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Linking Easily Measured Water Quality Variables to Microcystin Risk Using Decision Tree Models

Brian E. Haggard[1,3], ***Nazanin Abbasi***[2]

[1]Arkansas Water Resources Center, University of Arkansas Division of Agriculture, Fayetteville, AR, USA
[2]Department of Chemical Engineering, University of Arkansas, Fayetteville, AR, USA
[3]Biological and Agricultural Engineering Department, University of Arkansas, Fayetteville, AR, USA

Total microcystin poses a significant public health risk during harmful algal blooms, yet laboratory toxin measurements often lag behind rapidly changing lake conditions. This gap limits timely decision-making for recreational water advisories. We developed a decision tree to inform public harmful algal blooms advisories by translating easily measured lake variables into actionable toxin risk categories (e.g., low vs. high) using a recreational advisory threshold of 8 μg L^{-1} for total microcystins.

Paired observations of total microcystins and routinely measured field variables, such as temperature, pH, pigment fluorescence, conductivity, and related water quality indicators, were used to develop the decision-tree(s). This study evaluates the relationships between easily measurable lake variables and microcystin concentrations and assesses multiple tree-based approaches, including classification and regression trees, random forests, and gradient-boosted trees, for both concentration estimation and exceedance prediction.

Model performance was evaluated using k-fold cross-validation and public health–relevant metrics, including accuracy, sensitivity, specificity, and area under the curve, with particular emphasis on sensitivity to ensure reliable detection of elevated toxin conditions. The best-performing framework was subsequently simplified and translated into an advisory-oriented decision tree that generates transparent, implementable “if–then” rules to classify microcystin risk levels based on a defined threshold.

Abundance and Size Distributions of the Colonial, Bloom-forming Cyanobacteria, *Microcystis aeruginosa*, in Western Lake Erie

Ahammad Abdullah[1,2,3] *and Aditya R Nayak*[1,2,3]

[1] Department of Ocean and Mechanical Engineering, Florida Atlantic University, Boca Raton, FL 33431, USA
[2]Harbor Branch Oceanographic Institute, Florida Atlantic University, Fort Pierce, FL 34946, USA
[3]School of Environmental, Coastal, and Ocean Sustainability, Florida Atlantic University, Boca Raton, FL 33431, USA

Cyanobacterial harmful algal blooms (cHABs) are a frequent occurrence in Lake Erie, posing risks to ecosystem health and human well-being. Early detection and continuous monitoring are essential for mitigating cHAB impacts and improving our understanding of bloom dynamics and ecology. Here, we present a study employing a freestream, in situ digital holographic imaging system (AUTOHOLO) to characterize particle distributions, with a particular focus on *Microcystis aeruginosa* colonies, during a multi-year study in the western basin of Lake Erie. Over the course of multiple field campaigns, the AUTOHOLO was vertically profiled across different spatial transects in three regions of Western Lake Erie (Detroit River outflow, the Western Basin (WB) transect, and Maumee Bay) during both pre- and peak-bloom conditions. A convolutional neural network was trained on holographic imaging data to classify *Microcystis* colonies, facilitating characterization of their vertical abundance and size distribution in the water column. Simultaneous, co-located inherent and apparent optical property (IOP/AOP) measurements, including attenuation, backscattering and remote sensing reflectance, were also collected. During the pre-bloom period (June), inorganic particles, detrital matter and zooplankton dominated the image datasets. In contrast, the peak-bloom period (August) showed strong *Microcystis* dominance, particularly along the WB transect. The results demonstrated strong surface intensification of *Microcystis* colony abundance during peak-bloom conditions, along with a clear spatial gradient from nearshore to offshore regions. Particle size distributions (PSDs) indicated dominant colony sizes around ~200–300 μm and a tendency toward smaller sizes offshore. Additionally, using a recently developed empirical relationship, cell abundances are estimated from *Microcystis* colony sizes, and associated changes in optical properties driven by bloom presence are discussed. This integrated approach highlights the potential of combining digital holography with optical measurements for improved bloom monitoring and to address key scientific questions, with future long-term deployments offering new insights into bloom dynamics and cyanobacterial ecology.

Neurological Effects of Aerosolized Red Tide Neurotoxins

Abdullah L[1], *Aldrich G*[1], *Ferguson S*[1], *Helgager D*[1], *Garcia ME*[1], *Kirkpatrick B*[2], *Eric Milbrandt*[3], *Paris D*[1], *Crawford F*[1], *Mullan M*[1]

1) Roskamp Institute, Sarasota, FL, USA
2) Gulf of Mexico Coastal Ocean Observation System, College Station, Texas, USA
3) Sanibel-Captiva Conservation Foundation, Sanibel, FL, USA

In the Gulf of America, *Karenia* (*K.) brevis* blooms release aerosolized brevetoxin (PbTx), a known respiratory irritant. However, its neurological effects following inhalation remain unclear. This study evaluated the effects of PbTx inhalation on neurotoxic shellfish poisoning-like (NSPL) symptoms, examined interactions with apolipoprotein E (APOE) genotype, and assessed blood biomarkers. Participants were recruited across Southwest Florida, Gulf and Bay counties. A surrogate brevetoxin exposure (SBE_{air}) index estimated exposure to aerosolized PbTx based on the relationship between *K. brevis* cell counts in water and subsequent aerosolization. Data on past medical history and symptoms were collected from participants (n = 258) between June 2019 and August 2021 and from an additional cohort enrolled since September 2024 (n = 158). Participants in the latter cohort completed symptom surveys, Short Form-36 (SF-36) quality-of-life assessments, and the Montreal Cognitive Assessment (MoCA). Regression analyses adjusted for age and relevant covariates. A dose-dependent relationship between *K. brevis* cell counts and PbTx concentrations. Exposure to SBE_{air} was significantly associated with increased upper respiratory and NSPL symptoms. Social functioning scores on the SF-36 were reduced ($p < 0.05$). Cognitive performance on MoCA was largely preserved; however, higher exposure was associated with lower naming scores. Anti-PbTx antibodies in plasma correlated with exposure and symptom burden, supporting systemic absorption. Carriers of the APOE ε4 allele reported greater fatigue and memory-related symptoms. Aerosolized PbTx exposure is associated with respiratory and NSPL symptoms, along with subtle impacts on quality of life and cognition. Genetic susceptibility may increase vulnerability. These findings support the need for exposure thresholds and biomarker validation to inform public health responses to expanding HAB events.

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Co-occurrence of Microcystins and Emerging Peptides of Concern in Raw and Finished Drinking Waters in a Rural Community

Todd Miller[1], ***Anjana Adhikari***[1], *Amber Roegner*[2]

[1]University of Wisconsin-Milwaukee, Milwaukee, WI, USA
[2]University of Oregon, Eugene, OR, USA

Microcystin (MC) remains the most widely monitored and studied cyanotoxin, but it represents only a fraction of the cyanopeptide cocktail produced during freshwater cyanobacterial harmful algal blooms (cyanoHABs). The emerging cyanopeptides, such as anabaenopeptins (AP) and cyanopeptolin (CP), co-occur with MCs, often at equal or higher concentrations. This 2-year study examined the prevalence of MCs, APs, and CPs in raw and finished drinking water in the homes in a rural community using decentralized, at-home water treatment systems. Triple-quad LC-MS/MS was used to quantify 12 MCs, 3 APs, and 3 CPs. Our data show consistent co-occurrence of the emerging cyanopeptides AP and CP with MCs in both raw and finished drinking water. In raw lake water, mean concentrations were 0.51 ± 2.25 μg/L for MC (max: 23.1 μg/L), 15.2 ± 148 μg/L for AP (max: 2,221 μg/L), and 0.038 ± 0.10 μg/L for CP (max: 1.11 μg/L). In **finished drinking water**, MC concentrations averaged 0.21 ± 0.87 μg/L (max: 9.83 μg/L) while AP had a mean of 3.41 ± 19.4 μg/L (max: 191 μg/L). While the MC concentrations in finished water exceeded US-EPA health advisory guidelines in 8.5% of samples (>0.3 μg/L) and 2.8% of samples (>1.6 μg/L), the presence of emerging cyanopeptides AP was significantly higher. The ratio of the mean concentration shows that AP is approximately 16.6 times more prevalent than MC in the treated drinking water. The findings indicate that the total cyanopeptide burden exceeds that reported in current MC-centric monitoring.

Toxicity Screening and Gene Characterization of *Microcystis aeruginosa* Strains Using a Brine Shrimp Bioassay

Sahil Adtani[1], *Katelyn McKindles*[1,2]

[1] Department of Biology, Baylor University, Waco, Texas, USA
[2] Center for Reservoir and Aquatic Systems Research, Baylor University, Waco, Texas, USA

Cyanobacterial harmful algal blooms (cHABs) produce diverse secondary metabolites, many of which remain poorly characterized despite potential ecological and human health risks. We evaluated the relative toxicity of intracellular extracts from multiple *Microcystis aeruginosa* strains using a brine shrimp (*Artemia salina*) bioassay. Cyanobacterial biomass was harvested from laboratory cultures, lysed, and tested across multiple exposure concentrations (1, 10, and 100 µL). Mortality varied substantially among strains, allowing strains to be grouped into distinct toxicity categories based on dose-response patterns. To investigate potential genetic drivers of toxicity, DNA was extracted from cultured strains and screened using PCR primers targeting regions of the microcystin (*mcy*) operon and other cyanobacterial marker genes, followed by gel electrophoresis analysis. Preliminary results identified toxin-associated genes in most strains while also revealing substantial variation in observed toxicity. This work establishes a framework for linking cyanobacterial toxicity phenotypes with underlying genetic markers and screening novel bloom-associated metabolites.

Evaluation of a Novel Technique Used for Effective Mitigation of Harmful Freshwater Cyanobacteria

Joshua Alarcon[1]*, Pedram AziziHariri*[2]*, Vijay John*[2]*, Vince Lovko*[1]

[1]Mote Marine Laboratory, Phytoplankton Ecology Program, Sarasota, FL, USA
[2]Department of Chemical & Biomolecular Engineering, School of Science and Engineering, Tulane University, New Orleans, LA, USA

Cyanotoxins, as produced by various cyanobacteria, pose a threat to environmental and public health and therefore, management and mitigation of these toxins is an important topic of scientific investigation. Microcystin (MC), a hepatotoxin produced by cyanobacteria including *Microcystis* and *Anabaena*/*Dolichospermum*, has been associated with acute poisoning and cancer promotion via chronic exposure. The overall goals of this study are to (i) evaluate a novel foam delivery method for algaecides that enables a targeted intervention of *Microcystis* blooms via mitigation of dissolved and cell associated toxins , and (ii) scale-up experiments from a benchtop microcosm to mesocosms (80 L and 1400 L) to a future real-time field (pond or lake) application. Using data generated from the benchtop microcosm, the mesocosm experiments monitor physiochemical water parameters, photophysiology, cell abundance and cell viability using microscopy and PAM fluorometry post-administration of algaecidal treatments. Treatments consist of combinations of Tween-80 (polysorbate-80) and PAK® 27, a peroxide-based algae control. Results demonstrate that the recommended concentration of PAK® 27 (30 mg/L) is insufficient in effectively reducing algal concentrations in the benchtop studies, requiring a higher concentration (60 mg/L) to effectively reduce algal concentrations. However, in the 80L mesocosm experiment the lower concentration was found to be effective at cell and toxin removal. Results from additional ongoing studies, including 1,400L mesocosms, will be presented as available. Cumulatively, these results support this novel method for the enhanced delivery of algaecidal treatments to toxic freshwater cyanobacteria.

Development of ELISA and LC/MS Methods to Detect Plasma Brevetoxins Associated with Aerosolized Exposure

Aldrich GJ*[1]*, Shea JW[1], Evan JE[1], Ferguson S[1], Helgager D[1], Garcia ME[1], Kirkpatrick B[2], Paris D[1], Crawford F[1], Mullan M[1], Abdullah L[1]

[1]Roskamp Institute, Sarasota, FL, USA,
[2]Gulf of Mexico Coastal Ocean Observation System, College Station, Texas, USA

Aerosolized brevetoxins (PbTx) from Karenia brevis harmful algal blooms have been linked to neurologic and respiratory symptoms in coastal populations. Existing analytical methods lack the sensitivity and specificity to quantify low-level PbTx exposure in human samples. This study evaluated plasma PbTx detection by ELISA, developed a sensitive LC-MS assay for PbTx-3, and identified steps leading to PbTx extraction loss. Participants in Southwest Florida were enrolled from 2019 to 2021 as part of an ongoing cross-sectional study investigating health effects associated with red tide exposure. Plasma PbTx concentrations were initially analyzed by ELISA before LC-MS assay development; plasma samples and blanks were spiked with PbTx-3 standards prior to extraction. Recovery studies evaluated the impact of solvent composition, SPE cleanup, and biological matrix effects on PbTx-3 recovery using STRATA-X C18 and Waters HLB SPE cartridge. LC-MS analysis was performed using UHPLC with an Orbitrap mass spectrometer. ELISA analysis showed that currently available PbTx ELISAs can detect PbTx in biological samples; however, sensitivity (approximately 0.1 ng/mL) remained an issue when measuring low-level PbTx exposure. In addition, ELISAs do not distinguish between PbTx congeners, and background levels in plasma and urine matrices limit accurate quantification of low concentrations. LC-MS method development established a sensitive assay with a detection limit of approximately 75 pg/ml for PbTx-3. In solvent-only conditions, standard extraction protocols achieved ~80% recovery without SPE cleanup but incorporating SPE cleanup reduced recovery to about 50% with both STRATA-X C18 and HLB cartridges, and recovery decreased further in plasma samples, indicating substantial matrix-associated PbTx loss. These findings show the need for sensitive, congener-specific LC-MS methods for plasma PbTx at environmental levels and improved extraction workflows for biological samples.

Ultrasound Technology for Cyanobacteria Control

Viviana Almanza

SonicPure, Torrance, California, USA

Low-frequency ultrasound has been used for more than two decades as a chemical-free tool for controlling cyanobacteria in lakes, reservoirs, recreational waters, aquaculture systems, and industrial applications. The technology applies targeted ultrasonic frequencies that disrupt key cellular functions in cyanobacteria, including buoyancy regulation, morphology, and photosynthetic activity. By disrupting buoyancy, ultrasound causes cyanobacteria to sink out of the light they need for photosynthesis, controlling active growth and suppressing the formation of future blooms.

The benefits of ultrasonic treatment extend across a wide range of water uses. In recreational lakes and reservoirs, continuous treatment combats active blooms while suppressing future growth, improving water clarity and reducing reliance on chemical algaecides. In drinking-water sources, controlling algae and cyanobacteria upstream reduces the biomass entering treatment and eases the burden on filtration, chemical treatment, and taste-and-odor management. In aquaculture, controlling cyanobacteria reduces the conditions associated with off-flavors in cultured species. In industrial water and irrigation applications, lower cyanobacterial biomass reduces fouling of filters, equipment, and irrigation systems.

Ultrasound is not a substitute for nutrient management or other long-term restoration measures. Its value is providing continuous, chemical-free control of algae and cyanobacteria while those longer-term efforts move forward. This presentation will focus on how ultrasound works, the cellular mechanisms involved, how targeted frequencies disrupt cyanobacteria, and the practical factors that determine treatment effectiveness in real-world water bodies.

Ultrasound Technology for Cyanobacteria Control and Ecosystem Recovery in a Hypereutrophic Urban Lake

Viviana Almanza [1], *Rick Clark*[2], *Rob Slingerland*[3] *and George Hutchinson*[3]

[1]SonicPure, Concepcion, Biobio, Chile

[2]SonicPure, Havana, Florida, United States

[3]SonicPure, Torrance, California, United States

Ultrasound has been applied for over two decades as a physical, non-chemical approach for cyanobacteria control; however, evaluations under real field conditions remain limited. This study assesses its application for controlling cyanobacterial blooms in Laguna Lo Méndez, a hypereutrophic urban lake in southern Chile, where a major bloom in 2023 caused significant ecological impacts, including fish mortality and the death of local wildlife such as coypu (*Myocastor coypus*), generating strong community concern and demand for non-chemical restoration measures.

Following implementation, a significant reduction in bloom-forming taxa was observed. *Microcystis* was reduced by more than 90%, even under high summer temperatures (22 °C). Water transparency increased from approximately 40 cm to over 100 cm, while pH decreased from 8.5 to 7.2, consistent with reduced phytoplankton biomass. No increases in nutrient concentrations or sedimentation rates were detected during the study period. Community analysis indicated a shift in phytoplankton structure, with relative increases in green algae, diatoms, and dinoflagellates, accompanied by greater microalgal diversity. These changes were associated with improved ecological conditions, including evidence of recolonization by aquatic fauna and *M. coypus*.

These results suggest that ultrasound can contribute to cyanobacterial bloom control and to modifications in phytoplankton community structure under field conditions, promoting changes in trophic dynamics.

Social Amplification of Risk in Coastal Tourism Destinations with Harmful Algae Blooms (HABs)

Sergio Alvarez

University of Central Florida, Orlando, FL, USA

The social and economic impacts of HABs can be widespread, yet they remain understudied. When they occur in waterfront tourism destinations, the impacts may be of such magnitude and depth that they seem disproportionate for a hazard caused by a microorganism. The theory of social amplification of risk posits that social aspects could be responsible for the amplification or attenuation of risk. In other words, the magnitude of impacts from risk events could be increased or decreased depending on social factors. The theory highlights the role of information and communication as amplifiers of risk, but other social aspects of risk have been identified. Prior studies on perceptions of HAB risk have found differences in risk perceptions across different groups of people but have not established a theoretical framework to explain how risks of HABs may be amplified or attenuated by social factors. This study attempts to close this gap by exploring the case of Florida, a global destination renowned for extensive beaches and human-made attractions, integrating insights from recent studies of the social and economic impacts of HABs on this tourism destination to develop a theoretical framework of social amplification of risk in the context of waterfront tourism destinations plagued by HABs. There is growing evidence supporting the social amplification of HAB risks in waterfront tourism destinations. The mechanisms for social amplification of risk are varied and interact with one another, transcending short term economic impacts on the tourism industry and the housing market, and threatening the social fabric of the destination in the long term by becoming a motivator for social polarization and conflict. The common thread is the role of information and misinformation regarding HABs, which erodes the destination's image and encourages divergent and conflicting perceptions of the problem and motivations to address it.

Changing Biogeochemistry, Wildfires, and Anchovy: Evaluating Historic DA Events Relative to 40 Years of Observations

***Clarissa Anderson*[1]**, *Nathali Cordero Quiros*[1], *Rasmus Swalethorp*[1], *Julie Dinasquet*[1], *Melissa Carter*[1], *Andrew Thompson*[2], *Andrew Leising*[2], *Steven Bograd*[2], *Michael Jacox*[2], *Isaac Schroeder*[2], *Jayme Smith*[3], *Iliana Ruiz-Cooley*[4], *Mer Pozo Buil*[5], *Raphael Kudela*[5]

[1] University of California San Diego, Scripps Institution of Oceanography, La Jolla, California, USA
[2] Southwest Fisheries Science Center, La Jolla, California, USA
[3] Southern California Coastal Water Research Project, Costa Mesa, California, USA
[4] CICESE, Ensenada, Baja California, Mexico
[5] University of California, Santa Cruz, Santa Cruz, CA

This presentation synthesizes a suite of unique time series spanning multiple decades with the goal of answering long-standing questions pertaining to interannual variability in harmful algal blooms caused by the cosmopolitan diatom *Pseudo-nitzschia*. In coastal California, domoic acid (DA) production by toxigenic species of this group occurs almost annually, with varying intensity and duration, although prior to 2000, such events were much less frequent. Impacts from DA events across the ecosystem are even more variable year to year, presenting significant predictability challenges when moving from particulate DA levels to anticipating specific food web outcomes. In 2025, a major event struck central and southern California, leading to exceptional marine mammal and seabird mortality and extended shellfish closures. Here, we examine the interplay of bottom-up forcing (changing ocean biogeochemistry in the source waters of upwelling, nutrient levels measured at the land-sea interface, and land-based events, such as wildfires) with food web structure variability (presence and depth of forage fish, efficiency of DA transfer to higher trophic levels). Together with low frequency variability altering the vertical delivery of upwelled nutrients, some key “big years,” including 2025, can be better explained using this approach, which is expected to aid in improved prediction of impacts on public health and protected

Three Decades of Monitoring and Modeling Domoic Acid Events in California

Clarissa Anderson[1], *Kasia Kenitz[1], Melissa Carter[1], Henry Ruhl[2], Jayme Smith[3], Eric Bjorkstedt[4], Kendra Negrey[5], Dale Robinson[5], and Raphael Kudela[5]*

[1]University of California San Diego, Scripps Institution of Oceanography, La Jolla, California, USA
[2]Monterey Bay Aquarium Research Institute, Moss Landing, California, USA
[3]Southern California Coastal Water Research Project, Costa Mesa, California, USA
[4]Californoia State Polytechnic University Humboldt, Arcata, California, USA
[5]University of California, Santa Cruz, Santa Cruz, CA 95064

Decades of investment from NOAA NCCOS and IOOS have placed California at the forefront of monitoring and predictive model methods development followed by successful transition to operational systems. The fundamental purpose of these efforts was powerfully demonstrated during the 2022-2025 spate of marine mammal mortality events which required a coordinated response from academia, state and municipal government agencies, and non-profit rescue organizations. These close relationships are now germane to the CA HAB Early Warning System. Today's presentation will review the history of the California Harmful Algal Bloom Monitoring and Alert Program (HABMAP), its role in supporting forecast models like the California Harmful Algae Risk Mapping (C-HARM) System and ROMS-BEC, and the evolution of the CA Imaging FlowCytobot Network. The use of NASA satellite platforms, such as MODIS and PACE, has been critical to the success of blended approaches to HAB detection and forecasting. I will close by describing future plans for modernization, system and partner expansion, user-driven decision-support tools, and moving beyond domoic acid, we hope with continued NOAA guidance and support.

The Value of Hyperspectral Remote Sensing to HAB Detection: Fact or Fiction?

Clarissa Anderson[1], *Raphael Kudela[2], and Michelle Tomlinson[3]*

[1]University of California San Diego, Scripps Institution of Oceanography, La Jolla, California, USA
[2]University of California, Santa Cruz, Santa Cruz, CA
[3]National Oceanic and Atmospheric Administration, Silver Spring, MD

The promises of hyperspectral remote sensing for ocean color applications, including HAB detection, have been widely discussed in many publications and reports for years. During NOAA and NASA collaborative planning of the Geostationary Extended Observations (Geo-Xo) system of satellites, for instance, HAB detection was routinely advertised as the second most important application after short-term weather forecasts and severe storm warnings. The ocean color sensor on Geo-Xo would potentially revolutionize species-level detection such that we could monitor a bloom at sufficiently high spatial, temporal, and taxonomic fidelity as to provide a wholly new set of detailed early warnings for actionable solutions. Indeed, we are entering an era of rapid advancements in our ability to infer phytoplankton taxonomy, growth, ecophysiology, and trait-based metrics from space and other remote platforms with burgeoning hyperspectral capacity, however, the investment in research needed to deliver on these expectations cannot be overstated. While the first tranche of Geo-Xo satellites will, unfortunately, not be outfitted with ocean color sensors, NASA is already well into its second year serving daily PACE hyperspectral imagery of the coastal and open ocean. The NASA PACE and ESA Sentinel missions and many other planned small sat endeavors are fueling a new generation of inquiries deducing ocean process from space and airborne sensors. This presentation will describe the power of hyperspectral data for HAB science and provide examples of several opportunities and challenges facing the field over the next decade if we are to significantly improve upon the real-time and forecasted information delivered to decision-makers.

Dynamics of the Massive Cyst Beds of the Toxic Dinoflagellate *Alexandrium catenella* in the Rapidly Warming Pacific Arctic

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

[1]Woods Hole Oceanographic Institution, Woods Hole, MA, USA
[2]Shanghai Jiao Tong University, Shanghai, China
[3] Northwest Fisheries Science Center, National Marine Fisheries Service, NOAA, Seattle, WA, USA
[4]University of Alaska Fairbanks, Alaska Sea Grant Marine Advisory Program, Nome, USA
[5]Nome Eskimo Community, Nome AK USA
[6] University of Maryland Center for Environmental Science, Chesapeake Biological Laboratory, Solomons, MD, USA

The waters of western and northern Alaska are warming, increasing the risk of blooms of the toxic dinoflagellate *Alexandrium catenella*. This species produces a dormant cyst that accumulates in sediments and germinates to initiate surface blooms. This talk synthesizes eight years (2018–2025) of observations, focusing on cyst beds documented in U.S. waters of the Bering, Chukchi, and Beaufort seas that represent the largest and densest *Alexandrium* cyst deposit globally. These areas and cyst concentrations are 15–20 times greater than similar features elsewhere. The massive Chukchi cyst bed reflects repeated deposition from blooms originating in the northern Bering Sea that are transported northward through Bering Strait, with minimal germination in colder years; inputs often exceed losses, leading to high cyst abundances. During 2022 this dynamic was documented when a massive bloom entered Bering Strait, leading to a mass encystment and deposition event, while low bottom temperatures suppressed germination from the cyst beds in the area. The bloom documented in 2022 presumably originated from unidentified cyst beds in the Russian waters of the Gulf of Anadyr, northwestern Bering Sea. Similar blooms initiate in the southeastern Bering Sea, where another large cyst bed was recently characterized. A fourth cyst bed south of Nome was first observed in 2022 and has persisted since. It is now clear that cyst beds in the Bering, Chukchi, and Beaufort seas operate on different time frames, with bloom initiation and impacts varying dramatically annually and regionally due to variable bottom temperatures and transport pathways. The latter affect marine ecosystems and coastal communities far from bloom origins. These unprecedented cyst beds represent a significant and growing threat to marine ecosystems and coastal communities dependent on marine resources for nutritional, cultural, and economic well-being.

