambrosone[1], Julia Sandke[2]

(1) City University of New York, Advanced Science Research Center, 85 Saint Nicholas Terrace, New York, USA
(2) Queens College, School of Earth and Environmental Sciences, 65-30 Kissena Avenue, Flushing, USA

Urban estuaries, such as those surrounding New York City (NYC), tend to be chronically enriched by anthropogenic nitrogen (N) inputs from wastewater, runoff, and other sources. In the NYC region, much of this wastewater comes from combined sewer overflow (CSO) systems. CSOs discharge N-rich wastewater directly to adjacent rivers and embayments, causing multiple harmful algal blooms (HABs) as well as other ecosystem impairments. Previous work in Greenfield's lab has showed that dissolved inorganic N (DIN)-form, particularly elevated ammonia+ammonium, which is a primary component of effluent, can be associated with excessive growth of flagellated phytoplankton species in Long Island Sound (LIS), including HAB dinoflagellates. Conditions increasing DIN levels, such intense storms mobilizing N-rich wastewater inputs, may therefore favor dinoflagellate HABs over other taxa (e.g., non-toxigenic diatoms) that tend to be characteristic of 'healthy' ecosystems in LIS. Here we describe observations from multi-year, interdisciplinary research testing how proximity to wastewater, particularly inputs enriched with DIN, influences the incidences and relative abundances of HABs (emphasizing dinoflagellates and toxigenic diatoms) in NY/CT estuaries. Multiple systems (LIS and adjacent embayments) were surveyed for physical water quality, nutrients, HABs, chlorophyll a, toxin levels, and bacteria using both discrete water sampling and paired autonomous underwater surveys. HAB species identifications and cell abundances were quantified using light microscopy, sandwich hybridization assay, and fluorescent in-situ hybridization. Observations are placed within the context of storm-induced CSO events that deliver elevated bacteria, N, and pollutant contamination to receiving waterways. Results are broadly relevant to developing coastlines and nutrient management, globally.

**Keywords**: Nitrogen, urban estuaries, water quality management

**Financing**: Long Island Sound Study, New York/Connecticut Sea Grant

Poster Session 02: HABs in a Changing World & Emerging Issues
P-089 (Ignite Talk)

# Multi-stressor dynamics: Effects of marine heatwave stress and harmful algal blooms on juvenile mussel (*Perna canaliculus*) survival and physiology

**Hannah Greenhough**[1,2], Julien Vignier[1], Kirsty F Smith[1], Chris M Brown[2], Nathan J Kenny[2], Anne Rolton[1]

(1) Cawthron Institute, 98 Halifax Street East, Nelson, New Zealand
(2) University of Otago, Department of Biochemistry Te Tari Matū Koiora, School of Biomedical Sciences, Dunedin, New Zealand

Marine heatwaves (MHWs) and harmful algal blooms (HABs) are increasing in frequency and intensity around New Zealand, concurrently affecting regions where the green-lipped mussel (*Perna canaliculus*) is naturally abundant or commercially farmed. This study investigated the effects of MHW conditions and exposure to the toxic dinoflagellate *Alexandrium pacificum* on juvenile mussels (spat), both individually and in combination. Spat were exposed to control (17 °C) or MHW (22 °C) temperatures, along with two environmentally relevant concentrations of A. pacificum for four days, followed by a four-day recovery period.

The MHW temperature alone had no detrimental effect on mussel survival; however, exposure to A. pacificum at both temperatures led to reduced spat survival, especially at higher microalgal concentrations (< 90 % survival vs 100 % at the control temperature, no *A. pacificum).* In the combined exposure to the MHW temperature and A. pacificum, the stressors interacted synergistically to result in significantly reduced spat survival, dropping to 59%.

Exposure of mussels to *A. pacificum* alone showed marked reductions in byssal plaque production (up to four-fold), reduced growth (over 7.5-fold slower), tissue-level damage, and significant changes in gene expression, particularly in pathways related to lipid metabolism and detoxification.
These findings highlight the compounding effects of multiple environmental stressors and emphasize the need to better understand their combined impact, particularly in the context of climate change and the increasing prevalence of HABs in coastal ecosystems.

**Keywords**: *Alexandrium pacificum*, Climate change, Multiple stressors

**Financing**: Rutherford Discovery Fellowship RDF-UOO2001 from the Royal Society of New Zealand, MBIE funding (CAWX1801, CAW2438), University of Otago PhD Scholarship.

**Acknowledgments**: Rodney Roberts, Luke Johnston (SPATnz) for spat provision; Jordan Elvy, Carol Peychers for technical support; Otago Genomics Facility for sequencing assistance.

Poster Session 02: HABs in a Changing World & Emerging Issues
P-090

# *Pseudo-nitzschia* in Icelandic waters: Insights from long-term monitoring and sedimentary ancient DNA

**Sara Harðardóttir**[1], Kirstine Drumm[1], Kristín Valsdóttir[1], Steingrímur Jónsson[1], Nina Lundholm[2]

(1) Marine and Freshwater Research Institute of Iceland, Fornubúðum 5, Hafnarfjörður, Iceland
(2) University of Copenhagen, Natural History Museum of Denmark, Øster Voldgade 5-7, Copenhagen, Denmark

Shifts in oceanographic conditions have led to significant changes in the composition of phytoplankton communities across the North Atlantic and Polar regions, with a northward expansion of temperate phytoplankton. Iceland is positioned at the intersection of two waterfronts with different ecosystems making it an ideal place to study occurrences and bloom dynamics of HABs in a changing world. The spring bloom is a key event in the Arctic, and by long term monitoring of phytoplankton, we have collected samples at several coastal and oceanic sites since the 1950s during the spring bloom event. In this study, we investigate if there has been an increase in occurrences of the toxigenic diatom genus *Pseudo-nitzschia* in the North Atlantic water mass correlated to changes in water temperature and salinity. At several study sites. *Pseudo-nitzschia* spp. was enumerated and when possible, compared with eDNA results. We show the occurrences of *Pseudo-nitzschia* spp. over 15 years in spring at Selvogsbanki and Faxaflói, south and southwest of Iceland, respectively. By retrieving sedimentary ancient DNA from a dated sediment core from the Selvogsbanki area, we investigate occurrences *Pseudo-nitzschia* decades back in time. The results of this survey will provide a baseline for future assessment of *Pseudo-nitzschia* in the North Atlantic.

**Keywords**: North Atlantic, Diatoms, oceanographic conditions

Poster Session 02: HABs in a Changing World & Emerging Issues

P-091

# Coastal wildfires as a cause of increases in marine harmful algal blooms and phytoplankton

**Shauna Murray[1],** Penelope Ajani[1], Torrington Callan[1], Stephen Woodcock[1], Jaimie Potts[2], Peter Scanes[2], Matthew Tesoriero[1], Timothy M. Remaili[2], Arjun Verma[1], Hazel Farrell[3], Anthony Zammit[3], Steve Brett[4], William Maher[5], Wayne O'Connor[6], Mike Dove[6], Timotej Turk Dermastia[7], Janja Francé[7], Pamela Carbonell[8], Rebecca Gibson[2], Mia A. Bodycombl[2,3], Dóra Víg[1]

(1) University of Technology Sydney, School of Life Sciences, Sydney, PO Box 123, Broadway NSW 2007, Australia
(2) NSW Department of Climate Change, Energy, the Environment and Water, 480 Weeroona Rd, Lidcombe NSW 2141, Australia
(3) NSW Food Authority, NSW Department of Primary Industries and Regional Development, PO Box 232, Taree 2430, Australia
(4) Microalgal Services, 308 Tucker Rd, Ormond 3204, Australia
(5) Research School of Earth Sciences, Australia National University, Canberra, ACT.
(6) New South Wales Department of Primary Industries and Regional Development, Port Stephens Fisheries Institute, Taylors Beach, NSW, 2316, Australia
(7) National Institute of Biology, Marine Biology Station Piran, Fornače 41, 6330 Piran, Slovenia
(8) Fisheries Development Institute, Padre Harter 574, Puerto Montt, Chile

Globally, climate change is increasing the frequency and severity of wildfires, including along coasts, and in the process changing coastal marine phytoplankton communities. As phytoplankton places an upper limit on seafood production, modest increases in harmful algal blooms can cause large detrimental impacts, quantifying change is critical. Here, we determined wildfire severity in catchments using Fire Extent and Severity Mapping (FESM) and modelled wildfires of varying severity across ~1000 km of subtropical/warm-temperate Australian coasts and estuaries over 8 years. We found an ~100% increase in phytoplankton and a 38% increase in harmful *Dinophysis* spp. in the two months following high severity fires but not following low severity fires. When these models were extended to other warm-temperate zones in both hemispheres (Chile, north-western USA and Slovenia), post-fire changes in phytoplankton change following fires were predicted by fire severity in adjacent catchments. N and P increased following the fires but could not explain all observed changes in phytoplankton abundance, suggesting that a significant shift in pyrogenic trace metals, which are potentially limiting, may have been important. Model outputs suggest that wildfires alone may lead to an increase of 1.4% in coastal phytoplankton biomass this century, compounding already documented coastal HAB increases during peak Spring/Summer growth seasons.

**Keywords**: fire, harmful algal bloom, modelling

**Financing**: Bushfire Local Economic Recovery Fund, co-funded by the Australian and NSW Governments in association with the Food Agility CRC and the NSW Farmer's Association.

Poster Session 02: HABs in a Changing World & Emerging Issues
P-092 (Ignite Talk)

# CyanoHABs transfer along a freshwater-marine continuum and potential associated risks: Case of the Jacarepaguá Lagoon System (RJ, Brazil)

**Mauro Cesar Palmeira Vilar**[1], Suema Branco[1], Ricardo Rogers Paranhos[1], Michael Ribas Celano[1], Aloysio da Silva Ferrão-Filho[2], Sandra Azevedo[1]

(1) Federal University of Rio de Janeiro, Carlos Chagas Filho Institute of Biophysics, Laboratory of Ecophysiology and Toxicology of Cyanobacteria, Rio de Janeiro, Brazil
(2) Oswaldo Cruz Foundation, Oswaldo Cruz Institute, Laboratory of Environmental Health Evaluation and Promotion, Rio de Janeiro, Brazil

Eutrophication and climate change have increased harmful cyanobacterial blooms (CyanoHABs) worldwide, posing risks to environmental and public health. Some cyanobacteria produce toxins, especially microcystins (MCs), which are mainly studied in freshwater but less so in marine environments, especially in hydrological connections where cyanobacteria can be transferred from inland to coastal waters. This study assessed CyanoHABs transference risks along the Jacarepaguá lagoon system to the coastal zone in Rio de Janeiro, Brazil. Water samples were collected from 2020 and quarterly between 2022-2024 at seven sites, focusing on low tide to capture lagoon influence on the beach. Physical-chemical parameters ($O_2$, pH, salinity, temperature) were measured, and samples were analyzed for microcystins by ELISA and LC-MS. Phytoplankton biomass was assessed through chlorophyll-α and cell counts. A salinity gradient (1.3 to 34.6) was observed along the freshwater-marine continuum, with dissolved oxygen ranging 0.48-18.64 mg/L and temperatures from 20.4 to 31.6 °C. In 2020, *Microcystis aeruginosa* dominated (>90%), with MC-LR concentrations detected up to 37.3 µg/L near the coastal channel, exceeding WHO recreational risk levels. Between 2022-2024, *Planktothrix isothrix* predominated, with minimal *Microcystis* presence and low MC-LR detection (<1 µg/L). Cyanobacterial densities remained high (>$10^6$ cells/mL), and chlorophyll-α patterns indicated sustained biomass with WHO alert levels met for recreational exposure and fishing risks. The study confirms CyanoHAB contamination of the coastal zone, suggesting the beach was unsafe for fishing and water activities due to toxin exposure, recommending local warnings to limit contact and inhalation risks from cyanotoxin bioaerosols.

**Keywords**: Microcystins, Brackish waters, Cyanobacteria

**Financing**: FAPERJ (Carlos Chagas Filho Foundation for Research Support in the State of Rio de Janeiro).

Poster Session 02: HABs in a Changing World & Emerging Issues
P-093 (Ignite Talk)

# Implication of nitrogen and sulfur limitation on resources allocation and dimethylsulfoniopropionate (DMSP) production in toxic dinoflagellates

**Laura Pezzolesi**[1], Lorenzo Montalbetti[1], Giorgia Zoffoli[1], Andrea Facchin[2], Cristian Torri[2], Rossella Pistocchi[1]

(1) University of Bologna, Department of Biological, Geological and Environmental Sciences (BiGeA), Via Sant'Alberto 163, 48123 Ravenna, Italy
(2) University of Bologna, Department of Chemistry "Giacomo Ciamician", Via P. Gobetti 85, 40129 Bologna, Italy

In recent decades, the impacts of climate change on marine ecosystems have become increasingly evident, particularly in semi-enclosed basins such as the Mediterranean Sea. Notable effects include the rise in sea surface temperatures, reduced vertical mixing, and the consequent depletion of key nutrients, especially nitrogen (N) and sulfur (S), in the upper water layers. These alterations, combined with changes in light and temperature regimes, can significantly influence the growth dynamics of dinoflagellates and the synthesis of ecologically and climatically relevant compounds, such as toxins, dimethyl sulfide (DMS), and its precursor dimethylsulfoniopropionate (DMSP). These compounds play a crucial role in marine trophic interactions and atmospheric processes; a decrease in DMS/DMSP production could reduce the formation of cloud condensation nuclei (CCN), enhancing solar radiation penetration and contributing to further ocean warming.

This study investigates the effects of nitrogen and sulfur limitation on the growth, metabolic activity, and production of DMS/DMSP in two toxic dinoflagellate species, *Ostreopsis* cf. *ovata* and *Alexandrium minutum*. Experimental results demonstrate that nutrient availability strongly modulates cellular proliferation and the synthesis of osmoregulatory compounds. Under sulfur-limited conditions, cells appear to reallocate metabolic resources toward protein synthesis, leading to reduced DMSP production.

These findings underscore the importance of nutrient balance for optimal growth and metabolic regulation in dinoflagellates. Furthermore, they provide novel insights into the physiological strategies employed by these species under nutrient stress, with implications for understanding their ecological role and potential feedback in climate-relevant biogeochemical cycles, particularly during harmful algal bloom events intensified by climate change.

**Keywords**: nitrogen and sulfur deficiency, toxins, dimethylsulfoniopropionate

**Financing**: NRRP,Mission 4,Component 2,Investment 1.1,Call for tender No.104 published on 2.2.2022 by the Italian Ministry of University and Research,funded by EU–NextGenerationEU–Project INPHOMARE–CUP J53D23006610001.

**Acknowledgments**: We gratefully acknowledge Fondazione Centro Ricerche Marine, Italian NRL for Marine Biotoxins, for analytical support with the determination of dinoflagellate paralytic shellfish toxins.

Poster Session 02: HABs in a Changing World & Emerging Issues

P-094

# Plastisphere, the plastic “microcities” colonized by harmful microalgae

**Estela Pires**[1], Maria Carolina Slota Kutz[1], Ana Beatriz Mendes[2], Izabel Cristina Riegel-Vidotti[2], Luiz Mafra Jr[1]

(1) Federal University of Paraná, Center for Marine Studies, 83255-000, Pontal do Paraná, Brazil
(2) Federal University of Paraná, Chemistry Department, 81531-990, Curitiba, Brazil

The increasing presence of microplastics (MP) in the marine environment provides a surface area suitable for colonization by harmful benthic microalgae and the adsorption of their phycotoxins. Changes in the physicochemical characteristics of MP during their degradation, however, are expected to affect these interactions. To investigate how the composition, shape, size, and surface roughness of MP affect the colonization of benthic microalgae cells and dissolved phycotoxins, we conducted seven-day experiments with the okadaic acid (OA)-producing dinoflagellate *Prorocentrum lima*. Cell colonization began within 24 h, being more intense on ~750 µm polystyrene microspheres (mean=11.7 cells/mm$^2$) and 500×1000 µm cuboidal fragments (mean=7.0), and much reduced on 11,000×50 µm polypropylene microfibers (mean=0.28), which were probably too narrow and light to interact with these cells at the bottom. OA adsorption was greater on smaller (50 µm) MP (up to 8.0 pg mm$^{-2}$ in 168 h) than on 750 µm MP. Furthermore, adsorption was intensified on MPs with surface modified by abrasion, UV, or biodegradation. Our findings emphasize that surface area and size play a significant role in cell adhesion. Additionally, plastic pollution can worsen the adverse effects of harmful benthic algal blooms on marine organisms. During *P. lima* blooms, aged microplastics covered by adsorbed toxins or toxin-containing cells may increase the accessibility of these harmful substances to a variety of marine organisms. This is intensified through the formation of MP aggregates covered by harmful algal cells, which can reach benthic habitats, making the toxins more available to otherwise less exposed epifaunal and infaunal animals.

**Keywords**: Harmful Algae, Okadaic acid adsorption, Aged microplastic

**Financing**: Atomic Energy Agency (PHYTOPLASTOX - RC #23548): Coordination of Superior Level Staff Improvement (CAPES, Brazil) via a PhD scholarship granted to E.P

**Acknowledgments**: We thank Dr. Luciano F. Fernandes (Botany Department, UFPR) and Dr. Mathias Schramm (IFSC) for their assistance with micro-algal identification and sample preparation, respectively.

Poster Session 02: HABs in a Changing World & Emerging Issues
P-095

# Adapting to a changing Arctic: Investigating eco-physiological responses of the diatom *Pseudo-nitzschia delicatissima* to projected climate-driven pH and temperature shifts

**Erin Kathleen Redmond**[1,2], Einar Pétur Jónsson[2], Throstur Thorsteinsson[1], Sara Harðardóttir[2]

(1) University of Iceland, Environment and Natural Resources, Institute of Earth Sciences
(2) Marine and Freshwater Research Institute, Environmental Division, Iceland

Anthropogenic $CO_2$ emissions are altering ocean conditions, driving warming and acidification. These changes impact marine biodiversity, including phytoplankton growth, distribution, and the potential for harmful algal blooms (HABs). This study examined a phytoplankton spring bloom in Krossanes, East Iceland, in 2024, across three depths (0 m, 10 m, 30 m) at two stations (coastal and farther offshore). Species identification and enumeration revealed key bloom-forming taxa and the presence of harmful algal species at both stations. *Chaetoceros convolutus* and *Corethron* cf. *hystrix/pennatum* dominated at the coastal station, both capable of damaging fish gills. *Pseudo-nitzschia delicatissima*, detected at both stations but more abundant farther offshore, is generally considered low- or non-toxic; however, some strains can produce domoic acid, a potent neurotoxin, under changing conditions. This underscores the need for targeted research on P. delicatissima and its potential toxicity. To explore these dynamics, multi-stressor laboratory experiments were conducted on Krossanes strains of *P. delicatissima*, simulating ocean conditions projected for 2100. Growth responses—including changes in cell counts and chlorophyll a—were assessed under elevated temperature and $pCO_2$. pH, temperature, nutrients, total alkalinity, and domoic acid were also monitored at the start and end of each experiment. *P. delicatissima* exhibited enhanced growth under warming, slight inhibition under higher $pCO_2$, and no interaction between stressors. No domoic acid was detected; however, should future strains become toxic and warming promote blooms, there could be implications for ecosystems and human health. This work highlights the importance of monitoring phytoplankton communities and their responses to climate change in sub-Arctic waters.

**Keywords**: Climate change, Diatoms, Harmful algal blooms

Poster Session 02: HABs in a Changing World & Emerging Issues
P-096

# Unusual algal blooms during winter 2025 followed by accumulation of okadaic acid in molluscs in a lagoon of the Northern Adriatic Sea (Italy)

**Silva Rubini**[1], Barbara Bertasi[2], Sonia Dall'Ara[3], Martina Munari[1], Davide Ippoliti[4], Irene Servadei[3], Sara Arnaboldi[2,7], Giulia Magagna[2,7], Paolo Rizzi[5], Damiano Accurso[4], Elisa Massella[6], Monica Cangini[3]

(1) Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna (IZSLER), Sede di Ferrara, Via Modena 483, Ferrara, Italia
(2) IZSLER, Sede di Brescia, Via A. Bianchi 9, Brescia, Italy
(3) Fondazione Centro Ricerche Marine, National Reference Laboratory for Marine Biotoxins, Viale A. Vespucci 2, Cesenatico (FC), Italy
(4) IZSLER, Reparto chimico degli alimenti di Bologna, Via P. Fiorini 5, Bologna, Italy
(5) Azienda USL di Ferrara, Operational Unit "Food Hygiene of Animal Origin", Via A. Cassoli 30, Ferrara, Italy
(6) IZSLER, Sede di Piacenza, Strada Faggiola 1, Gariga di Podenzano (PC), Italy
(7) University of Parma, Parma, Department of Veterinary Science, Via Taglio 8, Parma, Italy

The northern Adriatic Sea is the most significant region in Italy for bivalve mollusc production. In this area, mussels (*Mytilus galloprovincialis*), clams (*Ruditapes* spp.) and, to a lesser extent, oysters (*Crassostrea gigas*) are commonly farmed.
Since the late 1990s, these production areas have been subject to systematic monitoring of microbiological, biotoxin and chemical hazards in bivalve molluscs intended for human consumption, in compliance with European legislation (updated Regulation (EU) 2017/625; Implementing Regulation (EU) 2019/627). Concurrently, phytoplankton monitoring is conducted to detect marine biotoxin-producing species in surrounding waters.
To date, no harmful algal blooms (HABs) involving potentially toxic species had been recorded in this area during the winter months. However, in January 2025, a bloom of *Dinophysis* cf. *ovum* was observed in a brackish lagoon, persisting for approximately two months. The bloom reached a maximum concentration of $1.74 \times 10^5$ cells per liter. Lipophilic toxin analysis performed on local bivalves revealed the presence of okadaic acid, with concentrations reaching up to 50 µg OA equivalents per kilogram in oyster samples.
Despite its brief duration, this atypical winter bloom may be indicative of the broader impact of climate change. Increasing water temperatures combined with extreme weather events, such as alternating periods of flooding and drought, are becoming increasingly frequent and may promote the development of HABs. Therefore, the implementation of enhanced and adaptive monitoring strategies in bivalve mollusc production areas is essential for the early detection and management of unexpected toxic algal blooms, driven by evolving climatic conditions.

**Keywords**: *Dinophysis* cf. *ovum*, northern Adriatic Sea, okadaic acid

**Financing**: Ministry of Health PRC 2022010

Poster Session 02: HABs in a Changing World & Emerging Issues
P-097 (Ignite Talk)

# How will rising ocean temperatures affect growth rates and toxigenicity of *Protoceratium reticulatum*, a yessotoxin-producing dinoflagellate

**Megan Schulz**[1,2], Misty B. Peacock[2], William P. Cochlan[2,3], Vera L. Trainer[1]

(1) University of Washington, 1410 NE Campus Pkwy, Seattle, United States
(2) Northwest Indian College, Salish Sea Research Center, 2522 Kwina Road, Bellingham, United States
(3) San Francisco State University, Estuary and Ocean Science Center, 3150 Paradise Drive, Tiburon, United States

Rising ocean temperatures are anticipated to have effects throughout marine ecosystems, including increasing phytoplankton's growth rates and potentially increasing toxigenicity. *Protoceratium reticulatum*, a dinoflagellate commonly found in coastal waters, produces yessotoxin, a lipophilic phycotoxin. While there is less research on human effects than other phycotoxins, yessotoxin has been identified as a contributing factor in shellfish mass mortalities worldwide. Shellfish provide economic value for commercial growers, promote tourism through recreational harvesting, and are culturally significant to Indigenous people. Despite this risk to shellfish, little is known of the ocean conditions that promote the growth and toxigenicity of *P. reticulatum* in the Salish Sea – the inland waters of the northwest coast of North America - where this dinoflagellate repeatedly forms toxic blooms. Preliminary experiments performed using a locally isolated culture of *P. reticulatum* (Blaine, WA, USA) at five temperatures in a temperature gradient bar incubator showed an increase in specific growth rates with increased temperature. To better understand the effect of temperature on this dinoflagellate, the same isolate was grown at three location-relevant temperatures (16, 19, and 22 °C) under macronutrient-replete and macronutrient-deficient conditions. Although specific growth rates increased with temperature, toxin concentrations and production rates (determined with daily dissolved and particulate yessotoxins samples) demonstrate variability with both temperature and growth phase. We have a particular interest in the relative increase of dissolved toxin concentrations with increased temperature, which may unexpectedly decrease the toxic risk to shellfish despite increased total (dissolved + particulate) toxin concentration.

**Keywords**: yessotoxin, dinoflagellate, shellfish

**Financing**: NOAA Award #NA22NOS4780166NOAA Award #NA23NOS4780171

Poster Session 02: HABs in a Changing World & Emerging Issues
P-098

# Warming waters and hurricane-driven inputs influence primary production and respiration rates in both *Karenia brevis* and phytoplankton communities on the West Florida Shelf

**Bruna Sobrinho**[1], Amanda Muni-Morgan[2], Cynthia Heil[3], Patricia Glibert[1]

(1) University of Maryland Center for Environmental Science, Horn Point Laboratory, 2020 Horns Point Rd, Cambridge, USA
(2) Ecosystem Insights LLC, St., Petersburg, FL, USA
(3) Mote Marine Laboratory, Sarasota, FL, USA

The ongoing ocean warming and expansion of hypoxia conditions in the Gulf of Mexico, combined with increasing riverine inputs of dissolved organic matter (DOM) into coastal areas due to hurricanes and storms can greatly impact primary production and respiration rates in phytoplankton communities. While recent studies have reported the presence of hypoxia during large *Karenia brevis* blooms, many questions remain regarding how the respiration rates of this species can influence hypoxia conditions. Here, we investigated the effects of temperature and humic acid enrichment on Gross Primary Production (GPP), Net Primary Production (NPP), and Gross Respiration (GR) in samples collected from Florida waters post-Hurricanes Helene and Milton during an ongoing *Karenia brevis* bloom. Primary production and respiration rates were measured using a new, rapid $H_2{}^{18}O$ enrichment technique with Membrane Inlet Mass Spectrometry (MIMS) and the characterization of DOM composition was identified using Spectrofluorometric analysis. Our results show that increasing temperature led to a decline in GPP and NPP, while GR increased and often exceeded GPP rates. Humic acid additions slightly enhanced NPP and reduced GR. Temperature increases also drove compositional changes in DOM. Terrestrial humic declined concomitant with increases in proteinaceous DOM in the K. brevis bloom sample, suggesting selective uptake or degradation by *K. brevis*. These findings highlight how warming and hurricane-driven DOM inputs can influence the rates of primary production and respiration on the West Florida Shelf, with implications for hypoxia development. Understanding these interactions is critical as extreme events become more frequent under climate change.

**Keywords**: Hypoxia, Hurricane-driven DOM, Karenia brevis

Poster Session 02: HABs in a Changing World & Emerging Issues
P-099

# Evaluating the co-occurrence of marine toxins and anthropogenic contaminants in marine sediment in a Ciguatera endemic region

**Katherine Yang**[1], Sarah Dietrick[1,2], Alison Robertson[1,2]

(1) Dauphin Island Sea Lab, 101 Bienville Blvd., Dauphin Island, United States
(2) University of South Alabama, The Stokes School of Marine and Environmental Sciences and Environmental Toxicology, 600 Clinic Dr., Mobile, United States

Ciguatera is a severe seafood poisoning syndrome that is caused by the consumption of fish contaminated with ciguatoxins (CTX), neurotoxins produced by benthic dinoflagellates such as *Gambierdiscus*. Despite its prevalence, ciguatera – and factors influencing CTX production and transfer – remains under researched. One such knowledge gap is the potential role of human pollution on CTX production and uptake. Anthropogenic contaminants, such as pesticides, pharmaceuticals, and trace metals, both co-occur with CTX in marine environments and have the potential to produce similar or confounding neurotoxic effects that could be associated with fish behavioral abnormalities. However, few studies focus on the coexistence of and possible interactions between these pollutants and natural toxins. Here, we developed methods to assess the distribution of various trace metals (Pb, As, Hg, Cd, Mn), organic contaminants, pesticides (neonicotinoids, organophosphates, pyrethroids, organochlorines), 6PPD-quinone, select pharmaceuticals, and natural toxins (CTXs, okadaic acid) in sediment from the Florida Keys. Using high resolution spatial sampling across multiple time points, we analyzed the spatial variability and persistence of these combined toxins in relation to sediment characteristics (pH, total carbon and organic carbon, total nitrogen). This study of the relative abundances of both anthropogenic contaminants and natural toxins provides a baseline for future analysis of their combined impacts on marine ecosystems and will form the basis of experimental studies. Moreover, this study will inform on the potential environmental contributions to the fish spinning phenomenon recently reported in the Florida Keys, where >50 fish species were exhibiting neurological and behavioral abnormalities.

Poster Session 02: Toxins & Other Microalgal Metabolites

P-100

# Assessing recovery rates of marine biotoxins in non-traditional matrices to support compliance with European Union regulations

**Mónica Cid Moure[1],** Pablo Sosa[1], Verónica García Morales[1], María Barreiro[1], Eva Eiriz[1,2], Lucía Soliño Alonso[1,2], Verónica Rey[1,2]

(1) EU Reference Laboratory for Monitoring of Marine Biotoxins (EURLMB), Spanish Agency for Food Safety and Nutrition (AESAN), Edificio CITEXVI, Fonte das Abelleiras 4, 36310 VIGO, SPAIN.
(2) Oceanographic Center of Vigo, Spanish Institute of Oceanography (IEO-CSIC), Subida Radio Faro 50, 36390 VIGO, SPAIN.

Regulated marine biotoxins groups such as lipophilic toxins (LT), paralytic shellfish toxins (PSTs) and amnesic shellfish toxins (ASTs), are produced by toxic phytoplankton, and can accumulate in edible filter-feeding marine organisms leading to human poisoning and food safety concerns. In response to this risk, European Commission (EC) Regulation 853/2004 (and its subsequent amendments) sets the maximum allowed levels in live bivalve mollusks and other seafood intended for human consumption, and specifies the methods that must be applied by official control laboratories. Although the analytical methods for extracting and quantifying marine biotoxin in marine bivalves are well established, the recovery rates and matrix effects for other widely consumed fishery products such as echinoderms and gastropods remain insufficiently characterized. Therefore, further studies on marine biotoxin recovery rates in these potential vectors are required to address this knowledge gap and to ensure compliance with legal requirements. For this purpose, blank tissues of the common limpet (Patella vulgata) and the sea urchin (Paracentrotus lividus) were spiked with commercially available standards of LTs, PSTs and ASTs at two concentration levels (1/2 and 1/4 of the legal limit or maximum validated level) and subsequently analyzed by the European Reference Laboratory for the Monitoring of Marine Biotoxins (EURLMB). The findings revealed that the recovery rates varied depending on the group of toxins and the matrices analyzed. Although these results are preliminary, they are relevant to laboratories involved in the monitoring of marine biotoxins and will contribute to enhancing seafood safety and the fulfilling EC regulatory requirements.

**Keywords**: Harmful Algal Blooms, shellfish poisoning, toxin quantitation

Poster Session 02: Toxins & Other Microalgal Metabolites
P-101 (Ignite Talk)

# Occurrence of phycotoxins and toxic microalgae in the Sea of Marmara, Türkiye

**Fuat Dursun**[1], Seyfettin Tas[1], Sebahat Semin[1], Bernd Krock[2], Rabia Sezgin[3], Turgay Durmus[4], Muharrem Balci[4], Dilara Kavus[1], Urban Tillmann[2]

(1) Institute of Marine Sciences and Management, Istanbul University, 34134, Istanbul, Türkiye
(2) Alfred Wegener Institut-Helmholtz Zentrum für Polar- und Meeresforschung, Ökologische Chemie, 27570, Bremerhaven, Germany
(3) Institute of Graduate Studies in Sciences, Istanbul University, 34134, Istanbul, Türkiye
(4) Department of Biology, Faculty of Science, Istanbul University, 34134, Istanbul, Türkiye

Harmful Algal Blooms (HABs) pose a significant global threat to both human health and the marine environment, including the ecosystem of the Sea of Marmara. The Sea of Marmara is an inland sea located entirely within Türkiye, connecting the Aegean Sea to the Black Sea via the Çanakkale and Istanbul Straits, respectively. Although there have been reports of potentially toxic microalgae in the Sea of Marmara, the presence of toxigenic species and their associated toxins are still understudied. A seasonal sampling campaign was conducted to investigate the diversity and distribution of toxigenic microalgae and phycotoxins by vertical net hauls in the northeastern Sea of Marmara between November 2023 and July 2024. The spatio-temporal distribution of toxic microalgae and toxin concentrations was associated with environmental variables. The dataset included 14 potentially toxic microalgae taxa in total. The genus Pseudo-nitzschia was the only representative of potentially toxic diatoms in the samples, but no associated toxins were found. Among toxic dinoflagellates, *Dinophysis spp., Protoceratium reticulatum, Lingulaulax polyedra*, and *Gonyaulax* spp. were frequently observed along with the related pectenotoxins and yessotoxins. These toxins were recorded for the first time in the region. A positive correlation was found between the cell abundance of *Dinophysis caudata, D. acuta, D. acuminata* and pectenotoxins, and between *Lingulaulax polyedra* and *Protoceratium reticulatum* and yessotoxins. The persistent presence of toxic microalgae and phycotoxins underscores the urgent need of regular monitoring in the Sea of Marmara.

**Keywords**: phycotoxin, Harmful algae, Sea of Marmara

**Financing**: This study was funded by the Scientific and Technological Research Council of Türkiye (TUBITAK, grant numbers: 122Y440 and 123N588).

**Acknowledgments**: We greatly acknowledge the technical support from Annegret Müller (DNA extraction) and Thomas Max (Toxin analyses).

Poster Session 02: Toxins & Other Microalgal Metabolites
P-102 (Ignite Talk)

# Culture optimisation of *Vulcanodinium rugosum* for biomass production and purification of portimine

**Philipp Hess**[1], Laurine Maurici[1], Simon Tanniou[1], Loic Plessis[1], Véronique Séchet[1], Léna Gouhier[1], Fabienne Hervé[1], Damien Réveillon[1], Gaël Bougaran[1]

(1) IFREMER, ODE, Phytox, Rue de l'Ile d'Yeu, Nantes, France

*Vulcanodinium rugosum* is a bentho-pelagic dinoflagellate that produces toxic cyclic imines, i.e. pinnatoxins and portimines, the latter have been linked to acute dermatitis (> 1,000 Senegalese fishermen, 2020 and 2021). To obtain purified toxins we established cultures of *V. rugosum* and analyzed the toxin profiles of four strains available. All four strains produced portimine, and only two additionally produced pinnatoxin G. However, for simplicity of purification and growth performance, a French strain producing only portimine analogues was selected. Accurately counting cells was a major challenge, due to mucus production and transitions between pelagic and benthic phases. To address this, we adapted the counting methods by combining microscopy and automated tools, thus clarifying the reliability of cell density measurements. Finally, biomass production was optimized for harvesting 8g every three weeks, resulting in 90 grams after 6 months. In parallel, the efficiency of previously published purification processes was independently assessed on small amounts of *V. rugosum* extract. These included liquid-liquid partitioning, size-exclusion chromatography, normal-phase silica SPE, and semi-preparative C18 chromatography. Recovery of these orthogonal techniques will be discussed as well as purification efficiency. The purified toxins will help the partners further understanding of portimines action mechanisms and increase their understanding of the resulting pathology. The optimized cultivation and purification processes could also ultimately be used to develop certified standards and reference materials for improved coastal zone management.

**Keywords**: natural products isolation, algal toxin, inflammation

**Financing**: This research was funded by the French National Research Project INFLAMATOX.

Poster Session 02: Toxins & Other Microalgal Metabolites

P-103

# Searching for the cylindrospermopsin producer in a Dutch estuarine shellfish production area

Els Faassen[1], **Mirjam Klijnstra[1],** Caroline Dirks[1], Margriet Hokken[1], Jorg Nijland[1], Jesper Lucassen[1], Alena Gsell[1]

(1) Wageningen Food Safety Research, Wageningen University and Research, Akkermaalsbos 2, Wageningen, The Netherlands

In the Netherlands, shellfish production areas are routinely monitored for regulated marine toxins. However, cylindrospermopsins (CYNs), which are currently not regulated, are frequently detected in shellfish harvested from estuarine areas between summer and winter. These occurrences raise potential food safety concerns. This study aimed to identify the source of CYNs in a hydrodynamically isolated shellfish production area. Mussels, water, seston, and epibiota were sampled regularly, and the organisms present were identified using light microscopy and molecular techniques. Between January and August, CYNs were detected in nearly all mussel samples, with peak concentrations at the time of harvest reaching 140 µg/kg wet weight for cylindrospermopsin and 74 µg/kg wet weight for 7-deoxy-cylindrospermopsin. Similar toxin profiles were observed in epibiota samples, though concentrations were substantially higher (15 mg/kg dry weight and 16 mg/kg wet weight, respectively). In contrast, no CYNs were found in water or seston samples. Microscopy revealed the presence of cyanobacteria, but no known CYN-producing species. Likewise, 16S rRNA gene sequencing and qPCR did not detect genes associated with CYN biosynthesis. Interestingly, amplicon sequencing revealed actinobacteria in the epibiota that correlated with toxin concentrations. Since some actinobacteria have been reported to carry CYN biosynthesis genes, they may represent a novel source. However, a definitive link could not be established. These findings suggest that CYNs are produced within the epibiota, although the exact producer organism has not been identified yet.

**Keywords**: cylindrospermopsin, shellfish, estuary

**Financing**: This work was performed within the statutory tasks Food Safety (WOT-VV) and financed by the ministry of Agriculture, Nature and Food Quality of the Netherlands.

Poster Session 02: Toxins & Other Microalgal Metabolites
P-104

# Toxins evaluation for the investigation of fish kills in the Kapchagai reservoir, Kazakhstan: Case study

**Galina Nugumanova**[1,2], Adina Zhumakhanova[2], Aiym Duisen[1,2], Natalie Barteneva[2]

(1) Nazarbayev University, NURA, 53 Kabanbay batyr Ave., Astana, Kazakhstan
(2) Nazarbayev University, Department of Biology, 53 Kabanbay batyr Ave., Astana, Kazakhstan

Nowadays, harmful algal blooms (HABs) have become an urgent environmental management problem in many regions, including Kazakhstan. In the present study, for the first time, we report the possibility that the toxic *Microcystis* spp. bloom in Kapchagai reservoir, Kazakhstan, may have contributed to a large fish kill in November 2022, affecting several fish species. Kapchagai is a major reservoir in southeastern Kazakhstan near Almaty. It was created in the 1960s by damming the Ili River, and is used for irrigation, fish farming, and recreation. Water samples were analyzed using UltiMate 3000 (Thermo Scientific, USA) liquid chromatography system (UHPLC-DAD). Microcystin-LR (MC-LR) was detected in a water sample collected near the «Ermin» recreation area with a concentration of 2.4 µg/l. Flowcam VS-4 (Yokogawa Fluid Imaging Technologies, USA) instrument detected *Microcystis* spp. colonies, which is correlated with the UHPLC-DAD results. Detection of toxins was also performed using an Impact II VIP (Bruker, Germany) ultra-high performance liquid chromatography quadrupole time of flight mass spectrometry (UHPLC-QTOF-MS) system. The results of the UHPLC-MS analysis confirmed the presence of MC-LR in a water sample from the Kapchagai Reservoir collected near the «Ermin» recreation base and its absence in the samples collected in the Fall of 2024. These findings support the possibility that cyanobacterial toxins contributed to fish mortalities in Kapchagai. We hope that our findings will contribute to the development of analytical methods for the timely detection of toxins and ecological monitoring in Kazakhstan, thereby significantly reducing risks to human health and the environment.

**Keywords**: cyanotoxins, microcystin-LR, UHPLC-MS

**Financing**: This research received funding from MES Kazakhstan grant AP23489214 to G.S.N. and Nazarbayev University FDCRGP grant #SSH2024005, and MES Kazakhstan grant AP14872028 to N.S.B..

**Acknowledgments**: We are thankful to the Core Facilities of Nazarbayev University for access to instrumentation, to Aleksey Rusanov for help with field expeditions to Kapchagai Reservoir.

Poster Session 02: Toxins & Other Microalgal Metabolites
P-105

# Mussels in fish feed – Are algal toxins a concern?

**Ingunn A. Samdal**[1], Amritha Johny[2], Karoline Sofie Gjelstad[1], Agnieszka Krzyszton[1], Christiane Fæste[1], Anita Solhaug[1], Gunnar Sundstøl Eriksen[1], Raoul V. Kuiper[1], Bente Ruyter[2], Gerd Marit Berge[2], Krista M. Thomas[3], Pearse McCarron[3], Christopher O. Miles[1]

(1) Norwegian Veterinary Institute, Ås, Norge
(2) Nofima, Norge
(3) National Research Council of Canada, Halifax, Canada

Sustainable salmon feed is crucial to the future of the Norwegian salmon farming industry. Today, feed accounts for more than 3/4 of the climate footprint of Norwegian salmon. Approximately 92% of the raw materials currently used in Norwegian aquaculture feed are imported. It is therefore a priority to increase the proportion of feed based on Norwegian resources and exclusively use sustainable ingredients by 2030. Shellfish is an ingredient of great interest in this context. Shellfish such as mussels are a valuable source of marine fatty acids, proteins, and astaxanthin which are important in fish feed. Mussels feed on algae in the marine environment by filtering large amounts of seawater. However, some species of algae can produce a wide variety of toxins, which can accumulate in the mussels, and then potentially in the fish.
The ShellFeed project is investigating the uptake and toxicity of algal toxins belonging to the DSP and PSP toxin groups in salmon. Salmon parr and post-smolt salmon have been fed using a specially prepared feed each spiked with purified toxins (STX, NEO, GTX, C-toxins, OA, DTX-1 and DTX-2). The feeding trials did not seem to influence the growth and wellbeing of the fish. The uptake and metabolism of which are being assessed using LC-MS-methods. Initial analysis indicates no transfer of PSP toxins to the salmon parr filet from the feed. Together, these results will provide the data required to perform the necessary risk assessments of algal toxins in new marine feed sources for salmon.

**Keywords**: Fish feed, DSP, PSP

**Financing**: FHF – Norwegian Seafood Research Fund, project: “Risk assessment of algal toxins in new marine feed sources for salmon” (ShellFeed - 901849)

Poster Session 02: Toxins & Other Microalgal Metabolites

P-106

# Quantification of azaspiracid-2 and characterization of analogous variability in mussels from the Central Adriatic Sea

**Ivana Ujevic**[1], Antonija Bulic[1], Ivana Pezelj[3], Tanja Bogdanovic[4], Stjepan Orhanovic[2]

(1) Institute of Oceanography and Fisheries, Laboratory of Plankton and Shellfish toxicity, Setaliste Ivana Mastrovica 63, SPLIT, Croatia
(2) University of Split, Faculty of Science, Department of Chemistry, Ruđera Boškovića 33, SPLIT, Croatia
(3) University of Split, Faculty of Science, Doctoral Study of Biophysics, Biophysics, Ruđera Boškovića 33, SPLIT, Croatia
(4) Croatian Veterinary Institute, Laboratory for Microbiology and Analytical Chemistry, Poljička cesta 33, SPLIT, Croatia

Marine Biotoxins are produced by some species of phytoplankton through the process of photosynthesis. Their main property is thermostability, so that they do not decompose during seafood preparation at any temperature and their toxicity remains unchanged. Marine organisms that feed by filtering seawater, such as mussels, can accumulate biotoxins during this process that are not harmful to their organism. Poisoning occurs in humans after eating contaminated organisms, and one of the types of poisoning is AZP poisoning (azaspiracid poisoning). Azaspiracids (AZA) are marine polyether biotoxins produced by dinoflagellates. This study represents the first comprehensive analysis of azaspiracid analogues in mussels from the central Croatian Adriatic Sea using high-resolution mass spectrometry. AZA-2 was quantified between January and May 2024, with the highest concentrations observed in early January. In addition to AZA-2, several known analogues (AZA-6, AZA-9, AZA-10, AZA-19, AZA-41, AZA-43) and a potentially new analogue (m/z 884.6066) were detected. The fragmentation patterns of this new analogue indicate a structural similarity to AZA-19, with a possible modification of the double bond. Possible pitfalls in the misinterpretation of spectra derived from molecules with $^{13}C$ atoms were identified. The presence of multiple analogues, some of which have high toxic potential, indicates that regulatory practise should consider the inclusion of more than three analogues in the monitoring program.

**Keywords**: AZA analogs, LC-QTOF, Adriatic Sea

**Financing**: Croatian Science Foundation project number HRZZ-IP-2024-05-9464 and “Young researchers’ career development project – training of doctoral students” (DOK -2021-02-7058), doctoral student Antonija Bulić.