The Scientific and Management Legacy of the ECOHAB Gulf of Maine and GOMTOX Programs

Donald M. Anderson[1]*, Dennis J. McGillicuddy*[1]*,Ruoying He*[2]*, Mike Brosnahan*[1]*,David Townsend*[3]*, Andy Thomas*[3]*, Neal Pettigrew*[3]*, Jefferson Turner*[4]*, Gregory Doucette*[5]*, Cynthia H. Pilskaln*[4]*, Jonathan R. Deeds*[6]*, Stacey Wiggins*[6]

[1]Woods Hole Oceanographic Institution, Woods Hole, MA, USA
[2]North Carolina State University, Raleigh NC USA
[3] University of Maine, Orono ME, USA
[4]University of Massachusetts, Dartmouth, North Dartmouth and New Bedford, MA USA
[5] NOAA National Ocean Service, Charleston, SC, USA (retired)
[6]US Food and Drug Administration Human Foods Program, College Park MD USA

The ECOHAB Gulf of Maine (ECOHAB-GOM) and ECOHAB-GOMTOX programs focused on the *Alexandrium catenella*, a species responsible for paralytic shellfish poisoning and recurring coastal and offshore fisheries impacts. From 1997 to 2013, these coordinated, multi-institutional efforts combined field observations, laboratory studies, and numerical modeling to resolve the physical, biological, and chemical controls on bloom dynamics and toxicity. ECOHAB-GOM established the first Gulf-wide understanding of bloom dynamics through large-scale surveys, cyst mapping, and coupled biophysical models, revealing the importance of alongshore transport, connectivity among regional populations, and the critical role of cysts in bloom initiation and persistence. The program produced the first realistic simulations of *Alexandrium* population dynamics, laying the foundation for predictive capability. ECOHAB-GOMTOX extended this work to offshore regions, particularly Georges Bank. A major advance was the development of a sustained, Gulf-wide cyst mapping program, now used to quantify bloom "inoculum potential" and initialize annual forecasts. The ECOHAB numerical model was also refined and transitioned into the operational NOAA Gulf of Maine HAB forecast system, now providing weekly real-time guidance for managers during the bloom season. Equally important were other management outcomes, such as a science-based onboard-screening, dockside-testing protocol that enabled the reopening of offshore surfclam and ocean quahog fisheries on Georges Bank, valued at approximately $10–15 million annually. These ECOHAB programs fostered enduring partnerships among scientists, managers, and industry stakeholders, with frequent interactions continuing to this day, including through the heavily attended annual Northeast HAB Symposium. Yet another outcome is that the knowledge, tools, and collaborative framework developed in the Gulf of Maine facilitated the rapid spin-up of another ECOHAB regional program focused on the emerging threat of *Alexandrium* in the Alaskan Arctic and the manner in which its toxins move through the food web, thereby enabling rapid progress in the development of region-specific management strategies.

Testing the Impact of Two New Clay Formulations on *Karenia brevis* Cell and Toxin Removal, Water Quality, and Benthic Organisms Using Mesocosm Tanks

John Kristoffer Andres[1], *Victoria Devillier*[2], *Emily R. Hall*[2], *Jessica D. Frankle*[2], *Susan Launay*[2], *Vincent J. Lovko*[2], *Jennifer H. Toyoda*[2], *Michelle R. Gaither*[1], *Donald M. Anderson*[3], *Kristy A. Lewis*[4]

[1]Department of Biology, University of Central Florida, Orlando, FL, USA
[2]Mote Marine Laboratory, Sarasota, FL, , USA
[3]Woods Hole Oceanographic Institution, Woods Hole, MA, USA
[4]University of Rhode Island, Graduate School of Oceanography, Narragansett, RI, USA

The application of clay to seawater has been shown to be an effective method for controlling marine Harmful Algal Blooms (HABs) with researchers testing new clay mixtures (termed modified clays) for increased efficacy. Here we investigated two clay formulations: Modified Clay II (kaolinite plus a polymer) plus curcumin (CUR) and GCO3.5 (GCO), a combination of two clay minerals, diatomaceous earth, and an oxidizer. We tested the ability of the two clay types to remove *Karenia brevis* (KB) cells and toxins from the water column and its effects on the physico-chemical properties of water, benthic organisms, and nutrient dynamics. We set up eighteen cylindrical mesocosm tanks and tested six different experimental conditions (KB only, Seawater only, CUR only, GCO only, KB + CUR, KB + GCO). Water samples were collected at T0, T2, T24, T48, and T72 hours. In addition, floc materials that settled in the bottom were collected for qPCR, toxin analysis, and nutrient analyses. The key findings in this study are: 1) both GCO and CUR were able to remove KB cells immediately after application with GCO removing more cells within 2 hours; 2) dissolved oxygen and pH were the physico-chemical parameters most influenced by clay application; 3) nutrients varied across treatments, but most changes were observed in tanks with the addition of KB; 4) both GCO and CUR are effective at removing toxins from water but toxin congeners changed throughout the study; and 5) organisms were not significantly impacted by clay application. Overall, the two new clay formulations were effective at significantly reducing cell number and removing toxins in our mesocosm. The next step would be to repeat these experiments in a natural system.

Assessing Use of Planet Satellite Data to Improve Harmful Algal Bloom Forecasts in Coastal Systems

Cynthia Arguijo[1]*, Michelle C. Tomlinson*[2]*, Xin Yu*[3]*, Sachidananda Mishra*[4]

[1]Smith College, Northampton, MA, USA
[2]NOAA, National Centers for Coastal Ocean Science, Silver Spring, MD, USA
[3]RPI, under contract to NOAA, Tallahassee, FL, USA
[4]Consolidated Safety Services Inc., under contract to NOAA, Fairfax, VA USA

Harmful algal blooms (HABs) pose a risk to human and ecological health in waterbodies around the US. In coastal and estuarine waters, these blooms are patchy, and change their extent hourly to daily, often occurring in small tributaries and near shorelines. To improve upon spatial resolution of model predictions, NOAA's National Centers for Coastal Ocean Science (NCCOS) is investigating the use of higher resolution Planet SuperDove imagery, which has 20 m spatial resolution, to better delineate bloom patchiness and monitoring at the coast. Current experimental forecasting efforts use the 300 m spatial resolution Ocean Land Colour Instrument (OLCI). In order to incorporate Planet imagery into NOAA's operational monitoring and forecasting efforts, an assessment of accuracy and potential forecast improvement is needed. This project will compare Planet SuperDove bloom detection products with OLCI, to evaluate its potential use in initiating forecast models, using *Margelefidinium polykrikoide*s bloom in the lower Chesapeake Bay for proof of concept. If successful, higher resolution satellite imagery will be used to initiate the bloom in the York River to determine improved transport and extent, to better guide management decisions in the region.

Holistic Management Practices in a Highly-Urbanized Watershed

Matthew Cerami[1], ***Tyler Arnold***[2], *Tom Warmuth*[3]

[1]Veolia Water NJ, Haworth, NJ, USA
[2]Veolia Water NJ, Haworth, NJ, USA
[3]BioSafe Systems, Charlotte, NC, USA

The Veolia Water New Jersey, Inc. Watershed Team addresses the challenge of protecting and managing 4,000 acres of forest and 8 billion gallons of raw water storage in a densely populated region. Watershed Area 5 (NJDEP) is highly urbanized, facing threats from harmful algal blooms, invasive species, ecosystem imbalance, overdevelopment, and overuse. Protecting the watershed and the Oradell, Lake Tappan, and Woodcliff Lake reservoirs is crucial, as nearly 900,000 people in Bergen and Hudson counties rely on them for clean drinking water. The VWNJ watershed team employs a unique blend of reservoir, forestry, and wildlife management to restore ecosystem balance and source water quality. Data-driven interventions include reservoir aeration, bio-manipulation, nutrient remediation/mitigation, floating wetlands islands, artificial fish habitat, reforestation, wetlands restoration, Canada geese control, remote water quality monitoring, and HABs forecasting and control with Greenclean Liquid 5.0 (peroxide/PAA algaecide). These efforts have resulted in improved water quality, including reduced Cyanobacteria, Chla, TOC, Geosmin, total phosphorus, and pH, alongside increased zooplankton population and ORP, and a reduction in overwintering Cyanobacteria and akinete spores. These changes have led to improved treatment plant performance, characterized by decreased chemical usage, increased filter performance, and reduced power consumption. This demonstrates that clean, safe drinking water originates at the source, and comprehensive watershed management, leading to more favorable water quality, alleviates strain on treatment plants and reduces operating costs.

Metagenomic Insights into Antimicrobial Resistance Gene Dynamics in Bloom-Impacted Freshwaters: A Seven-Year Western Lake Erie Basin Case Study

Naomy Avilés-Díaz, *Gregory J. Dick*

Department of Earth and Environmental Sciences, University of Michigan, Ann Arbor, Michigan, USA

Cyanobacterial harmful algal blooms (cHABs) in the Western Lake Erie Basin (WLEB) are well-characterized and monitored as a microcystin hazard, yet their potential intersection with environmental antimicrobial resistance remains poorly resolved. Blooms restructure aquatic microbial communities [1,2], alter nutrient concentrations, and generate oxidative and osmotic stress gradients [3], all conditions that can co-select for antimicrobial resistance genes (ARGs) and influence the mobility of stress-response. This raises the possibility that bloom development and resistome dynamics share environmental drivers, yet the two phenomena are rarely examined together. While LC-MS/MS and NMR platforms have transformed toxin discovery, parallel advances in metagenomic surveillance now enable longitudinal detection of both toxin genes and ARGs, opening a tractable path to test for co-occurrence. We applied a seven-year metagenomic time series (2016 to 2022, NOAA stations WE2, WE4, WE8, WE12) to characterize ARG dynamics across bloom development in WLEB. Across the time series, ARG abundances varied inconsistently from year to year, but detection rates have steadily increased, with a broader diversity of ARG subtypes recovered in more recent bloom seasons. Hierarchical generalized additive models with cyclic seasonal splines and site-level random effects revealed seasonal patterns in macrolide-lincosamide-streptogramin, bacitracin, and fosmidomycin resistance classes. A complementary spatial transect (2021 to 2022, ten NOAA sites from the Maumee River to the Detroit River) identified urban ARG hotspots and suggested that bloom community composition is associated with shifts in resistome structure. These findings complement a recently published characterization of bloom community succession in WLEB [4], supporting future integration of resistome and cyanobacterial community datasets. Together, these results position metagenomics alongside chemical analytical platforms as a complementary tool for examining the full spectrum of bloom-associated biological hazards and provide a foundation for exploring whether ARG dynamics and toxin-producing communities respond to overlapping environmental conditions in the Great Lakes.

Ground to Space: Operationalizing Integrated Sensor Monitoring

Dulcinea M. Avouris *[1], W. Josh Weiss[2], Elizabeth Crafton[3], Sahar Rezaei[2]*

[1]Hazen and Sawyer, Independence, OH
[2]Hazen and Sawyer, Baltimore, MD
[3]Hazen and Sawyer, Fort Collins, CO

Interest in remote sensing products that provide actionable data for water quality monitoring by water utilities is rapidly increasing. Of particular interest are reliable metrics for monitoring harmful algal blooms, early warning systems, and tools to identify hotspots for bloom development within source water bodies. Source water bodies are often managed for both drinking water and recreation, increasing the need for near real time data to inform safety warnings to the public, as personnel for "boots on the ground" sampling are not always available. The spatial extent of the rivers and reservoirs that feed utilities typically require 30m resolution at minimum, limiting applicable, publicly available, remote sensing data to missions such as Landsat or Sentinel 2. Water quality products from these two sensors have rapidly advanced to a sophisticated level, however, there is a large gap, often called the "valley of death", between remote sensing product development and tools for end users to implement for regular use. This is due to multiple factors, including knowledge and computing resource barriers on the part of utility personnel, lack of maintenance of online remote sensing access or tools, and the need for regional tuning of standard products. In addition to efforts by agencies that provide remote sensing data and products (e.g. NASA, NOAA, USGS, USEPA, ESA, EUMETSAT), water utilities and consulting companies that serve the water utilities sector are taking steps to leverage this data by partnering with governmental agencies, developing internal capabilities, and building tools to serve the expanding need for high quality, landscape scale monitoring of water quality. In this presentation, we will discuss the current landscape of actionable data and tools to support water utility planning and operations.

Hyperspectral Remote Sensing for Harmful Algal Bloom Detection: *Pseudo-nitzschia* in the Northeast Pacific

***Alexander Bailess*[1]**, *Nicholas Baetge[2], Andrew Barnard[1], Nicholas Tufillaro[3], Michael Behrenfeld[1], Brian Bill[4], Raphael Kudela[5], Jason Graff[1], Maria Kavanaugh[1]*

[1]Oregon State University, Corvallis, OR, USA
[2]Bermuda Institute of Ocean Sciences, Ferry Reach, Bermuda
[3]Aqualytics, Portland, OR, USA
[4]Environmental Chemistry Division, Northwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Seattle, WA, USA
[5]University of California Santa Cruz, Santa Cruz, CA, USA

Rapid identification of HABs is necessary to effectively manage marine resources, yet current identification methods are limited by expensive and labor-intensive in situ point sampling. Hyperspectral remote sensing enables scalable monitoring, but its ability to resolve taxonomic shifts within phytoplankton groups (e.g. diatoms) is largely unknown. To investigate this uncertainty, we cultured four dominant diatom genera from the California Current upwelling system, including this systems' most abundant harmful algae, *Pseudo-nitzschia*. The hyperspectral absorption and backscatter of these taxa were measured and used to model spectral reflectances that remote sensing platforms (satellites/drones) might detect. Differences between spectral fingerprints of these taxa were quantified using vector-based and statistical analyses. Mean spectral differences of 48% were observed between the most dominant diatom, *Thalassiosira*, and the most toxic diatom, P*seudo-nitzschia*. Differences of approximately 30% were found between *Pseudo-nitzschia* and the second and third most abundant diatoms, *Chaetoceros* and *Asterionellopsis*. Successful identification of P*seudo-nitzschia*'s reflectance fingerprint was driven by the presence of a unique feature around 560 nm. Preliminary validation work during a west coast cruise in fall 2025 found *Pseudo-nitzschia* blooms in the Monterey and San Francisco Bay to be discernible from adjacent phytoplankton communities based on this spectral feature. The distinct spectral fingerprint of *Pseudo-nitzschia* indicates that it may be distinguishable from benign diatom blooms using hyperspectral remote sensing platforms. This capability could provide a path for developing synoptic, spatially extensive early-warning monitoring frameworks for *Pseudo-nitzschia*.

What are US States Spending to Manage CyanoHABs and Can We Project Future Spending?

Eva M. Bailey[1]*, Lisa A. Wainger*[1]*, Emily Hoyt*[3]*, Elizabeth W. Price*[1]

[1]University of Maryland Center for Environmental Science, Solomons, MD, USA
[2]Independent Consultant, Corvallis, OR, USA
[3]Morgan State University, PEARL, St. Leonard, MD, USA

Every US state is experiencing cyanoHABs but the aggregate amount that they are spending to manage and respond is poorly quantified due to distributed responsibilities and inconsistent reporting. In this study, funded by the US Army Corps of Engineers, we are developing a national cost estimation model using data collected from structured interviews with state agencies across the continental United States and web/literature sources. We are using the model to fill in missing data to estimate current state-level management expenses and will also apply the model to estimate future management costs with and without control strategies. We use regression models to evaluate how expenditures respond to variation in cHAB event intensity, lake area, monitoring program type and state revenue. We distinguish fixed costs, e.g., coordinator salaries, from variable expenses, e.g., water sample testing and field personnel, to enable scaling of future spending to cyanoHAB intensity. We test alternative intensity metrics such as bloom area, bloom duration and total incidents, which are better constrained than toxicity. Results show substantial variation in management effort across states with responsibilities distributed among environmental quality agencies, health departments and fish and wildlife agencies. Most states conduct routine and response-based monitoring and invest in public communication through web dashboards and other outreach. Twenty states were found to conduct direct mitigation of blooms. Because we were not able to interview every agency and we omitted local government and private spending, our estimates will underestimate total management spending. Further, managers consistently reported insufficient dedicated funding to meet the management need. This work provides the first systematic national assessment of cyanoHAB management costs and establishes a framework for forecasting future spending under changing bloom conditions.

The Microbiome of a Freshwater Cyanobacterium Can Influence the Growth and Physiology of a Marine Eukaryotic Alga

***Eddie Bare**, Louie L. Wurch, Morgan M. Steffen*
James Madison University, Harrisonburg, VA, USA

Harmful algal blooms (HABs) are a major problem for aquatic ecosystems and water quality in both freshwater and marine environments. In freshwater systems, cyanobacteria like *Microcystis* form toxic blooms that can cause low oxygen conditions, fish kills, animal deaths, problems with drinking water, and devastation to tourism and fishery revenues due to annual bloom events. It is well-established that the cyanobacteria and algae in both freshwater and marine systems support a diverse and functionally important microbiome. What is not understood is whether the functional impact of individual microbiome members is specific to an individual host, or whether they can confer benefits to photobionts more broadly. Here, we investigated whether bacteria from freshwater *Microcystis* blooms in Lake Erie, Taihu, and multiple Virginia lakes influence the growth of the marine brown tide alga *Aureococcus*. Co-culture experiments between *Aureococcus* and bacteria isolated from *Microcystis* blooms indicate that freshwater bacteria from cyanobacterial blooms can change growth dynamics of marine eukaryotic algae. Specifically, *Aureococcus anophagefferens* reaches maximum growth rate more quickly and has significantly higher photosynthetic efficiency (Fv/Fm) when cultured with natives of the *Microcystis* bloom bacterial microbiome. These results provide new insight into the potential watershed-wide impacts of *Microcystis* blooms.

Advancing Sargassum Observation and Forecasting with Multi-Sensor Data Integration and Operational Models

*Joaquin A. Triñanes[1], **Brian Barnes**[2], Josefina Olascoaga[3], Julio Morel[4,5], Loraine Martell[4], Matthieu Le Henaff[6], Chuanmin Hu[2]*

[1]Universidade de Santiago de Compostela, Santiago de Compostela, Spain
[2] University of South Florida, St. Petersburg, FL, USA
[3] Rosenstiel School of Marine, Atmospheric, and Earth Science, University of Miami, Miami, FL, USA
[4]Caribbean Coastal Ocean Observing System (CARICOOS), Mayagüez, Puerto Rico, USA
[5]University of Puerto Rico at Mayagüez, Mayagüez, Puerto Rico, USA
[6]NOAA Atlantic Oceanographic and Meteorological Laboratory, Miami, FL, USA

Sargassum inundation events on Atlantic and Caribbean shorelines threaten coastal ecosystems, economies, and public health, and challenge existing observation and prediction capabilities. Satellite remote sensing and trajectory models have improved substantially since the Great Atlantic *Sargassum* Belt appeared in 2011. However, several limitations remain. Nearshore transport is poorly resolved, biomass is hard to quantify, and the integration of multi-sensor observations into consistent products is limited. Detection performance decreases in optically complex coastal waters, under cloud cover, near the Intertropical Convergence Zone, and at very low or very high biomass densities. Simplified drift representations and a single global biomass conversion factor can introduce systematic biases. The NOAA Sargassum Workshop identified priority actions to address these gaps. This effort integrates observations from multiple satellite platforms, including MODIS, VIIRS, OLCI, and MSI, as well as emerging sensors such as PACE OCI, with in situ measurements, drifters, autonomous platforms, and citizen reports. This approach would enable near-daily, higher-resolution views of *Sargassum* distribution, mat extent, thickness, and biomass. These products would then drive hybrid physical–biological models, including eBOMB, which represent ocean currents, winds, waves, and key biological processes such as growth, fragmentation, and decay. The objective is to improve the representation of transport pathways, retention, and coastal arrival timing, enabling forecasts actionable for mitigation. A stakeholder-led testbed will support the evaluation of new algorithms prior to operational use. Validation relies on regional observing networks and citizen science reports across the Caribbean and Gulf. Expected outcomes include improved forecast accuracy, more robust biomass estimates, reduced uncertainty, and reliable early warning products that support coastal management and decision making.

Improvements in *Sargassum* Detection and Monitoring Using Multi-Sensor Satellite Datasets

Brian B Barnes[1]*, Junnan Jiao*[1]*, Yuyuan Xie*[1]*, L Qi*[2,3]*, C Hu*[1]

[1]University of South Florida, St Petersburg, FL, USA
[2]NOAA Center for Satellite Applications and Research, College Park, MD, USA
[3]Global Science & Technology Inc., Greenbelt, MD, USA

Sargassum inundations on coastlines in the Caribbean Sea and southeastern United States have prompted the use of various remote sensing techniques in monitoring this brown macroalgae. Both coarse-resolution (300 – 1000m) and high-resolution (4 – 20m) datasets have critical roles, with the former providing long-term basin scale *Sargassum* abundance and distribution information. The latter enables *Sargassum* detection in nearshore waters, where individual patches may contribute to inundation events and subsequent harmful algae blooms. Here, we demonstrate improvements in satellite-based detection at both scales. Specifically, our findings reveal that data from the recently launched OCI sensor (1000m resolution) on the PACE satellite provide 47% more valid observations than the widely-used baseline sensor (MODIS, 1000m), while also identifying 51% more *Sargassum* pixels. These improvements result from PACE's tilted orbital design and OCI's higher radiometric quality. Other coarse-resolution sensors provide additional observations, with data merging facilitating more spatially complete maps of *Sargassum* abundance and distribution. These data may be further complemented using high-resolution monitoring, including datasets from Sentinel-2 MSI (20m) and the SuperDove (4m) constellation. Here, we demonstrate broad agreement between MODIS and MSI over the wider Caribbean region, with the latter providing significantly more observations in low-density months due to its finer spatial sampling. Additionally, satellite observation characteristics that previously precluded *Sargassum* detection and biomass assessment (especially unfavorable observation conditions) have been minimized through improved detection models and empirical correction algorithms. Together, these advancements have been implemented within the operational Sargassum Watch System, providing data at multiple scales in near-real time toward local ecosystem management and numerical forecasting of *Sargassum* transport.

Water Quality and Phytoplankton Dynamics in Los Olmos-Laguna Salada Tributary of Baffin Bay, TX

***Lucero Barraza**, Michael Wetz*

Harte Research Institute, Texas A&M University-Corpus Christi, Corpus Christi, Texas, United States of America

Since 1990, recurring blooms of the "brown tide" phytoplankton species, *Aureoumbra lagunensis,* have occurred in Texas' Laguna Madre and Baffin Bay. Findings from a 13-year time series suggest that one of the three tributaries of Baffin Bay, the Los Olmos Creek–Laguna Salada (LOLS) complex, regularly contains high biomass of *A. lagunensis*, even when biomass is low in the rest of the bay, indicating that it may function as an "incubator." This study aimed to characterize water quality and environmental factors influencing phytoplankton dynamics in the LOLS through biweekly sampling at three sites. The study found that the LOLS exhibits key characteristics that favor the proliferation of *A. lagunensis*. It is shallow (<1m), which enhances nutrient exchange from porewaters to the water column. Additionally, water circulation is primarily driven by wind, resulting in limited water exchange and prolonged residence times during calm periods. Moreover, all three LOLS sites consistently exhibited hypersaline conditions (41–130), which are conducive to the survival of salt-tolerant and slow-growing *A. lagunensis* over other phytoplankton species. The Los Olmos sites had elevated dissolved organic nutrient concentrations (LO1: 214.4 ± 87.6 µM; LO2: 209.2 ± 89.9 µM) that can be favorable for mixotrophic taxa such as *A. lagunensis*. Additionally, DIN:Si ratios above 1 and occasional phosphorus limitation at the Los Olmos sites create a nutrient regime less favorable to competing phytoplankton groups. *A. lagunensis* biovolume was significantly higher in upstream sites (LO1: 3.51×10^{7}–1.98×10^{8} μm^3/mL; LO2: 4.63×10^{7}–2.17×10^{8} μm^3/mL), peaking in spring and summer, compared to the downstream Laguna Salada (LS1: 7.57×10^{6}–3.98×10^{7} μm^3/mL). Results from this study contribute to our understanding of *A. lagunensis* bloom dynamics, aiding future monitoring efforts and helping to address water quality issues in Baffin Bay.

The Monitoring and Management of CyanoHABs in Shallow Dredged Material Containment Ponds

Lisa Barry[1], Colleen McMullen[2]

[1]Maryland Environmental Service, Poplar Island, Tilghman, Maryland, United States
[2] Maryland Environmental Service, Headquarters, Millersville, Maryland, United States

Maryland Environmental Service (MES), on behalf of the Maryland Port Administration (MPA), manages and operates multiple Dredged Material Containment Facilities (DMCFs) and Beneficial Use Ecosystem Restoration Sites in Baltimore Harbor and the Maryland portion of the Chesapeake Bay. This presentation focuses on four MPA sites: Cox Creek, Masonville, and Hart Miller Island DMCFs, and the Paul S. Sarbanes Ecosystem Restoration Project at Poplar Island. Nutrient-rich dredged material placed hydraulically or mechanically into containment cells can create eutrophic conditions that support rapid cyanobacterial proliferation, including the development of Harmful Algal Blooms (HABs). Resulting blooms may influence site operations and pose risks to human health and wildlife through elevated pH, increased turbidity, and cyanotoxin production. *Microcystis aeruginosa* blooms have affected Poplar Island in 2012–2014, 2020, and 2022–2024, and Masonville from 2016–2025, at times producing microcystin concentrations exceeding the established no-contact guidance levels. During these periods, additional CyanoHAB taxa, including *Anabaenopsis* sp., *Phormidium* sp., *Planktothrix* sp., *Synechocystis* sp., and *Aphanizomenon* sp., were identified, with several species producing toxins.

MES, in coordination with partner agencies, monitors and responds to algal blooms according to a Global HAB Response Plan and site-specific HAB Monitoring Plans. These plans guide sampling strategies, exposure reduction, and protective measures for human health, wildlife, and surrounding ecosystems. This presentation will summarize HAB data, explain why HABs occur within the DMCFs and restoration projects, and highlight how MES uses advanced monitoring tools and technologies to detect early bloom development and assess potential toxin production. It will also discuss collaborative monitoring efforts, treatment approaches, lessons learned, and recent advancements that allow MES to conduct onsite analyses to support timely, informed management decisions.

Lisa Barry, Senior Environmentalist Specialist II, and Colleen McMullen, Lead Environmental Specialist, with the Maryland Environmental Service (MES), supports the management and operation of dredged material containment facilities and large-scale ecosystem restoration projects on behalf of the Maryland Port Administration. Their work focuses on water quality monitoring, harmful algal bloom (HAB) assessment and response, regulatory compliance, and the application of advanced monitoring tools to support adaptive management decisions. They have extensive experience coordinating with state and federal partners to protect human health, wildlife, and aquatic ecosystems within the Chesapeake Bay and Baltimore Harbor.