Poster Session 02: Toxins & Other Microalgal Metabolites

P-107

# Characterization of allelochemicals from *Nitzschia closterium* and their allelopathic effects on *Prorocentrum donghaiense*

**Jiangtao Wang**[1], Hani Abdo[1], Bingbing Wang[1]

(1) Key Laboratory of Marine Chemistry Theory and Technology, College of Chemsitry and Chemical Engineering, Songling Road 23, Qingdao, China

This study explores the allelopathic interactions and chemical characterization of the diatom *Nitzschia closterium* and its impact on the harmful dinoflagellate *Prorocentrum donghaiense*. Using mixed culture and filtrate culture experiments, the allelochemicals released by N. closterium were shown to inhibit P. donghaiense growth in a concentration-dependent manner. These inhibitory effects were linked to disruptions in photosystem II efficiency. In addition, extracts from liquid-liquid extraction (LLE) including solvent of ethyl acetate, n-hexane, petroleum ether, dichloromethane and DMSO, and solid phase extraction (SPE) of filtrate of *N. closterium* cultures, were tested for their effects on *P. donghaiense*. Among these, only the n-hexane extracts from LLE significantly reduced algal growth, achieving a 78.1% inhibition at the highest concentration (50 µL). Fractionation of the n-hexane extracts via HPLC yielded twelve fractions, with fraction F-IV showing the most potent inhibition. Further GC-MS analysis identified several compounds, especially of 3-Acetoxy-7,8-epoxylanostan-11-ol, as a key allelopathic agent. These findings contribute to understand the ecological role of allelopathy in regulating harmful algal blooms and highlight the potential of *N. closterium* extracts for environmental management application.

**Keywords**: Allelopathy interactions; *Nitzschia closterium*; Extraction and isolation

Poster Session 02: Toxicity
P-108 (Ignite Talk)

# Toxic dinoflagellate *Ostreopsis* cf. *ovata* recorded for the first time in the area of Boka Kotorska Bay (South Adriatic Sea)

**Dragana Drakulovic**[1], Aleksandra Huter[1], Sandra Jokanovic[1], Danijela Joksimovic[1]

(1) University of Montenegro, Institute of Marine Biology, Put I Bokeljske brigade 68, Kotor, Montenegro

Diversity of phytoplankton community with focus on presence of potentially toxic and toxic phytoplankton species were researched on the mussel farms in small semi-enclosed Boka Kotorska Bay. Research was part of National monitoring of seawater quality at four mussel farms from January to December 2023.
Samples were taken at 5m depth using 5 L Niskin bottles according to MEST ISO 5667-9: 2020. Phytoplankton cells determination was carried out in accordance with Utermöhl (MEST EN 15204: 2014).
Total phytoplankton reached value up to $10^5$ cells/l. Values of dinoflagellates ranged up to $10^3$ cells/l and the highest abundance was recorded at the position Dražin vrt (BK1) reaching $6.96 \times 10^3$ cells/l.
The presence of the species from the genus *Ostreopsis* was noticed for the first time in the area of Boka Kotorska Bay and across the Montenegrin coast.. Species abundance reached $5.92 \times 10^3$ cells/l, while the total abundance of dinoflagellates at position Dražin vrt was $6.96 \times 10^3$ cells/l. This confirms that at position Dražin vrt (BK1) in the water mass species, *Ostreopsis* cf. *ovata* contributed mostly to dinoflagellates abundances. Additionally, the presence of dinoflagellates *Dinophysis acuta* and *Phalacroma rotundatum* was noticed
Mass appearances of the toxic dinoflagellate genus *Ostreopsis* can caused dangerous respiratory problems in humans exposed to aerosols. Also, *Ostreopsis* species produce different toxins that can be transferred to some fish and invertebrates and present a potential risk of food poisoning for humans. Therefore, as a result permanent monitoring is necessary to prevent risks to both human and environmental health.

**Keywords**: Toxic dinoflagellate, *Ostreopsis* cf. *ovata*, Adriatic Sea

Poster Session 02: Toxicity
P-109 (Ignite Talk)

# Mitochondria as environmental sensors: Unravelling the link between *Prymnesium parvum* biotoxins and mitochondrial network

**Zsuzsanna Neer**[1,2], Endre Kiss[3], Tamás Felföldi[2], Balázs Vajna[2], János Matkó[4], Elisabeth Varga[1]

(1) University of Veterinary Medicine Vienna, Clinical Department for Farm Animals and Food System Science, Centre for Food Science and Veterinary Public Health, Food Hygiene and Technology, Veterinärpl. 1, 1210 Vienna, Austria
(2) Eötvös Loránd University, Department of Microbiology, Faculty of Science, Pázmány Péter sétány 1/c, 1117 Budapest, Hungary
(3) Max Perutz Labs, BioOptics FACS Facility, Dr.-Bohr-Gasse 9, 1030 Vienna, Austria
(4) Eötvös Loránd University, Department of Immunology, Faculty of Science, Pázmány Péter sétány 1/c, 1117 Budapest, Hungary

The 2022 Oder disaster, caused by the toxic bloom of *Prymnesium parvum*, highlighted the fragility of freshwater ecosystems, which pose an increasingly significant threat due to anthropogenic effects and climate change.
Prymnesins are potent polyether biotoxins produced by *Prymnesium parvum*, exhibiting ichthyotoxic, hemolytic, and cytotoxic properties, making them significant contributors to fish kills and ecological disturbances.
Gill epithelial cells play a key role in respiration and ion regulation in aquatic organisms. The mitochondrial membrane potential (ΔΨm) is critical for ATP production via oxidative phosphorylation. Furthermore, maintaining adequate ATP levels is crucial for sustaining vital physiological functions.
Our work focused on setting up, optimizing and employing molecular and cellular bioassays using fluorescence microscopy and flow cytometry to map the onset and mechanisms of mitochondrial damage in rainbow trout gill cells exposed to extracts of *P. parvum* (PRM).
PRM induced disruption of the cells' mitochondrial network structure alongside collapse of mitochondrial membrane potential. These mitochondrial impairments compromise the energy metabolism and structural integrity of gill cells. Mitochondrial dysfunction in fish gill epithelial cells induced by prymnesin treatment could affect health and survival.
Loss of gill epithelial cells further compromises the barrier function of the gills, allowing toxins and pathogens to enter the fish's bloodstream. This phenomenon can explain why exposure to prymnesins leads to the massive deaths of fish populations.

**Keywords**: mitochondrial network, prymnesins, RTgill-W1

**Financing**: This research was funded in part by the Austrian Science Fund (FWF) [grant DOI:10.55776/I5707].

**Acknowledgments**: This research was supported using resources of the VetCore Facility (VetImaging) of the University of Veterinary Medicine Vienna.

Poster Session 02: Toxicity

P-110

# Controlled cultivation and anticancer activity of *Karlodinium veneficum* supernatant extracts on human tumor cell lines

**Alejandra Rivera**[1,2], Ghislayne Rivera[1], Allisson Astuya[1,2], Juan Jose Gallardo[3]

(1) Universidad de Concepción, Laboratorio de Biotoxinas UdeC, Facultad de Ciencias Naturales y Oceanografia, Concepcion, Chile
(2) Universidad de Concepción, Centro de Invetigación Oceanográfica COPAS COASTAL, Concepción, Chile
(3) Universidad de Almeria, ingieneria quimica, Centro de investigación CIAIMBITAL, Almeria, España

*Karlodinium veneficum* is a dinoflagellate commonly associated with Harmful Algal Blooms (HABs) and fish mortality, known for producing karlotoxins (KmTxs), potent bioactive compounds. In this study, *K. veneficum* was cultivated under controlled, scalable photobioreactor conditions to ensure reproducible biomass and metabolite production. Crude extracts were obtained separately from the biomass (intracellular) and culture supernatant (extracellular metabolites), collected during the late exponential phase.

The cytotoxic activity of these extracts was evaluated on two human cancer cell lines: MCF7 (breast adenocarcinoma) and HCT116 (colorectal carcinoma). Cells were exposed to concentrations ranging from 10 to 100 µg/mL for 24 and 48 hours. Cytotoxicity was assessed by MTT assay, while the mechanism of cell death was investigated using the ApoTox-Glo™ Triple Assay, evaluating apoptosis (caspase 3/7 activation) and membrane integrity.

The supernatant extract exhibited significant, dose-dependent cytotoxicity in both cell lines, with IC50 values below 50 µg/mL. In MCF7 cells, cytotoxicity was time-dependent and associated with early apoptotic features, while in HCT116 cells, cytotoxicity occurred rapidly, showing negligible caspase 3/7 activation and indicating necrotic mechanisms. Biomass extracts showed minimal cytotoxic activity under the same conditions.

These results demonstrate that extracellular metabolites secreted by *K. veneficum* exhibit anticancer effects that vary depending on the cell line evaluated. The reproducible photobioreactor system highlights the potential of *K. veneficum* as a scalable marine microalgal source of bioactive compounds for bioprospecting and anticancer research.

**Keywords**: *Karlodinium veneficum*, Photobioreactor cultivation, Cytotoxicity

Poster Session 02: Toxicity

P-111

# Further evidence for the persistent presence of yessotoxins in the Eastern Adriatic Sea

**Romana Roje-Busatto**[1], Ivana Ujević[1], Antonija Bulić[1], Nikša Nazlić[1], Roman Garber[1]

(1) Institute of Oceanography and Fisheries, Laboratory for Plankton and Shellfish Toxicity, Setaliste Ivana Mestrovica 63, Split, Croatia

The environmental quality of the mariculture areas, especially the mussel farming zones, in the eastern part of the Adriatic Sea has been intensively monitored over the last 25 years. However, the present study analyses natural populations in Croatian coastal waters that are not under anthropogenic influence and could be suitable for mussel farming. Samples of the blue mussel *Mytilus galloprovincialis* were collected at 21 stations in the warmer season of 2024, and in the colder season of 2025. LC-MS/MS analysis of the lipophilic toxin group showed that the mass fractions of yessotoxin (YTX) in 21 mussels sampled from May to July 2024 and January to March 2025, ranged from 0.0193 to 0.0967 and 0.011 to 0.046 mg/kg, respectively. The mean values for the years 2024 and 2025 were 0.0490 and 0.023 mg YTX eq./kg wet weight, while the mass fractions of nine and eleven mussel samples from the years 2024 and 2025 were < LOD. All results were below the EU Maximum Permitted Levels for YTX in bivalve molluscs. These results are consistent with those from 2019 to 2023 in the specified period indicated, as the same YTX derivatives were found in similar concentrations. The mass fractions of lipophilic toxins belonging to the azaspiracid (AZA1-3) and okadaic acid (OA, DTX1-2, PTX1-2) groups and hydrophilic toxins belonging to the amnesic (ASP; DA and epi-DA) and paralytic (PSP; 11 congeners) groups analyzed in samples collected in the coastal waters of the eastern Adriatic Sea were below the respective detection limits.

**Keywords**: mussel, biotoxin, Adriatic

**Financing**: Croatian Science Foundation project number HRZZ-IP-2024-05-9464 and “Young researchers’ career development project – training of doctoral students” (DOK -2021-02-7058), doctoral student Antonija Bulić

Poster Session 02: Toxicity

P-112

# Investigation into paralytic shellfish toxins and microcystins in seabirds from Portugal

**Lucía Soliño Alonso[1,2],** Andrew D. Turner[3], Begoña Ben-Gigirey[1], Ryan P. Alexander[3], Karl J. Dean[3], Robert Hatfield[3], Benjamin H. Maskrey[3], María V. Mena Casero[4,5]

(1) Centro Oceanográfico de Vigo (IEO-CSIC), Subida a Radio Faro, 50, 36390, Vigo, Spain
(2) EU Reference Laboratory for Monitoring of Marine Biotoxins (EURLMB, AESAN), CITEXVI, Campus Universitario de Vigo, 36310, Vigo, Spain
(3) Centre for Environment Fisheries and Aquaculture Science (Cefas),, The Nothe, Barrack Road, Weymouth, Dorset, UK
(4) Wildlife Rehabilitation and Research Center of Ria Formosa (RIAS), Ria Formosa Natural Park, 8700-194, Olhão, Portugal
(5) Instituto de Investigación en Recursos Cinegéticos (IREC), Junta de Comunidades de Castilla-La Mancha (JCCM, CSIC), Universidad de Castilla-La Mancha (UCLM), Ronda de Toledo 12, 13005, Ciudad Real,, Spain

Microalgae are the basis of marine food webs, essential in sustaining top predators including seabirds. However, certain species of microalgae synthesize biotoxins, which can accumulate in shellfish and fish and may cause harm to marine animals feeding on them. Toxins produced by dinoflagellates have been previously observed to be poisonous to seabirds. Also, in freshwater and brackish habitats, cyanobacteria have caused bird mortality events.
Wildlife hospitals are the front line when bird mortality events occur, although the causes of these events are frequently unknown. In South Portugal, several species of birds, mainly gulls, exhibiting a paretic syndrome were rescued by Wildlife Rehabilitation and Research Center of Ria Formosa – RIAS between 2018-2021.
In this work, the prevalence of six families of biotoxins (paralytic shellfish toxins (PSTs), microcystins (MCs), anatoxins, amnesic shellfish toxins (ASTs), cylindrospermopsin, and tetrodotoxins (TTXs) were analyzed in 340 samples from 193 wild birds admitted to RIAS. Furthermore, the clinical picture of 17 birds that presented quantifiable levels of biotoxins in their tissues, as well as the relationship between toxin burdens and the symptomatology observed were considered.
Bird tissue samples containing biotoxins were only found in yellow-legged gull (*Larus michahellis*), lesser black-backed gull (*Larus fuscus*), Audouin's gull (*Ichthyaetus audouinii*), Northern gannet (*Morus bassanus*), and sanderling (*Calidris alba*). Only PSTs or MCs were quantified.
Based on previously published research data, we conclude that, in these birds, the biotoxins are unlikely to be the only cause of death, but might contribute to some extent to a reduction in birds' fitness.

**Keywords**: seabird, Harmful Algal Bloom, paretic syndrome

**Financing**: This research was funded by the European Commission, through the project LIFE Ilhas Barreira, grant number LIFE18/NAT/PT/000927.

**Acknowledgments**: We acknowledge Rafael Mateo for his constructive comments.

Poster Session 02: Toxicity

P-113

# Toxicity of *Ostreopsis* cf. *ovata* and *O.* cf. *siamensis* from Basque (NE Atlantic) coast using bioassays on diatoms, oyster gametes and fish gill cells

**Lucie Souvignet**[1], Mathilde Madre[1], Audrey Duval[1], Fabienne Hervé[2], Hélène Hégaret[3], Damien Réveillon[2], Malwenn Lassudrie[1]

(1) Ifremer, COAST, LER-BO, Concarneau, F-29900, France
(2) Ifremer, PHYTOX, Metalg, Nantes, F-44000, France
(3) Univ. Brest, CNRS, Ifremer, IRD, IUEM, UMR 6539 LEMAR, Plouzané, F-29280, France

Since 2020, the Basque coast (France and Spain) has been experiencing co-occurring seasonal blooms of *Ostreopsis cf. ovata* and *O. cf. siamensis*, concomitantly with symptoms in humans and benthic fauna mortality. While *O. cf. ovata* is known to be toxic to some marine organisms, and produces ovatoxins, no toxin has been identified in *O. cf. siamensis*, and its toxicity remains poorly studied. These species are mucus producers, and during blooms, their benthic biofilms tend to detach into the water column. This study therefore investigated the toxicity of three *O. cf. ovata* and three *O. cf. siamensis* strains from the Basque coast on several aquatic organism models (diatoms, oyster gametes, and fish gill cells) and the role of mucus.
Toxicity of cultures was assessed on Pacific oyster gamete fertilization. Methanolic extracts were tested on RTgill-W1 fish gill cell viability. Allelopathic activity of both cultures and extracts were tested on *Chaetoceros* sp. Finally, mucus toxicity was evaluated using the allelopathic assay after successive filtrations (80 µm to 0.2 µm), producing filtrates with varying cells and/or mucus content.
Overall, *O. cf. ovata* was more toxic than *O. cf. siamensis*. Oyster and fish models were more sensitive than the diatom model. At bloom concentrations, strains from both *Ostreopsis* species were toxic to all models. Finally, culture filtrates exempt of cells displayed toxicity, which decreased as filter pore size (and hypothetically mucus content) decreased, suggesting mucus toxicity.
Although specific toxic mechanisms remain to be elucidated, the two *Ostreopsis* species from the Basque coast can affect marine life.

**Keywords**: Benthic, allelopathy, Ichthyotoxicity

**Financing**: This work was supported by the ANR HABIS project (22-CE20-0024), Région Bretagne (ARED), Ifremer, and the OstreoBila project funded by FEDER INTERREG POCTEFA.

Poster Session 02: Toxicity

P-114

# Bloom events of the *Alexandrium tamarense* species complex along the coast of Chubut Province (Argentina): health risks and ecological impacts (2022-2024)

**Noelia Mariel Uyua**[1], Alicia Viviana Sastre[1], Norma Herminia Santinelli[1], Germán Marino[2], Diego Saban[2], Marisol Montenegro[2], Jones Sofía[2], Emiliano Crippa[1,2], Brenda Pichaud[2]

(1) Laboratorio de Fitoplancton - Instituto de Investigación de Hidrobiología, Facultad de Ciencias Naturales y Ciencias de la Salud - Universidad Nacional de la Patagonia San Juan Bosco, Gales 48, Trelew, Argentina
(2) Dirección Provincial de Salud Ambiental, Gobierno de la Provincia del Chubut, Berwyn 226, Trelew, Argentina

Between 2022 and 2024, significant bloom events of the *Alexandrium tamarense* species complex were recorded along the coast of Chubut Province (Argentina).

In 2022, the species reached high relative abundances, with blooms occurring during September and October. The toxicity associated with these proliferations reached historically high levels: 215,000 µg STXdiHCl eq./kg in scallops, with cell concentrations up to 35,000 cells/L in San José Gulf, and 28,944 µg STXdiHCl eq./kg in mussels, with up to 800 cells/L in Nuevo Gulf.

During this period, significant mortality among marine birds and 30 southern right whales (*Eubalaena australis*) was reported. Analysis of intestinal contents in several specimens confirmed the presence of forms compatible with *A. catenella*.

In 2024, a similar event occurred in the southern sector of Chubut Province, associated with blooms of *A. catenella*. In March, cell concentrations reached up to 962,951 cells/L, and in April, maximum toxicity levels of 280,390 µg STXdiHCl eq./kg were recorded in mussels.

These events underscore the magnitude of the risk posed to public health and marine fauna. The implementation of the Provincial Plan for Red Tide Prevention and Control enabled timely communication with fishers and the community, effectively preventing cases of human intoxication.

The increasing frequency and intensity of these events raise important questions about the role of environmental conditions, with climate change emerging as a potential factor promoting the recurrence of such blooms along the Patagonian coast.

**Keywords**: toxicity, *Alexandrium tamarense* species complex, Argentine Patagonia

**Financing**: Government of Chubut Province, Provincial Plan for Red Tide Monitoring and Control
Acknowledgments: To the diving team and collaborators of the Provincial Plan for Red Tide Monitoring and Control.

Poster Session 02: New Methods & Technology (OMICS, chemical, bioassays, etc)
P-115

# In vitro assessment of saxiphilin C-lobe as a saxitoxin-neutralizing agent

**Ambbar Aballay González**[1,2,3], Jonathan Viveros[1,3], Verónica Avello[1], Maximiliano Figueroa[2], Allisson Astuya Villalón[1,3]

(1) University of Concepción, Biotoxins Laboratory, Faculty of Natural and Oceanographic Sciences, 4070386, Concepción, Chile
(2) University of Concepción, Molecular biophysics laboratory, Faculty of Biological Sciences, 4070386, Concepción, Chile
(3) University of Concepción, Center for Oceanographic Research COPAS COASTAL, Faculty of Natural and Oceanographic Sciences, 4070386, Concepción, Chile

Paralytic toxins of the saxitoxin (STX) type are a group of neurotoxins that block voltage-gated sodium channels (Nav), disrupting nerve impulse transmission and potentially leading to respiratory paralysis and death. Due to their high toxicity and the absence of effective antidotes, there is increasing interest in the development of neutralizing agents. Saxiphilin, a protein identified in certain amphibians and other animals, exhibits high affinity for STX and has been proposed as a potential therapeutic molecule. In this study, the C-lobe of saxiphilin, responsible for STX binding, was expressed in insect cells, yielding 3 mg $L^{-1}$ of culture medium. The saxitoxin-binding capacity of the recombinant protein was evaluated in vitro using a competitive binding assay with ouabain and veratridine. Recombinant protein concentrations ranging from 10 to 100 µg $mL^{-1}$ effectively reversed the effects of STX, preventing its interaction with Nav channels in the assay system. These findings highlight the potential of saxiphilin as a promising antidote candidate against STX-type paralytic toxins.

**Keywords**: Saxitoxin, in vitro, saxiphilin

**Financing**: Project Number VIU24P0097, FONDEF IDeA ID22I10218

**Acknowledgments**: The authors would like to thank Dr. Oliberto Sánchez and Dr. Frank Camacho,from the Faculty of Biological Sciences, Universidad de Concepción, Chile.

Poster Session 02: New Methods & Technology (OMICS, chemical, bioassays, etc)
P-116

# Towards a method for accelerating the discovery of unanticipated neurotoxins targeting nicotinic acetylcholine receptors to build functional molecular networks

**Rómulo Aráoz**[1], Elena Zindovic[1], Denis Servent[1], Vincent Guérineau[2], Laurence Jennings[3], Maggie Reddy[3], Olivier Thomas[3]

(1) CEA-Saclay, DMTS, SIMOS, Bâtiment 152, 91191 Gif sur Yvette, France
(2) CNRS, Insitut de Chimie des Substances Naturelles, 1 Av; de la Terrasse, 91191 Gif sur Yvette, France
(3) University of Galway, Marine Biodiscovery, School of Biological and Chemical Sciences, University Road, H91TK33 Galway, Republic of Ireland

Marine and freshwater neurotoxins target key cholinergic components of the neuromuscular junction like nicotinic acetylcholine receptors or acetylcholinesterase that are important for muscle contraction, respiration among other vital functions. Neurotoxins display a high affinity for their molecular targets; therefore, they were used for characterizing neuronal receptors and ion channels. Neurotoxins generally form large metabolic clusters, i.e., saxitoxins (> 80 congeners), cyclic imine toxins (> 40 congeners), palytoxins (>20 congeners). Non-targeted feature-based molecular networks may be used for the potential annotation of structurally related neurotoxins in complex mixtures. Most bioassays enable the detection of a given neurotoxin, but the chemical nature of the binder remains unknown. The present method allows the direct capture of a given ligand by the nicotinic acetylcholine receptor in solution and after elution, the chemical nature of the captured neurotoxin could be determined by mass spectrometry. Using the Irish marine biorepository, 750 fractions were screened by the microplate receptor-binding assay specific for detecting nicotinic acetylcholine receptor ligands. The positive fractions inhibiting more than 30 % of the toxin tracer binding were incubated with membranes rich in nicotinic acetylcholine receptors. Following elution, the analytes were concentrated by lyophilization prior to MALDI-TOF-MS analysis. The set-up was calibrated to detect small alkaloid and peptide-like molecules. To validate the target-fishing method, the eluted samples were analyzed by two-electrodes voltage clamp electrophysiology on Xenopus laevis oocytes expressing the human α7 nicotinic acetylcholine receptor. Hence, receptor-based bioassays allow the detection and potential annotation of non-anticipated neurotoxins to generate Bioactivity-Feature-Based Molecular Networks.