Integrating Field Data, Remote Sensing, and Water Quality Modeling to Forecast Harmful Algal Blooms

Melissa M. Baustian[1]*, Emily Lain*[2]*, Bingqing Liu*[3]*, Sibel Bargu*[4]*, Jacob Cheng*[4]*, Scott Mize*[5]*, Ryder Myers*[5]*, Francesca Messina*[6]*, Ioannis Y. Georgiou*[6]

[1]U.S. Geological Survey, Wetland and Aquatic Research Center, Baton Rouge, LA
[2]Cherokee Nation System Solutions, in contractual support of U.S. Geological Survey, Wetland and Aquatic Research Center, Lafayette, LA
[3]Florida State University, Tallahassee, FL
[4]Louisiana State University, Baton Rouge, LA
[5]U.S. Geological Survey, Lower Mississippi-Gulf Water Science Center, Baton Rouge, LA
[6]The Water Institute of the Gulf, Baton Rouge, LA

Aquatic ecosystems are undergoing changes due to shifts in climatic conditions (e.g., heavy rainfall events, warmer temperatures) that influence nutrient loading which often leads to increased growth rates of phytoplankton, including those that can be harmful. The increased frequency of harmful algal blooms (HABs) is problematic because they can affect wildlife, fisheries, and humans; reduce property values; and cause bottom-water hypoxia. The Lake Pontchartrain estuary in coastal Louisiana has over 1.5 million people who depend on it for commercial fishing, recreation, and aesthetics. Nutrient-rich water inputs from the Bonnet Carré Spillway openings, as well as from Lake Maurepas and the other local tributaries, can trigger the growth of cyanobacterial HABs (CyanoHABs) in Lake Pontchartrain estuary. Integrating field observations of algal pigments, including chlorophyll *a* and accessory pigments, with remote sensing technology and water quality modeling can provide innovative tools that learn from the past to forecast the temporal and spatial variation of CyanoHABs. Current monitoring includes monthly surface water collection at eight sites in the Lake Pontchartrain estuary over a two-year period to assess the phytoplankton biomass and composition. Preliminary analysis (November 2024 through May 2025) indicates the mean algal biomass ranges from 3.5 to 7.2 μg chlorophyll *a* L^{-1}, with high concentrations of accessory pigments—including zeaxanthin, fucoxanthin, alloxanthin, chlorophyll b, and peridinin—representing cyanobacteria, diatoms, cryptophytes, chlorophytes, and dinoflagellates, respectively. These pigments are used to validate ocean color remote sensing algorithms of algal pigment concentrations to estimate phytoplankton community composition. Generated maps of phytoplankton biomass and composition are then used to initialize conditions in a water quality model (Delft3D-BLOOM module of Delft3D-Flexible Mesh Suite) to forecast CyanoHAB events. These tools and results could help guide field practitioners in their efforts to detect and manage future CyanoHABs in the Lake Pontchartrain estuary, as well as other aquatic ecosystems.

Recurring Winter Blooms of Karenia selliformis near Matagorda Bay Texas

***Laura Beecraft*[1]**, *Dalton Tryba*[1], *Lucero Barraza Gomez*[1], *Mintu Chowdhury*[1], *Xinping Hu*[2], *Michael Wetz*[1]

[1]Harte Research Institute, Texas A&M University-Corpus Christi, Corpus Christi, TX, USA
[2]Marine Science Institute, University of Texas at Austin, Port Aransas, TX, USA

Karenia brevis has historically accounted for the majority of harmful algal blooms (HABs) along the Texas coast, with blooms typically occurring from ~July-November. However, recent observations suggest the emergence of a potentially novel winter HAB species, *Karenia selliformis*. Since 2022, *K. selliformis* has been detected in three of the last four December's at in the mouth of Matagorda Bay, raising questions about its population dynamics, environmental drivers and potential to become a species of concern in this region. In December 2025, high-frequency sampling using an Imaging FlowCytobot provided detailed temporal observations of a *K. selliformis* bloom. *K. selliformis* concentrations increased in early December, reached a peak around 600 cells/mL in mid-December, and returned to background levels (<1 cell/mL) by early January. Diurnal fluctuations suggest tidal influence and offshore sources at this location. *K. selliformis* was present across salinities ranging from 26-30. Cells were also observed at low concentrations 120 km to the south in Corpus Christi Bay, indicating the bloom may have at least spanned this geographic range and was transported to the upper estuary of Corpus Christi Bay through Aransas Pass. While toxicity is not confirmed in Texas populations and there are no known marine mortality events, *K. selliformis* has produced toxic blooms resulting in fish kills in other regions of the world, mainly through the toxin gymnodimine-A. These observations indicate that *K. selliformis* may represent an emerging HAB species in this region and the need for continued monitoring combined with toxin analyses to assess potential risk to marine life and ecosystems.

Validation of a Quantitative LC-MS/MS Method for Regulating Diarrhetic Shellfish Toxins Following ISSC Protocols

Christopher R. Beekman[1], *Brigid Carr*[2], *Stephen D. Archer*[2], *Tyler Spillane*[3], *Morgan Langis*[4], *Jeff Lahti*[4], *Shelley Lankford*[4] *Jonathan Deeds*[1]

[1]US Food and Drug Administration, Human Foods Program, College Park, MD, USA
[2]Bigelow Laboratory for Ocean Sciences, East Boothbay, ME, USA
[3]Maine Department of Marine Resources, West Boothbay Harbor, ME, USA
[4]Washington State Department of Health, Shoreline, WA, USA

In the US, the National Shellfish Sanitation Program (NSSP) is the federal/state cooperative program recognized by the U.S. Food and Drug Administration (FDA) and the Interstate Shellfish Sanitation Conference (ISSC) for the sanitary control of shellfish produced and sold for human consumption. The NSSP promotes public health protection and improves the sanitation of bivalve molluscan shellfish moving in interstate commerce through federal/state cooperation and uniformity of state shellfish programs. Under the NSSP, methods used for management of marine biotoxins must be validated according to a single laboratory validation scheme established by the ISSC. This work discusses the validation of an LC-MS/MS method for the management of diarrhetic shellfish poisoning (DSP) toxins in mussels in accordance with ISSC protocols. This work also covers the process for method extension to additional matrices of interest including oysters and clams in accordance with ISSC guidelines. Certified standards for okadaic acid (OA), dinophysistoxin-1 (DTX-1), and dinophysistoxin-2 (DTX-2) were spiked into 20 individual sources of matrix, each comprised of 12 homogenized animals, at a range of concentrations spanning the guidance level of 0.16 ppm OA equivalents Matrix-matched calibration curves were generated by diluting certified standards into pooled blank mussel matrix comprised of five previously tested blank matrix sources LC-MS/MS analysis was performed on a Sciex QTrap 5500+, with an electrospray ionization source, attached to a Shimadzu Nexera X2 UHPLC with a Waters Xbridge Premier BEH C18 (2.1 x 100 mm 3.5 µm) column, at a flow rate of 0.300 mL/min under acidic conditions. Ions were monitored in negative mode. An alkaline hydrolysis step converts fatty acid acyl-esters toxin metabolites back to the toxin for direct analysis. Overall, the method was found to be accurate, precise, specific, sensitive, and fit for the purpose of managing DSP toxins in mussels under the NSSP.

Interannual Variation in Freshwater and Marine Phycotoxins Quantified from Oysters Cultured Across Diverse Coastal Sites

Tal Ben-Horin[1] *and Astrid Schnetzer*[2]

[1]College of Veterinary Medicine, North Carolina State University, 303 College Circle, Morehead City, NC 28557, USA
[2]College of Sciences, North Carolina State University, 2800 Faucette Drive, Raleigh, NC 27695, USA

The expanding footprint of global aquaculture has pushed production systems into regions with unknown or limited baseline information about associated hazards and risks. Oyster (*Crassostrea virginica*) aquaculture, for example, has expanded throughout euhaline coastal sounds across the southeastern United States yet there exists limited information on phycotoxin levels in oysters cultured in these environments. Here we investigated domoic acid and microcystin accumulation in cultured oysters at three coastal sites in North Carolina, with all sites varying in surrounding land use. Oyster deployments throughout 2021 and 2023 were complemented by harmful algal bloom monitoring methods including the use of solid-phase adsorption toxin tracking devices and microscopy analyses to determine microalgal cell concentrations from water samples. Domoic acid was detected in 20% and 38%, and microcystin in 48% and 11%, of the tested oysters during 2021 and 2023 (N = 178 total oysters tested), with both toxins co-occurring in 7% of the animals. While domoic acid concentrations remained far below seafood safety action levels, maximum microcystin levels at some sites approached tolerable daily intake guidelines in 2021 but were nearly absent across all sites in 2023. This latter observation implicated environmental drivers of cyanotoxin production, transport, and accumulation in oysters operating at regional scales greater than individual oyster farms. Fully understanding the environmental drivers of phycotoxin production within a landscape context, including how and when these toxins accumulate in shellfish, therefore represents a critical research gap. Given the regional synchrony in phycotoxin concentrations observed in oysters, there holds considerable promise for developing adaptive sanitation and control programs in response to conditions when perceived toxin risks are high.

In-depth Comparisons of Extraction Methods for Natural Products of Cultured *Gambierdiscus* and *Fukuyoa*

Clayton T. Bennett[1]*, Sarah May*[2]*, Kirk Gaston*[2]

[1]VSG Contracting: Nitya, LLC, Gulf Coast Seafood Laboratory, Dauphin Island, AL, USA
[2]US Food and Drug Administration, Gulf Coast Seafood Laboratory, Dauphin Island, AL, USA

Marine dinoflagellates produce a variety of bioactive compounds, and several have been associated with the human illness ciguatera poisoning (CP). Recently, novel metabolites in the ciguatoxin (CTX), maitotoxin (MTX), and gambierone classes have been discovered in *Gambierdiscus* and *Fukuyoa*. These compounds range in polarity from very hydrophobic to hydrophilic. However, there is a knowledge gap in how extraction methods may impact recovery and isolation of these compounds, which affects downstream purification process. This study examines the changes in chemical profiles of extracts from cultured *Gambierdiscus* and *Fukuyoa* under different extraction methods using targeted low resolution and high-resolution mass spectrometry. Algae cultures established in the laboratory were extracted with varying conditions to provide chemically different fractions that were tested for activity using the mouse neuroblastoma (N2a) assay. The N2a assay results revealed voltage-gated sodium channel (CTX-like) and non-specific (MTX-like) toxicity, which was quantified using CTX3C and MTX-1 equivalence, respectively. The fractionation methods of the extractions can separate these types of toxicity. Further analysis of the toxic extracts using non-targeted LC-MS methods reveal novel toxins that will be further purified to study activity and structural elucidation.

Diversity and Toxicity of Planktonic, Tychoplanktonic, and Benthic Cyanobacteria from Freshwater Systems of Florida

***David E. Berthold*[1]*, Autumn Taylor*[1]*, Maria Carolina Ferreira*[1]*, Jéssica A.S. Moretto*[1]*, Forrest W. Lefler*[1]*, Sofia Iliakopoulou*[2]*, Alina Gialleli*[2]*, Triantafyllos Kaloudis*[2]*, H. Dail Laughinghouse IV*[1]

[1] Agronomy Department, Fort Lauderdale Research and Education Center, University of Florida / IFAS, Davie, FL, USA.
[2] Athens Water Supply and Sewerage Company - EYDAP SA, AquOmixLab - Laboratory of Organic Micropollutants, Water Quality Control Department, Menidi, Greece

CyanoHABs are increasing in frequency, duration, and severity across Florida and it is imperative to identify the cyanobacteria responsible for these blooms, their drivers and toxicity. Given their prevalence within (sub)tropical systems, their diversity is likely underestimated leading to research gaps regarding cyanobacteria taxonomy and systematics. In Florida, there is need for floristic studies that encompass both published and novel taxa along with their toxins and genetic potential. These toxins, coming from known or undescribed taxa pose risk to aquatic food webs, wildlife, and human uses. Consequently, a detailed characterization of the cyanobacterial taxa present across Florida freshwaters along with the identification of associated toxins, is critical for understanding bloom dynamics, assessing ecological and human health risks, and informing management strategies aiming to reduce cyanoHAB occurrence and toxicity within these systems. To complete this work, cyanobacteria were isolated from several freshwater systems around Florida from 2017-2026 and identified through morphology, genome sequencing, and phylogenenomics. Toxicity of isolated strains were evaluated using both ELISA and LC-qTOF. Results demonstrated that common planktonic, bloom-forming cyanobacteria produce toxins like microcystins, cylindrospermopsins, and anatoxin. Results also indicated that non-bloom forming cyanobacteria, e.g., benthic, tychoplanktonic and picocyanobacteria, are also sources for toxin production in these freshwater systems. This research also describes novel genera and species from well-known freshwater systems like Lake Okeechobee and Florida springs.

Floridanema, a Widespread Specialized Metabolite Producer Found in Lake Erie CyanoHABs

Aaditi Chopade,[1] Kaylin Hauck,[1] Terrance Meinardus,[1] Runjie Xia,[1] Mary-Candler Schantz,[1] David E. Berthold,[2] M. Carolina Fereira,[2] Forrest W. Lefler,[2] H. Dail Laughinghouse IV,[2] and ***Matthew J. Bertin***[1]

[1] Department of Chemistry, Case Western Reserve University, Cleveland, OH, USA

[2] Fort Lauderdale Research and Education Center, University of Florida – Institute of Food and Agricultural Sciences, Davie, FL, USA

Cyanobacterial harmful algal blooms (cyanoHABs) pose recurring risks to drinking-water sources and recreational waters, yet monitoring programs typically focus on a limited set of regulated toxins (e.g., microcystins). Increasing evidence indicates that blooms contain additional, under-monitored metabolites that may contribute to toxicity and complicate risk assessment. Here we report that the recently described cyanobacterial genus Floridanema encodes biosynthetic pathways for highly bioactive peptide families (including tychonamide- and pahayokolide-like compounds) that have historically been attributed to multiple cyanobacterial taxa. Using an integrated workflow that combines comparative genomics, LC–MS/MS and NMR-based structure elucidation, we link previously cryptic gene clusters to peptide products and identify conserved biosynthetic features associated with unusual β-amino acid residues (Atpoa and Athmu) that serve as diagnostic structural markers for this chemistry. Importantly, we isolated F. aerugineum BLCC-F306 from Lake Erie and detected a partial tychonamide biosynthetic gene cluster in a metagenome-assembled genome derived from Lake Erie cyanoHAB biomass. These findings suggest that Floridanema may be a previously underrecognized bloom-associated taxa with the capacity to produce potent metabolites in Great Lakes waters. Ongoing work will focus on determining the occurrence of Floridanema and its peptide markers across bloom samples and evaluating how these metabolites should be incorporated into expanded, mixture-aware cyanoHAB surveillance frameworks.

Evaluation of a Rapid Strip Test for Microcystin Detection in Recreational Waters

Takeda, SHK, ***Bertoni,*** *FM*

São Paulo State Environmental Company, São Paulo, SP, Brazil

This study evaluated the performance of a rapid strip test for semi-quantitative detection of microcystins in ultrapure and surface water samples fortified with microcystin-LR, using ELISA as the reference method. Samples covering concentrations from 0.4 to 15 µg/L were analyzed by visual interpretation performed by trained and untrained analysts, as well as by a strip reader.

The strip test showed consistent results for samples without detectable microcystins and for samples with higher toxin concentrations (>10 µg/L). Greater variability was observed at intermediate concentrations, particularly between 5 and 10 µg/L, where interpretation of the test line intensity was more subjective. Differences between operators were also more evident in this concentration range, especially for the non-specialist analyst. Results obtained with fortified surface water samples were similar to those observed in ultrapure water, suggesting limited matrix interference under the evaluated conditions. In general, the strip reader reduced variability compared with visual interpretation, mainly for intermediate concentrations. Overall, the rapid strip test proved to be a useful screening tool for the detection of microcystins in water samples, particularly for non-detectable samples and for concentrations above 10 µg/L, where the results were more consistent and easier to interpret. In contrast, intermediate concentrations required more careful evaluation due to greater variability in the interpretation of the test line intensity. These findings suggest that operator experience and the use of a strip reader may improve the consistency of results in this concentration range.

Changes in Cyanobacteria Abundance and Community Structure Following Aluminum Sulfate Treatments in Two Minnesota Lakes

Joe Bischoff[1]*, Terry Jeffery*[2]

[1] Barr Engineering Co., Minneapolis, MN, USA
[2]Riely Purgatory Bluff Creek Watershed District, Minneapolis, MN, USA

Lake Riley is a 297-acre recreational lake in the southwest suburbs of Minneapolis with historically poor water quality including nuisance algae blooms and poor water clarity. Cyanobacteria blooms frequently occurred in the lake with cyanobacteria cell counts approaching World Health Organization thresholds for a moderate probability of toxic blooms. Lake Riley has a large watershed (5,218 acres) with a large proportion discharging through Rice Marsh Lake, an 83-acre shallow lake that also exhibited poor water quality. Since 2016, the Riley Purgatory Bluff Creek Watershed District has focused restoration efforts on the two lakes including carp control, efforts to reduce Curly-leaf pondweed, and nutrient management. Both lakes demonstrated high internal phosphorus loading because of sediment phosphorus release. A series of sediment phosphorus inactivation projects began in 2018 using applications of aluminum sulfate to reduce sediment phosphorus release and minimize algal growth. Lake Riley was treated with alum in May 2016 and June 2020 while Rice Marsh Lake was treated in 2018 and 2024. Sediment P release was reduced by 83% between 2016 and 2021 in Lake Riley resulting in summer average chlorophyll-a concentrations consistently below 10 µg/L and Secchi depths exceeding 15 feet. Cyanobacteria abundance was significantly reduced following the alum treatments suggesting that internal phosphorus loading was a primary driver for the blooms. However, two toxic cyanobacteria blooms occurred in the lake in 2025 following five years of low phytoplankton abundance. Since hypolimnetic phosphorus concentrations remained relatively low, these blooms were likely driven by large spring storms and early spring warm temperatures. While reducing internal phosphorus loading minimized cyanobacteria abundance, reductions in watershed loading are still required to further minimize the potential for harmful algal blooms in Lake Riley.

Evaluating Efficacy and Ecological Implications of Peroxide-Based Algaecides in CyanoHAB Management

West M. Bishop

SePRO, Carmel, Indiana, USA

As cyanoHABs continue to increase and impede water use, options to rapidly restore systems are critical. A scalable and rapid acting mitigation strategy for HABs that has gained much awareness is use of USEPA registered peroxide technologies. Multiple research initiatives have greatly informed use patterns and environmental implications for operational field treatments. The influence of cyanobacterial cell density on peroxide degradation and subsequent efficacy is critical to guide use amounts. Comparison of multiple different formulated peroxide products in terms of efficacy and toxin dynamics allows selection of the most efficient product. In multiple operational treatments in near shore areas of Lake Okeechobee (FL, USA), control of *Microcystis aeruginosa* dominated blooms (> 90% decrease in cell densities) was consistently measured as well as decrease in total toxins. Some non-target bacterial communities decreased short-term after treatment though they recovered by 48HAT and eukaryotic algae increased. Routine and localized marina treatments in Utah Lake were also able to keep prioritized areas below risks levels of multiple cyanoHABs and associated toxins. Peroxide technologies can provide a scalable, ecologically compatible, and rapid acting approach to cyanoHABs even in localized areas and be part of integrated management programs.

High Frequency Monitoring of Phytoplankton Distribution with Special Reference to Cyanobacteriophyta, Dinoflagellata and Haptophyta

Tobias Boehme [1], *Anna Dahlhuas*[1], *Agnieszka Pasztaleniec*[2]

[1]bbe Moldaenke, Schwentinental, Germany

[2] Institute of Environmental Protection – National Research Institute, Warsaw, Poland

The growth of potentially harmful algae is increasingly threatening the water in reservoirs, lakes and oceans worldwide. Taxa belonging to various taxonomic groups (are known to produce toxins that pose a risk to fish, animals and humans. Therefore, an effective risk assessment is required in order to determine the occurrence and levels of the different classes of harmful algae. Climate change and human impact pose risks by helping harmful algae to advance in places where they did not pose a threat before like *Prymnesium* parvum N.Carter 1937 (Haptophyta) in the Oder River which killed masses of fish and aquatic life in a bloom in 2022.

The analysis of water samples is expensive due to the amount of manual labour involved. Here we present a real-time measurement of *in vivo* and *in situ* fluorescence with multispectral pigment excitation to determine different spectral classes of algae. We improved our fluorometric approach to determine additional algae classes, such as dinoflagellates and golden-brown algae in addition to cyanobacteria and higher algae classes. This method enables rapid, on-site assessment of potential ecological threats.

We apply this approach to two case studies: the development of *Prymnesium parvum* in the Oder River over few weeks period, and cyanobacterial dynamics in a freshwater Clear Lake, California, monitored over three years. As part of a pilot project in Clear Lake, we provide on-site and satellite data to visualize the development of phytoplankton. This knowledge enables the management of water treatment and reflects the condition of surface water in drinking water reservoirs and recreational areas along the lake.

Long-read Metagenomic Characterization of the Microbiome Associated with Karenia brevis Cultures from Manasota Key

***Nanushka M. Bonano-Collazo*[1]*, Anne Baldino*[1]*, Dr. Joaquín Martínez-Martínez*[2]*, Dr. Tsvetan Bachvaroff*[1]

[1] Institute of Marine & Environmental Technology - University of Maryland Center for Environmental Science, Baltimore, MD
[2]Horn Point Laboratory – University of Maryland Center for Environmental Science, Cambridge, MD

Karenia brevis is a marine dinoflagellate that causes Florida Red Tide harmful algal blooms (HABs), which produce brevetoxins harming marine ecosystems, public health, and coastal economies. Understanding factors driving *K. brevis* blooms can inform new control strategies. Laboratory cultures of *K. brevis* nurture diverse bacterial communities that may influence algal growth and nutrient exchange; however, their functional roles remain poorly understood. Nanopore long-read sequencing and metagenomic approaches were used to investigate interactions and characterize bacterial genomes associated with two *K. brevis* cultures from the Manasota Key isolate strain CCMP2229. The assembly recovered multiple bacterial genomes with metabolic capabilities and antimicrobial resistance genes. From 37 gigabases of sequence, the first isolate produced 11 bacterial genomes ranging from 3-9 megabases in length, and the second isolate, from 1-3 gigabases of sequence, produced three smaller partial assemblies of 10-50 kilobases. The first isolate contained a putative eukaryotic contaminant represented across 34 contigs ranging from 800 kilobases to 2.7 megabases. Bacterial taxonomic assignments based on BLASTn against the 16S rRNA gene database included *Shimia sediminis*, *Nioella ostreopsis* (Rhodobacteraceae), and *Oceanococcus atlanticus* (Oceanococcaceae), taxa previously associated with *K. brevis* cultures and marine environments. Comparative genomic analyses identified conserved pathways for amino acid biosynthesis, carbohydrate metabolism, and secondary metabolite biosynthesis, suggesting functional specialization across taxa. Biosynthetic gene cluster analyses revealed terpene and polyketide synthase pathways, indicating strong secondary metabolic potential. This study provides genomic insights into microbial communities associated with *K. brevis,* establishing a framework for investigating algal-associated microbial communities using culture-independent long-read sequencing approaches.

A Framework and Field Method for Quantifying Benthic Cyanobacteria Human Health Risk

Hannah Bonner[1]*, Ellen Bailey*[2]

[1]Brigham Young University, Provo, Utah, USA
[2]Utah Division of Water Quality, Salt Lake City, Utah, USA

Toxigenic benthic cyanobacteria mats pose an emerging and difficult-to-manage risk to recreational waters because exposure occurs primarily through direct contact with benthic material rather than through the water column. Traditional bloom-based metrics are therefore poorly suited for assessing human health risk from benthic mats. Here, we present an integrated guidance framework and standardized field method developed in Utah to support consistent, science-based management of benthic cyanobacteria in wadable rivers, streams, and lentic systems. The guidance establishes a hazard-based, exposure-oriented decision process centered on benthic mat presence, percent coverage, and site-specific recreational risk factors. It recognizes that toxin production is spatially and temporally variable and that in-mat toxin concentrations alone are insufficient for advisory decisions. As a result, percent benthic mat coverage is used as the primary quantitative indicator of risk, supported by qualitative considerations that elevate exposure potential. The field method proposed for quantifying benthic coverage employs a repeatable point-intercept method adapted from established plant ecology techniques. Quadrat-based presence/absence measurements are collected along five transects at a waterbody to generate reach-scale coverage estimates while minimizing observer bias and field time. Standardized observations of mat size, substrate, flow, and high-risk factors are collected to contextualize results. Together, the guidance and field method provide a practical, defensible approach for agencies managing recreational waters affected by benthic cyanobacteria. This poster highlights the scientific rationale, field implementation, and management relevance of the framework, offering a transferable model for jurisdictions facing similar challenges in assessing and communicating benthic cyanobacteria risk.

Disentangling *Karenia brevis* and Giant Virus Diel Interactions During an Active Bloom Along Coastal Florida

Anne Booker[1,2]*, Petra Byl*[1]*, and Joaquín Martínez Martínez*[1]

[1]University of Maryland Center for Environmental Sciences, Horn Point Laboratory, Cambridge, MD, USA
[2]Louisiana State University-Shreveport, Shreveport, Louisiana, USA

Seasonal blooms of the harmful alga *Karenia brevis* negatively impact southeastern USA coastal environments and their economy. We have recently shown that *K. brevis* are infected by, at least, six giant virus types within the *Imitervirales* order in the phylum *Nucleocytoviricota* (dsDNA), advancing understanding of *K. brevis*' microbial ecology. Viral interactions influencing *K. brevis* may be used as predictors to forecast bloom dynamics, aiding in monitoring and mitigation efforts. In this study, we employed single-virus genomics, metagenomics, and metatranscriptomics to investigate the diversity and activity of *K. brevis* viruses and their influence on host gene expression within a high-density *K. brevis* bloom off the western coast of Florida, collected over a 33-hour diel period. Our analyses uncovered 167 *Nucleocytoviricota* genomes, of which one falls within the same clade as *K. brevis* vOTU2 and twenty fall into the *K. brevis* vOTU6 clade. Previous work showed the vOTU6 NCLDV increased as *K. brevis* concentration increased in coastal Florida waters in 2021. With additional genomes, the vOTU6 clade represents a diverse viral population composed of nine subpopulations that share an average nucleotide identity of less than 75%. Whole genome alignments identified 45 shared genomic regions ranging in length from 1,600 to 23,000 base pairs located throughout the vOTU6 reference genome. Despite genomic differences, the presence of dinoflagellate viral nucleoprotein, carbonic anhydrase, and bacteriorhodopsin remain conserved in 16 of the newly sequenced genomes, providing continued evidence of their supportive role in *K. brevis* infection. The new vOTU6 phylotypes expand the genomic diversity represented by giant virus populations associated with *K. brevis*. Parallel metatranscriptomic analyses will provide insights into diel viral activity and the associated responses by *K. brevis* during a bloom's maintenance phase, increasing the understanding of giant virus influence on bloom dynamics.

Long-Amplicon Sequencing of Harmful Algal Bloom Formers

Paul D. Boudreau

University of Mississippi School of Pharmacy, Oxford, MS

Long-amplicon nanopore sequencing offers a promising new approach to harmful algal bloom monitoring by combining the low cost and rapid data generation of the nanopore platform with the specificity and sensitivity of targeted PCR amplification. Low-cost nanopore sequencing has revolutionized the study of organisms in their environment by allowing metagenomic sequencing of complex microbial communities. Though some advantages of older approaches, such as targeted PCR amplicon sequencing's ability to amplify limited substrate and target specific genes, have led to both techniques being used for harmful algal bloom monitoring. In this work, my lab has been developing PCR amplification methods to target long, >1.4 kb, amplicons from bloom formers. First, we mixed classical cyanobacterial 16S and 23S primers to produce ca. 4 kb ribosomal gene cluster amplicons that include the variable intergenic region. We view this as a compelling alternative to full-gene 16S sequencing because with nanopore sequencing, there is no need to limit the amplicon solely to the 16S gene. Then we developed primers targeting the microcystin toxin biosynthetic pathway. A key advantage of long-amplicon sequencing across the toxin biosynthetic gene cluster is that it can resolve between closely related pathways (e.g. microcystin and nodularin). While also holding the potential to detect changes indicative of evolutionary changes in these pathways. We intend to develop this approach of long amplicon sequencing as a new tool to monitor bloom formers in the environment. This will require effort to develop optimal template preparation, as well as the optimal primer pairings that minimize off-target amplification with environmental DNA samples.

Characterizing Harmful Algae and Phycotoxin Occurrences in San Francisco Bay, California

Keith Bouma-Gregson[1]*, Daniel Killam*[2]*, Katie Harding*[2]*, Timothy Otten*[3]*, Sean Jungbluth*[4]*, Raphael Kudela*[5]*, Zephyr Sylvester*[2]*, David Senn*[2]

[1]U.S. Geological Survey, California Water Science Center, Sacramento, CA, USA
[2]San Francisco Estuary Institute, Richmond, CA, USA
[3]Bend Genetics, Sacramento, CA, USA
[4]San Francisco State University, San Francisco, CA, USA
[5]University of California, Santa Cruz, CA, USA

Despite high nutrient inputs and concentrations, San Francisco Bay (SFB) has generally not experienced the severe or protracted water-quality impacts common to other nutrient-enriched estuaries, such as excessive phytoplankton blooms and low dissolved oxygen. However, there are concerns that resistance to eutrophication may be weakening and that harmful toxigenic phytoplankton may increase in the future. We analyzed phytoplankton, phycotoxin, and water quality data collected during 2015–2021 to characterize the spatial distribution and temporal trends of potentially harmful phytoplankton genera from multiple taxonomic groups identified in SFB. Preliminary analyses of the dataset found 23 genera in SFB that are on the International Oceanographic Commission Harmful Microalgae list, including *Alexandrium*, *Pseudo-nitzschia*, *Heterosigma*, and *Akashiwo*. Initial analyses of biweekly shellfish monitoring data for phycotoxins from 2015 through 2020 found that 63%, 53%, and 34% of mussel tissue samples contained microcystin, domoic acid, and saxitoxin, respectively. The frequency and magnitude of taxa and toxin detections varied among SFB subembayments. For example, saxitoxins and *Alexandrium* were detected most frequently in the central sub-embayment, near the mouth of SFB, consistent with the hypothesis that coastal ocean exchanges act as an important source of harmful algae in SFB. Additionally, seasonal abundances often varied among subembayments, suggesting spatially distinct populations of harmful algae within SFB. With the frequent occurrence of harmful algae and phycotoxins, these findings highlight that a deeper understanding of the response of phytoplankton communities in estuaries to global and regional change could help anticipate, prevent, and mitigate the degradation of aquatic ecosystems by harmful algae.

Aqusens: A Field-Deployable Holographic Imaging System for HAB Cell Detection

Holly A. Bowers[1]*, Maxim Batalin*[2]*, Kendra Negrey*[3]*, Raphael Kudela*[3]*, Alexis Pasulka*[4]*, Nicholas Soares*[4]*, Larkin Loewenherz*[1]*, Henry Ruhl*[5]*, Clarissa Anderson*[6]

[1]Moss Landing Marine Labs, Moss Landing, California, USA
[2]Lucendi, Inc., Los Angeles, California, USA
[3]University of California Santa Cruz, Santa Cruz, California, USA
[4]California Polytechnic State University, San Luis Obispo, California, USA
[5]Central & Northern California Ocean Observing System, Moss Landing, California, USA
[6]Southern California Coastal Ocean Observing System, La Jolla, 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 images 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 remotely and analyzes data in real-time. It 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 support of two CalHABMAP monitoring stations: Cal Poly Pier and the Santa Cruz Wharf (co-located with an IFCB). Other deployments include high throughput image generation for MBARI's Synchro test-bed program, underway operations in conjunction with an IFCB in San Francisco Bay (USGS cruises), and support of local citizen science (The Pacific Plankton Program). A host of classifiers are under development for various HAB species, with *Akashiwo sanguinea* serving as the inaugural test case. Pathways are being explored for image and data integration into processing pipelines with standardized metadata formats, long-term archival, and automated generation of management early-warning products.

Temporal Patterns in the Geographic Distribution of Dissolved Organic Nitrogen on the West Florida Shelf

Chelsie N. Bowman[1]*, Katherine A. Hubbard*[2]*, Kristen N. Buck*[3]*, Matthew J. Garrett*[2]*, Salvatore Caprara*[3]*, Angela N. Knapp*[1]

[1]Texas A&M University, College Station, Texas, United States
[2]Florida Fish and Wildlife Research Institute, St. Petersburg, Florida, United States
[3]Oregon State University, Corvallis, Oregon, United States

Despite persistently low inorganic nutrient concentrations, the West Florida Shelf (WFS) suffers from recurrent, often annual, blooms of the harmful alga *Karenia brevis* with cell concentrations of 10^5 to 10^6 cells/L or more. The concentrations of nitrate and nitrite ($[NO_3^-+NO_2^-]$) in samples from the inner and middle WFS (to the 20 and 50 m isobaths, respectively) are typically below the analytical detection limit of 0.05 μM. Dissolved organic nitrogen (DON) has been proposed as an alternative assimilative nitrogen source for *K. brevis* blooms, but data on its concentration on the WFS is minimal. Moreover, the short residence time of water in shelf environments is expected to lead to highly dynamic distributions of both inorganic and organic nutrients. Here we report surface and bottom water DON concentrations from three years of NOAA South Florida Ecosystem Restoration (SFER) cruises from June 2021 to November 2023. Surface and bottom water [DON] ranged from 3.0 to 29.4 μM. Concentrations were often highest near the mouths of bays and rivers on the west coast of Florida – near Charlotte Harbor, the Caloosahatchee River, and Florida Bay – and decreased westward across the inner and middle shelf. This pattern was common enough that for some cruises most of the variability in [DON] can be explained by simple two end-member mixing of margin sources and Loop Current/North Atlantic waters off the WFS using salinity as a conservative tracer. Several processes have been identified that cause data to fall off the mixing line for [DON] distribution: (1) additional sources of nutrients such as submarine ground water discharge, (2) additional sinks of nutrients such as DON consumption, and (3) salinity anomalies caused by excess precipitation or evaporation or the presence of river plumes.

Harmful Algal Blooms in the Great Lakes; NOAA's Support for their Detection, Management, and Prevention

Gregory L. Boyer

Department of Chemistry, State University of New York, College of Environmental Science and Forestry, Syracuse, NY 13210, USA

In 2000, Scott Brittain, Wayne Carmichael and colleagues published their report identifying the hepatotoxic microcystins in cyanobacteria collected from a bloom in Lake Erie. This seminar paper ushered in nearly thirty years of NOAA support for research on the harmful algal blooms in the Great Lakes region. Initial funding for the large regional project (MERHAB-Lower Great Lakes) in 2002 focused on better identifying the spatial distribution of toxic *Microcystis* in Lake Erie and Lake Ontario, as well as developing the essential tools, including mass spectrometry and molecular markers for microcystin biosynthesis, necessary to monitor for potentially toxic cells and toxin production. Since that initial effort, NOAA's Harmful Algal Bloom program has supported more than 14 projects and over 50 investigators in the Great Lakes region to determine how nutrients impact toxic bloom formation, the potential impact of a changing environment on these blooms, to evaluate and develop new tools to measure both existing and emerging toxins, to characterize the movement of these toxins through the food chain, and to look at mechanism to prevent their impact on the beneficial use of these important water bodies. This review will summarize some of the highlights and benefits to managers gained by this extensive body of research.

Remote Sensing Framework for Identifying Harmful Algal Bloom Hotspots in Managed River Systems

***Geneve Brady**, Brealynn Harper, John Moccio, Mindy Yeager-Armstead*

Marshall University, Huntington, West Virginia, USA

Large managed rivers are increasingly vulnerable to harmful algal blooms yet predicting where and when bloom-favorable conditions emerge remains difficult because riverine systems are spatially complex, temporally dynamic, and unevenly monitored. Traditional field sampling provides critical monitoring data, but it can be spatially and temporally limited by cost, labor, and access. Remote sensing offers an efficient and cost-effective complement by providing repeated, spatially continuous observations that can be automated to support routine monitoring across broad river reaches. The objective of this research is to use remote sensing to map algal and water quality patterns across large spatial areas and repeated time periods and to identify zones of high productivity and potential bloom initiation. High-resolution PlanetScope imagery, including eight-band SuperDove sensors with near-daily revisit capability, are used for the development and calibration of algorithms for estimating turbidity, chlorophyll-a, and phycocyanin. These satellite-derived metrics will be integrated into a hotspot framework to identify areas where bloom-favorable conditions are most likely to occur and inform HAB detection. In areas with limited in-situ data, the framework will rely on remote sensing, nearby monitoring stations, and transferable relationships among turbidity and algal indicators to support prediction. The resulting tools will support more reliable and cost-efficient monitoring while providing actionable information for community users, resource managers, and monitoring programs responding to harmful algal bloom threats.

Watershed-scale HAB Prevention Strategies for Lake Erie

Thomas Bridgeman[1], *Lauren Kinsman-Costello*[2], *Kenneth Anderson*[2], *Janice Kerns*[3]

[1]University of Toledo Lake Erie Center, Oregon Ohio, USA
[2]Kent State University, Kent, Ohio, USA
[3]Ohio Department of Natural Resources, Huron, Ohio, USA

The tremendous size (>500 mi^2) of HABs in western Lake Erie (WLE) places them beyond the scope of in-lake treatment technologies. Efforts to reduce blooms in WLE therefore focus on reducing nutrient loads to the lake, especially from the highly-agricultural Maumee River watershed. Because ¾ of this watershed is in Ohio, the state has invested heavily in reducing HABs through its H2Ohio program which seeks to reduce nutrient loadings to lake tributaries through agricultural best management practices (~2.2 million acres), land conservation (~137,000 acres), Wetland restoration (~20,000 acres), and other initiatives. Wetlands are especially effective in filtering nutrients on a per acre basis, but restored wetland acreage represents <1% of agricultural acreage. Since 2020, the approximately $680M invested in H2Ohio water quality projects has resulted in only a modest decrease in flow-weighted phosphorus loading to Lake Erie, indicating that further scaling-up of water quality projects will be necessary to achieve significant HAB reduction or prevention. In addition to watershed efforts, however, in-lake measures also have the potential to reduce Lake Erie HABs. In concept, physical structures placed to promote mixing between the nutrient-rich Maumee River plume and the nutrient-poor Detroit River plume could reduce average nutrient concentrations in WLE below levels that promote HAB formation. Preliminary hydrodynamic modeling studies suggest that in-lake mixing and dilution strategies are possible, but further research is needed to validate and refine the concept. A future vision of western Lake Erie includes both expanded watershed efforts and new in-lake improvements to produce reduced nutrient loads that are diluted and distributed more evenly in the lake to greatly reduce or prevent HABs while maintaining beneficial algal production and world-class fisheries.

The Three P's of Mixotrophy: Phosphorus, Phagotrophy, and Prey Selection in *Karlodinium veneficum*

Erik L. J. E. Broemsen[1,2]*, Allyson N. Underhill*[1,2] *Felipe M. Quintana*[1,2]*, Bryndan P. Durham*[1,2]

[1]Department of Biology, University of Florida, Gainesville, Florida, USA
[2]Genetics Institute, University of Florida, Gainesville, Florida, USA

The mixotrophic dinoflagellate *Karlodinium veneficum* occurs in estuaries worldwide where it can form toxic fish-killing blooms. Regulation of feeding in *K. veneficum* has largely been linked to inorganic nutrient limitation. However, laboratory observations have shown that feeding rates vary with prey nutritional quality (i.e. N:P ratio), suggesting a selective mechanism is present. In the Chesapeake Bay, populations often co-occur with cryptophyte microalgae, a preferred prey taxa, and field studies indicate that blooms of *K. veneficum* often follow and are likely initiated by cryptophyte blooms through mixotrophic consumption. We posit that prey-derived dissolved organic phosphorus compounds may act as indicators to reflect the nutritional condition of prey, ultimately triggering mixotrophic feeding and facilitating bloom initiation. Here we demonstrate the ability of *K. veneficum* to readily utilize organic phosphorus by comparing autotrophic growth on either PO_4 or various organic phosphorus compounds as sole phosphorus sources. We demonstrate mixotrophic feeding rates to correlate positively with the ratio of organic: inorganic phosphorus under phosphorus-replete conditions, and we test the concentration-effect of organic phosphorus on feeding rates. To further investigate the role of these compounds in prey detection/selection, we determine the chemotactic response of *K. veneficum* towards organic phosphorus. We explore inorganic phosphorus as an inhibitor of phagotrophic behavior and dissolved organic phosphorus as a potential signal of prey availability, with both as potential regulators on the balance of autotrophy and mixotrophy in natural populations.

HABON-NE: Advancing HAB Science and Management in a Changing Coastal Ocean

Michael Brosnahan[1], *Donald Anderson*[1], *Gregory Doucette (retired)*[2], *Katherine Hubbard*[3], *Bruce Keafer*[1], *Mindy Richlen*[1], *Collin Roesler*[4], *Aleck Wang*[1], *Jake Kritzer*[5], *Dennis McGillicuddy*[1], *Christina Mikulski*[2], *Juliette Smith*[6], *Robert Olson*[1], *Heidi Sosik*[1], *Daniel Ward*[7], *Mrunmayee Pathare*[1], *Serena Sung-Clarke*[1], *Michael Staiger*[1], *Vanessa Haggans*[1], *Ethan Andrews*[1], *Ryan Govostes*[1], *Nathan Figueroa*[1], *Cristian Swift*[1], *Nour Ayache*[8], *David Beaudoin*[1]

[1]Woods Hole Oceanographic Institution, Woods Hole, MA, USA
[2]NOAA National Ocean Service, Charleston, SC, USA
[3]Florida Fish and Wildlife Conservation Commission-Fish and Wildlife Research Institute, St. Petersburg, FL, USA
[4]Bowdoin College, Brunswick, ME, USA
[5]Northeast Regional Association of Coastal Ocean Observing Systems, Portsmouth, NH, USA
[6]Virginia Institute of Marine Science, Gloucester, VA, USA
[7]Ward Aquafarms, Falmouth, MA, USA
[8]French Research Institute for Exploitation of the Sea, IFREMER, Nouméa, New Caledonia (FR)

Over the past three decades, ECOHAB and MERHAB investments have transformed understanding of harmful algal bloom (HAB) dynamics in the Gulf of Maine while also driving development of new observing technologies that record these events in unprecedented detail. Increasingly, advances in HAB science and HAB management are inseparable: the same automated observing systems that protect public health and fisheries resources are also reshaping understanding of bloom ecology, transport, life-history dynamics, and ecosystem response to environmental change.

Expanded HAB observing has become increasingly urgent as climate change, coastal development, and shifting circulation patterns alter established seasonal and biogeographic patterns of HAB occurrence and impact. Blooms are emerging in new locations, starting earlier, persisting longer, and increasingly involving multiple toxin syndromes. These changes pose growing risks to public health and coastal economies while challenging assumptions about environmental controls governing bloom initiation, transport, persistence, and toxicity. Addressing these questions requires observations with substantially greater temporal, spatial, and biological resolution than can be achieved through traditional survey methods.

This presentation highlights HABON-NE and related efforts to establish coordinated networks of automated biological sensors and adaptive observing platforms across the northeast U.S. Sustained observations from these systems have revealed ecological behaviors and bloom dynamics that were previously hidden from conventional observing approaches, including previously unrecognized links between life-cycle dynamics and bloom persistence, as well as major disconnects between organism behavior in situ and in laboratory culture. Through high-frequency, near-continuous sampling, these systems are substantially advancing mechanistic understanding of how HAB species and plankton communities respond to environmental variability and long-term ecosystem change. Continued progress will require sustained investment in observing infrastructure, mobile sensing, open data systems, and regional coordination capable of resolving rapidly changing HAB dynamics across interconnected coastal ecosystems.

Understanding Ecosystem-scale Impacts of Sargassum Inundation Events to Guide Coastal Research and Management

Max Brown[1]*, Felipe Arzayus*[2]*, Rachel Brewton*[3]*, William J. Hernández*[4]*, Clifford Louime*[5]*, Brigitta Van Tussenbroek*[6]*, Mya Garrison*[7]

[1]CSS Inc. under contract to NOAA National Centers for Coastal Ocean Science, Silver Spring, MD, USA
[2]NOAA National Centers for Coastal Ocean Science, Silver Spring, MD, USA
[3]Florida Atlantic University, Boca Raton, FL, USA
[4]Environmental Mapping Consultants LLC, Mayagüez, Puerto Rico
[5]University of Puerto Rico Río Piedras, San Juan, Puerto Rico
[6]National Autonomous University of Mexico, Mexico City, Mexico
[7]University of Miami, Coral Gables, FL, USA

This presentation synthesizes the consequences of large-scale *Sargassum* strandings on the natural environment to establish a comprehensive state of the science to support coordinated management strategies. As part of a NOAA-lead workshop held in May 2025 this effort focuses on identifying critical knowledge gaps to inform a federal research strategy addressing the negative effects of *Sargassum*. While the immediate effects of *Sargassum* inundation events (SIEs) on coastal and nearshore zones are partially understood, their long-term and broad-scale impacts remain largely uncharacterized. SIEs are the accumulation of large mats of *Sargassum* on or along a coastline due wind and current transport. These landing events are natural phenomena, however since 2011 large and more frequent SIEs are commonplace in the Caribbean and the Gulf. These events have transformed a vital habitat for juvenile fish, sea turtles, and migratory birds into a recurring coastal hazard, with significant negative consequences for the natural environment. SIEs physically change benthic ecosystems by smothering coastal habitats -- leading to light attenuation, altered sediment transfer, and shifts in tidal dynamics. Resulting oxygen depletion, eutrophication, and acidification; contaminant transfer (heavy metals, PCBs, PAHs etc), and decay (releasing H_2S, CH_4) have also been documented. These changes have acute impacts on flora and fauna, but it is unclear when or how cascading and interconnected effects may lead to ecosystem shifts and potential regime changes. A research strategy contributing to a mechanistic understanding of the linkages between *Sargassum* biomass and residence time on overall ecosystem health in different systems (coral reefs, seagrass meadows, mangrove forests, beach-dune systems) can bridge the gap between monitoring and management efforts, helping guide coastal stakeholders decide when and where intervention and mitigation efforts are needed.

Trace Metal Micronutrients over the West Florida Shelf and in *Karenia brevis*

Kristen N. Buck[1,2]*, Delfina Navarro-Estrada*[2]*, Salvatore Caprara*[1]*, R. Ben Freiberger*[1]*, Yida Gao*[3,4]*, Eric Muhlbach*[3]*, Julie Koester*[3]*, Matt Garrett*[3]*, Katherine Hubbard*[3]

[1]Oregon State University, Corvallis, OR, USA
[2]University of South Florida, St. Petersburg, FL, USA
[3]Florida Fish and Wildlife Research Institute (FWC-FWRI), St. Petersburg, FL, USA
[4]Woods Hole Oceanographic Institution, Woods Hole, MA, USA

Trace metals serve as important micronutrients for phytoplankton and marine microorganisms. Here we present results from a multi-year survey of dissolved (<0.2 µm filtered) and total dissolvable (unfiltered) concentrations of the trace metals manganese (Mn), iron (Fe), cobalt (Co), nickel (Ni), copper (Cu), zinc (Zn), cadmium (Cd), and lead (Pb) in surface waters over the West Florida Shelf. We also leverage field and experimental studies to explore trace metal incorporation in communities of the harmful algal species *Karenia brevis*. Results highlight drivers of inshore-offshore gradients in trace metal concentrations across the shelf and changes in dissolved and particulate trace metal distributions during local *K. brevis* blooms. Altogether, these results provide insights into trace metal sources, sinks, and biogeochemical cycling on the West Florida Shelf, and potential roles of these trace metals in regional harmful algal blooms.

Brevetoxins and Emergency Department Visits among Children: A Case-Crossover Study of Florida Red Tides

Erik M. Rizzo[1]; Bianca I. Dowling[1]; Ananya Ranganagoudar[2], Justin K. Arnold[3,4,5]; Barbara Kirkpatrick[6]; ***Catherine M. Bulka[1]***

[1] Department of Epidemiology, College of Public Health, University of South Florida, Tampa, FL
[2] Judy Genshaft Honors College, University of South Florida, Tampa, FL
[3] Department of Emergency Medicine, College of Medicine, University of South Florida, Tampa, FL
[4] Florida Poison Information Center, Tampa, FL
[5] Tampa General Hospital, Tampa, FL
[6] Gulf of America Coastal Ocean Observing System (GCOOS), Department of Oceanography, Texas A&M University, College Station, TX

Blooms of the harmful alga *K. brevis* produce brevetoxins that contaminate seawater and aerosolize, exposing humans via ingestion and inhalation. While adult exposures are linked to respiratory and gastrointestinal illness, children—who may be more vulnerable—remain understudied. We investigated whether short-term brevetoxin exposures trigger pediatric emergency department (ED) visits.

We analyzed ED visits for coastal southwest Florida residents aged 0–18 years in the OneFlorida+ Clinical Research Network (2012–2019) using a time-stratified case-crossover design. Two brevetoxin exposure indices were estimated for the 14 days before each visit: (1) waterborne, based on spatially interpolated *K. brevis* concentrations linked to residential ZIP codes, and (2) aerosolized, further incorporating wind speed and direction. Conditional logistic regression estimated odds ratios per interquartile range increase in exposure, adjusting for federal holidays, heat index, ozone, and PM2.5. Models were stratified by diagnosis; a negative control group (trauma) assessed confounding.

Overall associations with ED visits were null, as were associations in the negative control group. However, stratified models revealed diagnosis-specific effects. Same-day increases in both indices were associated with ~50% higher odds of respiratory visits (n=216). Waterborne exposures 12–13 days prior were modestly associated with ear, nose, throat, dental, and mouth diseases (n=321). Aerosolized exposures 6–9 days prior were associated with ~50% higher odds of eye diseases (n=53).

Brevetoxins from *K. brevis* blooms may trigger pediatric ED visits for respiratory, ocular, and ear–nose–throat complaints in coastal southwest Florida. As blooms intensify, these results underscore the need for public health guidance tailored to children.

First Report of Anabaenopeptins in New York Finger Lakes: Translating Untargeted HRMS into Routine Monitoring

Alexander Levine[1], ***Gabriel T. Bullis***[1], *Zac Triumph*[1], *Nicholas C. Pflug*[1], *Gregory L. Boyer*[1]

State University of New York College of Environmental Science and Forestry (SUNY ESF), Syracuse, NY, United States

Harmful algal blooms have become a persistent problem in the New York Finger Lakes. Fluidity of site conditions and algal species lead to highly variable toxin types and levels, and some toxin classes are being increasingly reported in the Great Lakes. Anabaenopeptins (APs) are a class of hepatotoxic cyclic peptides that share many characteristics with the more studied microcystins (MCs) including extreme structural variability and disparate toxicity based on congener. APs are increasingly being reported in blooms in the great lakes including Lake Erie and Lake Michigan, often alongside MCs, and APs have recently been shown to have synergistic toxic effects with MCs. APs have much more potential for structural diversity than MCs, but far fewer congeners have been identified. These recent developments in the field highlight the urgency in expanding routine monitoring techniques to include APs as well as documenting which congeners are common in new and historic blooms in the Finger Lakes. Here, we use untargeted high resolution mass spectrometry (UPLC-MS/Orbitrap) to identify known and potentially novel APs. This is the first report of APs in the Finger Lakes. Previous studies have used HRMS for this purpose, but we seek to expedite classification and standardize the identification process for APs. Using relative retention times, m/z ratios, and diagnostic UV spectra, we lay a framework for incorporation of these APs into existing analytical methods targeting MCs that use different columns and less sophisticated detectors for high-throughput routine monitoring. Overall, this work provides a bird's eye view of APs in Upstate New York and demonstrates the need for more research on and monitoring of APs in the Finger Lakes and beyond.

Bridging the Benthic Gap: Sediment and Groundwater Nutrient Fluxes on the West Florida Shelf

Emma J. Bullock[1]*, Emily R. Hall*[1]*, James K. Culter*[1]*, Bruce E. Kurtz*[2]*, James E. Landmeyer*[3]

[1] Mote Marine Laboratory, Sarasota, FL, USA
[2] New College of Florida, Sarasota, FL, USA
[3] U. S. Geological Survey, Lutz, FL, USA

This study investigates the influence of submarine groundwater discharge and sediment nutrient fluxes from the southern West Florida Shelf to determine their importance for harmful algal blooms in the region. Despite the recognized importance of sediments and groundwater in nutrient cycling, the heterogeneous nature of benthic fluxes makes it challenging to quantify their significance for harmful algal blooms. To facilitate better understanding of how diverse benthic environments on the West Florida Shelf contribute to nutrient fluxes, this study combines large-scale integrative methods, including radium isotopes and water column chemistry surveys, with traditional sediment core incubations. This study also investigates the importance of localized inputs from seafloor features. Submerged springs and sinkholes on the West Florida Shelf, known as blue holes, may expose breaks in geological confining layers and facilitate groundwater discharge. Given the potential significance of these seafloor anomalies to overall benthic fluxes, a monthly time series was conducted at a representative blue hole, complementing the seasonal shelf surveys. Together, these methods allow for a better understanding of how significant groundwater and sediment contributions of nutrients are for bloom formation and maintenance on the southern West Florida Shelf and whether localized inputs or diffuse, large-scale processes are more impactful.

Aqua-Bot: Removal of Cyanobacteria using an Aquastream Algae Skimmer Bot

***Devin Burris*[1], *Erik Heidt*[2], *Cynthia Heill*[1], *William Scott*[1], *Dominic DeMarco*[1], *Jennifer Toyoda*[1]**

[1]Mote Marine Laboratory, Sarasota, Florida USA
[2]Innovation Heights, Inc., Sarasota, Florida USA

Microcystis aeruginosa poses a significant threat to aquatic ecosystems, wildlife, and drinking water supplies due to its toxin production and influence on water quality. Current mitigation strategies often rely on chemical compounds which introduce additional compounds into water bodies, may not be effective against toxins and may have unintended ecological impacts. Alternatively, physical controls, though challenging in open systems such as oceans, may be better suited for closed or semi-closed water bodies. Closed or semi-closed water bodies, such as lakes, provide an advantage for strategies as they experience reduced influence from wind and wave action, which allows for a more controlled and targeted removal. In this study, we present the development and evaluation of the Aqua-Bot, a semi-autonomous prototype designed to physically remove cells of *M. aeruginosa*. The Aqua-Bot operates using a conveyor mechanism coupled with an adjustable intake platform, to lift the algal cells from the water surface and transfer it through a hose into a storage reservoir. Various prototypes were constructed and tested to assess removal efficiency over a range of cell concentrations and environments, as well as associated toxins. Removal of moderate cell concentrations (5×10^9 cells L^{-1}) of cultured *M. aeruginosa* occurred at a rate of 142.99 ($\pm$4.25) mg L^{-1} h^{-1} in 1,400 L controlled raceway mesocosms. Results presented here demonstrate the potential of a scalable physical mitigation control, as well as the unique methodological challenges that come with cyanobacterial removal.