**Keywords**: Bioactivity-Based Molecular Networks, Nicotinic acetylcholine receptor, Cyclic imine toxins

**Financing**: French National Research Agency ANR-21-CE34-0024 ICH-NEURO-MET to RA and INTERREG Atlantic Area EAPA-0032/2022 BEAP_MAR to DS and OT.

Poster Session 02: New Methods & Technology (OMICS, chemical, bioassays, etc)
P-117 (Ignite Talks)

# Advancing HABs monitoring in Ireland: An in-house qPCR-based toolkit for detecting *Pseudo-nitzschia* species

**Nicolè Caputo**[1], Dave Clarke[2], Fiona Kavanagh[1], Luca Mirimin[1]

(1) Atlantic Technological University, Marine and Freshwater Research Centre, Dublin Road, H91 T8NW, Galway, Ireland
(2) Marine Institute, Marine Environment and Food Safety, Rinville, Oranmore, H91 R673, Galway, Ireland

*Pseudo-nitzschia* is a genus of cosmopolitan marine pennate diatoms that includes species capable of producing domoic acid, a neurotoxin responsible for Amnesic Shellfish Poisoning (ASP). In Ireland (North-East Atlantic Ocean), Amnesic Shellfish Toxin (AST) events typically occur in spring, with smaller additional events observed during summer. These events have resulted in short-term shellfish harvesting closures along the South-West and West coasts due to toxin concentrations exceeding regulatory limits. Despite improved monitoring contributing to the perceived global increase in AST events, severe cases and their large-scale ecosystem impacts highlight the growing need for efficient early detection strategies.
This study evaluates a scalable molecular approach using a flexible qPCR-based toolkit. The approach combines three molecular assay types, designed and adapted to offer either rapid broad-spectrum screening or species-/toxin-specific detection:
(i) High-Resolution Melting (HRM) assays enabling fast and cost-effective detection of seven key *Pseudo-nitzschia* species (*P.pungens, P.multiseries, P.australis, P.fraudulenta, P.delicatissima, P.subpacifica,* and *the P.pseudodelicatissima/cuspidata* complex) in isolated strains;
(ii) TaqMan qPCR assays redesigned from an established FRET assay and optimized with single hydrolysis probes for enhanced species-specific detection of selected taxa;
(iii) EvaGreen qPCR assay developed to target the dabA gene in *P.multiseries*, providing molecular insight into potential toxin production.
The preliminary results of this study aim to demonstrate the applicability of a modular and scalable molecular toolkit for the efficient detection of *Pseudo-nitzschia* species in both cultured and field samples. The toolkit represents a valuable step toward advanced molecular integration within the Irish National Monitoring Programme for Harmful Algal Blooms conducted by the Marine Institute.

**Keywords**: *Pseudo-nitzschia* spp., quantitative PCR (qPCR), dabA gene

**Financing**: This project (Grant-aid Agreement No. CS-21-007) is carried out with the support of the Marine Research Programme by the Irish Government.

Poster Session 02: New Methods & Technology (OMICS, chemical, bioassays, etc)
P-118 (Ignite Talks)

# A loop-mediated isothermal amplification method (LAMP) for detecting toxic *Microcystis*

**Carolina Croci**[1], Gabriela Martínez de la Escalera[1], Paola Scavone[2], Carla Kruk[3,4], Angel Segura[4], Claudia Piccini[1]

(1) Laboratorio de Ecología Microbiana Acuática, Departamento de Microbiología, Instituto de Investigaciones Biológicas Clemente Estable, Montevideo, Uruguay.
(2) Laboratorio de Biofilms, Departamento de Microbiología, Instituto de Investigaciones Biológicas Clemente Estable, Montevideo, Uruguay.
(3) Instituto de Ecología y Ciencias Ambientales, Facultad de Ciencias, UdelaR, Montevideo, Uruguay.
(4) Departamento de Modelación Estadística de Datos e Inteligencia Artificial, Centro Universitario Regional del Este, UdelaR, Rocha, Uruguay

One of the major concerns about cyanobacterial blooms is that some of them are capable of producing metabolites that are toxic to animals and humans (cyanotoxins). Thus, their presence in water affects human uses, from direct consumption, irrigation, aquaculture, to recreational uses. In Uruguay, the cyanobacteria most frequently associated with these events are species of the genus *Microcystis*, which includes toxic (carrying the mcyA-J cluster) and non-toxic populations. Since microscopy-based methods are not able to distinguish between them and analytic methods are time-consuming, the development of early detection techniques to generate early warnings and avoid health risk is straightforward. In this work, we developed a method for monitoring toxic *Microcystis* quickly, at low cost and without specific or expensive equipment to read the results. A loop-mediated isothermal amplification protocol (LAMP) was designed using the mcyJ gene, which has not been described to suffer recombination and is present in single copy in toxic populations, as a target. The detection of mcyJ gene was achieved for natural samples by LAMP reaction and was confirmed by real-time quantitative PCR. The limit of detection showed that it was able to detect 28 pg/µL of DNA (corresponding to 3.65 x $10^4$ toxic cells of *Microcystis*) in 19 min with 100% sensitivity. By extending the incubation time to 40 min, ca. 5000 toxic *Microcystis* cells could be detected but with lower sensitivity (< 80%). This method constitutes a promising tool for early warning that could be used to ttake monitoring and water management decisions.

**Keywords**: LAMP, Microcystis, monitoring

**Financing**: ANII FMV_1_2021_1_166354 and FCE_3_2022_1_172223

Poster Session 02: New Methods & Technology (OMICS, chemical, bioassays, etc)
P-119

# Validating the use of high-throughput digital PCR methods for monitoring the presence of *Alexandrium* species in environmental samples

**Amanda Curtin**[1], Francesca Cucchi[2], Patrick Costello[1], Nicolè Caputo[2], Dave Clarke[1]

(1) Marine Institute, Rinville, Oranmore, H91 R673, Galway, Ireland
(2) Atlantic Technological University, Marine and Freshwater Research Centre, Dublin Road, H91 T8NW, Galway, Ireland

The Harmful Algal Bloom (HAB) genus *Alexandrium* and its production of Paralytic Shellfish Toxins (PSTs) has caused significant negative impacts on the aquaculture industry with potential risks and impacts to human health in Ireland. While PST occurrences in Ireland are routinely monitored, ongoing research is evaluating molecular methods for increased faster detection and enhanced identification accuracy with greater sensitivity. This study investigated the transferability of Alexandrium specific assays from traditional real-time quantitative PCR (qPCR) to digital PCR (dPCR) platform, a technology known to have greater sensitivity to low-abundance targets and greater tolerance to inhibitors. Three previously published assays were validated on dPCR: two probe–based assays targeting *Alexandrium* genus and *A. minutum*, and one dye-based assay targeting the sxtA4 gene associated with PST biosynthesis. Samples were taken from the South-West Coast of Ireland, an area known to experience re-occurring PST events. As the quantifiable range is usually assessed in controlled environments, field samples (surface, net and filtered water) were used to assess the capability of dPCR to perform absolute quantification across a wide range of target concentrations. The results of this study demonstrate the feasibility and practicability of using dPCR technology and highlight the advantages of absolute quantification and species level identification when monitoring morphologically complex HAB species like Alexandrium in both routine monitoring programmes and research. The dPCR platform provides higher and faster throughput analysis with greater sensitivity and limits the effects on analysis of the potential presence of inhibitors.

**Keywords**: *Alexandrium*, dPCR, Validation

**Acknowledgments**: Amanda Curtin1, Francesca Cucchi2, Patrick Costello1, Nicolè Caputo2, Dave Clarke1

Poster Session 02: New Methods & Technology (OMICS, chemical, bioassays, etc)
P-120

# Development, validation, and application of automated SPE-based LC-MS/MS method for quantification of microcystins in water samples

Christos Tagkidis[1,2], Nikoletta Xanthopoulou[3], Chrysa Gkementzoglou[3], Despoina Alexiadou[3], Vasileios Alampanos[1,2], Georgia Seretoudi[3], **Dimitra Lambropoulou[1,2]**

(1) Center for Interdisciplinary Research and Innovation (CIRI-AUTH)„ Aristotle University of Thessaloniki, Balkan Center, Thessaloniki, GR-57001, Greece, THESSALONIKI, Greece, Greece
(2) Aristotle University of Thessaloniki, Chemistry, Science, Campus of University, Thessaloniki, Greece
(3) EYATH S.A., Thessaloniki Water Supply & Sewerage Company, Thessaloniki Water Treatment Plant, Thessaloniki, Greece, Thessaloniki, Greece

Microcystins (MCs) are hepatotoxic cyanobacterial metabolites commonly found in surface waters during harmful algal blooms, posing risks to public health through drinking water exposure. A sensitive and robust analytical method was developed and validated for the monitoring of four microcystins (MC-LR, MC-YR, MC-RR, MC-LA) in raw and treated drinking water from the city of Thessaloniki, using solid phase extraction (SPE) and ultra-performance liquid chromatography tandem mass spectrometry (UPLC-MS/MS). Comprehensive validation of the method was performed in line with accreditation requirements, ensuring its suitability for regulatory monitoring. Validation was carried out using automated SPE with HLB 12cc/500 mg cartridges, following the OASIS HLB SPE protocol. For the elution step, methanol containing 0.1% trifluoroacetic acid (TFA) was chosen to enhance elution efficiency. Chromatographic analysis was performed using multiple reaction monitoring (MRM) with a gradient of methanol and 5 mM ammonium acetate. LODs ranged from 0.023–0.024 ng/mL (drinking water) and 0.011–0.032 ng/mL (surface water), with LOQs of 0.069–0.073 ng/mL and 0.032–0.097 ng/mL, respectively. Recoveries at 0.1 and 1 µg/L were between 91.03–105.17% (drinking water) and 80.21–108.99% (surface water). Repeatability (%RSD) was between 4.79 and 13.88% while reproducibility (%$RSD_R$) ranged from 7.89 to 18.26% across both matrices. Monthly monitoring showed no detectable microcystins in raw water from Aliakmonas River or in drinking water, in agreement with microscopic analysis showing absence of cyanobacteria. The method's precision, sensitivity, and robustness demonstrate its suitability for routine monitoring, with TFA improving linearity across the 0.1–1000 ng/L calibration range.

**Keywords**: Automated SPE, Microcystins, Water safety

Poster Session 02: New Methods & Technology (OMICS, chemical, bioassays, etc)
P-121 (Ignite Talk)

# Survey of cyanotoxins from various isolates from around the United States

**Stuart Oehrle**[1], Avery Tatters[2]

(1) Northern Kentucky University, Chemistry Department, Waters Lab 100 Nunn Dr, Highland Heights, USA
(2) U.S. Environmental Protection Agency, Office of Research and Development, Gulf Ecosystem Measurement and Modeling Division, Gulf Breeze, USA

Algal blooms have been the source of many toxic events throughout the world. Typically, animal killings are one such common event. Targeted monitoring using Liquid Chromatography/Tandem-Mass Spectrometry (LC/MS/MS) is commonly used to monitor a wide variety of compounds in differing matrices. What is especially attractive about LC/MS/MS is its sensitivity and selectivity. Using a small particle (sub 2um particle size) column and a simple gradient method and that was developed for the original toxins (6 microcystins at the time, anatoxin and cylindrospermopsin) it has been expanded to include over 30 additional microcystins, variants of anatoxin and cylindrospermopsin, as well as several dermatoxins, various anabenopeptins, euglenopyhycin, okadaic acid and others. In addition, backward (precursor) monitoring can provide a useful screening tool for the detection of any unusual toxins. This talk will cover several examples of toxin analysis of waters from a variety of locations to show how you can “see” (detect) additional compounds (anabaenopeptins, aeruginosamide, anatoxin variants, etc) and how you can “search” for others with some basic knowledge. We will show examples of the usefulness of additional toxin screening of samples from a wide variety of lakes, rivers and ponds.

**Keywords**: Freshwater HABS, LC/MS/MS

Poster Session 02: New Methods & Technology (OMICS, chemical, bioassays, etc)
P-122

# Digital PCR for detection of *Alexandrium* saxitoxin genes in Icelandic waters

**Line Roager**[1], Guðbjörg Ólafsdóttir[2], Erin Kathleen Redmond[1], Sophie Jensen[2], Davíð Gíslason[2], René Groben[2], Sara Harðardóttir[1]

(1) Marine and Freshwater Research Institute, Environmental Division, Fornubuðum 5, Hafnarfjörður, Iceland
(2) Matís, Vínlandsleið 12, Reykjavík, Iceland

Harmful algal blooms (HABs) caused by saxitoxin-producing *Alexandrium* spp. are becoming more frequent in Icelandic waters, however, current monitoring still depends on labor-intensive microscopic identification of the species. This method is time-consuming and dependent on taxonomic expertise, hence costly and limiting for shellfish aquaculture producers as well as the development of a recreational monitoring program, which currently does not exist in Iceland.

In this project, we develop a molecular detection method for rapid, low-cost detection of toxigenic *Alexandrium* spp. in Icelandic waters based on digital PCR (dPCR). The assay targets the sxtA gene, an essential component of the saxitoxin biosynthesis pathway, enabling detection of toxic genotypes directly from environmental DNA (eDNA), independent of taxonomy. Furthermore, dPCR provides higher accuracy and sensitivity compared to classical quantitative PCR (qPCR) and is much less labor-intensive.

This method offers a scalable solution for real-time monitoring of toxic *Alexandrium* blooms in Iceland and has strong potential for an integration into existing shellfish safety programs and future recreational HAB initiatives. Its low cost, speed, and minimal training requirements makes it a practical tool for improving HAB response and public health protection.

**Keywords**: digital PCR, *Alexandrium*, Iceland

**Financing**: The Icelandic Centre for Research

Poster Session 02: In Situ Monitoring and Remote Observing Systems

P-123

# Seasonal dynamics of HAB-forming phytoplankton communities across coastal habitats in the Philippines

**Hazel Alvarez**[1], Deo Florence Onda[1]

(1) The Marine Science Institute, College of Science, University of the Philippines, Diliman, 1101, Quezon City, Philippines

Harmful Algal Blooms (HABs) have been a recurrent problem in the Philippines. Bloom duration and onset of HABs-associated phytoplankton communities has been linked to monsoon shifts and anthropogenic pressures. This study investigates the seasonal dynamics of phytoplankton across three distinct habitat types: mangrove, mariculture, and offshore. Biweekly sampling was conducted from March 2023 to March 2024 at nine stations located in Bolinao (Luzon), Cancabato Bay (Leyte), and Dumanquillas Bay (Zamboanga Peninsula). Each site includes one station per habitat type. Phytoplankton samples were analyzed using the Imaging FlowCytobot (IFCB), which enables high-resolution, image-based detection of cell abundance, morphology, and potential HAB-forming taxa such as *Alexandrium, Prorocentrum*, and *Pseudo-nitzschia*.

Data processing and image annotation are currently underway. The study aims to reveal spatial and temporal patterns in phytoplankton communities across seasons and habitats, with particular attention to the occurrence and variability of HAB-associated groups. This research will provide baseline data to understand phytoplankton phenology in Philippine coastal ecosystems and support early warning strategies for HAB events.

**Keywords**: Seasonal dynamics, Imaging flow cytometry, HABs

**Financing**: The authors will apply for a travel grant from the university.

Poster Session 02: In Situ Monitoring and Remote Observing Systems

P-124

# Hyperspectral characterization of phytoplankton species: effect of algal species and cell concentration

**Pilar Aparicio-Rizzo**[1,2], Cristian Vera-Bastidas[1], Vicente Aguilar[1], Daniel Varela[1]

(1) Centro i~mar, Universidad de Los Lagos, Camino Chinquihue, km 6, Puerto Montt, Chile
(2) Centro de Ciencia del Clima y la Resiliencia (CR2), Universidad de Chile, Santiago de Chile, Chile

The impact of harmful algal blooms (HAB) in the different coasts of the world promotes a permanent development of new technologies for monitoring and early warning, especially in areas where fishing and aquaculture practices are intensive such as in the Chilean Patagonia (~40°-56°S). One of these technologies is the use of hyperspectral sensors in the recognition of harmful algae. In this context, we are trying to identify the optical fingerprint of eight HAB species and explore the effects of bio-optical properties of these species on the spectra. The results show that the reflectances are similar among heterokontophyte species (H. *akashiwo*, P. cf. *verruculosa, Pseudo-nitzschia* sp., *Skeletonema* sp. and *T. pseudonana*), although within this group it is still possible to distinguish Pseudo-nitzschia sp. from the other two diatoms. Likewise, the dinophyte species *(A. catenella*, *H. triquetra, P. reticulatum*) show also similar spectra among each other. Regarding cellular and pigments concentrations, both variables displayed a direct relation with the reflectance at red spectral bands (655-720nm), but an inverse relation at blue (400-485nm), green (495-580nm) and orange (585-650nm) bands. These single species cultures spectra are possible to segregate in two main groups, each one sub-grouped by abundance, pigment and phylum. On the other hand, the reflectance from cultures with mixed species in different proportions show variable spectrum shapes, where the spectral reflectance shape is more similar to the dominant species, regardless of total abundance. The results obtained are discussed in relation to their usefulness in the implementation of algal bloom monitoring using hyperspectral sensors.

**Keywords**: harmful microalgal species, reflectance signal, cellular concentration

**Financing**: FONDEF ID20I10369 and ID24I10271

Poster Session 02: In Situ Monitoring and Remote Observing Systems

P-125

# Decoding the hyperspectral signals from phytoplankton species and non-biological particles

**Pilar Aparicio-Rizzo[1,2],** Camilo Rodriguez-Villegas[1,3], Cristian Vera-Bastidas[1], Vicente Aguilar[1], Matthew Lee[1], Daniel Varela[1]

(1) Centro i~mar, Universidad de Los Lagos, Camino Chinquihue, km 6, Puerto Montt, Chile
(2) Centro de Ciencia del Clima y la Resiliencia (CR2), Universidad de Chile, Santiago de Chile, Chile
(3) Center for Biotechnology and Bioengineering (CeBiB), Universidad de Los Lagos, Casilla 557, Puerto Montt, Chile

Hyperspectral optical technology provides information about suspended particles in water, becoming a potential tool for phytoplankton monitoring. However, coastal waters are optically complex, so it is necessary to decode the signals of absorbance/reflectance spectra between biological and non-biological particles, as both could differentially affect the optical properties of the water. To characterize and decode the spectral signal of biological and non-biological particles, a comparative laboratory study was conducted on five species of harmful microalgae, at different cell densities, and sediments collected from four locations in northern Chilean Patagonia (~41°S), using a hyperspectral imaging sensor. The results show that the reflectances of the seawater with sediments displayed a similar pattern each other, describing a progressive increase in reflectance from the blue (400-485nm) to the green (495-580nm) bands, reaching the highest values at ~560-580nm. In contrast, the reflectance spectra of the species-only cultures are clearly different from those of the sediment. When comparing the spectral signals of the species cultures and the species-sediment mixtures, the dominant pattern coincides with the species-specific reflectance. However, differences were detected along the spectral magnitude in a specific range of the spectrum, with higher reflectance in the species-sediment mixture along the blue-green band, which was also affected by cell concentrations. In both cases, species-only cultures and species-sediment mixtures, reflectance between 400 and 680nm increases when cell concentrations decrease, but between 680 and 720nm, reflectance increases when cell concentrations are higher. We discuss the usefulness of these results for distinguishing microalgae from sediments in coastal waters.

**Keywords**: harmful species, suspended particulate matter, hyperespectral signal

**Financing**: FONDEF ID20I10369 and ID24I1027

Poster Session 02: In Situ Monitoring and Remote Observing Systems
P-126 (Ignite Talk)

# Phytoplankton integrated multiscale monitoring in the English Channel and North Sea: Automated/high throughput approaches for characterizing changes in phytoplankton assemblies and Harmful Algal Blooms

**Luis Felipe Artigas[1],** Zeline Hubert[1], Veronique Creach[2], Alain Lefebvre[3], Guillaume Wacquet[3], Arnaud Louchart[1,4], Fabrice Lizon[1], Sebastien Monchy[1], Emilie Poisson Caillault[5], Pascal Claquin[6], Klaas Deneudt[7], Klas Owe Moeller[8], Hedy Aardema[9], Melilotus Thyssen[10], Clementine Gallot[1,10], Luis Chomienne[1], Aurélie Libeau[1], Valentine Szrama[1], Orane Levoy[1], Sophie Brasseur[1], Kevin Robache[1], Emma Mayette[1], Betty Gubri[1], Maialen Palazot[1], Florine Verghaeghe[1], Eve Golfier[1], Lucie Fauvel[1], Lisa Jeabert[1,11], Lucinda Lanoy[1], Muriel Crouvoisier[1], Arnaud Cauvin[1], Claire Dedecker[1], Alexandre Epinoux[1,12], Raed Halawi Ghosn[3], Jean-Valery Facq[13], Michel Repecaud[14], Maxime Navon[15], Tania Hernandez Farinas[15], Pierre-Alexandre Hebert[5], Rune Lagaisse[7], Jonas Mortelmans[7], Ankita Vaswani[8], Khatarina Kordubel[8], Lumi Haraguchi[16], Kaisa Kraft[16]

(1) CNRS - ULCO - U Lille - IRD, Laboratory of Oceanology and Geosciences, Wimereux, France
(2) Center for Environment, Fisheries and Aquaculture Science, Lowestoft, United Kingdom
(3) Institut Français pour l'Exploitation de la Mer - IFREMER, Observation et écologie de la restauration des écosystèmes littoraux (COAST), Laboratoire Environnement Ressources,, Boulogne sur Mer, France
(4) Netherlands Institute of Ecology - NIOO-KNAW, Department of Aquatic Ecology, Wageningen, The Netherlands
(5) ULCO, Laboratoire d'Informatique Signal et Image de la Côte d'Opale, Calais, France
(6) CNRS - University of Caen, Marine Ecosystems and oRganisms Laboratory, Caen, France
(7) Vlaams Instituut voor de Zee - VLIZ, Ostende, Belgium
(8) Helmholtz-Zentrum Hereon GmbH, Institute of Coastal Research, Geesthacht, Germany
(9) Max Planck Institute for, Otto Hahn Institute, Mainz, Germany
(10) CNRS - IRD - AMU, Mediterranean Institute of Oceanology, Marseille, France
(11) CNRS - SU, Laboratoire d'Océanographie de Villefranche, Villefranche sur Mer, France
(12) LMD/IPSL, ENS, PSL University, École Polytechnique, Institut Polytechnique de Paris, Sorbonne Université, CNRS, Paris, France
(13) Institut Français pour l'Exploitation de la Mer - IFREMER, Laboratoire Hydrodynamique Marine, Unité Recherches et Développements Technologiques, Boulogne sur Mer, France
(14) Institut Français pour l'Exploitation de la Mer - IFREMER, Laboratoire Détection, Capteurs et Mesures - PDG-REM-RDT-LDCM, Plouzané, France
(15) Institut Français pour l'Exploitation de la Mer - IFREMER, Laboratoire Environnement Ressources, Observation et écologie de la restauration des écosystèmes littoraux - COAST, Port en Bessin, France
(16) Finnish Environment Institute SYKE, Marine Ecology Measurements - Research Infrastructure Unit, Helsinki, Finland

## Poster Session 02: In Situ Monitoring and Remote Observing Systems

### P-126 (Ignite Talk)

Phytoplankton integrated observations combine innovative automated/high throughput approaches at high spatial and temporal resolution, to decipher intricate community dynamics. For more than a decade, these techniques have been deployed on a variety of monitoring networks and platforms, dedicated research surveys, fixed stations and moorings and measurements of opportunity, supported by national or international projects. The eastern English Channel and southern North Sea show significant connectivity to adjacent ocean and seas, strong hydrodynamics and are submitted to high riverine inputs and anthropogenic pressure, leading to high productivity and recurring phytoplankton blooms, including some Harmful Algal Blooms-HABs of potential impact on marine food webs, human health and economy. Automated/high throughput approaches provide information on the distribution and dynamics of phytoplankton functional groups (automated flow cytometry) and main taxa (imaging, metabarcoding), community changes, and productivity (variable fluorometry), at high spatial and/or temporal resolution, assigning bloom states and pelagic habitat characteristics based on physical, biogeochemical, and biological variables. In addition to presenting updated results on integrated monitoring, we discuss the relevance of implementing some of these techniques to follow spatial and temporal variability of marine coastal ecosystems and tracking some HABs at different spatial and temporal scales. We underline the importance of ongoing advances in the harmonization of operational practices, data pipelines, automated treatment and analytical and synthesis tools that should allow the inclusion of automated/high throughput data into integrated modelling, building scenarios of ecological trends in coastal marine ecosystems under multiple local to global pressures.
Keywords: Phytoplankton monitoring - Automated and High throughput approaches – English Channel and North Sea

**Financing**: CPER MARCO-IDEAL, ANR-France2030 PPR RiOMar/FutureOBS, IFSea graduate school, French MTES-INSU MSFD convention, European H2020 JERICO NEXT-S3, OBAMA NEXT and DTO BioFlow Horizon projects, EuroMarine grant

**Acknowledgments**: The authors thank all students, technicians, engineers, scientists of laboratories/institutions and research vessels crews who participated in the sample collection, treatment and analysis of the data.