Advancing Harmful Algal Bloom (HAB) Management Through Digital Innovation

Ibrahim Busari, *Kendall Kirk, Heather Nix, John Hains, Franklin Ott McAlhany III, Debabrata Sahoo*
Clemson University, Clemson, SC, USA

Harmful algal blooms (HABs) in lentic systems negatively impact pets, livestock, wildlife, humans, and the ecosystem. Their early identification could likely aid in reducing their detrimental impacts on water quality, aquatic life, recreational values, and overall ecosystem health. Increased nutrient loading and changing weather patterns are driving an increase in aquatic weeds and planktonic growth, leading to more phone calls, and requests for Extension agents by pond owners and livestock farmers who need help identifying aquatic plant growth in their ponds to initiate effective management actions. Currently, pond owners and agents send pond samples to a lab for HAB identification, which requires transport that can make the process lengthy. We believe digital tools have a critical role to play in this sphere. We are developing a web-application that would accelerate a preliminary HAB identification and streamline the confirmation processes for common genera such as Microcystis, Dolichospermum, Cylindrospermopsis, Aphanizomenon, and Lyngbya. The web-app will include common HAB genera to assist Extension agents and their clients with identification. Upon completion of the development of the application, several training sessions will be conducted across different platforms for different stakeholders to instruct the applicability of the tool. This presentation will highlight the process behind the development of the web-app and explain how the tool works. We believe that the tool will be a valuable resource for the users, shortening the HAB identification process, thereby supporting the efforts to minimize damage and efficiently manage HAB.

Empirical Dynamic Modeling Approach to Investigate Chlorophyll-a Timeseries as an Indicator of Harmful Algal Blooms

Ibrahim Busari, *Debabrata Sahoo*
Clemson University, Clemson, SC, USA

Chlorophyll-a concentration in lakes and ponds has long been used to monitor harmful algal blooms (HABs). However, forecasting and interpreting Chlorophyll-a concentrations is challenging because growth depends on numerous complex and changing environmental factors. This study used empirical dynamic modeling to uncover the presence and degree of chaotic dynamics in chlorophyll-a concentration data observed during 2015–2021 in Boyd Millpond, an upstate lake in South Carolina, USA. We applied the phase space reconstruction, average mutual information, false nearest neighbor algorithm and nonlinear prediction of chlorophyll-a for the entire time series. We found evidence of chaotic behavior throughout the entire series, as well as in some individual years, suggesting that algal dynamics vary in complex and unpredictable ways. This suggests that HABs management action may need to be flexible and responsive rather than relying on fixed seasonal expectations. By understanding the complexity in the chlorophyll-a time series, bloom events can be predicted accurately to promote effective implementation of targeted interventions, reducing ecological and economic impacts and enhancing the resilience of aquatic ecosystems.

Sediment Conditions May Support Unexpected Benthic Cyanobacteria Bloom Formation

***John Buster**, Sarah Roley*

School of the Environment, Washington State University, Richland, WA, USA

Benthic cyanobacteria blooms (cyanoHABs) have become more common in systems with low surface water nutrient concentrations. Because benthic cyanobacteria grow on top of sediments, we hypothesized that sediment phosphorus (P) release was the primary P source for benthic cyanoHAB formation and that higher temperatures accelerate P release, leading to this contemporary phenomenon. We tested our hypothesis in the Hanford Reach of the Columbia River, where recent benthic cyanoHABs killed dogs and sickened humans. We collected surface water and porewater from several sites. Surface water P concentrations were generally low (mean = 0.018 mgP/L, range = below detection to 0.125 mgP/L), with pore water P concentrations generally higher (mean = 0.484 mgP/L, range = 0.012 to 4.943 mgP/L). We calculated diffusive flux and found that P flux to surface water ranged from 0.71 to 339 mg P m^{-2} d^{-1}. Based on the Redfield ratio, we calculated the hypothetical algal biomass that could be supported by porewater P diffusing into the benthos. It ranged from 0.03 to 13.55 g m^{-2} d^{-1}, likely sufficient to support cyanobacteria blooms. We used P fractionation to identify potential P sources. Releasable P fractions varied by site, but, in general, pH-sensitive and organically bound P dominated (redox-sensitive range = 8% to 28%, pH-sensitive range = 31% - 65%, organically bound range = 18% - 61%). These fractions will potentially release more P with higher temperatures. Microbial decomposition rates increase with temperature, releasing P from the organic fraction, while also decreasing oxygen concentration and causing P release from the redox-sensitive fraction. Photosynthesis increases daytime pH, which causes P desorption from pH-sensitive pools. Our findings suggest that surface water eutrophication may not be necessary to fuel benthic cyanoHABs; their formation might, instead, depend on internal loading of P from sediments, accelerated by increasing global temperatures.

Comparative Genomics of *Pseudo-nitzschia* Genomes Reveals a Wide Diversity of Endogenized Viral Elements

Petra Byl *[1,4], Zoltán Füssy[2,3], Steffaney M. Wood-Rocca[2], Monica Thukral[2], Frederik Schulz[4], Andrew E. Allen[2,3], and Joaquín Martínez Martínez[1]*

[1]University of Maryland Center for Environmental Sciences, Horn Point Laboratory, Cambridge, MD
[2]Scripps Institution of Oceanography, University of California, San Diego, La Jolla, CA
[3]J Craig Venter Institute, La Jolla, CA
[4]US DOE Joint Genome Institute, Berkeley, CA

The widespread diatom genus *Pseudo-nitzschia* includes bloom-forming and toxin-producing species. Blooms of toxigenic species cause severe wildlife fatalities and economic losses for fisheries. Viral lysis acts as a competing top-down control of phytoplankton, including *Pseudo-nitzschia*. Beyond lytic infections, host genomes can carry complete or fragmented viral genomes, *i.e*. endogenized viral elements (EVEs), which can be transcriptionally active and potentially confer beneficial or detrimental traits to their host. EVEs are mainly retroviral, but the role of non-retroviral RNA and DNA viruses is increasingly recognized in algal protist evolution. In microalgae, EVEs from dsDNA giant viruses in the phylum *Nucleocytoviricota* can expand their host's functional repertoire of stress response proteins. Due to the diversity of potential EVEs in algal protists, we leveraged five bioinformatic tools to screen 10 near-complete genomes of *Pseudo-nitzschia*, representative of seven species, five of which are reported to be toxigenic, for virus endogenization. Half of the *Pseudo-nitzschia* representatives contained ssDNA EVEs and three had ssRNA EVEs. All ten *Pseudo-nitzschia* representatives encoded homologs of the *Nucleocytoviricota* marker gene, DNA-directed RNA polymerase beta subunit (RNAPs) (E-value < 1×10^{-11}), identified by Hidden Markov Model-based analyses in two software tools. Additionally, three *Pseudo-nitzschia* representatives encoded homologs of the Poxvirus Late Transcription Factor 3 (VLTF3) (E-value < 1×10^{-6}). The copy number of these *Nucleocytoviricota* annotations varied depending on the stringency of the bioinformatic tool, but across both tools *P. arenysensis* and *P. hasleana* had the highest number of *Nucleocytoviricota* EVE predictions, and *P. hasleana* had the widest diversity of EVE predictions including ssRNA virus phylum *Kitrinoviricota*. These diverse viral footprints broaden our understanding of *Pseudo-nitzschia*-virus interactions, which is currently limited to lytic infections of ssDNA and ssRNA viruses, and underscore the importance of developing research workflows to detect viruses with different nucleic acid types for insight into virus-host co-evolution.

Genomic Approaches to Understanding HABs roles on Pacific Oyster's Mortalities in the US Pacific Coast

Bernarda Calla[1,2]*, Darren deSilva*[2]*, Alexander Langley* [2]

[1]USDA-ARS Pacific Shellfish Research Unit, Newport, Oregon, USA
[2]Oregon State University, Coastal Marine Experimental Station, Oregon, USA

The value of the Pacific oysters (*Magallana gigas,* a.k.a. *Crassostrea gigas*) industry in the U.S. has been estimated at 149-million-dollars in 2023 (National Agricultural Statistics Service). Mass oyster mortality events, associated with complex and yet unclear environmental factors including higher summer temperatures, have resulted in heavy yearly losses and continue to threaten this important aquaculture product. Current and historical datasets point at a strong correlation between HABs occurrence and Pacific oyster mortality by secondary factors including viral and bacterial diseases; but this indirect causality has not been confirmed.

Some of the most prevalent HAB species in the Northern hemisphere belong to the *Alexandrium* genus. Several species within this genus can produce and secrete saxitoxin, a potent neurotoxin responsible for Paralytic Shellfish Poisoning (PSP) in humans, fish, and birds. Saxitoxin and its derivatives might affect several physiological and behavioral processes in Pacific oysters with very high variability in toxin accumulation in tissues. Currently, little is known about saxitoxin effects on Pacific oysters' susceptibility to mortality.

To better understand how HABs and their toxins influence immunity and defense response mechanisms in Pacific oysters, we are using transcriptomics to study the molecular and physiological effects of exposure to a toxic *Alexandrium* sp. isolated in the Pacific Northwest. RNA was isolated from exposed oysters and whole-body tissues were sampled to quantify saxitoxin levels. In addition, oysters exposed to saxitoxin will be challenged with *Vibrio aestuarianus*, a pathogenic bacteria found on dying oysters to assess oyster differential susceptibility. Preliminary results from these experiments will be presented.

Microcystins in Maine Lakes: LC-MS/MS and eDNA Monitoring Approaches

Brigid Carr[1]*, Claire Thompson*[2]*, Brooke Robbins*[3]*, Robin Sleith*[1]*, Peter Countway*[1]*, Stephen D Archer*[1]

[1]Bigelow Laboratory for Ocean Sciences, East Boothbay, Maine, USA
[2]St. Mary's College of Maryland, St Mary's City, Maryland, USA
[3]University of Nebraska-Lincoln, Nebraska, USA

Microcystin monitoring can be a challenge, with cost and infrastructure hurdles limiting monitoring efforts. The gold standard for microcystin quantification is liquid chromatography triple quadrupole mass spectrometry (LC-MS/MS), however this approach is often unable to keep up with the growing need for quick and low-cost measurements. This research aims to expand access to microcystin monitoring by validating alternative approaches such as the use of eDNA targeting toxin biosynthesis pathways. Water samples from several lakes in Maine were analyzed using both LC-MS/MS and eDNA approaches in order to compare and validate the use of eDNA as part of the microcystin monitoring toolkit. Preliminary data indicates that eDNA could be used for routine monitoring, and once eDNA indicates a bloom then LC-MS/MS or another recognized analytical approach should be used to confirm microcystin levels.

Toxicokinetic and Physiological Alterations in Blue Crabs Exposed to Domoic Acid and Okadaic Acid

***Isabelle Castro**, Marta P. Sanderson, Juliette L. Smith*

William & Mary's Batten School of Coastal and Marine Science at Virginia Institute of Marine Science, Gloucester Point, VA, United States of America.

Blue crabs, *Callinectes sapidus*, are a valuable fishery across the Mid-Atlantic. As omnivorous scavengers, blue crabs are innately at risk of consuming phycotoxins through their diet, and therefore, may be a possible vector of these toxins to higher trophic level organisms including humans. Domoic acid and okadaic acid are present and of growing concern in the region. To test sublethal stress and toxin distribution patterns in blue crabs following oral exposure, two experiments were conducted. The first, a dose response experiment in which crabs were fed ascending doses of either okadaic acid or domoic acid, sacrificed 24 hours later, and hepatopancreas dissected for antioxidant biomarker analyses. Domoic acid and okadaic acid provided a dose-response increase in total superoxide dismutase activity in hepatopancreas tissue. A second experiment was conducted in which crabs were fed an oral dose of okadaic acid, domoic acid or both toxins, with sacrificial sampling (n=6) at 24, 48, 72, and 96hr. Hepatopancreas, gill, and muscle tissues were analyzed using UPLC-MS/MS to establish toxicokinetic profiles. Overall, there was less of each toxin in muscle and hepatopancreas tissues in crabs that were co-exposed to domoic acid and okadaic acid, relative to crabs exposed to either toxin alone. Across treatments, domoic acid was found to be accumulating during the initial 72-hours at a rate of 156.6 ng toxin g tissue^{-1} day^{-1}. By 24 hours, free okadaic acid was slowly depurating or bio-transforming in the hepatopancreas at a rate of 2.34 ng toxin g tissue^{-1} day^{-1}. Total okadaic acid equivalents were increasing in crabs exposed to only okadaic acid (15.20 ng toxin g tissue^{-1} day^{-1}) but remained nearly unchanged across time in co-exposed crabs. This study addresses foundational toxicokinetic and physiological data necessary to assess whether current blue crab harvest practices adequately protect blue crab and public health when blooms occur.

Strategies for Detecting Harmful Algal Blooms and Paralytic Shellfish Toxins in Alaska's Mariculture Industry

Rebecca Cates[1]*, Jordan Hollarmsith*[1]*, Spencer Lunda*[3]

[1]NOAA Alaska Fisheries Science Center, Juneau, Alaska, USA
[2]Alaska Sea Grant, Juneau, Alaska, USA

Harmful algal blooms of *Alexandrium catenella* are an extreme public health concern for people who consume shellfish and can lead to lengthy and costly shutdowns of Pacific oyster farms in Alaska due to the risk of paralytic shellfish poisoning. Often, oyster farmers become aware of a bloom only when a tissue sample is identified as containing unsafe levels of paralytic shellfish toxins (PSTs) in the Alaska Department of Environmental Conservation (DEC) lab, thereby shutting down commercial harvest on the farm until samples are identified as not toxic over multiple sampling events. This current approach is economically costly and could preclude industry expansion, especially as climate change may increase the temporal and spatial variability of blooms. While the DEC lab currently uses the mouse bioassay to test commercial sales of Pacific oysters, other methods could be used to assess risk and modify farm practices. We reviewed multiple approaches to managing or identifying elevated risk of PSTs for shellfish farmers including net tows and microscopy, rapid field tests, depuration chambers, and co-culture with seaweed. Establishing monitoring and mitigation methods allows farmers to make more informed choices about when to harvest and provides critical advancements for the mariculture industry in Alaska.

Capacity Building and Data Generation by Alaskan Tribal Efforts

Shannon Cellan[1]*, Esther Kennedy*[2]*, John Harley*[2]*, Nicole Filipek*[1]*, Matteo Masotti*[1]*,*

[1]Sitka Tribe of Alaska, Sitka, AK, USA
[2]University of Alaska Southeast, Alaska Coastal Rainforest Center, Juneau, AK, USA

Southeast Alaska, known for its many islands and vast coastline, has long been susceptible to HAB events. Paralytic shellfish toxins (PSTs) are a growing concern across the state and PSP fatalities are in recent memory for many. While toxin testing efforts across the state have grown, so have concerns that changing ocean conditions are increasing the risk of HAB events and shellfish poisonings. The Sitka Tribe of Alaska (STA) Environmental Research Laboratory is trying to better understand these concerns from the perspective of Indigenous science, which takes many lifetimes to gather, while observing these rapidly changing scenarios through the lens of laboratory-based analysis. Implementing shellfish toxin testing methodologies in Sitka has provided clear benefits to the region, but it is not without challenges. Individuals and tribal partners utilize critical toxin information to make informed decisions about harvesting and shellfish consumption. STA supports both “harvest and hold” and community shellfish testing to inform harvesters about active PST risks in shellfish, while also engaging in significant competitive and novel research with university, nonprofit and government partners. STA hopes to showcase just some of the work that tribes and tribal programs can do when provided equity and access in research spaces. Although STA is a federally recognized government working to advance the health and safety of its Tribal citizens, research funds are exclusively acquired through competitive granting agencies, creating challenges in program expansion; a challenge also faced by many other tribal efforts happening in the state. Despite these challenges, STA’s community collaborations, PST testing, and research objectives continue to grow, demonstrating the capacity and strength of Tribally led programs.

Anabaenopeptins and Microcystins in Lake Erie

Justin D. Chaffin[1]*, Judy Westrick*[2]*, Thomas Bridgeman*[3]

[1]The Ohio State University, Put-in-Bay, Ohio, USA
[2]Wayne State University, Detroit, Michigan, USA
[3]The University of Toledo, Toledo, Ohio, USA

Lake Erie cyanobacterial bloom research and advisory limits have focused on microcystins. However, with recent detections of non-microcystin toxins, researchers are beginning to investigate other bioactive peptides produced by cyanobacteria. One such group of peptides are the anabaenopeptins. We conducted a two-year investigation into anabaenopeptins in the western basin of Lake Erie during the 2024 and 2025 bloom season and compared anabaenopeptins to microcystins. We analyzed 163 samples for anabaenopeptins collected weekly to biweekly (June through mid-October) from waters near the Maumee River to the Bass Islands. Anabaenopeptins were detected before microcystins, and anabaenopeptins' peak concentrations were four times higher than microcystins. Anabaenopeptins were primarily in the cellular phase. Collectively, these suggest that anabaenopeptins can serve as an early warning for microcystins, and that removing intact cells is the best approach for water treatment. The congener anabaenopeptin-F accounted for more than 80% of all anabaenopeptins; therefore, previous studies that did not include anabaenopeptin-F could have drawn misleading conclusions. In five incubation experiments conducted throughout early to late bloom, anabaenopeptins concentrations were not affected by enrichments of phosphorus and/or nitrogen. However, in the same experiments, the highest cyanobacterial biomass and microcystin concentrations occurred in treatments with phosphorus and nitrogen enrichment, suggesting that the environmental trigger for microcystins and anabaenopeptins differs. Further research and monitoring of the anabaenopeptins are needed.

Shifting Bloom Biomass in Sandusky Bay, Lake Erie: Lessons Learned in a Shallow Hypereutrophic Lacustuary

Gillian Champoir, *Margaret Rettig, Ryan Wagner, Christopher Ward, Riley Ralph, Michelle Neudeck, Kate Brown, and George Bullerjahn*

Biological Sciences, Bowling Green State University, Bowling Green OH, USA

Sandusky Bay is the drowned mouth of the Sandusky River in the southwestern portion of Lake Erie. The bay is a popular recreation location and a regional source for drinking water. Like the western basin of Lake Erie, Sandusky Bay is known for being host to summer cyanobacterial harmful algal blooms (cHABs) year after year, fueled by runoff from the predominantly agricultural watershed and internal loading of legacy nutrients (primarily phosphorus). Since at least 2003, Sandusky Bay has harbored a microcystin-producing bloom of *Planktothrix agardhii,* a species of filamentous cyanobacteria that thrives in low light conditions. Long-term sampling (2003 – 2018) of Sandusky Bay revealed regular *Planktothrix*-dominated blooms during the summer months, but in recent years (2019-2024), 16S rRNA gene community profiling revealed that *Planktothrix* has largely disappeared. From 2017-2024, microcystin decreased well below WHO guidelines, yet there were no statistically different shifts in water temperature. With the exception of the high bloom of *Planktothrix* in 2018, there was no statistical difference in chlorophyll during all other years. The only significant change in water chemistry was a decline in total phosphorus post 2019 to the present. Concurrent with disappearance of *Planktothrix*, *Cyanobium* spp. have become the dominant cyanobacterial group, although *Microcystis* made a brief appearance in 2025 that warrants further monitoring. The appearance of other potential toxigenic genera (i.e., *Aphanizomenon*, *Dolichospermum*, *Cylindrospermopsis*) may motivate monitoring of new toxins of concern in Sandusky Bay. Here, we document the regime shift in the cyanobacterial community and hypothesize that the decline in the *Planktothrix* bloom was linked to the removal of an upstream dam on the Sandusky River in late 2018.

Elevated N_2 Fixation Rates on the Shallow West Florida Shelf: Implications for HABs

***P. D. Chappell*[1]**, *A.N. Knapp[2], K.N. Buck[3], S. Caprara[3], C. Parente[1], R. Boiteau[4], T. Conway[1], H. Hunt[1], J. Tamborsk[5], A. Lindgren[5], C. Smith[6], E.A. Webb[7], K. Hubbard[8], K.A. Confesor[1]*

[1]University of South Florida, Tampa, FL, USA
[2]Texas A&M University, College Station, Texas, USA
[3]Oregon State University, Corvallis, OR, USA
[4]University of Minnesota, Minneapolis, MN, USA
[5]Old Dominion University, Norfolk, VA, USA
[6]USGS, St. Petersburg, FL, USA
[7]University of Southern California, Los Angeles, CA, USA
[8]Florida Fish and Wildlife Research Institute, St. Petersburg, FL, USA

Dinitrogen (N_2) fixation is an important process performed by diazotrophs, converting N_2 gas into bioaccessible forms. Studies of marine N_2 fixation and diazotroph community composition have primarily focused on the open ocean, with less attention paid to coastal areas. The West Florida Shelf (WFS) is an oligotrophic, nitrogen (N)-limited coastal region known for blooms of the cyanobacterial diazotroph genus *Trichodesmium* and the harmful algal species *Karenia brevis*. While N_2 fixation has been hypothesized as a potential N source that fuels *K. brevis* blooms, little is known about the magnitude of N_2 fixation, the distribution of diazotrophs on the shelf, or how they change seasonally. This study addresses this knowledge gap by quantifying the absolute abundance of nine different diazotroph groups (*Trichodesmium thiebautii*, *Trichodesmium erythraeum*, *Crocosphaera watsonii*, Gammaproteobacteria, UCYN-A1, UCYN-A2, and three different *Richelia* symbionts of diatoms) with qPCR from samples collected on two cross-shelf cruises conducted in different seasons, and comparing surface abundances with *in situ* surface N_2 fixation rates and other environmental data, including *K. brevis* gene abundance. N_2 fixation rates were highest in the summer. Both cruises measured rates exceeding 100 nmol N/L/d in the nearshore region of the WFS. In this February cruise, these high rates were measured within a *K. brevis* bloom. Differences in diazotroph community composition were also found, with UCYNA groups and *Richelia* dominating coastal regions in February amid a *K. brevis* bloom; only *Richelia* dominated nearshore in summer; and *T. thiebautii* consistently dominated offshore stations and correlated with open-ocean parameters. Understanding the distribution of diazotrophs and their sensitivities is crucial for better constraining sources of new N on the shelf and the potential for that new N to impact harmful algal blooming species like *K. brevis*.

Identifying Nutrient Reductions Needed to Mitigate *Alexandrium* and *Dinophysis* Harmful Algal Blooms

***Lucas Chen**, Jen Goleski, Christopher J. Gobler*

School of Marine and Atmospheric Sciences Stony Brook University, Southampton, NY, USA

Approximately 40% of the world's population lives within 100 km of a coastline, triggering intense nutrient loading to coastal zones. Nutrient loading can promote harmful algal blooms (HABs) that can be harmful to humans and the ecosystem. *Alexandrium catenella* is a HAB-forming dinoflagellate that produces saxitoxins, compounds that accumulate in shellfish and can result in paralytic shellfish poisoning (PSP). *Dinophysis acuminata* is another HAB-forming dinoflagellate which produces toxins that cause diarrhetic shellfish poisoning (DSP) and has been linked to DSP events worldwide. Both HAB-species blooms have been linked to eutrophication and excess nutrients such as nitrogen (N) and nutrient reductions needed to mitigate these HABs are unknown. We monitored eight sites across NY from 2022-2026 for HABs and performed incubation experiments to assess the impact of enhanced and reduced N and phosphorus (P) concentrations. We found that nutrient enrichment with N and P consistently increased total algal biomass but only occasionally enhanced HABs as background nutrient levels were high. Nutrient reduction of 75% to 90% were capable of significantly reducing the intensity of *Alexandrium* and *Dinophysis*. These findings, therefore, provide specific managerial targets that can be implemented to mitigate these HABs.

Assessing Spatial and Temporal Coverage of Harmful Algal Bloom Sampling on the Florida Gulf Coast

Mugdha Chiplunkar[1]*, Kari St.Laurent*[2]*, Caroline Owens*[2]

[1]University of Washington, Seattle, WA, USA
[2]NOAA NOS National Centers for Coastal Ocean Science, MD, USA

Harmful algal blooms (HABs), such as Florida red tides, are caused by the toxin-producing dinoflagellate *Karenia brevis* along the Gulf Coast. The toxins produced through these blooms are harmful to human health, fisheries, and tourism in Florida's coastal communities. NOAA's National Centers for Coastal Ocean Science (NCCOS) produces HAB forecasts along the Gulf coastline to predict red tide events and provide an early warning of respiratory irritation at beaches in this region. NCCOS and partners have the ultimate goal to forecast "every beach, every day" to provide beachgoers with the best available information for which beaches to explore, and which to avoid, during an active *K. brevis* bloom event. These forecasts rely on in-situ cell counts collected by a suite of state, federal, and local partners. However, whether the available cell count data aligns with the bloom's spatial and temporal location remains unexplored. In this project, we will analyze patterns in cell count data availability, namely the timing and location of cell count data, and the relationship of these patterns to areas that experience frequent bloom impacts. These analyses will reveal how sampling efforts can be best directed for maximum efficiency and coverage, as well as the effectiveness of the forecast itself, by highlighting gaps and strengths in the areas where forecasts have previously issued high risk alerts. This information will help inform new sampling areas to target, such as by citizen science tools like the existing HABscope and in development BloomSCOPE networks.

Role of Freshwater Inflow Events in Shaping Estuarine Phytoplankton Community Composition in Texas Bays

Mintu Chowdhury*, Michael S. Wetz*

Harte Research Institute, Texas A&M University, Corpus Christi

Pulsed freshwater inflow events have been hypothesized to play an important role in shaping estuarine phytoplankton community composition and diversity. To better understand the influence of pulsed freshwater inflow events on estuarine phytoplankton communities, we conducted high temporal resolution sampling before and after discrete inflow events in Baffin Bay and Lavaca Bay, Texas. Chlorophyll *a* concentrations increased significantly in ≤1 week after rain events in both systems, likely due to increased nutrient inputs. Preliminary finding suggests that under low inflow, hypersaline conditions in Baffin Bay, the phytoplankton community was dominated by the brown tide species, *Aureoumbra lagunensis*, and other small phytoplankton taxa. However, following a rainfall event in March 2025, a pronounced diversification of the phytoplankton community occurred. Similar response was observed in Lavaca Bay in June 2025, after a rain event triggered a community shift in the phytoplankton population. This transition highlights the sensitivity of phytoplankton assemblages to short-term hydrological perturbations and underscores the role of freshwater pulses in restructuring estuarine community composition. These findings highlight the importance of wet-dry cycles in shaping estuarine phytoplankton community composition and diversity, and specifically the potential for *A. lagunensis* blooms and their persistence.