Poster Session 02: In Situ Monitoring and Remote Observing Systems
P-127 (Ignite Talk)

# Next generation sequencig applied to toxic algae monitoring in the Adriatic Sea in Italy, the experience of Emilia Romagna and Marche regions

**Barbara Bertasi**[1], Silva Rubini[1], Laura Ragni[1], Giulia Magagna[1,5], Sara Arnaboldi[1,5], Michela Tilola[1], Marina Nadia Losio[1], Laura Pezzolesi[3], Marika Ubaldi[2], Francesca Neri[2], Stefano Accoroni[2], Stefania Milandri[4], Monica Cangini[4]

(1) Istituto Zooprofilattico Sperimentale della Lombardia ed Emilia Romagna, Food Safety Department, 7/9 via Antonio Bianchi, Brescia, Italia
(2) Università Politecnica delle Marche, Life and Environmental Science department, via Brecce Bianche, Ancona, Italia
(3) Università degli Studi di Bologna, Biological, Geological and environmental Science, via S. Alberto 163, Ravenna, Italia
(4) Fondazione Centro Ricerche marine, National Reference Laboratory for Marine Biotoxins, V.le A. Vespucci, 2|47042, Cesenatico (FC), Italia
(5) Università degli Studi di Parma, Department of Veterinary Science, via Università 12, Parma, Italia

The Adriatic Sea is characterized by a shallow depth and high riverine inputs, consequently more affected to the extremely variable climate changes, but most of the nation's bivalve mollusc farms are concentrated there. In recent years, changes in the phytoplankton composition and emerging problems related to the new microorganism appearances and early detection of well-known toxic algae have become of great concern for human safety, also from the One Health perspective. Marine water samples were collected respectively from different farm sites of Emilia Romagna and Marche region. Samples collections were conducted from 2023 to 2024 (still progressing) in the LTER (Long-Term Ecological Research station) of Senigallia in the Marche region and across all coastal sites in the Emilia Romagna region, areas that are highly appealing to mollusc farmers. Samples were amplified and sequenced using Illumina instrument DNA metabarcoding (targeting V4 and V9 regions of the 18S rRNA gene, using PR2 and SILVA as reference databases). The results obtained were compared with microscopical detection conducted by Utermöhl method. Comparison between microscopy and metabarcoding revealed significant differences, as the two methods produced only partially overlapping results; in most cases Dinophyceae were detected by sequencing, despite the absence or low cells of Dinophysis spp. detection by microscopy. For instance, many potentially toxic Alexandrium species were detected exclusively by metabarcoding, likely due to the difficulty of detecting them with microscopy after fixing methods. Consequently, NGS sequencing can be a powerful system to verify water sample compositions in terms of potentially toxic microorganisms, to support microscopical analysis conducted to carry out official monitoring.

**Keywords**: Adriatic Sea, toxic algae, NGS sequencing

Poster Session 02: In Situ Monitoring and Remote Observing Systems

P-128

# Operational and functional evaluation of the SuiteCase Lab System for molecular detection of *Alexandrium catenella* using LAMP

**Gonzalo Icaza Zuleta**[1], Alejandra Aguilera-Belmonte[1,2], Miriam Seguel[1], Juan Manosalva[1], Felipe Tucca[3], Gustavo Roselott[1]

(1) Universidad San Sebastián, Programa de vigilancia *Alexandrium catenella*., Sede Patagonia, Lago Panguipulli 1390, Puerto Montt, Chile
(2) Universidad San Sebastián, Facultad de Ciencias, Lago Panguipulli 1390, Puerto Montt, Chile
(3) Instituto Tecnológico del Salmón (INTESAL)„ Independencia n° 50 of 8, Puerto Varas, Chile

In response to the need for rapid, sensitive tools to monitor harmful algal blooms (HABs), a molecular detection method was evaluated in collaboration with the Salmon Technology Institute (INTESAL, Chile). INTESAL provided the portable Suitecase Lab, an integrated unit containing all necessary supplies, reagents, and equipment for molecular detection of *Alexandrium catenella* using Loop-Mediated Isothermal Amplification (LAMP).

The study aimed to evaluate the operational and functional status of the Suitecase Lab. Its base protocol was modified by replacing the original polymerase and optimizing reaction temperatures. Conventional PCR targeting the *A. catenella* 28S rRNA gene (primers AC2245R/AC1976F) served as the reference method. LAMP assays used DNA extracted via two methods: a commercial kit for complex environmental matrices and the Chelex-100 resin protocol from the device's manual. DNA sources were *A. catenella* cultures (1, 6, 26, and 100 cells·mL$^{-1}$) and environmental samples from priority monitoring areas.

LAMP assays showed a gradual increase in amplicon absorbance over time for both culture and environmental samples, including successful detection at the minimum tested concentration of 1 cell·mL$^{-1}$. Environmental sample amplification curves exhibited steeper slopes, indicating higher efficiency compared to cultured samples. Due to its rapidity and sensitivity, this LAMP method presents a valuable complement to traditional microscopy for *A. catenella* detection.

**Keywords**: *Alexandrium catenella*, Loop-mediated isothermal amplification (LAMP), Molecular detection

**Financing**: This research was funded by the monitoring, detection, and control program for Alexandrium catenella. San Sebastián University.

**Acknowledgments**: We thank INTESAL for providing the Suitecase Lab equipment used in this study.

Poster Session 02: In Situ Monitoring and Remote Observing Systems
P-129

# Evolution of toxic ban management affecting *Aequipecten tehuelchus* and *Mytilus edulis* in the San José Gulf, Valdés Peninsula, Chubut, Argentina

**Dario Ezequiel Litterio Sassaroli**[1], Noelia Mariel Uyua[1], María Eva Góngora[1]

(1) Instituto de Investigación de Hidrobiología, Universidad Nacional de la Patagonia San Juan Bosco, Facultad de Ciencias Naturales y Ciencias de la Salud, Gales 48, Trelew, Argentina

Harmful algal blooms (HABs) pose serious ecological and socio-economic challenges to coastal communities worldwide. In Chubut Province, Argentina, the first recorded case of shellfish poisoning occurred in 1980, resulting in the deaths of two sailors who consumed toxin-contaminated mollusks near the Valdés Peninsula.

In response, local authorities initiated harvesting bans to mitigate public health risks. Over the past three decades, these bans have evolved in scope and regulation, with the current framework governed by the Provincial Plan for Red Tide Control and Prevention (PPCPMR). This plan establishes monitoring zones and protocols along Chubut's maritime coast to regulate the extraction of bivalve mollusks.

This study analyzes the historical evolution of HAB-related harvesting bans from 1985 to the present in the San José Gulf. We focus on two economically important species: the Tehuelche scallop (*Aequipecten tehuelchus*) and the blue mussel (*Mytilus edulis*), both of which are vital to local fisheries. We identify temporal patterns in ban duration and frequency by examining data across the PPCPMR's three regulatory zones.

Our findings reveal shifts in management strategies over time, reflecting advances in monitoring capacity, toxin detection, and policy adaptation. These changes have had direct implications for the sustainability of mollusk fisheries, as well as for the livelihoods of coastal harvesting communities.
Understanding how HAB management has evolved in this region contributes to the broader discussion on adaptive strategies for mitigating the impacts of toxic algal events under changing environmental conditions.

**Keywords**: HABs, toxic bans, management strategies

**Financing**: Consejo Nacional de Investigaciones Científicas y Técnicas (CONICET, Argentina)Secretaría de Ciencia y Tecnología de la Provincia de Chubut.

**Acknowledgments**: We thank Viviana Sastre, Norma Santinell, and the Fisheries Secretariat of Chubut for their invaluable contributions and access to essential documents supporting this research.

Poster Session 02: In Situ Monitoring and Remote Observing Systems
P-130 (Ignite Talk)

# Development of a satellite-based algorithm for green *Noctiluca* discrimination in the upper Gulf of Thailand using in-situ bio-optical observations

**Jutarak Luang-on**[1], Eko Siswanto[1], Joji Ishizaka[2], Akihiko Morimoto[3], Anukul Buranapratheprat[4], Jitraporn Phaksopa[5]

(1) Japan Agency for Marine-Earth Science and Technology, Tohoku University and JAMSTEC Advanced Institute for Marine Ecosystem Change (WPI-AIMEC), Yokohama, Japan
(2) Institute for Space-Earth Environmental Research (ISEE), Nagoya, Japan
(3) Ehime University, Center for Marine Environmental Studies (CMES), Japan
(4) Burapha University, Department of Aquatic Science, Faculty of Science, Thailand
(5) Kasetsart University, Department of Marine Science, Faculty of Fisheries, Thailand

Green *Noctiluca scintillans*, a heterotrophic dinoflagellate containing photosynthetic endosymbionts *(Pedinomonas noctilucae)*, is a recurrent harmful algal bloom (HAB) species in the upper Gulf of Thailand (uGoT). Its high biomass alters seawater color to a characteristic milky green and can trigger hypoxic conditions, leading to widespread fish mortality. However, distinguishing green *Noctiluca* blooms from other phytoplankton species using satellite ocean color data remains challenging due to limited in-situ validation. This study develops a satellite-based discrimination algorithm specifically for identifying green *Noctiluca* blooms. The algorithm was developed and calibrated using in-situ bio-optical datasets collected between 2017 and 2023, including chlorophyll-a concentrations, phytoplankton community structures derived from HPLC-CHEMTAX, and hyperspectral remote sensing reflectance (Rrs) measurements obtained using a RAMSES radiometer (320–950 nm). Distinct spectral features of green *Noctiluca* were extracted and used to formulate a robust classification approach applicable to multispectral satellite sensors such as MODerate-resolution Imaging Spectroradiometer-Aqua (MODIS) and the Second-Generation Global Imager (SGLI) on the Global Change Observation Mission-Climate. The resulting algorithm enables improved detection and monitoring of green *Noctiluca* blooms from space, supporting early warning systems and marine ecosystem management in the uGoT.

**Keywords**: Remote sensing, Algal bloom detection, Green *Noctiluca*

**Financing**: ISEE, Nagoya University (2023-13-009); JAXA GCOM-C contract: 24RT000233; KAKENHI JP21H05317 and 22KK0167, Sasakawa Scientific Research Grant of the Japan Science Society (JSS-29-714)

**Acknowledgments**: We gratefully acknowledge the data support provided by the Department of Marine and Coastal Resources (Thailand).

Poster Session 02: In Situ Monitoring and Remote Observing Systems

P-131

# Strengthening harmful algal blooms monitoring in the Subantarctic Region: The CHIC Red Tide Laboratory as a model for integrated Environmental Surveillance in Cape Horn, Chile

**Vanessa Monge**[1,2,3], Maximo Frangopulos[1,3,4], Gemita Pizarro[5], Francisca Massardo[1,6], Claudia Zamora[5], Maria Carolina Zuñiga[2,3,5], Eduardo Barros[1,6]

(1) Centro Internacional Cabo de Hornos (CHIC), Universidad de Magallanes, Puerto Williams, Chile
(2) Programa de Magíster en Ciencias con Mención en Conservación y Manejo de Recursos Naturales en Ambientes Subantárticos, Universidad de Magallanes, Punta Arenas, Chile
(3) Instituto Milenio Biodiversidad de Ecosistemas Antárticos y Subantárticos (BASE), Universidad de Chile, Santiago, Chile
(4) Centro de Investigación Gaia-Antártica (CIGA), Universidad de Magallanes, Punta Arenas, Chile
(5) Centro de Estudios de Algas Nocivas (CREAN), Instituto de Fomento Pesquero (IFOP), Enrique Abello 0552, Punta Arenas, Chile
(6) Parque Etnobotánico Omora, Universidad de Magallanes, Puerto Williams, Chile

Due to climate change and other environmental factors, **Harmful algal blooms (HABs)** are becoming more frequent, intense, and widespread, posing significant risks to marine ecosystems, human health, and local economies. In response to these challenges, the CHIC Red Tide Laboratory has been established in Cape Horn, Chile, a remote and ecologically significant area recognized as one of the southernmost and pristine coastal regions on the planet. Situated within the Cape Horn Biosphere Reserve, this location is a global biodiversity hotspot and a sentinel region for monitoring oceanic changes caused by climate variability.

The laboratory was established as part of a **planned and integrated strategy** to strengthen the subantarctic region`s long-term HAB surveillance capacity. It is equipped with high-performance liquid chromatography systems (HPLC-FLD/DAD) for detecting paralytic shellfish toxins (PSTs) and amnesic shellfish toxins (ASTs), operating under analytical protocols that align with national and international standards. Beyond infrastructure, the initiative involves multi-level coordination with public institutions, local communities, and national monitoring networks. Addressing a longstanding gap in toxin detection and early warning systems in extreme southern latitudes, the project enhances data availability, scientific sovereignty, and local response capacity in an underserved territory, while promoting sustainable socioeconomic development and supporting ecotourism by safeguarding marine resources and coastal communities.

This project represents a **strategic model** for integrated environmental surveillance in remote coastal ecosystems. It provides a framework that can be replicated in other biosphere reserves and vulnerable regions that are facing emerging threats from harmful algal blooms in the context of global change.

**Keywords**: Harmful algal blooms, Marine toxins monitoring, Subantarctic region

**Financing**: ANID/BASAL FB210018

**Acknowledgments**: ANID/BASAL FB210018

Poster Session 02: In Situ Monitoring and Remote Observing Systems
P-132

# Monitoring, detection and control of *Alexandrium catenella* in NW Patagonia: A Program Overview (2018-2025)

**Miriam Seguel**[1], Alejandra Aguilera-Belmonte[1,2], Juan Manosalva[1], Gonzalo Icaza Zuleta[1], Gustavo Roselott[1], Patricio Díaz[3]

(1) Universidad San Sebastián, Programa de vigilancia *Alexandrium catenella*, Sede Patagonia, Lago Panguipulli 1390, Puerto Montt, Chile
(2) Universidad San Sebastián, Facultad de Ciencias, Lago Panguipulli 1390, Puerto Montt, Chile
(3) Universidad de Los Lagos, Centro i~mar & CeBiB, Casilla 557, Puerto Montt, Chile

Blooms of *Alexandrium catenella* have affected coastal activities of northwestern Patagonia in the last 30-years. The most affected activities have been the shellfish aquaculture, benthic fisheries and the public health. To prevent the transport of vegetative cells to unaffected areas north of 43°22'S, Chile established the *Monitoring, Detection, and Control Program for Alexandrium catenella* in 2016. Managed by the Chilean National Fisheries and Aquaculture Service (SERNAPESCA) and implemented by Universidad San Sebastián since 2021, this program employs systematic monitoring of wellboats transporting live salmon. The protocol involves collecting water samples from onboard holds and conducting microscopic analysis in situ. The detection of a single *A. catenella* cell is considered a positive result, requiring the wellboat to either recirculate the water south of latitude 43°34.9' S or discharge it at an authorized processing facility equipped with a deactivation system. Between 2018 and 2025, 22,749 samples were analyzed, revealing 237 positives (1% positivity rate). The highest rate occurred during summer 2018 (6%), coinciding with an intense bloom in the Aysén region, where cell densities reached 643,500 cells·$L^{-1}$. Subsequent years showed consistently lower positivity rates (0.2–0.6%).

To date, the program has achieved 100% verification of wellboats transiting from Aysén to Los Lagos regions, establishing itself as an international model for controlling *A. catenella* dispersal risks associated with aquaculture.

**Keywords**: *Alexandrium catenella*, Chilean north Patagonia, monitoring and mitigation

**Financing**: This research was funded by the monitoring, detection, and control program for Alexandrium catenella. San Sebastián University.

**Acknowledgments**: We thank all professionals who work in the Monitoring, Detection, and Control Program for Alexandrium catenella.

Poster Session 02: In Situ Monitoring and Remote Observing Systems

P-133

# Enhancing automated detection of HABs in Alaskan and Atlantic waters: Evaluation of strategies for improving CNN model accuracy

**Cristian Swift**[1,2], Mrunmayee Pathare[1], Vanessa Haggans[1], Ethan Andrews[1], Mike Brosnahan[1]

(1) Woods Hole Oceanographic Institution, Biology, 266 Woods Hole Road, Woods Hole, United States of America
(2) Massachusetts Institute of Technology, 77 Massachusetts Avenue, Cambridge, United States of America

The rapid adoption of automated in situ microscopy for HAB monitoring is driving near-exponential growth of plankton image data. Still, a major bottleneck for use of these records for HAB monitoring and science is taxonomic annotation of images, a task that requires machine classification. Convolutional neural networks (CNNs) are a leading class of models being applied to this task due to their high classification skill and computationally efficient inference. Still, development of models that can be generalized reliably for detection of HABs across different regions has been a challenge. This study characterizes the growth and geographic expansion of plankton image data created by Imaging FlowCytobots (IFCB), a leading platform for collection of phytoplankton images. A series of experiments are described that evaluate the effects of instrument, geographic origin, year, and model architecture on model skill and generalizability through comparison of inferences to human annotations of >15 taxonomic classes from records collected in Alaska and the northwestern Atlantic regions. Additional experiments explored the effects of training image augmentation through supplementation of training sets (through annotation of target training sets) and training image manipulation (e.g., rotation, brightness variation, and artificial noise). The results of these experiments are guiding development of new image classification models that more reliably detect the presence and abundance of HAB cells in plankton image observations.

**Keywords**: Image Classification, IFCB, CNN

**Financing**: Woods Hole Center for Oceans and Human Health

**Acknowledgments**: Biology Department, Woods Hole Oceanographic Institution Department of Earth Atmospheric and Planetary Sciences, MITAlaska Ocean Observing SystemNSF Graduate Research Fellowships ProgramAlaska Sea Grant.

Poster Session 02: HAB's Social Dimensions
P-134 (Ignite Talk)

# Adaptive governance for sustainable fisheries: Insights from the scallop fishery of the Eastern English Channel (France) faced with HAB and emerging challenges

**Sarra Chenouf**[1]

(1) IFREMER, Unité d'Economie Maritime de l'IFREMER, UMR 6308 AMURE, Brest, France

Harmful algal blooms (HAB) have been particularly intense in the Eastern English Channel over the past two decades. This cyclical and unpredictable phenomenon, represents a major driver for the dynamics in the fisheries sector, including economic, social, and governance-related changes.

As a key fisheries activity, the scallop fishing is subject to specific exploitation conditions through binding management measures. This management framework includes a set of technical and access regulations aimed at preserving and sustainably managing this resource. Furthermore, following the emergence of HAB-related public health and socio-economic issues, a risk mitigation approach, based on continuous monitoring and commercial restrictions, has gradually been implemented through a series of regulatory reforms. Consequently, HAB have triggered significant challenges and changes in fishery governance and the operational strategies of fishermen.

The evolution of this social-ecological system requires particular attention to ensure its sustainability and resilience in the face of growing pressures, including those induced by HAB. These challenges extend beyond environmental concerns, as the sector is currently subject to a complex combination of cumulative effects within a continuously evolving context. Although scallop stocks in the Eastern English Channel remain generally in good condition and Amnesic Shellfish Poisoning (ASP) toxicities have not been reported since the 2012 crisis, fragmentation of governance continues to hinder the sector's ability to respond effectively to emerging challenges and uncertainties.

This research explores decision-support mechanisms to foster a more adaptive, resilient, and collaborative governance approach, that meets the fishing community's needs.

**Keywords**: Scallop fishery, sustainability, HAB

Poster Session 02: HAB's Social Dimensions

P-135

# Microalgae for kids: Storytelling as a tool for harmful algal bloom outreach in Chile

**Anita Flores Lenero**[1], Francisca Prieto[2], Teresa Huneeus[3]

(1) Scottish Association for Marine Science (SAMS), Scottish Marine Institute, PA37 1QA, Oban, United Kingdom
(2) Colegio Puerto Varas, Artes Visuales, Camino Viejo a Llanquihue, Puerto Varas, Chile
(3) Without affiliation

In the last decade, there has been a notable increase in science outreach initiatives, reflecting the growing recognition of the importance of connecting research with non-academic audiences. In Chile, harmful algal blooms (HABs) pose a recurrent threat to marine ecosystems and human health. Therefore, public activities play a key role in raising awareness and promoting prevention strategies. This project created the first Chilean children's book focused on microalgae, using a story-based learning approach to communicate scientific concepts in an accessible way. The book title *Microcuentos: grandes historias para pequeños organismos*, consists of fictional stories that introduce children to the ecological role and potential risks of microalgae. Each story is followed by a simple scientific explanation that connects the narrative to natural phenomena. The objective was to explore a creative method for introducing complex environmental topics to young audiences, encouraging curiosity. Before publication, the stories were tested with a group of 30 children between the ages of 3 and 11, to assess comprehension and engagement. After printing, the project includes *kamishibai* (Japanese-style theater) storytelling sessions on schools and libraries, involving directly more than 900 children across different regions of Chile and indirectly impacting more than 12,000 children. This project was a novelty in using stories with scientific background as an innovative strategy for communicating environmental challenges such as HABs to younger generations. Future efforts must continue developing innovative outreach tools to inform, prevent, and protect the Chilean population, against the ongoing risks of HABs in a changing climate.