Assigning Dinoflagellate PKS/NRPS Proteins to Sterolysin Toxin Biosynthesis Using Toxic and Non-Toxic *Amphidinium carterae* Strains

***Sam Christenson**, Anne Baldino, Tsvetan Bachvaroff, Allen Place*

IMET, University of Maryland Center for Environmental Science, Baltimore, Maryland, USA

Amphidinium carterae is a photosynthetic, cosmopolitan, benthic dinoflagellate that produces complex polyhydroxy-polyene compounds, known as amphidinols, that form pores in sterol-containing membranes. Also synthesized by this species is the polyunsaturated fatty acid octadecapentaenoic acid, (18:5n-3), which is a crucial component of the chloroplast membrane. Both compounds are believed to be synthesized by modular polyketide synthase (PKS) machinery, in which glycolate is progressively lengthened with 2-carbon units and modified by a multi-domain protein or protein complex. Previous Oxford Nanopore long-read sequencing efforts have resulted in the assembly and annotation of a near-complete genome of *A. carterae* strain NCMA 1314. Analysis of this genome has identified both single- and multi-domain proteins with potential roles in amphidinol and 18:5n-3 biosynthesis, including non-ribosomal peptide synthases (NRPS), ketosynthases, acyl transferases, and reductases. The exact mechanisms by which these proteins interact and produce toxins and 18:5n-3, however, remain unknown. The *A. carterae* strain NCMA 2980, isolated from the Gulf of Mexico, has been documented to produce neither amphidinol nor 18:5n-3 with no apparent detriment to growth or performance. Oxford Nanopore long-read DNA-seq and Illumina RNA-seq data were collected from NCMA 2980 and compared to previously published data obtained from NCMA 1314. Gene assembly and annotation revealed differences in the composition and expression of polyketide synthase genes between these two strains, providing insight into the mechanisms of toxin biosynthesis in dinoflagellates. Future experiments will use these two strains as a wild-type vs. mutant pair to investigate this process and attempt to determine the missing component in toxin and 18:5n-3 biosynthesis in the nontoxic mutant.

Decadal Nutrient and Flushing Time Analysis in the Chowan River Estuary: Implications for CyanoHAB Reappearance

Mingying Chuo, *Nathan S. Hall*

University of North Carolina at Chapel Hill, Earth Marine and Environmental Sciences, Institute of Marine Sciences, Morehead City, NC, USA

Chowan River is a eutrophic, blackwater estuary in northeastern North Carolina that has been plagued by nuisance cyanobacterial blooms during the 1970s and over the past decade. The reappearance of blooms after several decades warrants investigation into its underlying causes. Nutrients and light are fundamental resources regulating phytoplankton growth, while freshwater flushing time, a proxy for transport time, also modulates biomass accumulation. Trend analysis based on generalized additive models indicated that the decline in blooms during the 1970s-1980s may be attributed to nutrient management, particularly phosphorus reduction, suggesting that phytoplankton were phosphorus-limited during that period. However, in recent years, only intermittent nitrogen limitation has been observed. The dominance of diazotrophic cyanobacteria may alleviate nitrogen limitation through nitrogen fixation, thereby sustaining blooms even when ambient nitrogen was scarce. Phytoplankton biomass responses to flushing time exhibited strong seasonal dependence, characterized by a pronounced saturating increase in summer and minimal winter sensitivity. These patterns likely reflected interacting mechanisms: longer flushing times increased phytoplankton retention; cyanobacterial nitrogen fixation may have prevented declines in biomass despite dissolved inorganic nitrogen depletion under prolonged flushing times; low light was likely the dominant constraint on phytoplankton growth during winter, resulting in weak biomass responses to flushing time. Overall, phytoplankton biomass in the Chowan River appeared to be jointly regulated by flushing time, nitrogen fixation, and light limitation. These findings provide important insight into the coupled physical-biogeochemical controls on estuarine productivity and will support the development of mechanistic models aimed at understanding estuarine responses to changing climate and human activities.

Model Validation and Satellite Integration to Predict Toxic Cyanobacteria Blooms at Ohio Inland Lakes

Jessica Cicale *and Erin Stelzer*

USGS, Ohio-Kentucky-Indiana Water Science Center, OH

Limited scientific understanding of the frequency, spatial extent, and magnitude of cyanobacterial harmful algal blooms impedes accurate and consistent prediction of toxic cyanobacteria blooms in water bodies. Current prediction tools based on pigments (chlorophyll and phycocyanin), nutrients, biomass, and satellite algorithms, lack the ability to measure the potential toxicity of the bloom. Consequently, advanced monitoring and modeling techniques are needed to reliably identify toxic blooms. The Cyanobacteria Assessment Network is a collaboration between the Environmental Protection Agency, National Aeronautics and Space Administration, National Oceanic and Atmospheric Administration, and the U.S. Geological Survey to develop a nationwide warning system using satellite data to detect cyanobacterial harmful algal blooms in freshwater. At inland lakes in Ohio, the presence of harmful algal blooms and associated cyanotoxins have increased, along with the need to predict their occurrence and to protect the public and drinking water systems. Critical *in situ* water-quality, biological, and environmental data were collected during satellite overflights at two Ohio lakes for the Cyanobacteria Assessment Network to ground-truth satellite algorithms and develop predictive models to assess the level of toxicity of a bloom. Statistical models were developed by integrating discrete sample, environmental, and satellite cyanobacteria estimate data to predict the probability of exceeding an advisory-level cyanotoxin threshold using the prediction software, Virtual Beach. Top-rated models were evaluated for fitness, predictive power (cross-validation), accuracy, sensitivity, and specificity to build robust models for use as a potential tool for management decisions. Advanced warning of a cyanotoxin threshold exceedance allows recreational and drinking water managers to provide timely advisories and/or implement cost-effective treatment to remove toxins and protect public health.

Financial and Economic Aspects of New HAB Control Technologies

Kevin Claridge

Mote Marine Laboratory, Sarasota, Florida, USA

The Florida Red Tide Mitigation and Technology Development Initiative is a partnership between Mote Marine Laboratory and the State of Florida that established an independent and coordinated effort among public and private research entities to develop control technologies to decrease the impacts of red tide on the environment, economy and quality of life in Florida. After over seven years of collaborative research with dozens of local, state, national, and international partners, this Initiative has successfully navigated pioneering scientific, regulatory, and deployment challenges to now face the hurdle of leading the development of incident command and financial structures for routine red tide control. This presentation will share experiences and examples on the costs of the development of the HAB controls (lab/field research and regulatory steps – including efforts underway through the US Harmful Algal Bloom Control Technologies Incubator to assist future work across the U.S.) and the likely costs to the users of the controls, while also raising the concern about the restrictions that the overall approval process has on allowing possibly highly effective and safe options to come to market. The frequency of blooms, geographic location (canal/marina vs. open water), scalability of tools and technologies, and financial emergency management structure all dictate costs that are now being assessed and considered for the first time.

Quantifying Clay Technology Efficiency for Harmful Algal Bloom and Toxin Mitigation in Field Bioreactors

Lucas Clark Burnette[1], *Denesh Karunakaran*[1], *Yuan Li*[1], *Miki Hondzo*[1], *Ardeshir Ebtehaj*[1], *Justin Chaffin*[2]

[1]Saint Anthony Falls Laboratory and Department of Civil, Environmental, and Geo-Engineering, University of Minnesota – Twin Cities, Minneapolis, Minnesota, USA

[2]Stone Laboratory, Ohio State University, Put-In-Bay, Ohio, USA

Harmful algal blooms (HABs) pose significant ecological and public health risks in freshwater ecosystems. This study examines the effectiveness of removal of *Microcystis aeruginosa* through clay-algae aggregation. We tested two types of clay, naturally occurring kaolinite and synthetically produced laponite. The experiment was conducted in 2300 Liter mesocosms filled with cyanobacteria-contaminated lake water at the Stone Laboratory on Lake Erie. We tested three clay concentrations—low, medium, and high doses—for removing HABs and the cyanotoxin microcystin. Due to their smaller size and higher encounter rates, laponite was found to aggregate and remove algae from the water column more quickly and at lower dosages compared to kaolinite. The medium laponite dose (0.05 g/L) achieved a higher removal efficiency (88%) compared to 71% at the medium dose of kaolinite (4 g/L), indicating laponite removed more algal biomass despite requiring 80x less clay material input. Laponite also formed larger aggregates ($D50_{laponite}$ = 184μm, $D50_{kaolinite}$ = 111μm) in shorter times; kaolinite exhibited an aggregation rate of $\beta_{kaolinite}$ = 3.69 μm/h, whereas laponite aggregated at a rate of $\beta_{laponite}$ = 60 μm/h. Removal of the cyanotoxin *microcystin* followed similar trends. These findings provide initial guidance for the application of clay-based mitigation strategies and highlight the potential for engineered clay materials to improve the efficiency of HAB and toxin removal in freshwater environments.

CyanoDetector: Improving Minnesota's Cyanobacteria Toxin Detection Technologies

Nora Conzemius[1,2], *Chan Lan Chun*[1,2], *Chris Filstrup*[1,2], *Britta Larson*[1,2], *Shawnee McMillian*[1,2]

[1]Natural Resources Research Institute, Duluth, Minnesota, United States
[2]University of Minnesota, Duluth, Minnesota, United States

As anthropogenic climate change and excess nutrient inputs accelerate, cyanobacteria harmful algal blooms (cHABs) are projected to intensify. These blooms pose significant threats to public health, ecosystem welfare, freshwater resources, and local economies through production of excessive biomass and sometimes toxins. Current methods of detecting cHAB toxins often struggle with generating timely results for management purposes and lack standardized monitoring protocols. Such drawbacks make decisions on beach closures, water treatment needs, and other mitigation practices more difficult, as people can be exposed to toxins before warnings are posted. This project aims to improve forecasting of cyanotoxin levels and develop a toolbox for local water resource management groups to use, allowing them to better communicate risks of cHABs with the public. Working in collaboration with project partners, samples will be collected from across Minnesota lakes and analyzed for cyanotoxin concentrations, toxin-encoding genes, and water quality parameters. Encoding genes are of particular interest, as the gene codes have experimentally acted as an indicator for future toxin concentrations. From these data, correlations between toxin presence and bloom formation will be analyzed to develop a predictive test for cyanotoxins before they are present in water bodies. These analyzed results will be used in developing a field-deployable cyanobacteria testing kit. The kit will comprise of portable laboratory tools, which use molecular biology methods, allowing for genomics and microbial testing in the field. Kits will be tested and evaluated by researchers initially to ensure effectiveness for beta-testing with partners. To further engage water resource managers, workshops will be conducted to demonstrate the kit and obtain feedback on its practicality and limitations. This project will provide improved data on early-detection of cyanotoxins, thereby creating a proactive strategy for cHAB mitigation to protect public and environmental health.

Distribution and Co-Occurrence of Cyanotoxins in Iowa Lakes

Katie Cope[1], *William Crumpton*[1], *Charlie Loewen*[1,2]

[1]Department of Ecology, Evolution and Organismal Biology, Iowa State University, Ames, Iowa, United States
[2]Department of Biological Sciences, University of Calgary, Calgary, Alberta, Canada

Waterbodies in Iowa and other agricultural regions often receive elevated nutrient loads from runoff containing fertilizer and livestock manure. These conditions can promote harmful algal blooms (HABs), including those of cyanobacteria, many of which produce potent cyanotoxins. Microcystin is a common cyanotoxin that is frequently monitored at the state and municipal levels because it is highly toxic and poses a direct threat to public health. However, microcystin is not the only cyanotoxin of concern and others have been detected at lakes across the Midwest, although reporting is limited. Here, we sought to address a major gap in our understanding of the occurrence of multiple cyanotoxins and the risks they may pose in Iowa's lakes and reservoirs. We leveraged the existing Iowa DNR Ambient Lake Monitoring Program to collect samples from 145 lakes across the state three times over the summer of 2025 (May–October). Microcystin was already sampled as part of the monitoring program, and we measured concentrations of four additional cyanotoxins at each lake, including anatoxin-a, saxitoxin, cylindrospermopsin, and anabaenopeptin. All cyanotoxins were analyzed using the ELISA method. Microcystin was detected in 75% of samples, and anabaenopeptin was detected in 56% of samples. Anabaenopeptin was frequently detected at high concentrations. cylindrospermopsin, anatoxin-a, and saxitoxin were detected in less than 20% of samples.

Samples containing multiple toxins with shifting patterns across the summer offer novel insights into the spatial and temporal distributions of cyanotoxins and their co-occurrence on Iowa's uniquely agricultural landscape.

Design and Pilot Validation of a Bilingual Instrument to Assess HAB Exposure Awareness

***Cunill Flores JM*[1]*, Smith LE*[2]*, Popendorf K*[3]*, Solo-Gabriele H*[4]*, Shaefer-Solle N*[2,5]*, Maizel D*[3]*, Swanson E*[6]*, Klatt N*[6]*, Caban-Martinez AJ .*[2]

[1] Abess Center for Ecosystem Science and Policy. Rosenstiel School of Marine, Atmospheric and Earth Science. University of Miami, Coral Gables, FL, USA
[2] Department of Public Health Sciences, Leonard M. Miller School of Medicine, University of Miami, Miami, FL, USA
[3] Department of Atmospheric Science, Rosenstiel School of Marine, Atmospheric and Earth Science, University of Miami, Miami, FL, USA
[4] Department of Chemical, Environmental, and Materials Engineering, University of Miami, Miami, FL, USA
[5] Department of Medicine, Leonard M. Miller School of Medicine, University of Miami, Miami, FL, USA
[6] Department of Surgery, Medical School. University of Minnesota, Minneapolis, MN, USA

Harmful algal blooms (HABs) represent a growing environmental and public health concern in Florida, especially in agricultural regions where outdoor workers may encounter airborne and waterborne cyanotoxins. Approximately 77% of agricultural workers in the United States identify as Latino, underscoring the importance of culturally relevant environmental health research. Despite this, awareness of environmental exposures within Latino agricultural communities remains limited. To address this gap, a culturally tailored participatory instrument was developed and piloted to assess awareness of HABs and related exposures. The instrument was administered through a structured workshop conducted entirely in Spanish, integrating team-based activities with an individual assessment component. Participants engaged in group exercises involving discussion and drawing to explore environmental concepts, followed by an individual activity designed to identify and represent personal exposure to contaminants. Data collection utilized worksheets that captured both written and visual responses, including perceptions of contaminants, understanding of microalgae and HABs, identification of exposure pathways, and spatial representations of community water bodies. Individual responses were systematically evaluated using structured coding sheets. Visual and textual data were analyzed to identify recurring themes, exposure pathways, and levels of conceptual understanding. Participant drawings were synthesized into a “living hazard map” that represented shared perceptions of environmental risks and exposure landscapes. The pilot study included 26 participants in Immokalee, Florida. All participants identified as Latino or Hispanic. Results indicated strong awareness of general occupational exposures such as pesticides, dust, and smoke, but limited familiarity with HAB-related risks. Visual responses frequently linked contamination to water quality and agricultural activity. These findings reveal gaps in HAB risk communication and support the implementation of participatory, culturally grounded approaches to assess environmental exposure awareness in agricultural communities.

NASBA for Detecting Saxitoxin Synthesis in *Pyrodinium bahamense* Populations in the Indian River Lagoon, FL

Kathleen Cusick[1]*, Robert Ulrich*[2]

[1]Florida Atlantic University Harbor Branch Oceanographic Institute, Ft. Pierce, FL, USA
[2] Clife Sciences Advanced Technologies, St. Petersburg, FL, USA

Pyrodinium bahamense is toxic, bioluminescent dinoflagellate that forms annual recurring blooms along Florida's east coast. It produces the potent neurotoxin saxitoxin (STX). Monitoring of *P. bahamense* is typically via cell counts from water samples collected when a bloom is occurring or at random. However, cell counts do not inform as to bloom toxicity. Molecular and ELISA data from the Cusick lab over the past few years showed that *Pyrodinium* populations are consistently producing toxin, yet these levels vary spatially and temporally. We developed a NASBA-based isothermal amplification assay that detects toxin synthesis activity via detection of *sxtA4* transcripts. *SxtA4* is a key gene in the *P. bahamense* STX biosynthesis pathway that is essential for toxin synthesis. The sxtA4 NASBA utilizes a molecular beacon (MB) as the source of fluorescence. Following optimization with the MB format, reactions were performed using the 3x NASBA buffer mix, 6x nucleotide mix, and NASBA enzyme mix from Life Sciences Advanced Technologies along with 200 nm each forward and reverse primer, 100 nm MB2, and 1.5ul each RNA template. Based on standard curves, the assay detects as little as 500 copies, or 37.5 copies ul^{-1}, of *sxtA4* transcripts in <55 minutes. The assay was then performed on a subset of field samples for comparison with toxin measurements (ELISA) and *sxtA4* transcripts identified via a qRT-PCR assay. Overall, the NASBA was able to detect *sxtA4* transcripts, which serve as molecular proxy for STX biosynthesis in *P. bahamense* populations. It detected them more quickly than the qRT-PCR assay, and does not require the additional separate reverse transcription reaction. All samples that tested positive via the ELISA also generated a fluorescent signal with the NASBA. These results demonstrate NASBA based on *sxtA4* transcription provides a rapid, diagnostic tool for determining if *P. bahamense* populations are actively producing toxin.

HABs in the High Desert: State of New Mexico's Monitoring and Advisement Strategies

***Savannah Cutler**, Miguel Montoya, Lynette Guevara, Nathan Reynolds*

NMED SWQB Monitoring, Assessments, & Standards Section, Santa Fe, NM, USA

The New Mexico Environment Department's Surface Water Quality Bureau began monitoring and creating advisement thresholds for Harmful Algae Blooms (HABs) in lakes and reservoirs across the state in 2025. Monitoring last season was primarily in response to field observations in our ambient water quality monitoring survey areas, information provided by land management partners and recreationists, and/or satellite imagery. Heightened monitoring frequencies began late Fall 2025 (weekly to bi-weekly) in response to toxin results in multiple lakes exceeding state adopted standard for Microcystin (8 µg/L). The USFS decided to close Quemado Lake in the Gila National Forest from November – end of December 2025 due to sustained Microcystin results ranging between 500 µg/L – 2,000 µg/L. A closed basin system and extreme drought conditions are suspected to have combined to decrease water volume, concentrate nutrients, and increase water temperatures in Quemado Lake – the perfect storm for intensification of blooms. A buoy equipped with a multi-parameter sonde and three thermographs attached to the anchor line were deployed in Quemado April 2026 for the field season. The equipment will produce a long-term dataset for dissolved oxygen, temperature, specific conductivity, turbidity, and phycocyanin (BGA-PC) to help the SWQB understand what might be driving HABs in Quemado Lake. The toxin results along with species identification will be used to inform and generate HAB advisories based on thresholds developed for microcystin, cylindrospermopsin, anatoxin, saxitoxin and/or cyanobacteria biovolume. Development of threshold values considered health effects related to toxin levels specific cyanobacteria species, informed by the examination of established arid western states' HABs Advisory Programs. Current advisories for 2026 will be displayed via a web map that will be updated as new data is reported, streamlining communication of HABs advisories to the public and stakeholders.

The Effect of Ciguatoxins on Sea Urchin, *Lytechinus variegatus*, Reproductive Success

Ashley Dalleske[1,2] *and Alison Robertson*[1,2]

[1]University of South Alabama, Mobile, AL
[2]Dauphin Island Sea Lab, Dauphin Island, AL

Gambierdiscus is an epiphytic, benthic dinoflagellate found in tropical regions with the potential to produce potent neurotoxins such as ciguatoxins (CTXs). Marine herbivorous invertebrates, like sea urchins, have been found to accumulate CTXs in their gonads; but the effects of these toxins on invertebrates are poorly understood. Meanwhile, urchins serve as an essential link between macroalgae and higher-trophic-level organisms and play a key role in regulating benthic community structure. The decline in urchin populations following mass mortality events throughout the Caribbean in recent years (2022-2024) has promoted shifts in reef biodiversity, resulting in macroalgal-dominated reefs. Despite increased food availability under macroalgal dominance, urchin populations have shown limited recovery. This suggests other environmental stressors may be involved. Shifts toward algal-dominated reefs enhance substrate availability for *Gambierdiscus* spp., potentially increasing the risk of CTX exposure. Urchin populations are heavily driven by reproduction, with gamete production and larval development acting as bottlenecks for population growth. This study evaluates how dietary exposure to CTXs disrupts urchin reproduction. Laboratory exposure experiments were conducted with the variegated sea urchin, *Lytechinus variegatus* (n=45 each control vs. treatment). Gametes were collected through induced spawning and used for in-vitro fertilization. Fecundity, fertilization, and larval development were assessed for exposed and control groups. Preliminary findings indicate that CTX exposure disrupts fertilization and larval development in the F1 generation compared to controls. Also, CTX-exposed larvae were found to develop more rapidly than controls, and with a greater frequency of morphological defects. These effects may have meaningful long-term impacts on reproduction, and therefore population success of urchins in coral reef ecosystems where CTX-producing *Gambierdiscus* thrive.

Cyanobacterial Harmful Algal Blooms in Arkansas: From Monitoring to Advisories

***Grace Davenport**, Felicia Osburn*

Arkansas Division of Environmental Quality, North Little Rock, Arkansas, USA

Cyanobacterial harmful algal blooms (cHABs) present an escalating challenge for states seeking to protect public health and aquatic ecosystems. The Arkansas Division of Environmental Quality, Office of Water Quality (OWQ) has established a monitoring and advisory program for cHAB occurrences that is designed to provide timely, science-based decisions to protect public health. This program integrates routine environmental monitoring, public education and outreach, and interagency collaboration to detect cHABs, assess cyanotoxins, and communicate with the public through standardized advisory protocols. Currently, the OWQ performs routine water quality monitoring at approximately 90 public lakes including measuring cyanotoxins, primarily total microcystins (MCX) and cylindrospermopsin (CYL). These routine lake samples are creating a robust, publicly available dataset for the status of MCX and CYL in Arkansas. Additionally, the OWQ has a protocol for responding to publicly reported cHABs. Over the past four years, the OWQ has seen an increase in both the number and average duration of cHAB advisories in Arkansas. Continued monitoring and expansion of this program is vital to safeguarding public health through gaining a better understanding of conditions under which cHABs occur, increasing public awareness of negative health and ecological effects, and increasing the public's ability to accurately identify, avoid, and report cHABs.

Research Update on the Novel Diarrhetic Shellfish Poisoning (DSP) Toxin Dihydrodinophysistoxin-1 (Dihydro-DTX-1)

Jonathan R. Deeds[1], *Christopher R. Beekman*[1], *Nour Ayache*[2], *Callie J. McAulay*[3], *Elliott J. Wright*[3], *Aurelia Tubaro*[4], *Silvio Sosa*[4], *Tyler Spillane*[5], *Pearse McCarron*[3], *Vera L. Trainer*[6], *Michael Brosnahan*[2], *Juliette L. Smith*[7]

[1]US Food and Drug Administration, Human Foods Program, College Park, MD, USA
[2]Woods Hole Oceanographic Institute, Woods Hole, MA, USA
[3]National Research Council Canada, Biotoxin Metrology, Halifax, Canada
[4]University of Trieste, Department of Life Sciences, Trieste, Italy
[5]Maine Department of Marine Resources, West Boothbay Harbor, ME, USA
[6]University of Washington, Olympic Natural Resources Center, Forks, WA, USA
[7]Virginia Institute of Marine Science, Gloucester Point, VA, USA

In 2016 and 2018, discrepancies between protein phosphatase inhibition assay (PPIA) screening and targeted confirmatory analysis by liquid-chromatography tandem mass-spectrometry (LC-MS/MS) led to the discovery of a new toxin in the Diarrhetic Shellfish Poisoning (DSP) toxin complex, dihydrodinophysistoxin-1 (dihydro-DTX1). Thus far, *Dinophysis norvegica* from the northeastern Atlantic coast of the United States is the only known producer of this toxin, while also producing a rare congener in the pectenotoxin (PTX) group, PTX-12 (dehydro-PTX2). Broad SPATT sampling in Puget Sound and the outer coast of Washington State (northeastern Pacific coast of the United States) as well as the analysis of isolates of *D. norvegica* from Washington State, confirmed dihydro-DTX-1 not to be present, even though *D. norvegica* is commonly found in this region. Since 2018, large-scale blooms of *D. norvegica* have not occurred again in the Gulf of Maine, but dihydro-DTX-1 continues to be found in low concentrations in several shellfish species when *D. norvegica* is present, often mixed with dinophysistoxin-1 (DTX-1) and okadaic acid (OA) from co-occurring *D. acuminata*. For the proper management of this new DSP toxin risk, a toxicity equivalency factor (TEF) must be determined, and dihydro-DTX-1 must be added to the LC-MS/MS method currently approved for regulatory use in the National Shellfish Sanitation Program (NSSP). To aid in these efforts, dihydro-DTX-1 from shellfish collected during the *D. norvegica* blooms in 2016 and 2018 in the Gulf of Maine was purified and is currently in the process of being evaluated for toxic potency relative to OA, DTX-1, and DTX-2 assessing both their ability to inhibit protein phosphatase and their cytotoxicity in an intestinal cell line. A large-scale SPATT pumping system has also been developed that can be deployed in the event of future *D. norvegica* blooms to acquire additional toxin for continued research efforts.

Plasma-laser Mitigation of Dinoflagellate Cysts

Dominic DeMarco[1], *William Scott[1], Devin Burris[1], Cynthia Heil[1], Josh Mangum[2]*

[1]Mote Marine Laboratory, Sarasota, FL, USA
[2]Southwest Research Institute, Sarasota, FL, USA

Current harmful algal bloom (HAB) mitigation technologies focus exclusively on vegetative cells and their toxins in the water column. These efforts can eliminate current blooms, but do not address cysts that have accumulated in benthic sediments which have the potential to bloom at later dates. Current approaches to cyst mitigation often include costly practices or the use of potentially hazardous methods. We have developed a plasma-laser (532 nm) that can target and destroy dinoflagellate cysts. The laser uses various treatment mechanisms to destroy the cysts, including powerful oxidative species like hydroxyl radicals (•OH, 2.8V), ozone (O_3, 2.1V), pressure waves, and hydrogen peroxide (H_2O_2, 1.8V), which are able to penetrate and disrupt the protective sporopollenin and cellulose walls that make these cysts resistant to many other treatment approaches. Preliminary testing has been two-fold with a focus on the need to generate cysts predictably in the lab for experimental purposes and the construction and testing of a laser system to mitigate these cysts. We utilized diethylamine NONOate (DEA), a nitric oxide (NO) donor, to trigger cyst formation in *Alexandrium monilatum* in benchtop experiments. Additions of 0.5 to 2.0 μM DEA had no impact on cyst formation over 24 hrs, however additions of ≥5.0 μM DEA increased encystment from 11.99 (+1.40)% in controls to 87.35 (+5.12)% with DEA additions within 48 hrs. Preliminary experiments with a prototype plasma-laser and *Karenia brevis* demonstrated a 98% reduction in *Karenia brevis* cell concentration and associated brevetoxins within 10 minutes of application. Looking forward, the plasma-laser could be manually deployed in areas of high cyst density in open water - with the goal of autonomous deployment at later dates - to mitigate the cysts and prevent future HABs from forming; effectively acting as a preventative and mitigative measure simultaneously.

Light, Microcystin Content, and Vertical Migration of *Microcystis* in a Shallow Eutrophic Lake

Dominique Derminio[1,2]*, Zacharias J. Smith*[1,3]*, and Gregory L. Boyer*[1]

[1]Department of Chemistry, State University of New York, College of Environmental Science and Forestry, Syracuse, NY, USA
[2]Department of Environmental Resources Engineering, State University of New York, College of Environmental Science and Forestry, Syracuse, NY, USA
[3]USDA-ARS, Hydrology and Remote Sensing Laboratory, Beltsville, MD, USA

The cyanobacterium *Microcystis* vertically migrates in response to cellular nutrient needs and to optimize its light environment. Samples were collected at 0.5 m intervals from shallow, hypereutrophic Lake Neatahwanta during a 1-day diurnal study under windy (2016) and low-wind (2017) conditions to examine the vertical migration of *Microcystis* when nutrients were in excess. Light irradiance, cellular pigments, PSII photosynthetic efficiency (F_v'/F_m'), and cyanotoxins were measured at 2 hr intervals from dawn to dusk. On the high-wind day, there was a homogeneous distribution of cells within the top meter of the water column. In 2017, the cells moved deeper in the water column during the day. Cells near the surface had a lower photosynthetic yield (~0.15) than cells deeper in the water (~0.3), indicating that these cells were subject to light stress, which decreased with depth. There was no change in chlorophyll-*a* or phycocyanin cell quota throughout the day, indicating that cyanobacteria did not photoacclimate by changing their bulk pigments. The microcystin cell quota did not change with depth, but the toxin quota showed a midday maximum. These results have implications for monitoring HAB events as cells migrate away from the surface during hours of peak irradiance.

Nanobubble Oxygenation – An Emerging Technology for HABs Mitigation

Denise Devotta, *Shane Hoyt*
Moleaer, Hawthorne, CA

Nanobubble oxygenation is an emerging technology applied to mitigate/prevent harmful algal blooms (HABs) in lakes by reducing anoxia, improving redox conditions at the sediment-water interface, and reducing internal nutrient loading. Unlike bubbles produced by conventional aeration, nanobubbles exhibit neutral buoyancy, long residence times, and enhanced gas transfer efficiency in the water column, enabling sustained oxygen delivery to benthic environments. Three lakes across California and Minnesota characterized by recurring HABs, underwent nanobubble treatment over 3.5 to 18 months. In each lake, changes in dissolved oxygen (DO), oxidation–reduction potential (ORP), total nitrogen (N) and phosphorous (P) concentrations, cyanobacterial biomass, phytoplankton cell counts, and algal toxin levels were monitored. Across all sites under nanobubble treatment, bottom-water DO levels increased by 2-4x, reducing lakebed exposure to anoxia by up to 90%. Aligning with this, under treatment across all sites, ORP often doubled within the first month and remained above +150 mV for the remainder of treatment duration. Under no treatment, ORP remained persistently negative, indicating continued reducing conditions. Consistent with this, total P and N levels were 36-64% and 44-65% lower under treatment vs. no treatment, respectively. Also, reduced cyanobacterial biomass and algal toxin levels under nanobubble treatment were detected. Specifically, cyanobacterial cell densities and microcystin concentrations were > 50% lower under treatment than no treatment. Additionally, under nanobubble treatment, the relative abundance of eukaryotic algae was 264-382% higher than under no treatment, potentially reflecting altered competitive dynamics. Collectively, these results demonstrate that nanobubble oxygenation modifies benthic redox conditions, reduces internal nutrient loading, and thereby helps mitigate HAB development in lake ecosystems.

Exploring the Role of Episodic Events on Phosphorus Dynamics and Bloom Progression in Western Lake Erie

Anshula Dhiman[1], *Trevor Holm[1], Forough Naali[1], Audrey Ciochetto[1,2], Brice K. Grunert[1]*

[1]Department of Biological, Geological and Environmental Sciences, Cleveland State University, Cleveland, OH, USA
[2]Graduate School of Oceanography, University of Rhode Island, Narragansett, RI 02882, USA

Harmful algal blooms in freshwater systems threaten drinking water supplies, fisheries, industry, and recreation. These impacts have driven operational forecast development to better understand bloom dynamics and support nutrient mitigation efforts. In western Lake Erie, current bloom severity forecasts rely on spring bioavailable phosphorus loads from the Maumee River. However, severity and timing of blooms often deviate from predictions, with internal phosphorus loading from sediments remaining a major under-quantified source of variability. Ecological forecasts treat internal loading as a steady diffusive flux and do not resolve episodic wind-driven resuspension or hypoxic events. To understand their role in bloom progression, we build on prior work identifying sediment resuspension as a basin-wide internal phosphorus source. We examine how combined hypoxia and resuspension events can influence bloom progression and maximum biomass in western Lake Erie in a given year. We focus on algal bloom progression in 2025, when a large hypoxic event occurred from July 09 to 18 during typical bloom intensification. Spring 2025 Maumee River discharge was below the recent average, and observed severity reached 2.4, lower than predicted. Peak bloom was delayed by about one month relative to 2020–2024 and covered a smaller spatial extent. Bottom hypoxia persisted for 5–10 days at offshore stations before strong winds reoxygenated and mixed the water column. The post-event increase in soluble reactive and total phosphorus, estimated at ~0.7–88 mg $m^{-2}$and ~1.5–12 mg m^{-2}, represents a notable phosphorus pulse during a critical bloom period. Using satellite datasets, we assess expected bloom progression under below-average Maumee discharge and evaluate whether the phosphorus released explains bloom progression divergence from climatological patterns. We also examine how timing and cumulative episodic loading shape harmful algal bloom dynamics and inform nutrient management efficacy in the Great Lakes.

Semi-Targeted LC-MS and Assay-Guided Characterization of *Gambierdiscus silvae* Cultures

***Sarah Dietrick*[1,2], *Michael L. Parsons*[3], *Deana L. Erdner*[4], *and Alison Robertson*[1,2]**

[1]University of South Alabama, Mobile, AL
[2]Dauphin Island Sea Lab, Dauphin Island, AL
[3]Florida Gulf Coast University, Fort Myers, FL
[4]University of Texas. Port Aransas, TX

Ciguatera poisoning can occur following consumption of tropical or subtropical fish that have accumulated potent neurotoxins known as ciguatoxins. Ciguatoxins are large polyether compounds produced by several species of the dinoflagellate genera *Gambierdiscus* and *Fukuyoa*. The toxicity and metabolomic profiles of *Gambierdiscus* can vary across species and strains due to environmental factors such as water temperature, salinity, wave action, and light. Through collaborative efforts, a toxigenic strain of *G. silvae* 1602 SH-6, previously led to the discovery of C-CTX-5, a toxic metabolic precursor to the dominant piscine metabolite, C-CTX-1/2. CTX-like sodium channel activation of both culture and isolated compounds were assessed by cell-based assay and high resolution mass spectrometry analysis. From this, semi-purified C-CTX-5 was confirmed to produce CTX-like sodium channel activity and was the dominant C-CTX identified, while low levels of C-CTX1/2 were also detected in culture. However, this did not fully account for the CTX-like activity (1.4 ± 0.2 pg CTX3C eq. cell−1) found in extracts of the 1602 SH-6 strain. As a follow-up study, we investigated contributors to this total CTX-like pool, including another novel C-CTX, synergistic enhancement of toxicity, or additional secondary metabolites with functional overlap. To address this, larger scale cultures (3-5 L) were prepared and extracted to identify additional analogues or toxins responsible for enhanced bioactivity. In addition to larger biomass, we employed techniques such as flash chromatography for enhanced separation, allowing assay-guided fractionation with targeted LC-MS/MS and high resolution MS/MS profiling. This workflow has been applied to extensive *Gambierdiscus* culture collections to aid chemometrics, enabling extraction of hidden metabolite information from complex analytical profiles to improve signal quality, build predictive models, and optimize chemical experiments which will be discussed.

Bringing Small Water Bodies into View: How to Incorporate Satellite-based Monitoring for Freshwater HABs

Emily Dorne

DrivenData, San Francisco, CA, USA

Satellite-based HAB monitoring data is widely available to U.S. federal and state water-quality programs through projects such as EPA's CyAN, but HAB detection in small inland water bodies is still limited by spatial resolution constraints. Sentinel-3's 300m pixel spatial resolution is too coarse to reliably detect blooms in inland water bodies, such as lakes and reservoirs that are smaller than 250–300 acres, yet these constitute approximately 98% of all U.S. water bodies.

A relatively new system, CyFi (Cyanobacteria Finder), utilizes machine learning and higher-resolution Sentinel-2 satellite imagery with 10–30m spatial resolution to accurately detect cyanobacteria blooms in freshwater bodies under 250 acres. CyFi extends coverage to 10 times as many water bodies as Sentinel-3-based methods, with comparable or higher accuracy.

This powerful HAB monitoring tool is freely available to water quality managers. This presentation describes how CyFi works, how to test and tune it to local conditions, and how to integrate CyFi data into the dashboards and day-to-day workflows of HAB monitoring programs. The goal is to help water quality managers improve HAB monitoring in small water bodies by leveraging high-frequency, large-area satellite coverage that complements field monitoring and autonomous buoy systems.

Introduction & Background: Transforming HAB Science and Management through Three Decades of Competitive Research

Quay Dortch[1]*, Marc Suddleson*[1]*, Maggie Broadwater*[1]*, Felix Martinez*[1]*, Brittany King*[1]*, Sarah Pease*[1]*, and Bruna Fernanda Sobrinho*[1,2]

[1]NOAA, NOS, NCCOS, CRP, Silver Spring, MD, USA
[2]University of Maryland Center for Environmental Science, Horn Point Laboratory, Cambrigde, MD, USA

Guided by the 1995 community plan, The Ecology and Oceanography of Harmful Algal Blooms: A National Research Agenda, the Ecology and Oceanography of Harmful Algal Blooms (ECOHAB) program was established and funded the first projects in 1997. The Harmful Algal Bloom and Hypoxia Research and Control Act (HABHRCA) was enacted in 1998, reauthorized in 2005, 2011, 2019. It authorizes NOAA's National Competitive HAB programs, including ECOHAB, Monitoring and Event Response for HABs (MERHAB), Prevention, Control, and Mitigation of HABs (PCMHAB), and Social, Cultural, and Economic Impacts of HABs (SEAHAB). Two innovative programs, HAB Event Response and the HAB Control Technologies Incubator (HAB-CTI) were established. Besides research, NOAA's Competitive Research Program has also funded, led, or participated in many regional, national, and international community building and outreach efforts (e.g. establishing U.S. National Office for HABs, supporting national HAB research and response planning (HARRNESS 2005-2015, 2024-2034), and creating the National HAB Committee (NHC).

Success can be measured by new or improved HAB forecasting on all coasts; extraordinary advances in HAB monitoring; increased regional, state, tribal, and local HAB response capacity; many new HAB control methods currently being evaluated; increased public HAB literacy; and enhanced understanding of public health, environmental, economic, social, and cultural impacts of HAB events. Factors that have contributed to the success of these programs include

1. Long term, multidisciplinary ecosystem research focused on improved HAB management;
2. HAB Event Response support to collect data during ephemeral events;
3. HAB research-to-management plans, community-building activities, and outreach.

This talk covers the history of the NOAA competitive HAB programs and introduces presentations in plenaries and sessions that will address the scientific accomplishments and their application to management from a regional perspective and analyze and summarize competitive HAB funding.

Periphyton Blooms and Algal Toxins in Yosemite and Sequoia and Kings Canyon National Parks

***Thea M. Edwards*[1]**, *Kelly M. Martin*[2], *Alissa M. Chrisekos*[2], *Brittany Perrotta*[1], *Satomi Kohno*[3], *James Soldenwagner*[4], *Catherine Fong*[4], *Michael Templeton*[1], *John Carroll*[1], *Olivia Jenks*[5], *Zach Laughrey*[5], *Keith A. Loftin*[5], *Ashley Lopez*[5], *David Lutin*[5], *Erik Meyer*[6]**

[1]US Geological Survey, Columbia Environmental Research Center, Columbia, MO, USA
[2]National Park Service, Sequoia National Park, Three Rivers, CA, USA
[3]Department of Biological Sciences, Fort Hays State University, Hays, KS, USA
[4]National Park Service, Yosemite National Park, CA, USA
[5]US Geological Survey, Kansas Water Science Center, Lawrence, KS, USA
[6]National Park Service, Natural Sounds and Night Skies Division, Fort Collins, CO, USA

Drought, increased temperatures, and atmospheric nutrient deposition are linked to increasing periphyton blooms in Yosemite (YOSE) and Sequoia and Kings Canyon (SEKI) National Parks, California, USA. To better understand the bloom distributions, environmental drivers, potential for toxin production, and taxonomic structures, we surveyed 30 sites in SEKI and 12 sites in YOSE, each four times during 2023 and 2024. Composite periphyton and water samples were collected from transects at each site, along with water quality metrics and data on habitat characteristics. Bacterial community analysis, based on 16S DNA sequencing, revealed high levels of biodiversity in both Parks, with relative abundance of Cyanobacteria higher in YOSE, compared to SEKI, possibly because more lower elevation sites were sampled in YOSE. Microcystins were detected in 19% of SEKI and 13% of YOSE samples, with a range of 0.9 to 86.3 µg of toxin per square meter of river substrate. Anatoxin-a was detected in 11% of SEKI and 11% of YOSE samples, with a range of 1.2 to 9.0 µg/m^2. Saxitoxin was detected in 2% of SEKI and 5% of YOSE samples, with a range of 0.2 to 7.8 µg/m^2. Cylindrospermopsin was not detected at either park. Furthermore, in SEKI, 55% and 34% of water samples exceeded total phosphorus and dissolved phosphorus criteria (10 ug/L), respectively, to prevent algae growth; 1% exceeded nitrate-nitrite criteria (1.0 mg N/L). In contrast, YOSE water quality exceeded criteria less often: 8% of samples exceeded the total phosphorus criterion, and none exceeded dissolved phosphorus or nitrate-nitrite criteria. Relationships among water quality metrics, aquatic habitat characteristics, geography, elevation, bacterial taxa, and toxin concentrations will be presented. This study expands National Park infrastructure to monitor periphyton biodiversity, predict algal toxin potential, and protect visitor health.

Cyanophage-Mediated Infection of *Microcystis* Blooms in Lake Erie

Richardson Egyirifa[1], *Rebecca Tietze*[1], *Jeff Martin*[3], *Michael Sommerville*[3], *Katelyn McKindles*[1,2]

[1] Department of Biology, Baylor University, Waco, Texas, USA
[2] Center for Reservoir and Aquatic Systems Research, Baylor University, Waco, Texas, USA
[3] Collins Park Water Treatment Plant, Toledo, Ohio, USA

Viral infection of bloom-forming *Microcystis* has been associated with pulses of dissolved toxin release, but the ecological timing and consistency of these events remain poorly resolved. To better understand host-cyanophage dynamics relevant to water quality, we partnered with Collins Park Water Treatment Plant to characterize *Microcystis*-specific cyanophages and associated bacterial communities in Lake Erie from June to September 2024 at the plant intake and surge well. Sampling increased from biweekly to daily following detection of microcystin in raw plant samples to capture rapid changes associated with potential viral lysis dynamics. During this period, *Microcystis* abundances peaked, then declined and fluctuated, while cyanophage abundance increased following host decline. This coupled host-virus transition occurred within 25 days, between August 6 and August 30. Viral-host activity ratios increased during this interval, indicating viral gene expression became more prominent relative to declining host activity, consistent with active phage involvement in bloom dynamics. *Microcystis* marker gene amplicon sequencing revealed shifts in population structure, with dominant clades declining while previously rare clades increased during the viral infection period. Microbial community composition also shifted during this interval, with principal coordinate analysis indicating directional community changes and 16S rRNA sequencing showing declining relative abundance of *Microcystaceae* over time. Cyanophage amplicon sequencing revealed high sequence identity to known *Microcystis* cyanophages, with minor sequence variation suggesting previously undescribed genetic diversity. Together, these findings demonstrate that cyanophages are dynamic components of Lake Erie harmful algal blooms that may drive host turnover, mediate clade succession, and restructure microbial communities, with implications for bloom prediction and managing toxin exposure in drinking water systems.

Integration of Multi-Omic Time Series Data to Identify Viral Infection and Lysis During an Algal Bloom

Claire E. Elbon*[1]*, Emma Timmins-Schiffman*[1]*, Michael Riffle*[1]*, Gabriella Chebli*[2]*, Julia Kubanek*[2]*, Tatiana A. Rynearson*[3]*, Brook L. Nunn

[1]University of Washington, Seattle, Washington, USA
[2]Georgia Institute of Technology, Atlanta, Georgia, USA
[3]University of Rhode Island, Narragansett, Rhode Island, USA

Harmful algal blooms (HABs) disrupt marine ecosystems, restructure microbial communities, and threaten public health, yet the mechanisms driving bloom-associated mortality remain poorly resolved. Viral infection likely shapes bloom decline, but its in situ timing and contribution remain unclear. Because algae-infecting viruses and bacterial phage are captured in >0.22 µm size fractions, integrated metagenomic, metatranscriptomic, and metaproteomic time series can track viral abundance, infection dynamics, and host mortality across bloom progression. Here, I resolve viral dynamics across ecological niches, tracking distinct viral groups as they shift from free-living states to algal- and bacterial-associated populations, and linking these transitions to bloom initiation, collapse, and functional ecosystem responses. Samples were collected every 4 hours over 22 days from East Sound, WA, across two size fractions (0.22–1 µm and >1.2 µm), capturing bloom initiation, peak, decline, and the initiation of a second bloom. In 0.22 µm metagenomes, two clear patterns emerged. First, free-living dsDNA giant algal viruses, Phycodnaviridae, peaked in estimated gene copies 48 hours before bloom initiation and declined as the bloom developed, consistent with a transition from free-living viral reservoirs to host-associated infection. Second, bacterial dsDNA phages, Caudoviricetes, tracked bacterial cell abundance; estimated gene copies declined and rebounded by an order of magnitude before and after the HAB. In >1.2 µm metatranscriptomes, Phycodnaviridae transcripts peaked during the chlorophyll maximum, suggesting active infection and replication within an algal host.This demonstrates how multi-omic time series approaches can validate genetic potential to active physiology revealing cross-kingdom controls on ecosystem dynamics (bloom-bust cycles). Integration of the full time series metaproteomics dataset will further our understanding of these dynamics. This complex integrated framework will help determine whether Phycodnaviridae directs bloom termination, whether free-living viral reservoirs seed infection at bloom onset, and whether bacteriophage dynamics provide predictive signals of ecosystem state change before and after bloom collapse.

The Interplay of Acidification, Warming, and Nutrient Availability on cHAB Growth and Toxin Production in the Great Lakes

Reagan M Errera[1], *Greg Dick*[2, 3], *Rachel Eveleth*[4], *Jenan Kharbush*[2], *Ben Kramer*[5,6], *Cody Sheik*[5], *Trisha Spanbauer*[7], *Kevin Yeager*[8]

[1]NOAA Great Lakes Environmental Research Laboratory (GLERL), Ann Arbor, MI, USA
[2]University of Michigan, Ann Arbor, MI, USA
[3]Cooperative Institute for Great Lakes Research (CIGLR), Ann Arbor, MI, USA
[4]Oberlin College, Oberlin, OH, USA
[5]University of Minnesota – Duluth, Duluth, MN, USA
[6] USGS Great Lakes Science Center, Ann Arbor, MI, USA
[7]University of Kentucky, Lexington, KY, USA
[8]Old Dominion University, Norfolk, VA, USA

The Great Lakes face a complex array of threats necessitating a multivariate approach to understanding ecosystem dynamics. The synergistic impacts of acidification, warming, and nutrient availability alter aquatic systems, leading to significant shifts in phytoplankton community dynamics. Despite a decade of intensive research into cyanobacterial HABs (cHABs), the role of acidification has been largely overlooked, leaving a critical gap in our understanding of Great Lakes ecology. While the ability of cyanobacteria to effectively utilize inorganic carbon (C_i) is thought to provide a competitive advantage during periods of C_i scarcity, *Microcystis*, the primary cHAB-forming genus in the Great Lakes, comprises a diverse array of genotypes with varying carbon-concentrating mechanisms (CCMs). Through a series of experiments, we have explored the impacts of acidification, temperature, and nitrogen source on the growth rates and physiology of three *Microcystis* strains isolated from Lake Erie, representing distinct C_i -uptake genotypes. Our results showed that high C_i/low pH conditions enhanced the growth rate of the high-HCO_3^- affinity ecotype (GLCC LE18 22.4), regardless of temperature or nitrogen source. In contrast, the high-HCO_3^- flux ecotype (GLCC LE19 84.1) was primarily influenced by temperature, with C_i availability having little effect. The generalist ecotype, capable of leveraging both acidic and basic conditions, exhibited the highest growth rates across all C_i levels, with a significant growth increase at a pCO_2 [1000]. For toxin producing strains, toxin production increased with higher C_i availability (elevated pCO_2). Experiments on Lake Erie plankton community were also performed in 2024 and 2025. Results suggest that *Microcystis* took advantage of increased C_i conditions, though the whole community suffered under higher temperatures. These results suggest that C_i availability and temperature during early periods of the bloom may be key drivers in bloom initiation.

Particle-assisted Delivery of Curcumin for Mitigation of *Karena brevis*

Alana L. Espinosa *, Vincent J. Lovko*

Mote Marine Laboratory, Phytoplankton Ecology Research Program, Sarasota, FL, USA

Harmful Algal Bloom mitigation is increasingly important due to the frequent occurrence of Florida Red Tide (*Karenia brevis*) along the Gulf Coast. Current mitigation strategies include physical, chemical, and biological approaches, with prominent focus on chemical algaecides and physical cell removal. Natural algaecides such as curcumin show promise as environmentally benign mitigation agents and are effective against *K. brevis*. However, curcumin's low water solubility requires dissolution in solvent, limiting scalability. Previous work has shown that coagulant-amended modified clays (ex. MCII clay with PAC) effectively remove algal cells through flocculation and sedimentation, though removed cells may remain viable. Adsorptive materials such as biochar similarly promote sedimentation when modified with a coagulant while also adsorbing algal toxins, potentially improving mitigation outcomes. Previous work has also shown that curcumin binds with MCII clay and effectively kills *K. brevis* cells (>80% @ 24hrs) at concentrations as low as 1.0mg/L, suggesting clay can serve as a solvent-free curcumin carrier. However, curcumin combined with unamended kaolinite or biochar has not been evaluated. This study evaluates whether pairing curcumin with an adsorptive material (biochar) or sedimenting mineral (kaolinite) enhances mitigation of *K. brevis*. Laboratory experiments compared control, single-component, and particle-bound curcumin treatments. Endpoints included cell concentrations, photosynthetic efficiency, and removal efficiency. Curcumin-only treatments produced rapid, sustained reductions (>99% by 48 h), with cell densities declining from ~5.8 x 10^5 at 3 h to ~5.0 x 10^3 cells/L through 96 h. Curcumin with kaolinite achieved similarly high removal (99.9%), with complete elimination at 48 h and no significant recovery, suggesting synergy between sedimentation and inactivation. In contrast, curcumin with biochar showed lower removal (~86-95%) and persistent cells (~6.4 x 10^5 cells/L at 96 h), suggesting adsorption may limit curcumin bioavailability. These findings demonstrate that particle type strongly influences curcumin efficacy.

Developing Global Risk Maps for Fish-killing Harmful Algal Blooms

Esther Garrido Gamarro[1], Alfonso Sanchez-Paus Diaz[1], Nicholas R Record[2], ***Johnathan Evanilla[2]***

[1]Food and Agriculture Organization of the United Nations, Viale delle Terme Caracalla, Rome, Italy
[2]Bigelow Laboratory for Ocean Sciences, East Boothbay, ME, USA

Harmful algal blooms that kill fish can pose a risk to fisheries, aquaculture and public health. While HAB monitoring takes place in many regions of the world, some areas are not covered, which allows fish killing events to take place with little to no warning and without follow-up. This project aims to develop a methodology for modeling the global risk of fish-killing HAB species presence in both well-monitored and undersampled regions. Observations of species were queried from the Ocean Biodiversity Information System (OBIS). The data was then matched with environmental covariates such as sea surface temperature, mixed layer depth, etc. Multiple approaches were tested to model the risk distribution of target species, from a climate envelope to machine learning. The former considers the possibility that a taxon can occur within the range of environmental conditions in which it has been observed. The latter used randomly generated background points, in combination with the presence observations, to fit and tune a suite of machine learning model types. The performance of each model was validated using fish-killing events found in the Harmful Algal Event Database (HAEDAT), in addition to expert opinion from members of the Intergovernmental Panel on Harmful Algal Blooms task teams. Risk maps were deployed onto a prototype online interactive mapping tool, Earth Map – a climate data analysis tool developed by the Food and Agriculture Organization of the United Nations. Maps feature species of interest, oceanographic covariates, and the plotting of harmful algal events listed in HAEDAT. High skill was achieved from all approaches tested, but some trade-offs exist between them considering the deployment and long-term maintenance of each method, and regarding extrapolation into undersampled regions. The next steps of the project include modeling additional species, refining the prototype online tool, and incorporating end-user feedback.

From Ship to Shore: Growing Capacity for HAB Response in the Alaskan Arctic

Evangeline Fachon[1]*, Gay Sheffield*[2]*, Emma Pate*[3]*, Thomas Farrugia*[4]*, Chris Whitehead*[5]*, Kathi Lefebvre*[6]*, Patrick Charapata*[7]*, Mrunmayee Pathare*[1]*, Michael Brosnahan*[1]*, Don Anderson*[1]

[1]Woods Hole Oceanographic Institution, Woods Hole, MA, USA
[2]Alaska Sea Grant, Marine Advisory Program, University of Alaska Fairbanks, Nome, AK, USA
[3]Nome Eskimo Community, Nome, AK, USA
[4]Alaska Ocean Observing System, Anchorage, AK, USA
[5]Ocean and Earth Environmental, Jacksonville, FL, USA
[6]NOAA/Northwest Fisheries Science Center/Environmental and Fisheries Science Division/WARRN-West, Seattle, WA, USA
[7] Center for Species Survival, Georgia Aquarium, Atlanta, GA, USA

Until recently, Alaskan Arctic waters have been considered too cold for significant harmful algal bloom (HAB) development, but regional warming and loss of sea ice are increasing the likelihood of HAB occurrence in this region. The impacts of HABs on environmental health, food security, and seafood safety are of great concern to the peoples of northern and western Alaska who comprehensively utilize the marine food web for nutritional, cultural, and economic well-being. These threats were brought to the forefront during summer 2022, when a massive and highly toxic bloom of *Alexandrium* was detected by a shipboard Imaging FlowCytobot (IFCB) during an offshore research cruise in the northern Bering and Chukchi seas. Since then, shipboard HAB observing has expanded across the region, and IFCB deployments aboard cruises of opportunity have been used to characterize and communicate subsequent offshore HAB events. In each case, real-time data collection and HAB assessment are used to craft risk advisories in collaboration with shore-based rural Alaskan entities; these advisories are used to mobilize regional community response. In addition to recent successes, this presentation will highlight challenges and limitations of these efforts, as well as the importance of synergy between shipboard observing and shore-based communication networks. Building from these collaborations, regional seawater monitoring and educational programs have been implemented, and public awareness about harmful algal toxin impacts in northern waters continues to grow. These efforts include the development of algal and toxin testing laboratory resources operated by coastal Arctic environmental and tribal governments. Looking forward, continued engagement and capacity-building at the community level alongside further investment in sustained observing technology will be essential in mitigating the risks of Alaskan Arctic HABs.