**Keywords**: Children, Story-based learning, Public engagement

**Financing**: Project financed by the Public Science program of the Ministry of Science, Technology, Knowledge and Innovation of Chile

**Acknowledgments**: We sincerely thank all collaborators, with special recognition to the Centro de Investigación Dinámica de Ecosistemas Marinos de Altas Latitudes (IDEAL) and Ediciones Mis Raíces.

Poster Session 02: HAB's Social Dimensions

P-136

# Enhancing marine and coastal resilience through scientific communication on stressors: The case of harmful algal blooms in Latin America and the Caribbean

**Isabela Katime**[1,2], Paola Obando[1,2], Luisa F. Espinosa[1,2]

(1) Marine and Coastal Research Institute, INVEMAR, Scientific Communication / Marine Quality Water Program, Calle 25 # 2-55, Santa Marta, Colombia
(2) Marine-Coastal Stressors Research Network (REMARCO)

Harmful algal blooms (HABs) are an increasingly frequent marine-coastal stressor in Latin America and the Caribbean (LAC), impacting food security, public health, and coastal economies. Addressing this complex issue requires not only scientific expertise, but also effective public communication and community participation. The **Marine-Coastal Stressors Research Network (REMARCO)** is a voluntary, interdisciplinary, and non-profit initiative involving 18 countries in the region. Established through the International Atomic Energy Agency (IAEA) and ARCAL, REMARCO uses nuclear, isotopic, and complementary techniques to monitor stressors like HABs. Crucially, REMARCO integrates scientists and communicators to ensure that scientific knowledge is accessible to decision-makers, coastal communities, and the general public. One of REMARCO's core strengths lies in its communication strategy, which promotes science literacy and public engagement. Since 2009, six regional projects have enhanced national capacity for HAB monitoring and communication. These projects have strengthened science-based responses while empowering communities to understand and act on environmental threats. Its knowledge dissemination efforts include accessible reporting formats, open data, training courses, and citizen-focused content. In countries like Colombia, monitoring activities support the development of early warning systems where citizen observations contribute to data collection and risk response. By promoting citizen science and transparent communication, REMARCO contributes to the UN Sustainable Development Goals 14 and 17, and the Ocean Decade. It demonstrates how regional collaboration and public engagement can transform scientific data into actionable knowledge that protects both people and ecosystems from the risks of HABs.

**Keywords**: Scientific communication, HABs

**Financing**: International Atomic Energy Agency (IAEA) / RLA7028 project

**Acknowledgments**: To the International Atomic Energy Agency (IAEA), to scientists and communicators as REMARCO members. The Marine and Coastal Research Institute, INVEMAR

Poster Session 02: HAB's Social Dimensions

P-137

# Inhalation of microcystin-producing cyanobacteria associated with pulmonary toxicity

**Dail Laughinghouse[1],** David Berthold[1], Jessica Moretto[1], Sarah Bisesi[2], Kevin Kroll[2], Tamas Jilling[3], Maria Garzon-Ramirez[3], Claire Fisher[3], Tara Sabo-Attwood[3], Nancy Denslow[2]

(1) University of Florida, Agronomy Department, Ft. Lauderdale Research and Education Center, Davie, FL, USA
(2) University of Florida, Department of Physiological Sciences, Center for Environmental and Human Toxicology, Gainesville, FL, USA
(3) University of South Carolina, Department of Environmental Health Sciences, Arnold School of Public Health, Columbia, SC, USA

Cyanobacterial harmful algal blooms (cyanoHABs) pose global environmental and public health risks, particularly due to microcystin production (MCs). While aerosolized MCs may primarily impact the lung, their potential to induce systemic toxicity via extracellular vesicles (EVs) remains poorly characterized. This study investigates MC-driven changes exosomes from lung epithelial cells and their functional implications. Lyophilized *Microcystis* (high MC), *Dolichospermum* (intermediate MC), and *Floridanema* (negligible MC) biomass were resuspended in PBS, subjected to freeze-thaw cycles to release toxins, and applied to human small airway epithelial cells (SAECs) at 0–200 µg/mL biomass for 48 hours. Exosomes were isolated for lipidomic profiling, while RNA-seq analyzed cellular transcriptomic changes. Flow cytometry revealed dose-dependent reductions in viability and increased apoptotic/dead cells proportional to MC levels. Lipidomics identified significant shifts in exosomal ceramides, lysophospholipids, and ether-linked phospholipids, suggesting altered membrane fluidity and function. These findings support the hypothesis that MC exposure modifies EV composition, potentially disrupting intercellular communication and contributing to systemic toxicity.

**Keywords**: aerosol, *Microcystis*, *Dolichospermum*

**Financing**: Florida Department of Health

Poster Session 02: HAB's Social Dimensions

P-138

# A book with two women in an ocean of stories in the Southeastern Pacific coast

**Vivian Montecino**[1], Doris Oliva[2]

(1) Universidad de Chile, Ciencias Ecológicas, Ciencias, Las Palmeras 3425, Santiago, Chile
(2) Universidad de Valparaíso, Instituto de Biología, Ciencias, Av. Gran Bretaña 1111 Playa Ancha, Valparaíso, Chile

In Chile, oceanography starting with important explorations, developed in the early XX century, due to naturalists and diverse marine sciences professionals in response to the needs of the country along a large eastern boundary current with seasonal or permanent upwelling. Knowledge of the coastline, shelf, the open ocean, fjords and channels, oceanic islands and the Southern Ocean has gradually been accomplished by academic and public institutions in relation to physical, chemical, and biological oceanography and fisheries. We communicate academic experiences, scientific questions, problems, and describe investment in science and infrastructure. The stories come from "women of sacrifice and courage" (masculine attributes?). We refer to contemporary marine sciences (1960-1972) characterized by the first marine biologist, Mar-Chile Expeditions, Marine Science Committee, first man graduated in marine sciences in Chile (woman 10 years later); and creation of iconic scientific institutions (Instituto Antártico Chile, Instituto de Fomento Pesquero, Comisión Nacional de Ciencia y Tecnología and Comité Oceanográfico Nacional). Today women work in remote areas, participating in national and international cruises, modeling in supercomputers, and creating leadership. From biology and taxonomy to molecular science, from archaea to large cetaceans, living particles of all sizes, physical oceanography, climate variability, biogeochemistry, ecology, fisheries, and a permanent monitoring program in harmful algal species (HAB´s). We refer to HAB's and fisheries and aquaculture generating political, social, and economic conflicts to encourage young researchers for new scientific knowledge, multiple discipline interactions, and a growing need to coexist with the ocean as part of the solution for humanity and climate change.

**Keywords**: Chilean and Humboldt-Current marine-sciences

**Financing**: IEB-Chile, Facultad de Ciencias & Departamento Ciencias Ecológicas U. Chile, Proyecto Inés Género & Ciencia 2030 U. Valparaíso

**Acknowledgments**: María Teresa Infante, René Durán, Anelio Aguayo, Rodolfo Iturriaga, and Eduardo Tarifeño.

Poster Session 02: HAB's Social Dimensions

P-139

# ADICFito: A platform for public engagement and AI-supported taxonomic awareness in HAB monitoring

**Stephanie Sáez**[1], Carmen G Brito[1], Álvaro Jorquera[1], Carlos Flores[1], Pablo Nahuelpán[1], Rodrigo Gibson[1], Laura Latorre-Melín[1], Nicole Correa[1], María J Calderón[1], Carla Palma[1], Francisca Muñoz[1], Felipe Zerené[1], Alejandro Clément[1]

(1) Plancton Andino SpA., Terraplén 869, Puerto Varas, Chile

Effective HAB monitoring requires not only expert data collection, but also accessible communication tools and platforms that engage a broader scientific and public audience. ADICFito is a web-based application designed to support phytoplankton identification through collaborative image sharing and taxonomic catalog building.

A central feature of ADICFito is the shared image repository, composed of microscopic cell images submitted by users with varying expertise. This results in a practical visual catalog that combines high-resolution reference images with day-to-day operational samples, making it especially useful for regional monitoring teams, early-career taxonomists, and citizen scientists.
Recently, the platform has been enhanced with Large Language Model (LLM) technology to automatically generate descriptive content for over 50,000 phytoplankton taxa. These AI-generated descriptions improve the accessibility and educational value of the catalog, helping bridge the gap between expert knowledge and public understanding.

ADICFito encourages collaboration among specialists while opening the door to broader participation in phytoplankton research. By combining technology, public access, and expert networks, it represents a new model for science communication and citizen science engagement in the context of HABs.

**Keywords**: ADICFito, phytoplankton images, web-based platform

**Financing**: Plancton Andino SpA.

**Acknowledgments**: To the team at Plancton Andino, for all their hard work.

Poster Session 02: HAB's Social Dimensions
P-140 (Ignite Talk)

# Local perceptions of the HABs impacts in Chilean Patagonia

**Rodolfo Sapiains**[1,2,3], Aldo Barreiro[6], Gabriela Azócar[1,3], Ana Maria Ugarte Caviedes[3], Máximo Jorge Frangopulos Rivera[4,5]

(1) Universidad de Chile, Ciencias Sociales, Santiago, Chile
(2) Centro de Investigación GAIA Antártica (CIGA) Universidad de Magallanes, Punta Arenas, Chile
(3) Center for Climate and Resilience Research (CR)2, Santiago, Chile
(4) Cape Horn International Center (CHIC), Cabo de Hornos, Chile
(5) Millenium Institute Biodiversity of Antarctic and Subantarctic Ecosystems (BASE), Chile
(6) Centro Interdisciplinar de Investigação Marinha e Ambiental (CIIMAR ), Matosinhos, Portugal

Chilean Patagonia is significantly affected by HABs, yet there is limited research on how local coastal communities perceive the impacts of these events. This study presents a survey conducted in three HAB affected Provinces in southern Chile, using AI techniques for sampling and online platforms for data collection. The survey had a large sample size (n=1718). Results show that 79% of respondents have experienced at least one HABs episode in their lifetime, with health and economic dimensions being the most affected. The overall level of preparedness for future episodes is generally low, with participants feeling more prepared for economic than for health impacts. Some 66% of respondents believe that it is likely or very likely that a HABs episode will occur in their area within the next five years; 56% express a high level of concern about such an event. Respondents were also divided into two groups based on the variability of their responses. The first group (37%) with participants from the northern Patagonia region (Chiloe Island and Llanquihue Province), whose income is heavily dependent on marine resources, showed greater knowledge of HABs symptoms and associated impacts. In contrast, the second group (63%) included people from the three provinces with lower economic dependence on the sea and varying levels of knowledge about HABs. These findings highlight the importance of understanding local perceptions of HABs for policy-making and interdisciplinary research. Such knowledge can contribute to the development of more informed responses and interventions to mitigate the local impacts of future HABs events.

**Keywords**: HABs impacts, local perceptions, Chilean Patagonia

**Financing**: FONDAP/ANID 1523A0002

Poster Session 02: HAB's Social Dimensions

P-141

# Advances in monitoring harmful qlgae and phycotoxins in Santa Catarina – Brazil: From mouse bioassay to mass spectrometry

**Mathias Alberto Schramm**[1], Thiago Pereira Alves[1], Thatiana de Oliveira Pinto[1], Luiz Laureno Mafra Jr.[2], Rodrigo Barcellos Hoff[3], Cristian Rafael Kleemann[4], Carolina Turnes Pasini Deolindo[4], Pedro Sesterhenn[5], Robson Ventura Souza[6]

((1) Federal Institute of Santa Catarina, Laboratory of Harmfull Algae and Phycotoxins, Itajaí, Brazil
(2) Federal University of Paraná, Center for Marine Studies, Pontal do Paraná, Brazil
(3) Ministério da Agricultura e Pecuária, Laboratório Federal de Defesa Agropecuária, Seção Laboratorial Avançada em Santa Catarina, São José, SC, Brasil (4) Instituto Catarinense de Sanidade Agropecuária (ICASA), Florianópolis, SC, Brasil
(5) Companhia Integrada de Desenvolvimento Agrícola de Santa Catarina (CIDASC), Florianópolis, SC, Brasil
(6) Agricultural research and rural extension company of Santa Catarina, Aquaculture and Fisheries Development Center (CEDAP/EPAGRI), Florianópolis, SC, Brazil

Shellfish aquaculture began in Santa Catarina in the late 1980s and now accounts for >90% of the country's bivalve production (~7,000 tons/year). Research on harmful algal blooms (HABs) and phycotoxins started in 1990, following a suspected diarrhetic shellfish poisoning (DSP) outbreak. Initial efforts focused on phytoplankton microscopy and toxin detection using mouse bioassay (MBA) and HPLC. In 2012, an official HAB monitoring program was launched. A major advancement occurred in 2018, with the adoption of a unified LC-MS/MS protocol as the Brazilian reference method for toxin analysis. Monitoring data indicate that *Dinophysis* spp., particularly the *D. acuminata* complex, are the most frequent toxin producers, reaching densities of 580,000 cells $L^{-1}$ and accounting for >95% of shellfish harvesting closures since 2007. Okadaic acid and dinophysistoxin (OA+DTX) levels reached 6,867 µg/kg in farmed *Perna perna*, 1,102 µg/kg in *Crassostrea gigas*, and 30,065 µg/kg in wild *Mesodesma mactroides*. Paralytic shellfish toxins (PSTs) are rare, with regulatory exceedances recorded only twice—during *Gymnodinium catenatum* (2006) and *Alexandrium tamarense* (2017) blooms. Domoic acid (DA) contamination is also infrequent, despite recurrent blooms of low-toxicity *Pseudo-nitzschia* spp. Exceedance of the DA limit appears to require ≥$10^6$ cells $L^{-1}$ and ≥75% Pseudo-*nitzschia* dominance, as estimated during a P. *pseudodelicatissima*-dominated bloom in 2009. The 2018 methodological shift was key to accurately characterizing toxin profiles, including emerging compounds. MBA previously required sacrificing hundreds of animals monthly and yielded ambiguous results near regulatory thresholds. LC-MS/MS surveillance enabled more precise harvest bans and geographic targeting, benefiting producers and helping reduce poisoning cases.

**Keywords**: Seafood Safety, Regulatory Programs, Shellfish Poisoning

**Financing**: Resources from the Ministry of Fisheries and Aquaculture, Ministry of Agriculture, CIDASC, EPAGRI and IFSC.

**Acknowledgments**: Thanks to all institutions that collaborated in carrying out the work, including the Ministry of Fisheries and Aquaculture, Ministry of Agriculture, CIDASC, EPAGRI and IFSC.

Poster Session 02: HAB's Social Dimensions
P-142

# Harmful algae and phycotoxin research in Brazil: 35 years of advances and challenges

**Mathias Alberto Schramm[1],** Thiago Pereira Alves[1], Thatiana de Oliveira Pinto[1], Luis Antônio de Oliveira Proença[1], Luiz Laureno Mafra Jr.[2], Carlos Eduardo Junqueira de Azevedo Tibiriçá[3], Rodrigo Barcellos Hoff[4], Clarisse Odebrecht[5]

(1) Federal Institute of Santa Catarina (IFSC), Laboratory of Harmfull Algae and Phycotoxins, Itajaí, SC, Brazil
(2) Federal University of Paraná (UFPR), 2- Center for Marine Studies (CEM), Pontal do Paraná, PR, Brazil
(3) Instituto do Meio Ambiente de Santa Catarina (IMA-SC), Florianópolis, SC, Brasil
(4) Ministério da Agricultura e Pecuária, Laboratório Federal de Defesa Agropecuária, Seção Laboratorial Avançada em Santa Catarina (SLAV/SC/LFDA/RS), São José, SC, Brasil
(5) Universidade Federal do Rio Grande (FURG), Rio Grande, RS, Brasil

Harmful algal blooms (HABs) have been reported along the Brazilian coast since 1900, as early described by Vieira-da-Rosa (1905) in the "*Chrorographia de Santa Catharina*". Early events were often associated with water discoloration, fish kills, and/or the presence of toxic species. The expansion of bivalve mollusk aquaculture in the 1990s increased the need for HAB monitoring. However, an official national monitoring program was only implemented in 2012 and updated in 2024. Phycotoxin research in Brazil began in 1990 using mouse bioassays and high-performance liquid chromatography (HPLC), leading to the identification of the most common toxin groups causative of human intoxication: domoic acid (DA) by *Pseudo-nitzschia* spp. (ASP), okadaic acid (OA) by *Dinophysis acuminata* (DSP), paralytic shellfish toxins by *Gymnodinium catenatum* and *Alexandrium* spp. (PSP). Over the past 35 years, other pelagic and benthic harmful algae have been documented, including species belonging to *Azadinium, Chattonella, Coolia, Fibrocapsa, Gambierdiscus, Gonyaulax, Heterosigma, Lingulodinium, Ostreopsis, Phaeocystis, Prorocentrum, Synechocystis*. DSP is the most frequent intoxication in the South, and, since 2022, Ciguatera poisoning has become recurrent in the Northeast. Numerous phycotoxins have been detected in coastal water and marine organisms, regardless of reported human intoxication, including AZAs, BTX-like compounds, DA, DTXs, OA, OvTXs, PLTX, PSTs, PTXs, SPXs, YTXs, and, recently, CTXs. Research groups have played a crucial role in advancing knowledge, developing postgraduate training, supporting the establishment of the mollusk health program, and collaborating with the Ministries of Agriculture and Health in investigating foodborne poisoning linked to seafood from marine and freshwater sources.

**Keywords**: HABs in Brazil, Phycotoxins in Brazil, Public Health

**Acknowledgments**: Thanks to all funding agencies, institutions, universities and research groups that in one way or another contributed to HABs research.

Poster Session 02: HAB's Social Dimensions

P-143

# Spatiotemporal patterns of lipophilic toxins in filter-feeding from NW Patagonia

**Sergio A. Triviño**[1], Carlos Molinet[2], Gonzalo ÁLvarez[4], Michael Araya[3], Patricio A. Díaz[5]

(1) Universidad Austral de Chile , sede Puerto Montt, Programa de Magister en Medio Ambiente y Bioseguridad en Acuicultura, Puerto Montt, Chile
(2) Universidad Austral de Chile , Campus Puerto Montt, Instituto de Acuicultura y Medio Ambiente, Puerto Montt, Chile
(3) Universidad Catolica del Norte, Departamento de Acuicultura, Facultad de Ciencias del Mar, Larrondo 1281, Coquimbo, Chile
(4) Universidad Catolica del Norte, Centro de Investigación y Desarrollo Tecnológico en Algas (CIDTA), Facultad de Ciencias del Mar, Larrondo 1281, Coquimbo, Chile
(5) Universidad de Los Lagos, Centro i~mar & CeBiB, Casilla 557, Puerto Montt, Chile

Harmful algal blooms of lipophilic toxin-producing species represent a growing global threat to public health and marine resources with severe socioeconomic impacts on coastal communities. Shellfish resources in Chilean Patagonia are subject to chronic contamination with lipophilic toxins such as okadaic acid (OA), dinophysistoxins (DTXs), pectenotoxins (PTXs), yessotoxins (YTXs) and their analogs, which are related to *Dinophysis*, mainly *D. acuta* and *D. acuminata*, and *Protoceratium reticulatum* blooms. In this study, we used filter-feeding shellfish samples collected monthly at 75 monitoring stations in the Aysen region during 2024 and analyzed them by LC-MS/MS to study the occurrence and diversity of lipophilic toxins and their spatiotemporal distribution. Our results revealed marked spatial patterns in shellfish contamination. The area with the greatest influence from ocean waters to the west of the Moraleda Channel showed absence or low toxin concentrations. Nevertheless, to the east of the Moraleda Channel, where strong haline stratification is almost permanent, highly contaminated areas were identified, such as the Jacaf Channel and Puyuhuapi Fjord. The maximum concentrations of 567 and 482 mg/kg of OA and DTX1, respectively, were recorded in the ribbed mussel, *Aulacomya atra*, in April 2024. These shellfish also contained concentrations of 2.25 mg/kg of YTX. This fjord has been classified as a hotspot for this type of toxin in the last decade because it has been the site of intense blooms of *D. acuta* and *P. reticulatum* owing to their high residence times. The results of this study can be used to develop evidence-based management strategies.

**Keywords**: Lipophilic Toxins, Okadaic acid, LC-MS/MS

**Financing**: My participation will be funded through support from the ISSHA Student Travel Awards, the UACh Master's Program in Environment, and my own funding.

**Acknowledgments**: To the Master's Program in Environment and Biosecurity in Aquaculture, collaborating universities and monitoring program that facilitated the development of this research.

Poster Session 02: Prevention, Control and Mitigation (PCM-HABs)
P-144

# CYANOACTION: COST Action CA23160, effective Lake management: reducing cyanobacteria by actions in the catchment

**Maria G. Antoniou**[1], Claudia Wiegand[2], Petra Visser[3], Christine Edwards[4], Zenepe Dafku[5], Spyros Gkelis[6], Nikoletta Tsiarta[1], Sevasti Kyriaki Zevrou[7], Theodoros Triantis[7]

(1) Cyprus University of Technology, Department of Chemical Engineering, Limassol, Cyprus
(2) University of Rennes, ECOBIO (UMR 6553 CNRS), Rennes, France
(3) Institute for Biodiversity and Ecosystem Dynamics, Free University of Amsterdam, Amsterdam, The Netherlands
(4) Robert Gordon University, Pharmacy & Life Sciences, CyanoSol Research Group, Aberdeen, UK
(5) Agricultural University of Tirana, Faculty of Economy and Agribusiness, Tirana, Albania
(6) Aristotle University of Thessaloniki, School of Biology, Thessaloniki, Greece
(7) NCSR Demokritos, Institute of Nanoscience and Nanotechnology, Athens, Greece

The increasing occurrence of toxic cyanobacterial blooms globally as a consequence of anthropogenic activities in freshwater threatens not only aquatic balance, but also water security and quality. Moreover, blooms cause significant economic losses to the water, health, tourism, and fishing industries. The implementation of thorough monitoring strategies for cyanobacteria, along with the evaluation of the risks of bloom incidents, and a plan for prevention and control measures, have become a necessity. With an array of in-lake control methods available, but little guidance on their efficiency, makes it difficult to choose. Long term prevention through decreasing nutrient input from the catchment is crucial in reducing blooms and would be possible by the transition towards more sustainable agricultural practices, but it requires implementation strategies. The COST action, CYANOACTION, started in the autumn of 2024, aims to increase and broaden capabilities throughout Europe for effective and sustainable management of water resources using a catchment-wide approach. To achieve this, CYANOACTION seeks to establish a unique network of experts, end users, and stakeholders. Gathering and distributing information on early warning detection methods and experience in the effectiveness of both long and short-term control methods will underpin Decision Support Tools for water managers and authorities. These tools will ensure the selection of appropriate methods tailored to specific water bodies. The overarching goal is to increase the mutual exchange between scientific knowledge and management practices to decrease cyanobacterial blooms, while considering the diverse characteristics of water bodies, their catchment, and the regulatory frameworks across Europe.

**Keywords**: Prevention, monitoring, control methods

**Financing**: CYANOACTION, CA-23160 is supported by COST (European Cooperation in Science and Technology).

**Acknowledgments**: CYANOACTION, CA-23160 is supported by COST (European Cooperation in Science and Technology).

Poster Session 02: Prevention, Control and Mitigation (PCM-HABs)

P-145

# National surveillance and control program of poisoning by harmful algal blooms "Red Tide" – Role of the Institute of Public Health of Chile

**Lorena Delgado**[1], Natalia Acuña[1], Natalia Valerio[1], Carlos Choque[1], Soraya Sandoval[1], María Natalia Gutierrez[1], Francis Alarcón[1], Paola Cornejo[1], Marcelo Soto[1], Andrea Rivera[2]

(1) Institute of Public Health, Chile, Environmental Health Department, Marathon 1000 Nunoa, Santiago, Chile
(2) Ministry of Health, Chile, Food and Nutrition, Healthy Policies Division, Enrique Mac Iver 541, Santiago, Chile

The Chilean Ministry of Health develops and coordinates the National Surveillance and Control Program of Poisoning by Harmful Algal Blooms ("Red Tide"), todetect the presence of marine biotoxins and prevent poisoning in the population resulting from the consumption of contaminated seafood. The Regional Health Secretariats and the Institute of Public Health of Chile (ISP) participates in this program. The ISP, in its role as the National Reference Laboratory of Chile, performs biotoxin analysis in seafood from regions lacking analytical capacity. It also conducts training and technology transfer activities, coordinates proficiency testing programs, and supervises laboratories that perform biotoxin analysis. In the last decade, the ISP Marine Toxins Laboratory performed 9989 analyses: 3584 for Paralyzing Shellfish Toxins (PST), 3167 for Diarreic Shellfish Toxins (DST), and 3238 for Amnesic Shellfish Toxins (AST), covering the Regions of Arica and Parinacota to Bío Bío. Additionally, it has provided 11 supervision sessions, 17 training sessions, and 2 technology transfers. Furthermore, since 2007, the ISP Metrology Subdepartment has organized the SP6 and SP13 proficiency tests annually, corresponding to the determination of PST and AST, respectively, providing a valuable external quality assurance tool to the national laboratory network. All of the above has allowed the ISP to accomplish a fundamental contribution to ensuring food safety regarding the potential presence of marine toxins in seafood consumed by the Chilean population.

**Keywords**: Biotoxins, Surveillance, Chile

**Financing**: Institute of Public Health of Chile

**Acknowledgments**: Institute of Public Health of Chile - Ministry of Health, Chile.

Poster Session 02: Prevention, Control and Mitigation (PCM-HABs)
P-146

# Integrated evaluation of nanobubble ozone for cyanobacterial bloom control: From ecosystem impact to molecular mechanisms

**H. Dail Laughinghouse**[1], Justin Chaffin[2], Forrest Lefler[1], David Berthold[1], Rachel Gabor[2], Linda Weavers[2], Heather Raymond[2]

(1) University of Florida, Davie, FL, USA
(2) The Ohio State University, Columbus, USA1) National Oceanic and Atmospheric Administration

Cyanobacterial harmful algal blooms (cyanoHABs) pose a significant threat to freshwater ecosystems worldwide, driving the need for effective and environmentally responsible control strategies. Nanobubble ozone technology (NBOT) is a promising alternative to traditional algaecides, offering rapid treatment with potentially lower ecological impact. This study evaluated NBOT effectiveness in suppressing Planktothrix-dominated blooms through controlled mesocosm experiments and field-scale applications in Grand Lake St. Marys (Ohio, USA). In mesocosms, medium and high NBOT doses ($O_3$:DOC ratios of 1.21 and 2.04) reduced chlorophyll-a and phycocyanin by 98–99%, and microcystins by up to 92%. In contrast, limited effectiveness in field trials was attributed to lower ozone delivery, higher biomass, and reduced treatment coverage. Replicate mesocosm trials demonstrated that NBOT had fewer adverse effects on native zooplankton communities compared to copper- and peroxide-based algaecides, with taxa such as Daphnia and Bosmina declining under chemical treatments but remaining stable or increasing under NBOT. Transcriptomic analyses of Planktothrix-dominated blooms revealed rapid gene expression changes within four hours of NBOT exposure, including upregulation of genes involved in oxidative stress response and protein repair (e.g., DnaK, ClpB), and downregulation of photosynthesis-related genes. These responses indicate a metabolic shift toward stress mitigation and cell death pathways. These findings demonstrate that NBOT effectively suppresses cyanoHABs while minimizing impacts on non-target organisms. Molecular data provide insight into its mode of action, supporting NBOT as a viable and scalable technology for cyanoHAB management.

**Keywords**: cyanoHABs, control, treatment.HAB Control

**Financing**: Funded by National Oceanic and Atmospheric Administration - National Centers for Coastal Ocean Science (#NA22NOS4780172).

Poster Session 02: Prevention, Control and Mitigation (PCM-HABs)

P-147

# United States harmful algal bloom control technologies incubator

**Lizabeth Longstreet**[3], Taylor Armstrong[2], Allen Place[2], Kevin Claridge[3], Felix Martinez[1]

(1) National Oceanic and Atmospheric Administration
(2) University of Maryland Center for Environmental Science- Institute of Marine and Environmental Technology
(3) Mote Marine Laboratory

Strategies to control HABs are lagging research into the prevention and management of blooms. Technologies are needed to treat active blooms to reduce immediate environmental, health and socio-economic impacts. However, it is difficult to identify control solutions that will be effective and permitted for use in the United States. The United States Harmful Algal Bloom Control Technology Incubator (US HAB-CTI) is a partnership between National Oceanic and Atmospheric Administration, University of Maryland Center for Environmental Science - Institute of Marine and Environmental Technology, and Mote Marine Laboratory, to streamline the vetting process of novel HAB control ideas. The US HAB-CTI is a source of funding, research equipment, and regulatory guidance to accelerate the development and application of control technologies. The incubator funds small, short-term projects of freshwater and marine HAB control technologies still in the initial stages of research. This allows more control tools to be tested for their potential to be 1) effective, 2) scalable, 3) feasible, and 4) economical. Additionally, US HAB-CTI is developing a clearinghouse website to provide guidance to end users and stakeholders on navigating the relevant licensing and permitting processes, and environmental compliance requirements that apply to both potential and existing technologies in the United States.

**Keywords**: HAB Control

**Financing**: Funded by National Oceanic and Atmospheric Administration - National Centers for Coastal Ocean Science (#NA22NOS4780172).

Poster Session 02: Prevention, Control and Mitigation (PCM-HABs)
P-148

# Overview of IAEA capacity building and collaborative projects on HABs and biotoxins: Technical cooperation (TC) and coordinative research projects (CRPs)

**Kristof Möller**[1]

(1) International Atomic Energy Agency Marine Environment Laboratories, Department of Nuclear Sciences and Applications, International Atomic Energy Agency, 98000 Monaco, Principality of Monaco

The International Atomic Energy Agency (IAEA), through its Marine Environment Laboratories, supports Member States (MS) in addressing harmful algal blooms (HABs) and marine biotoxins through capacity building and research activities. Technical cooperation (TC) projects and coordinated research projects (CRPs) leverage nuclear and isotopic techniques to improve monitoring, risk management, and mitigation strategies. Currently, the IAEA is implementing several international, regional, and national TC projects focused on HABs. These programs provide MS with expert missions, training courses, fellowships, technical manuals, equipment, and funding for participation in scientific conferences. For instance, under TC project INT7022, the IAEA organized a workshop on the harmonization of marine algal and toxin sampling and analysis, involving 19 countries. Key barriers preventing the establishment of monitoring programs, such as limited access to standards and certified reference materials, were identified and procurement support is now being provided. In another initiative, the IAEA conducted a training course on the application of the radioligand receptor binding assay (RBA) for saxitoxin detection from cyanobacteria. Preliminary results indicate the RBA's potential for monitoring saxitoxin in drinking water in alignment with the WHO guidelines. Additionally, the IAEA sponsored participation for 13 scientists from 12 countries in the IOC-HAB certification course on HAB-species identification and plans continued support. Finally, a new CRP, launched this year, focuses on using isotopic tools to assess eutrophication and its role in the development of HABs in coastal systems. Through these efforts, the IAEA fosters long-term capacity, scientific exchange, and the development of HAB monitoring programs globally.

**Keywords**: Capacity building, Monitoring and Management, Funding

**Acknowledgments**: The IAEA is grateful to the Government of the Principality of Monaco for the support provided to its Marine Environment Laboratories.

Poster Session 02: Prevention, Control and Mitigation (PCM-HABs)

P-149

# The efficacy of solubilized curcumin for mitigation of *Alexandrium* and *Pseudo-nitzschia* species

**William Scott**[1], Cynthia Heil[1], Devin Burris[1], Victoria Vossler[1], Emily Hall[1], Jessica Frankle[1], Susan Launay[1]

(1) Mote Marine Laboratory, Red Tide Institue, 1600 Ken Thompson Parkway, Sarasota, USA

Curcumin, a phytochemical and the primary bioactive compound found in turmeric (*Curcuma longa*), a member of the ginger family (Zingiberaceae), has been shown to be effective in the mitigation of *Karenia* brevis cells and associated brevetoxins. Less is known of the efficacy of curcumin on other harmful algal bloom (HAB) species, however. We investigated the influence of a range of curcumin additions (10 mg , 20 mg , 30 mg and 50 mg solubilized in ethanol) on cell concentrations in a series of laboratory experiments with the dinoflagellate species, *Alexandrium monilatum* and *Alexandrium tamarense*, and the diatoms *Pseudo-nitzschia multiseries*, and *Pseudo-nitzschia australis*. Additions of 50 mg $L^{-1}$ of curcumin were optimal for both *Alexandrium* species. With respect to the controls, cell concentrations of *A. monilatum* and *A. tamarense* reduced by 48% and 40% in 24 hrs, and 96% and 68% in 48 hrs, respectively. These responses, in comparison with an optimal dose of 5 mg $L^{-1}$ for K. brevis, suggest that higher doses may be required for thecate dinoflagellates and diatoms. In addition, optimum curcumin doses for HAB species may be species specific and should be evaluated on an individual species basis.

**Keywords**: Curcumin, *Pseudo-nitzschia*, *Alexandrium*

**Financing**: Mote Marine Laboratory, Red Tide Institute, HAB-CTI

**Acknowledgments**: We would like to thank Mote Marine Laboratory for their help and support. Funding for this project was provided by the Mote Red Tide Institute.

Poster Session 02: Prevention, Control and Mitigation (PCM-HABs)
P-150 (Ignite Talk)

# Cyanobacteria disruption with ozone: Insights into dose-dependent and culture age effects

**Nikoletta Tsiarta**[1], Efthymia Chatziathanasiou[1], Andreas Hadjicosti[1], Hanna Mazur-Marzec[2], Maria G. Antoniou[1]

(1) Cyprus University of Technology, Department of Chemical Engineering, 30, Archiepiskopou Kyprianou, Limassol, Cyprus
(2) University of Gdańsk, Division of Marine Biotechnology, Faculty of Oceanography and Geography, Gdynia, Poland

Harmful cyanobacterial blooms (HABs) are a growing global concern, driven by nutrient enrichment and intensified by climate change. These blooms threaten water quality and public health through the release of toxic metabolites, as cyanotoxins, such as microcystins and anatoxins, which can cause liver damage, gastrointestinal distress, and neurological symptoms. As HABs pose a growing threat to freshwater sources, scalable and effective mitigation technologies are urgently needed. Ozonation, an advanced oxidation process, offers a dual-function approach by targeting both cyanobacterial cells and their associated toxins. This study investigates the effectiveness of ozone as a pre-oxidation treatment under controlled conditions using three toxin-producing cyanobacteria (*Microcystis* sp., *Aphanizomenon* sp., and *Cylindrospermopsis* sp.) and one green alga (*Scenedesmus obliquus*). Cultures were exposed to ozone concentrations ranging from 0.5 to 4 mg/L at 20°C. Results showed that cyanobacteria were more sensitive to ozone exposure compared to green algae, with a 4 mg/L dose effectively disrupting cyanobacterial biomass and preventing regrowth. Furthermore, microcystin-LR was also totally degraded. Lower doses allowed partial recovery, depending on the species and cell age. Older cyanobacterial cultures were more susceptible to ozone, whereas younger cells displayed greater resilience, especially at sub-lethal doses. These findings highlight ozonation's potential as a promising, environmentally friendly mitigation strategy for drinking water treatment plants. By effectively degrading both biomass and toxins, ozonation supports proactive management of toxic HABs, offering a practical solution aligned with global goals for safe water access and ecosystem protection.

**Keywords**: cyanobacteria, cyanotoxins, ozonation

**Financing**: This research was part of the project CYANOTECH-EXCELLENCE/ 0421/0212, co-financed by the European Union and the Republic of Cyprus through the Research and Innovation Foundation.

**Acknowledgments**: The authors would like to thank Dr. Robert Konkel, Mrs. Despoina Kyriazi, Mrs. Kyproula Georgiou, and Mrs. Christiana Tsiarta for their contributions.

Poster Session 02: Prevention, Control and Mitigation (PCM-HABs)

P-151

# Mitigation of *Karenia brevis* using natural products

**Victoria Vossler**[1], Cynthia Heil[1], Devin Burris[1], Sarah Klass[1], Sara Turner[1], Will Scott[1], Victoria Devillier[1], Richard Peirce[1], Kevin Claridge[1]

(1) Mote Marine Laboratory & Aquarium, 1600 Ken Thompson Pkwy, Sarasota, FL 34236, USA

Natural plant-derived pesticide products have been increasingly explored as eco-friendly alternatives to synthetic chemical pesticides for the mitigation of harmful algal blooms (HABs). We conducted an extensive literature review investigating the inhibitory properties of several minimum-risk natural pesticide products and tested the mitigation potential of cinnamon, garlic, flaxseed, eugenol, clove, and thyme against the harmful dinoflagellate *Karenia brevis.* Diluted cultures (~1.0 x 10^6 cells·$L^{-1}$) were exposed to a range of concentrations of each product for 48 to 72 hours in triplicate 1.5 L beakers and responses were tracked by changes in cell and toxin concentration. Of the compounds tested, additions of 500 uL·$L^{-1}$ cinnamon, garlic, eugenol, and clove oil were the most effective, reducing cell concentration by 44-88% in 2 hours, and by 83-99% in 24 hours. These data suggest that natural products hold potential for successful in situ mitigation of *K. brevis* and other HAB species in Florida. Additional tests with varying treatment concentrations will determine optimal dose ranges for potential large-scale laboratory mesocosm experiments and in situ limnocorral trials.

**Keywords**: Mitigation, Control, Algecide

**Financing**: Florida Red Tide Mitigation and Technology Development Initiative

**Acknowledgments**: Mote Marine Laboratory & Aquarium, Florida Fish and Wildlife Conservation Commission.

Poster Session 02: Prevention, Control and Mitigation (PCM-HABs)
P-152 (Ignite Talk)

# Specification for field control of HABs in different scenarios by using Modified Clay

**Yongquan YUAN**[1], Xihua CAO[1], Xiuxian SONG[1], Zhiming YU[1]

(1) Institute of Oceanology, Chinese Academy of Sciences, Nanhai Rd 7, Qingdao, China

In field practices of HAB control using a promising technology, it's essential to make reasonable and applicable specifications toward different scenarios. The Modified Clay (MC) technology, which has been proved environmental-friendly and efficient to suppress HAB organisms, thus needs specifications for the application of which in different waters. Regarding this aspect, we initialized the "Dosage-effectiveness" theory of MC, a theorical model to quantitative relationships between MC dosage and its effectiveness to control various-sized HAB organisms was built, the theoretical flocculation "saturation" point of MC and optimal dosage for which was thus identified. Guided by the theory, an estimation approach of field MC dosage for HAB control in typical enclosed and semi-enclosed waters was further proposed. In the meantime, we also summarized the imperial dosage for HAB control in open waters. Based on these findings, a specification for field control of HABs was proposed, including the SOP using MC in field, recommended specific equipments, etc. As for practices, the removal efficiency of various-sized HAB organisms by MC in different scenarios could reach 80%, or even 90% within hours, e.g., over 90% of cyanobacterial cell removal in tilapia aquaculture farms of Temonggor lake in Malaysia, over 90% of *Phaecystis globosa* colonies removal in a nuclear cooling water pond in China, and nearly 80% of *Noctiluca scintillans* cell removal in Van Phong Bay, Vietnam, etc. In summary, the field control of HABs using MC has been standardized toward different scenarios, thus can be applied in much broad areas globally.

**Keywords**: Modified Clay, Dosage-effectiveness theory, Field application specification

**Financing**: This work was financially supported by Laoshan Laboratory (LSKJ202203700), the National Key Research and Development Program of China (2024YFF0506902).

**Acknowledgments**: We acknowledge the efforts and contributions of other HAB control team members of Institute of Oceanology, Chinese Academy of Sciences to this work.

Poster Session 02: Prevention, Control and Mitigation (PCM-HABs)
P-153 (Ignite Talk)

# AlgicideDB: A comprehensive database enhanced by large language models for algicide management and discovery

**Zhangqi Zuo**[1], Jing Hu[2], Chaowei Zhang[1], Zuoqi Wang[1], Lei Chen[1], Fei Li[1], Xi Xiao[1]

(1) Zhejiang University, Hangzhou, China
(2) City University of Hong Kong, Hong Kong, China

Harmful algal blooms (HABs) are increasing in frequency and intensity worldwide, posing significant threats to aquatic ecosystems, fisheries, and human health. While chemical algicides are widely used for HABs control due to their rapid efficacy, the lack of systematic data integration and concerns over environmental toxicity limit their broader application. To address these challenges, we developed AlgicideDB, a manually curated database containing 1,672 algicidal records on 542 algicides targeting 110 algal species. Using this database, we analyzed the physicochemical properties of algicides and proposed an algicide-likeness scoring function to facilitate the exploration of compounds with antialgal properties. Additionally, we evaluated the acute toxicity of algicidal compounds to non-target aquatic organisms of different trophic levels to assess their ecological risks. The platform also incorporates a large language model (LLM) enhanced by retrieval-augmented generation (RAG) to address HAB-related queries, supporting decision-making and facilitating knowledge dissemination. AlgicideDB, available at http://algicidedb.ocean-meta.com/#/, serves as an innovative and comprehensive platform to explore algicidal compounds and facilitate the development of safe and effective HAB control strategies.

**Keywords**: algicide, harmful algal blooms, large language model

Poster Session 02: Modeling, Early Warning and Forecasting

P-154

# Application of a quantitative PCR method to characterize abundance and distribution of *Alexandrium* cysts in three regions: Gulf of Maine, Puget Sound and Kodiak, Alaska

**Cheryl Greengrove**[1], Julie Masura[1], Steve Kibler[2], Julie Matweyou[3], Courtney Hart[4], Mark Vandersea[2], Tyler Harman[5], Lynn Wilking[5]

(1) University of Washington Tacoma, SIAS/SAM, Environmental Science, 1900 Commerce Street, Tacoma, WA 98402, USA
(2) NOAA Beaufort Laboratory, 101 Pivers Island Road, Beaufort, NC 28516, USA
(3) University of Alaska Fairbanks, Alaska Sea Grant, 118 Trident Way, Kodiak AK 99615, USA
(4) Port Gamble S'Klallam Tribe, 31912 Little Boston Road NE, Kingston, WA 98346, USA
(5) CSS Inc., NOAA-NOS NCCOS, Contractors, 1305 East-West Highway, Silver Spring MD 20910, USA

*Alexandrium catenella* is a paralytic shellfish poisoning-causing toxic dinoflagellate that overwinters as a benthic cyst and germinates into the water column in the spring to establish the next bloom. *A. catenella* forms annual blooms along portions the Pacific and Atlantic coastlines of the U.S and Canada. To help mitigate human health risks and economic effects of shellfish closures, winter cyst distribution has been used to develop forecast tools in the Gulf of Maine (GOM) and as an early warning system in Puget Sound, Washington. The current protocol for cyst enumeration by fluorescent microscopy is time consuming and requires extensive training for accurate cyst identification. This MERHAB project, funded by NOAA, includes development of a new quantitative polymerase chain reaction (qPCR) methodology for *A. catenella* cysts that was evaluated against the standard microscopy protocol with the goal of producing more rapid and accurate cyst abundance data. Assay development has shown the importance of using a qPCR standard curve based on cysts instead of a diluted amplicon, necessitating concentration of a large number of *A. catenella* cysts from the environment. Furthermore, interannual, seasonal and regional variability in rDNA gene copy number requires new standard curve construction for each cyst survey. The work presented here includes comparison of rDNA copy number content among *A. catenella* strains and resting cysts from The Gulf of Maine, Puget Sound and Kodiak, Alaska, a seasonal analysis of cyst rDNA copy number from Puget Sound, and a comparison of microscopy-based and qPCR-based cyst abundances for all three regions.

**Keywords**: *Alexandrium*, cyst, qPCR

**Financing**: NOAA NCCOS NA19NOS4780188

**Acknowledgments**: We would like to thank all the ships' crews, students and our NOAA NCCOS program officer Marc Suddleson for their support.

Poster Session 02: Modeling, Early Warning and Forecasting
P-155 (Ignite Talk)

# BloomPredictor: Integrating AI and ecological data for harmful algal bloom risk prediction

**Alvaro Jorquera**[1], Alejandro Clement[1], Vicente Fernández[1], Nicole Correa[1], Mónica Gomez[2], Rodrigo Gibson[1], Francisca Muñoz[1], Carmen Brito[1], Laura Latorre-Melín[1], Stephanie Saez[1], Carlos Flores[1], Carla Palma[1], Pablo Nahuelpan[1]

(1) Plancton Andino, Terraplen 869, Puerto Varas, Chile
(2) Skretting Chile, Ruta 5 Sur #775, Osorno, Chile

HABs pose major ecological and economic risks, especially for aquaculture. *BloomPredictor* is a machine learning-based forecasting tool designed to support short-term (1–6 days) risk prediction of HAB events by integrating ecological variables and environmental data. The core objective is to enhance predictive accuracy by aligning artificial intelligence methods with the biological and physical processes that influence phytoplankton dynamics in southern Chile.
The model was developed using a nine-year daily dataset (2016–2025) from a long-term monitoring program in southern Chile called POAS. This dataset includes laboratory-analyzed phytoplankton samples, meteorological observations, and weather forecasts from the Global Forecast System. Site-specific models were trained for three distinct marine inlets, incorporating multiple environmental indicators to forecast the $HAB_f$ INDEX — an ecological algorithm that quantifies risk based on a weighted sum of species-specific ratios between observed concentrations and critical thresholds.
A key innovation in *BloomPredictor* is the use of quantile regression, which enables probabilistic forecasting and the generation of risk-based alerts. Additionally, the model incorporates custom performance metrics that go beyond standard error measures — including the model's precision in forecasting the first occurrence of a bloom and its ability to detect whether a bloom is in decline. These metrics are essential for operational decision-making in fish aquaculture.
By showcasing case studies across diverse ecological and geographical settings, *BloomPredictor* demonstrates the value of combining AI with ecological indicators to support early warning systems and improve short-term planning in aquaculture.

**Keywords**: Forecast, Machine Learning, HAB

**Financing**: Skretting Chile

Poster Session 02: Modeling, Early Warning and Forecasting
P-156 (Ignite Talk)

# Algal bloom prevention and management through end-user driven forecasting and seasonal planning apps

**Lisa Krimsky**[1], Mauricio Arias[2], Osama Tarabih[2], Darlene Saindon Velez[3], Nathan Swain[4], James Dolinar[4], Michael Souffront[4]

(1) University of Florida, Florida Sea Grant, Lisa Krimsky, 2199 S. Rock Rd, Ft. Pierce, United States
(2) University of South Florida, Civil and Environmental Engineering, 4202 E. Fowler Avenue, Tampa, United States
(3) University of Florida, Water Institute, Darlene Saindon Velez, 1949 Stadium Road, 570 Weil Hall, Gainesville, United States
(4) Aquaveo, 3210 N. Canyon Road, Suite 300, Provo, UT, United States

Traditional approaches to dealing with algal blooms in lakes and rivers are often expensive, labor-intensive, and/or ineffective. An alternative to these approaches involves modifying water infrastructure operations, an economical, low-risk method that could prevent algal blooms by deterring excessive amounts of nutrients and phytoplankton from reaching sensitive downstream waters. The goal of our project is to develop a digital toolbox that water resource managers can use to prevent algal blooms in the short term (2 weeks) and long term (1 year). The toolbox engine is the Lake Operations Optimization of Nutrient Exports (LOONE) model, a documented open-source software that couples water, nutrient, and phytoplankton processes to help optimize operation rules based on desired environmental and societal goals. LOONE has been adapted to serve two specific lake management goals: For short-term management (up to 14 days), the model allows the end-user to visualize predicted water levels and concentrations at lake monitoring stations, as well as predicted discharges and loads. For long-term planning (up to a year), an easy-to-operate guided user interface was developed, which allows the user to explore expected nutrient and phytoplankton loads as a function of desirable or regulatory monthly discharge rates. This project has intentionally incorporated end-users in the tool development process to ensure it meets the needs of state and federal water resource managers. This presentation will provide an overview of the end-user engagement process and a short demonstration of the toolbox.

**Keywords**: bloom forecasting, stakeholder engagement, prevention and management

**Financing**: USACE through the project: Integrating Modeling Tools and Observations for Prediction and Management of Harmful Algal Blooms in the St. Lucie Estuary and Watershed, 2023-2025.

**Acknowledgments**: This interdisciplinary partnership includes the University of South Florida, University of Florida, US Army Corps of Engineers, South Florida Water Management District, and Aquaveo.

Poster Session 02: Modeling, Early Warning and Forecasting
P-157 (Ignite Talk)

# Forecasting cyanobacteria cell counts for inland water: A hybrid approach

**Duy Nguyen**[1], Klaus Joehnk[1]

(1) CSIRO, CSIRO Environment Research Unit, Black Mountain Science and Innovation Park, Canberra, Australia

This study develops a short-term forecasting framework for cyanobacteria bloom formation in Australian inland freshwater systems by incorporating in-situ observations, emerging hyperspectral remote sensing, and coupled hydrodynamic and algal growth models.
On three Australian lakes with different limnological conditions, the distribution of a buoyant cyanobacteria species was simulated using an algal growth model driven by forecasted meteorological conditions, and a one-dimensional k-epsilon turbulence hydrodynamic model that represented temperature stratification and mixing dynamics. To enhance model accuracy, cyanobacteria cell counts were re-initialized daily using estimates derived from hyperspectral reflectance data based on a linear relationship between hyperspectral cyanobacteria indices and simulated cell count values. The novel approach demonstrates the viability of short-term forecasting for cyanobacterial blooms.
Simulations of cyanobacteria concentrations captured the dynamic mixing processes within the lakes, characterized by daily near-surface accumulation followed by redistribution driven by wind-induced turbulence or nocturnal cooling. Accurate estimation of cyanobacteria surface concentrations at sub-daily timescales necessitates the integration of high-resolution water temperature profiling, hyperspectral reflectance measurements, and hydrodynamic modeling to quantify mixing dynamics. This comprehensive study improves risk assessment for cyanobacterial blooms and supports informed water management strategies, contributing to AquaWatch Australia's initiative to establish an integrated ground-to-space national water quality monitoring system to support water management with accurate data and predictive forecasting.

**Keywords**: Cyanobacteria Bloom Forecasting, Hybrid Modelling, AquaWatch

**Financing**: We gratefully acknowledge funding from the Murray–Darling Basin Authority, SmartSat CRC, Hunter Water Corporation, and the CSIRO AquaWatch Australia.

**Acknowledgments**: We acknowledge our colleagues at Northeast Water, Hunter Water, Water NSW, ACT Government, Environmental Sensing Systems, and CSIRO for their invaluable contributions.

Poster Session 02: Modeling, Early Warning and Forecasting
P-158

# Seasonality of cyanobacterial toxins in and associated with farmed mussels from the Baltic Sea

**Manuela Seehauser**[1], Manne Larsson[2], Johanna Hofrén[3], Martin Reutgard[3], Martin Karlsson[3], Elin Dahlgren[2], Malin Olofsson[1]

(1) Swedish University of Agricultural Sciences, Department of Aquatic Assessment and Sciences, Uppsala, Sweden
(2) Swedish University of Agricultural Sciences, Department of Aquatic Resources, Uppsala, Sweden
(3) Ecopelag, Trosby gammelväg 10, 139 51 Värmdö, Sweden

Cyanobacterial blooms occur recurrently in the Baltic Sea, particularly during summer, often resulting in the production of cyanotoxins—bioactive metabolites with negative ecological and health impacts. While the toxicological effects of compounds such as nodularin, microcystin, and cylindrospermopsin are well studied, their bioaccumulation in farmed marine organisms remains poorly understood. This study investigated the seasonal presence and accumulation of cyanotoxins in the blue mussel *Mytilus edulis* at mussel farms in the Baltic Sea.
Samples were collected over an entire year to encompass both peak bloom periods and off-season conditions. By combining liquid chromatography–mass spectrometry (LC-MS) and immunoassays (ELISA), we quantified cyanotoxins in water, phytoplankton biomass, and mussels. Cyanobacterial community composition and abundance were analyzed through microscopy and metagenomic sequencing, while genomic and transcriptomic tools were used to identify toxin-related genes and their expression patterns. Environmental parameters, including temperature, salinity, and nutrient levels, were concurrently monitored and correlated with toxin concentrations and cyanobacterial community data.
Initial results showed that toxin types and concentrations varied throughout the year in water, phytoplankton, and mussels, with peaks of microcystin and nodularin during the warmer months. These patterns largely coincided with increased cyanobacterial abundance and environmental conditions conducive to bloom formation. In contrast, cylindrospermopsin appeared more frequently in the cooler early spring, although its producer in the Baltic Sea remains unidentified.
Overall, this research provides new insights into cyanotoxin dynamics and bioaccumulation in aquaculture environments, contributing to the development of effective monitoring strategies to ensure safe and sustainable mussel farming in the Baltic Sea.

**Keywords**: Cyanotoxins, Baltic Sea, Mussel farming

**Financing**: The project was funded by the Board of Agriculture and the European Union (grant nr. 2023-1281).

**Acknowledgments**: I acknowledge Susanna Minnhagen, Anna-Pia Molander, Kristian Molander, Erik Bergström, Fanny Persson and Oscar Juvall for helping with the sampling during the season!

Poster Session 02: Modeling, Early Warning and Forecasting

P-159

# Observations from Scotland's Monitoring Programme support the *Dinophysis* trigger level as an effective early warning for diarrhetic shellfish toxin accumulation in mussels

**Sarah Swan**[1]

(1) Scottish Association for Marine Science, Oban, Argyll, PA37 1QA, UK

The potentially harmful dinoflagellate genus *Dinophysis* is regularly detected in Scottish coastal waters, and the accumulation of diarrhetic shellfish toxins (DSTs) presents a significant challenge for the shellfish industry, often resulting in harvesting area closures that may persist for several months. Within the regulatory monitoring program, *Dinophysis* cell counts are used to guide the testing of bivalve molluscs for DSTs. An exploratory analysis of the relationship between *Dinophysis* and DSTs in common (blue) mussels was conducted using 14 years of regulatory monitoring data, with particular focus on toxic events preceded by weekly time-series observations of both *Dinophysis* and DST concentrations. Of the 217 cases in which DST concentrations in mussels were detected above the regulatory threshold of 160 µg OA eq./kg, 166 (76.5%) were preceded by *Dinophysis* cell densities equal to or greater than 100 cells/L in the previous week. In approximately two-thirds of these instances, *Dinophysis* concentrations were below 500 cells/L, with 27% less than 200 cells/L. These findings show that the current *Dinophysis* trigger level of 100 cells/L used within the monitoring program remains a reliable early warning indicator for initiating additional biotoxin testing.

**Keywords**: HABs, risk assessment

**Financing**: The regulatory monitoring program for phytoplankton and biotoxins is funded by Food Standards Scotland.

Poster Session 02: Modeling, Early Warning and Forecasting

P-160

# A study on the prediction model of cyanobacterial cell counts in the Nakdong River basin using public data

**Seungjae Yeon**[1], Hyun Je Oh[1], Jusuk An[1], Changseog Oh[1], Juwon Lee[1], Bokjin Lee[1]

(1) KOREA INSTITUTE of CIVIL ENGINEERING and BUILDING TECHNOLOGY, Department of Environmental Research, 283, Goyangdae-Ro, Ilsanseo-Gu, Goyang-Si, Gyeonggi-Do, Korea

From the perspective of drinking water treatment, algal blooms can reduce the availability of water resources and increase the operational challenges of treatment processes. Odor and taste compounds produced by cyanobacteria not only cause discomfort but may also be toxic, requiring specialized treatment methods. Current water quality monitoring systems often respond only after algal blooms occur, underscoring the need for a more proactive and efficient water quality management framework. AI-based algal bloom prediction models offer a viable alternative to address this issue.
The Nakdong River in South Korea provides favorable conditions for algal growth due to its high nutrient levels, slow flow velocity, elevated water temperatures, and abundant sunlight. Water quality in the Nakdong River basin is continuously monitored, and the relevant data is publicly available.
This study serves as a foundational effort to establish a predictive framework for responding to algal bloom–related issues by forecasting cyanobacterial cell concentrations using public data from the Nakdong River basin.
Based on public data collected from May 2014 to 2024, the model predicts an average cyanobacterial cell count of 10,039 cells/mL. The period during which cell counts are expected to exceed the early warning threshold for drinking water sources (1,000 cells/mL) is widely distributed from May through as late as December. According to the model predictions, the Nakdong River basin experiences algal concentrations exceeding the threshold level for approximately eight months each year, indicating a clear need for proactive measures.

**Keywords**: Modelling, algalbloom, bigdata

**Financing**: Supported by Korea Environment Industry&Technology Institute(KEITI) through Project for developing innovative drinking water and wastewater technologies Project, funded by Korea Ministry of Environment(MOE)(2020002700003).

**Acknowledgments**: Supported by Korea Environment Industry&Technology Institute(KEITI) through Project for developing innovative drinking water and wastewater technologies Project, funded by Korea Ministry of Environment(MOE)(2020002700003).

Poster Session 02: Biotechnology & Natural Products

P-161

# Toxicity and miscibility study of algae carrageenan blends as effective Tolterodine L-Tartrate release carriers

**Dimitrios Bikiaris**[1], Evangelos Karavas[2]

(1) Aristotle University of Thessaloniki, Chemistry, Laboratory of Polymer Chemistry and Technology, Thessaloniki, Greece
(2) Pharmathen S.A., Athens, Greece

Polymeric matrices of ι-, κ- and λ-carrageenans and ι-, κ- and λ-carrageenans blends, prepared by simple mixing and solvent evaporation technique, have been tested for controlled release delivery of Tolterodine L-Tartrate. X-ray diffraction (XRD), infrared spectroscopy (FT-IR), scanning electron microscopy (SEM) and viscometry measurements showed that although all weight ratios of carrageenans blends were immiscible, carrageenans formed complexes with the drug through hydrogen bonding. In solid dispersions formulations, although the drug was almost immediately dissolved (due to its amorphous character), an amount remained absorbed into polymer matrix and was not released, probably due to hydrogen bonding. When physical mixtures of pure carrageenans and Tolterodine L-Tartrate were prepared, release rate was slower and when κ-carrageenan was used, an almost controlled release formulation was achieved. However, real controlled release formulations were achieved only when physical mixtures of ι-/κ-carrageenans and Tolterodine were used. Thus, the combination of different types of carrageenans could change the carrier's behaviour. The cytotoxicity of copolymers was evaluated by measuring the viability of human umbilical vein endothelial cells (HUVEC), in the presence of different polymer concentrations and comparing results with those obtained from poly(lactic acid) (PLA). Cell viability was determined by means of the MTT assay. Although ι-, κ- and λ-carrageenans cannot form miscible blends, they can still be used in the development of a controlled release Tolterodine L-Tartrate formulation, due to their ability to form hydrogen bonds with the drug. The synthesized blends exhibit low cytotoxicity and are appropriate for drug release carriers.

**Keywords**: Algae carrageenans; toxicity; drug release carriers.

Poster Session 02: Biotechnology & Natural Products

P-162

# Synthesis and characterization and properties of isocyanate-modified red seaweed carrageenans

**Nikos Bikiaris**[1], Dimitroula Lambropoulou[2]

(1) Aristotle University of Thessaloniki,, Department of Chemistry,, Laboratory of Polymer Chemistry and Technology,, GR-541 24 Thessaloniki, Greece, Thessaloniki, Greece
(2) Aristotle University of Thessaloniki, Department of Chemistry, Laboratory of Environmental Pollution Control, GR-541 24, Thessaloniki, Greece

Carrageenans are sulfated galactans extracted from red seaweed (Rhodophycae), mostly of the genus Chondrus, Eucheuma, Gigartina and Iridaea. Different seaweed produces different carrageenans. They are composed of D-galactose residues linked alternately in 3-linked-b-D-galactopyranose and 4-linked-a-D-galactopyranose units and they are classified according to the degree of the substitution that occurs on their free hydroxyl groups. They are traditionally identified by aGreek prefix: ι- (iota) carrageenan (mono-sulfate), κ- (kappa) carrageenan (di-sulfate), and λ- (lambda) carrageenan (three-sulfate). In the present study, two isocyanate-modified carrageenan polymers based on kappa-carrageenan (κ-CAR) and iota-carrageenan (ι-CAR) have been synthesized using tolylene diisocyanatoe (TDI). The polymer materials were characterized using Fourier transform infrared spectroscopy (FTIR), X-ray diffraction (XRD), Thermal Gravimetric Analysis (TGA) and Scanning Electron Microscopy (SEM). It was found that κ-CAR and ι-CAR have smooth surfaces while the modification with TDI caused more rigid and hard surface. FTIR spectra of modified carrageenans with TDI revealed that a new peak at 3248 $cm^{-1}$ owing to >N–H stretching vibrations was formed indicating that the -OH groups of carrageenans were successful reacted with isocyanate groups of TDI. From XRD patterns, it was found that TDI modification did not affect the amorphous physical state of carrageenans. However, the modified polymers showed reduced thermal degradation stability due to –NCO– groups. Modified carrageenans can be used as extraction sorbents of pharmaceutical contaminations in aqueous media.

**Keywords**: Red seaweed carrageenans; modification; properties.

Poster Session 02: Biotechnology & Natural Products

P-163

# Sodium alginate-chitosan hydrogel sponge: A multifunctional biopolymer matrix for hemostasis and wound healing

**Rizos Evangelos Bikiaris**[1], Nikolaos Iosif Matschek[1], Ioanna Koumentakou[2], George Kyzas[2]

(1) Aristotle University of Thessaloniki, Chemistry, Chemistry, Thessaloniki, Greece
(2) Democritus University of Thrace, Chemistry, Chemistry, Democritus University of Thrace, Kavala, Greece

This study introduces a multifunctional biopolymer hydrogel sponge composed of sodium alginate (SA) and chitosan (CS), enhanced with arginine (Arg) and tannic acid (TA) to promote rapid hemostasis, infection control, and tissue regeneration. Traditional wound dressings often lack these combined properties, necessitating the development of a versatile hydrogel matrix. Sodium alginate played a key role in enhancing structural integrity, water absorption, and biocompatibility, creating an optimal moist environment for wound healing. Arginine, acting as a green crosslinker, reinforced mechanical strength, improved hemostatic efficiency, and facilitated cellular interactions, while its antioxidant properties (>90%) helped mitigate oxidative stress. The ionic crosslinking mechanism and freeze-drying process resulted in a highly porous, absorbent sponge with superior water retention and structural resilience. SEM imaging confirmed an interconnected porous network, ensuring efficient cell infiltration and nutrient diffusion. The hydrogel's hemostatic performance, assessed via the Blood Clotting Index (BCI), demonstrated significant clotting ability, with excellent hemocompatibility (2.08% hemolysis rate). These findings highlight the critical role of sodium alginate and chitosan as a biopolymer matrix, making this hydrogel sponge a promising candidate for advanced wound care applications in both emergency and clinical settings.

**Keywords**: Sodium alginate, Chitosan, Hydrogel sponge

Poster Session 02: Biotechnology & Natural Products

P-164

# Investigation of carrageenan blend miscibility and their potential as sustained release carriers

**Evi Christodoulou**[1], Dimitrios N. Bikiaris[1], Evangelos Karavas[2]

(1) Aristotle University of Thessaloniki, Department of Chemistry, Faculty of Sciences, Thessaloniki, Greece
(2) Pharmathen SA, Pharmaceutical Industry, Dervenakion Str. 6, Pallini Attikis, GR-153 51, Greece

Carrageenans, sulfated polysaccharides extracted from red seaweeds, are widely used in food and pharmaceutical applications due to their gelling, thickening, and stabilizing properties. Their ability to form hydrogels makes them promising candidates for controlled drug delivery systems. This study investigates the miscibility of carrageenan blends (L-, K-, and λ-carrageenans) and evaluates their potential as sustained release carriers for Tolterodine L-Tartrate, a drug used in the treatment of overactive bladder, by providing insights into their structural interactions and release behavior.

More specifically, the carrageenan-based polymeric matrices were prepared by simple mixing and by solvent evaporation technique and tested for controlled release delivery of Tolterodine L-Tartrate. X-ray diffraction (XRD), infrared spectroscopy (FT-IR), scanning electron microscopy (SEM) and viscometry measurements indicated that all weight ratios of carrageenan blends were immiscible; however, strong hydrogen bonding interactions between carrageenans and the drug were observed, leading to complex formation. In solid dispersion formulations, the drug exhibited rapid dissolution due to its amorphous nature, yet a portion remained absorbed within the polymer matrix, likely retained by hydrogen bonding. In contrast, physical mixtures of pure carrageenans with Tolterodine L-Tartrate resulted in slower drug release rates.

**Keywords**: carrageenan, miscibility, oligosaccharides

Poster Session 02: Biotechnology & Natural Products

P-165

# Taxonomic and biochemical characterization of a novel Altericista cyanobacterial strain from the Mondego River, Portugal

Guilherme Scotta Hentschke[1], **Flavio Luis de Oliveira[1,2],** Graciliana Lopes[1], Aimone Duarte[1,2], Raquel Silva[1], Vitor Vasconcelos[1,2]

(1) CIIMAR/CIMAR LA – Interdisciplinary Centre of Marine and Environmental Research, University of Porto, Avenida General Norton Matos s/n, 4450-208, Matosinhos, Portugal
(2) University of Porto, Department of Biology, Faculty of Science, Rua do Campo Alegre 1021, 4169-007, Porto, Portugal

A novel cyanobacterial strain was isolated from Mondego River, Coimbra, Portugal and subjected to a comprehensive taxonomic and biochemical characterization. Morphological and molecular analyses, based on scanning electron microscopy (SEM) and transmission electron microscopy (TEM), 16S rRNA and ITS gene sequencing, confirmed the distinct phylogenetic position within the *Altericista* genus, supporting the description of a new species under LEGE 17690 code. Recent studies highlight the antioxidant potential of cyanobacteria, largely attributed to the presence of carotenoids, fatty acids (FA), phycobiliproteins (PBPs), and phenolic compounds. Dry biomass of LEGE 17690 was used for biochemical analysis. Extracts of different polarities were prepared through a sequential extraction process with acetone and water, and chemically characterized by spectrophotometry and high-performance liquid chromatography (HPLC-PDA). Acetonic extracts were mainly composed of β-carotene with 56.1 mg $g^{-1}$ DW extract (25%) and chlorophyll-a with 152.8 mg $g^{-1}$ DW extract (71%). Aqueous extracts showed a higher concentration of PBPs, namely phycocyanin (129.7 µg $mg^{-1}$ DW extract), allophycocyanin (181.4 µg $mg^{-1}$ DW extract), and phycoerythrin (96.5 µg $mg^{-1}$ DW extract). Chlorophylls were also determined, with 25.2 µg $mg^{-1}$ DW extract. Total sugars content was obtained using glucose standard according to Masuko method, with 48.5 µg of glucose equivalents $mg^{-1}$ DW extract. Additionally, total phenolic content was determined by Folin-Ciocalteu method, with 9.3 µg of galic acid equivalents $mg^{-1}$ DW extract. These results highlighted its potential for biotechnological applications, and the new species of *Altericista* sp. LEGE 17690 as a valuable source of bioactive compounds with antioxidant potential.

**Keywords**: Carotenoids, Phycobiliproteins, Cyanobacterial taxonomy

**Financing**: This research was funded by FCT Projects UIDB/04423/2020, UIDP/04423/2020, WP9-Portuguese Blue Biobank (C644915664-00000026), and FO thanks to FCT scholarship UI/BD/06241/2021.

**Acknowledgments**: Graciliana Lopes thank FCT for the financial support through the Scientific Employment Stimulus - Individual Call (https://doi.org/10.54499/2021.01768.CEECIND/CP1665/CT0007).

ICHA

PUNTA ARENAS • CHILE 2025

21st International Conference on HARMFUL ALGAE

# From HAB Science to Environmental Resilience