Modified Clay (MCII) Effects on Suspended Brevetoxins and Bacterial Profiles

***Catherina Fagan*[1]*, Jennifer H. Toyoda*[1]*, Vic Simons*[1]*, Nicholas Ohnikian*[1]*, Christopher Sibley*[1]*, Kirstie Francis*[1]*, Bayne Landreth*[1]*, Donald M. Anderson*[2]

[1]Mote Marine Laboratory, Sarasota, Fl, USA
[2]Woods Hole Oceanographic Institution, Woods Hole, MA, USA

Clay dispersal has been shown to remove *Karenia brevis* cells and toxins from the water column. Clay flocculates with itself and with cells which sink to the seafloor, removing intracellular toxins, however the effect of clay on extracellular toxins is not well understood. This study investigated the fate of extracellular brevetoxins after application of modified clay II (MCII) in a closed saltwater system containing *K. brevis* lysate. Untreated controls and MCII-treated tanks were sampled 0, 5, 24, 48, and 72 hours after treatment. Brevetoxin partitioning and degradation were analyzed within the water column, floc-associated water, and settled floc material. Concurrently, bacterial community composition was identified by 16S amplicon sequencing and bacterial abundance was quantified by quantitative polymerase chain reaction (qPCR) targeting the 16S rRNA gene. MCII treatment altered both brevetoxin distribution and microbial dynamics. Brevetoxins were reduced by 28.3% and 67.9% within 72 h in treated and untreated tanks, respectively, suggesting treatment prevented brevetoxin degradation. Toxins in floc decreased over time and brevetoxin concentrations were lower in floc-associated water than in the water column, indicating MCII has a direct effect on toxins in close proximity. Sequencing data showed changes in bacterial community composition after clay treatment. Bacterial abundance increased in both treatments over time; however, MCII-treated tanks exhibited a lower relative increase (4.93-fold) versus control tanks (11.94-fold). This suggests suppression of microbial proliferation in the presence of MCII, which may inhibit bacteria-mediated toxin degradation. These data indicate brevetoxins do not adsorb to clay during flocculation but may be degraded in close association with clay in floc. Additionally, effects on bacterial communities can influence the fate of toxins after clay application. This highlights the importance of evaluating microbial communities when assessing ecological impacts of HAB mitigation technologies. This work was supported by NOAA National Centers for Coastal Ocean Science PCMHAB grant.

Recent Discovery of Recurring *Alexandrium* Blooms in the Southeast Bering Sea

Thomas J. Farrugia[1]*, Evie Fachon*[2]*, Kathi Lefebvre*[3]*, Michael Brosnahan*[2]*, Donald Anderson*[2]

[1]Alaska Ocean Observing System, Anchorage, Alaska, USA
[2]Woods Hole Oceanographic Institution, Falmouth, Massachusetts, USA
[3]NOAA, Northwest Fisheries Science Center, Environmental and Fisheries Science, Seattle, Washington, USA

Marine living resources are a primary source of food throughout Alaska, 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 becoming more frequent and expanding into new areas leading to 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 make HAB monitoring and research difficult. Imaging FlowCytobots (IFCBs) facilitate the detection of HABs and can help alert nearby communities of potential threats to their marine resources. During the summers of 2024, 2025 and 2026, the Alaska Ocean Observing System (AOOS) deployed multiple IFCBs aboard research vessels to monitor for HABs in the Gulf of Alaska, Aleutian Islands, and the Bering, Chukchi and Beaufort Seas. Several potential HAB species were detected at low levels by these IFCBs with blooms of *Alexandrium catenella* detected multiple years in the Southeast Bering Sea region. As part of a communication plan established before the initiation of research cruises, rapid advisories were sent to coastal communities in the region to alert them of blooms and of potential steps they can take to mitigate the impact of the bloom (e.g. modifying harvesting behaviors). Although the discovery of a recurring bloom in the Southeast Bering Sea is relatively recent, its location coincides with the presence of a large *Alexandrium* cyst bed, indicating that the changing ocean conditions may now be ripe for these annual summer blooms to continue into the future.

Machine Learning-Based Prediction of Microcystin Across Multi-Use Pond Systems in South Carolina

Morolake M. Fatunmbi, *Debabrata Sahoo*

Clemson University, Clemson, South Carolina, USA.

Ponds are constructed and used for a variety of purposes, including irrigation, livestock watering, recreation, and stormwater control, and the different functions they serve can strongly influence nutrient inputs and overall water quality. Given such variability, understanding how these factors affect harmful algal bloom dynamics, particularly microcystin production, is critical for protecting human health, livestock, and aquatic ecosystems. This study will apply machine learning approaches to predict microcystin concentrations across diverse pond systems in South Carolina. A total of 75 ponds, representing irrigation, livestock, recreational, and stormwater uses, were sampled, and water quality parameters were measured to characterize physicochemical and biological conditions. Currently, these variables are being used as input features to develop predictive models using multiple machine learning algorithms, including multiple linear regression, random forests, support vector machine, light gradient boosting, and extreme gradient boosting. Model development involves data preprocessing, feature engineering, and hyperparameter optimization via cross-validation. To improve predictive performance and model robustness, an ensemble modeling framework will be implemented by integrating outputs from individual models. Model performance will be assessed using standard evaluation metrics, including the coefficient of determination (R^2) and root mean square error (RMSE), on independent validation datasets. A feature importance analysis will be conducted to identify key water quality drivers that primarily influence microcystin prediction. This study aims to improve the understanding of the factors controlling microcystin occurrence in multi-use pond systems. The outcomes will provide insight into dominant predictors of toxin production and support the development of data-driven management strategies to mitigate risks associated with harmful cyanobacterial blooms in freshwater ponds.

From Harmful Blooms to Agricultural Resources: Valorization of Cyanobacterial Biomass from a Tropical Reservoir

Maria Carolina Capellini, Éryka Almeida, Gabriel Schimmelpfeng Passos, Dominique Stenico, Ernani Pinto, and ***Kelly Afonsina Fernandes***

Center for Nuclear Energy in Agriculture, University of São Paulo, Piracicaba, São Paulo, Brazil

Harmful cyanobacterial blooms generate large amounts of biomass in eutrophic freshwater systems, yet the potential valorization of this environmental biomass remains poorly explored. This study evaluated the chemical, taxonomic, and agronomic characteristics of cyanobacteria-rich biomass collected from the Tietê River Basin, São Paulo, Brazil. Biomass processing and drying conditions were evaluated, followed by chemical characterization of nutrients, amino acids, potentially toxic metals, and cyanotoxins. Microbial composition was assessed through taxonomic and metataxonomic analyses, and agronomic potential was investigated in greenhouse experiments using lettuce seeds and seedlings. The biomass showed high total nitrogen content (8.06 g/100 g) and contained nutritionally relevant amino acids, including glutamic acid, aspartic acid, leucine, valine, and alanine. Relevant macro- and micronutrients included calcium (672 mg/100 g), iron (321 mg/100 g), phosphorus (276 mg/100 g), potassium (148 mg/100 g), and magnesium (112 mg/100 g). Potentially toxic metals were below regulatory limits for organic fertilizers, while relevant cyanotoxins were not detected in the analyzed samples. Metataxonomic characterization showed Cyanobacteriota (*Microcystis* sp. and *Pseudoanabaena* sp. or *Limnothrix* sp.) as a major component of the microbial community, together with diverse bacterial and fungal groups. Greenhouse assays evaluated plant responses to the processed environmental biomass. Complementary analyses are ongoing to investigate potential cyanotoxin transfer to lettuce tissues and enzymatic activity in exposed plants. These findings demonstrate the nutritional potential of naturally occurring cyanobacterial bloom biomass and support further evaluation of its agricultural use within circular strategies for eutrophic freshwater management.

Evaluation of Novel Biobased Algaecides for the Control of Microcystin-Producing Cyanobacteria

Maria Carolina Ferreira, *David E. Berthold, Autumn Taylor, Jéssica A.S. Moretto, Forrest W. Lefler, Israel Urcuyo, H. Dail Laughinghouse IV*

Agronomy Department, Fort Lauderdale Research and Education Center, University of Florida / IFAS, Davie, FL, USA.

Cyanobacterial harmful algal blooms (cyanoHABs) are an increasing concern due to their adverse effects on aquatic ecosystems, drinking water resources, and public health, due to their production of cyanotoxins such as microcystins (MC). This study evaluated the efficacy of two novel biobased algaecide formulations for mitigating toxic *Microcystis*-dominated cyanoHABs under both controlled laboratory and environmentally relevant mesocosm conditions. Laboratory experiments used *Microcystis* sp. BLCC-F108, while mesocosm trials utilized bloom material collected from Lake Okeechobee. Low- and high-density bloom cultures were exposed to multiple algaecide application rates and monitored over 72 hours for changes in abundance and MC concentrations. Both formulations rapidly reduced abundance within 24 hours compared to untreated controls. Total MC concentrations were generally lower in treated cultures; however, aqueous MC concentrations increased following treatment, indicating toxin release associated with cellular lysis. Mesocosm experiment designed to simulate natural bloom and field treatment conditions supported laboratory findings. The mesocosms containing bloom material from Lake Okeechobee showed substantial reductions in cyanobacterial abundance and photosynthetic efficiency within 48 hours of treatment. Similar to laboratory observations, treatment-induced cellular lysis resulted in a shift from intracellular to aqueous MC, highlighting the importance of understanding toxin dynamics during bloom mitigation. Overall, these findings demonstrate that biobased algaecides have strong potential for suppressing toxic *Microcystis* blooms while emphasizing the need for optimized application strategies and post-treatment toxin monitoring to support safer and more sustainable cyanoHAB mitigation approaches.

Automated In Situ Nutrient Monitoring: Connecting Nutrient Dynamics to HAB Response and Management Actions

***Alexis D. Fischer**, Scott Shuler, Max Milone, Vince Kelly*

EutroPHIX, Carmel, IN, USA

Nutrient forms, concentrations, and ratios can influence harmful algal bloom (HAB) initiation, termination, and toxin production. These dynamics can unfold over hours to days, but traditional nutrient monitoring often occurs at much longer intervals. High-frequency biological sensors, including imaging-in-flow cytometry, have transformed our ability to observe phytoplankton dynamics in near-real time. Yet nutrient measurements have not kept pace. In most monitoring programs, nutrients are measured from infrequent grab samples analyzed later in the laboratory, producing isolated snapshots of rapidly changing systems. This temporal mismatch limits our ability to connect nutrients to biological response, inform management actions, and evaluate the results of those actions. The NuLAB platform addresses this gap by bringing established wet-chemical nutrient analyses into the field. This autonomous “chemistry robot” quantifies nitrate + nitrite, soluble reactive phosphorus, ammonia + ammonium, total nitrogen, total phosphorus, and silicate in situ with near-real time data access. To date, shore-based NuLAB deployments in the coastal ocean, lakes, and rivers have been used to build long-term nutrient time series, quantify external loading when paired with flow data, and support adaptive nutrient management. Here, we introduce the first NuLAB buoy prototype, which samples surface and bottom waters and pairs nutrient measurements with co-located multiparameter sonde data. This allows nutrient concentrations to be interpreted alongside water column stratification, oxygen dynamics, algal fluorescence, and other parameters. Deployed in a Utah waterbody, the buoy captured seasonal sediment nutrient release and tracked the response to sediment phosphorus mitigation. By resolving nutrient dynamics as they happen, this approach opens new opportunities to investigate how complex nutrient conditions drive HABs and to evaluate management responses in near-real time.

Towards a Unifying Harmful Algal Bloom Hazard and Risk Framework

Lisa R. Fogarty[1]*, Jennifer L. Graham*[2]*, Daniel K. Jones*[3]*, Tyler V. King*[4]

[1]U.S. Geological Survey, Lansing, Michigan
[2]U.S. Geological Survey, Troy, New York
[3]U.S. Geological Survey, Salt Lake City, Utah
[4]U.S. Geological Survey, Boise, Idaho

Perceived, potential, or actual harms serve as the foundational motivation for a rich body of harmful algal bloom research. While our ability to detect hazards such as algal biomass or toxins at potential levels of concern has advanced, the linkages between these hazards and ecologic, economic, or public health harms often remain implicit. As such, decision-makers are faced with evaluating consequences and managing tradeoffs using incomplete information about potential future harms. The U.S. Geological Survey is advancing a coordinated national program to improve harmful algal bloom prediction, monitoring, and mitigation through integrated research spanning detection technologies, exposure pathways, algal bloom dynamics, and decision-support tools. To guide this effort, a structured framework is needed to evaluate hazards, characterize vulnerabilities, and support transparent, defensible mitigation and management strategies. The U.S. Geological Survey is developing a harmful algal bloom hazard and risk framework to serve as a roadmap for research and development that ultimately results in tools to directly inform decisions. The framework will facilitate knowledge transfer and empower proactive, transparent, and efficient harmful algal bloom risk management. Collaboration with state, Federal, Tribal, and academic partners will broaden the framework's applicability across diverse freshwater systems. This poster presentation is an opportunity to begin critical conversations as the framework is being developed and the applications are being discussed.

Permitting Challenges for Field Testing Novel Marine Harmful Algal Bloom Control Technologies

Siena Fouse

National Sea Grant Law Center, Oxford, MS, USA

Testing harmful algal bloom (HAB) control technologies in marine environments is uniquely challenging due to environmental factors and overlapping jurisdictions, statutes, and regulations. Before last year, no one had successfully gone through the permitting process to test a marine HAB control product in the United States since the 1972 enactment of the Clean Water Act. With funding from US HAB-CTI, the National Sea Grant Law Center conducted legal research, engaged in conversations with agency staff, and developed case studies to map out the regulatory framework of the permitting process. This information will be shared through a publicly accessible website to provide guidance to researchers. This presentation will provide an overview of challenges to permitting the field testing of marine HAB control technologies. Crucially, marine environments are publicly controlled open systems with moving water used for fishing and swimming and home to threatened and endangered species and critical habitat. Researchers have more limited ability to conduct studies when testing HAB control products in marine settings than in, for example, a privately-owned isolated artificial pond. In inland settings it is often easier to isolate species, ensure no one swims or fishes in the area, and have a lower risk of impeding navigation. In marine waters, without that control and isolation, researchers must ensure compliance with a host of laws and regulations including the Federal Insecticide, Fungicide, and Rodenticide Act (FIFRA); the Federal Food, Drug and Cosmetic Act (FFDCA) tolerance requirements; the Clean Water Act (CWA); the Marine Protection, Research, and Sanctuaries Act (MPRSA); the Rivers and Harbors Act (RHA); and the Endangered Species Act (ESA). My team and trailblazing researchers are working to develop relationships that strengthen interagency coordination and improve awareness of the regulations and permits required for experimental use through commercial expansion.

Evaluation of In Situ Chlorophyll Fluorescence Sensors for Detecting Cyanobacterial Colonies

Nicholas Framsted[1]*, Tim Baxter*[1]*, Keith Bouma-Gregson*

U.S. Geological Survey, California Water Science Center

Continuous in situ chlorophyll fluorescence (fCHL) sensors are essential for providing real-time phytoplankton data for the early detection of cyanobacterial blooms. However, the colonial morphology of some bloom forming taxa may be difficult for these sensors to detect. In the Sacramento-San Joaquin Delta of California, the colonial cyanobacterium *Microcystis* often forms large (~1 cm diameter) colonies that are sparsely distributed. There are often discrepancies between field observations and in situ fCHL concentrations, with fCHL concentrations often underestimating the biomass of colonial cyanobacteria compared to other sampling methods. Using laboratory experiments, we evaluated several factors that may affect the detection capability of fCHL sensors, such as sampling volume, sampling rate, colony size and density, and mixing intensity. Preliminary results indicate that the sensors could detect *Microcystis* colonies with recorded high fCHL concentrations over 300 µg/L. This suggests that the sensor excitation and emission wavelengths are sufficient, but other elements in the design and operation may prevent detection. The sensors had small sampling volumes, and fCHL concentrations declined by 80% below their maximum concentration when colonies were moved 1 centimeter from the sensor face in the best performing sensor. In simulated field conditions, detection frequencies of colonies were less than 50%. Detection frequencies improved when colonies were mechanically disaggregated to smaller sizes (<1 mm diameter) and increased to 100% in the best performing sensor with fCHL values that matched laboratory chlorophyll-a values. We also found that the detection frequency increased with colony density and higher mixing intensity. Overall, the preliminary results reveal that larger sampling volumes and faster sampling rates led to improvements in detecting colonial cyanobacteria and help identify design improvements for the early detection of *Microcystis* colonies.

Forecasting Domoic Acid Depuration in the U.S. West Coast Dungeness Crab Fishery Empowers Adaptive Monitoring, Management, and Business Decisions

Christopher M. Free[1]*, Andrew O. Shelton*[2]*, Stephanie K. Moore*[2]*, Daniel S. Holland*[2]

[1] University of California, Santa Barbara, CA, USA
[2] Northwest Fisheries Science Center, Seattle, WA, USA

Harmful algal blooms (HABs) that produce biotoxins often force the closure of socioeconomically important fisheries to protect public health. Improved understanding of *in situ* biotoxin depuration rates would allow the fishing industry to make business decisions that mitigate the socioeconomic impacts of such closures and fishery managers to make decisions that facilitate more efficient monitoring and management of biotoxin risk. On the U.S. West Coast, *Pseudo-nitzschia* blooms that produce the potent neurotoxin domoic acid are causing more frequent and extended closures in the highly lucrative Dungeness crab (*Metacarcinus magister*) fishery. Here, we use data from state-run biotoxin monitoring programs to quantify *in situ* temperature-dependent rates of domoic acid depuration in Dungeness crab. We find that, on average, wild Dungeness crab depurated domoic acid at a rate of 1.05% a day, equivalent to a half-life of 65.7 days. This is more than 10 times slower than the 6.2 day half-life reported by a published lab study in which crabs were fed uncontaminated clams after obtaining peak toxicity. Depuration rates were faster when bottom temperatures were warmer. We use these results to develop a web tool that predicts when domoic acid levels will fall below the food safety threshold based on recent toxicity and temperature observations. The tool and its predictions can empower the fishing industry to make business decisions about when and where to fish, and can empower coastal resource managers to make informed decisions about the implementation of closures versus other mitigation strategies (e.g., evisceration or removal of the guts) and where to prioritize monitoring.

Marine Biotoxin Depuration rates: Management Applications, Research Priorities, and Predictions for Unstudied Species

Christopher M. Free*, Yutian Fang*

University of California, Santa Barbara, CA, USA

Monitoring and managing the public health risk posed by marine biotoxins is a daunting challenge. With expansive coastlines, 1000s of seafood species, and dozens of biotoxins, monitoring cannot occur everywhere at once. Improving the cost-effectiveness of biotoxin monitoring is thus critical to expanding coverage to include more species, toxins, and locations. Notably, understanding the rate at which seafood species depurate biotoxins can be used to optimize the cadence of monitoring. We conducted a systematic review to collate marine biotoxin depuration rates and synthesize the factors that influence them; identify knowledge gaps, best practices, and research priorities; and generate predictions of depuration rates for unstudied species. We found that only 85 marine species have been studied for their biotoxin depuration rates. Depuration rates for non-bivalves and for toxins besides paralytic shellfish toxins (PSTs) are especially understudied. Depuration half-lives varied from 0.03 to 1269 days based on species, toxin, tissue, and environmental conditions. In general, depuration accelerates with increased temperature and food availability, with implications for aquaculture siting, depuration enhancement, and biotoxin monitoring. We identified unstudied bivalve and finfish species that are highly produced and vulnerable to HABs that are high priorities for future research. Finally, we used a Bayesian regression model to predict PST depuration rates for 102 unstudied bivalve species, the only clade-syndrome with sufficient training data. These predictions can guide efficient monitoring and management until laboratory- or field-based depuration rates become available. We recommend that future studies directly estimate depuration rates to ensure their comparability across studies and utility to managers.

Principles of Effective, Efficient, and Adaptive Biotoxin Monitoring and Management: Lessons from the U.S. West Coast

Christopher M. Free

University of California, Santa Barbara, CA, USA

Harmful algal blooms (HABs) that produce biotoxins that accumulate in seafood pose an increasing threat to public health, aquaculture, commercial, recreational, and subsistence fishing. Given limited resources for spatially, temporally, and taxonomically expansive biotoxin testing, biotoxin monitoring and management must become more efficient and adaptive to protect public health while simultaneously minimizing impacts on coastal food systems. The U.S. West Coast states of California, Oregon, and Washington have monitored and managed seafood biotoxins since the 1960s, though often with different approaches and outcomes. The review of these programs for their strengths and weaknesses thus offers a unique opportunity to curate a set of broadly applicable best practices for effective biotoxin monitoring and management. We reconstructed the spatial-temporal history of biotoxin monitoring and management across the U.S. West Coast and identified and exemplified nine best practices for effective, efficient, and adaptive biotoxin monitoring and management: (1) conduct regular monitoring to detect unexpected risk; (2) optimize the cadence of monitoring based on toxicokinetics; (3) trigger seafood testing in response to other indicators of biotoxin risk (e.g., HAB abundance/toxicity, seabird or marine mammal strandings, oceanographic risk indicators); (4) define clear, relevant, and small biotoxin management zones; (5) when safe, use alternative management actions (e.g., processing requirements, preparation advisories) to protect public health while avoiding closures; (6) ensure that monitoring covers all vulnerable species or manage unmonitored species using indicator species; (7) prioritize toxins, species, regions, and seasons with greatest risk to limit costs while protecting public health; (8) partner with fishermen to collect samples, especially when likely to open fisheries; and (9) clearly communicate both what is known and unknown about biotoxin risk to support informed food safety decisions. These principles are applicable to other regions seeking to more effectively, efficiently, and adaptively monitor and manage the growing risk posed by HABs and seafood biotoxins.

Cyanotoxins and Inflammation: Cellular and Molecular Mechanisms Driving HAB-Associated Organ Damage

Andrew Fribley

University of Toledo College of Medicine and Life Sciences, Toledo, OH, USA

Cyanobacterial harmful algal blooms generate a complex mixture of toxins and bioactive metabolites that may trigger inflammatory responses in exposed tissues. This presentation will focus on cellular and molecular mechanisms that link cyanotoxin exposure to organ damage. We will discuss how microcystins and other bloom-associated compounds can disrupt cellular homeostasis, alter stress response pathways, impair mitochondrial function, and promote immune activation. Particular emphasis will be placed on inflammatory signaling, oxidative and endoplasmic reticulum stress, mitochondrial dysfunction, barrier injury, and cell death pathways that may contribute to tissue pathology. The talk will also consider how exposure context, including toxin mixtures, repeated low-dose exposure, and pre-existing disease, may shape the biological response to cyanotoxins. By integrating mechanistic cell biology with preclinical and community health observations, this presentation will highlight candidate pathways and biomarkers that can be used to connect environmental exposure with clinically relevant outcomes. These mechanistic insights are essential for identifying susceptible populations, refining risk assessment, and developing strategies to prevent or reduce harmful algal bloom-associated organ injury.

A Milestone in Water Restoration: The Multifunctional Power of Lake Guard® Oxy

Jessica R. Frost[1,2*]*, Amanda Foss*[3]*, Cynthia Heil*[4]*, Jennifer Toyoda*[4]

[1]Emerge Marine, Sarasota, Florida, USA
[2]Formerly with BlueGreen Water Technologies, Gainesville, Florida, USA
[3]Greenwater Laboratories, Palatka, Florida, USA
[4]Mote Marine Laboratory, Sarasota, Florida, USA

Harmful algal blooms (HABs) present severe ecological, economic, and public health threats across global aquatic systems. Conventional algaecides often suffer from poor scalability and high environmental toxicity, necessitating targeted, eco-friendly remediation alternatives. Lake Guard® Oxy, a proprietary granular formulation developed by BlueGreen Water Technologies, was used for mitigating toxic algae blooms in distinct aquatic environments like freshwater cyanobacteria (e.g., Microcystis spp.) and marine dinoflagellates (Karenia brevis). Lake Guard® Oxy uses the active ingredient sodium percarbonate that is encapsulated within a patented, biodegradable, hydrophobic coating. This specialized formulation provides buoyancy, allowing the granules to float and dynamically drift with winds and currents to aggregate specifically where high-density surface HABs can occur. When mixed with water, the granules slowly release hydrogen peroxide (H2O2), which acts as an oxidizing agent. In freshwater environments, cyanobacteria exhibit an exceptionally high sensitivity to oxidative stress caused by reactive oxygen species (ROS) like H2O2 as compared to non-toxic eukaryotic green algae. Their physiological response involves distinct photosynthetic disruption and degradation to the cellular membrane. In marine environments, this same oxidative mechanism affects Karenia brevis, the dinoflagellate responsible for devastating Florida red tides. The chemically induced oxidative stress disrupts cellular membranes and paralyzes photosynthetic activity resulting in complete elimination and viability of K. brevis cells. Lake Guard® Oxy also significantly reduces extracellular brevetoxins produced by K. brevis resulting in mitigating the danger of aerosolized toxins. Notably, Lake Guard® Oxy decomposes entirely into harmless water and oxygen molecules, leaving no toxic chemical residues or persistent environmental footprint. Lake Guard® Oxy represents a highly scalable, safe, and dual-action technology capable of mitigating HABs in both fresh and marine environments.

Comparison of Two Passive Samplers for Monitoring of 25+ Toxins across the U.S. Marine-to-Freshwater Continuum

***J.A. Garber*[1]*, A.O. Tatters*[2]*, D. Shea*[3] *R.M. Kudela*[4]*, A.R. Place*[5]*, J.L. Smith*[1]

[1]Virginia Institute of Marine Science, Gloucester Point, VA, USA
[2]University of Washington, Forks, WA, USA
[3]Statera, Raleigh, NC, USA
[4]Ocean Sciences & Institute for Marine Sciences, University of California, Santa Cruz, CA, USA
[5]Institute of Marine & Environmental Technology, University of Maryland Center for Environmental Science, Baltimore, MD, USA

Harmful algal blooms are becoming an increasingly complex concern as they continue to grow in terms of distribution and frequency. They are a phenomenon which occur in freshwater, brackish, and marine environments producing numerous classes of toxins ranging in size and polarity. Monitoring programs must account for this physicochemical diversity when implementing policies to track toxin presence and identify emerging toxins of concern. A national field study was conducted to evaluate the performance of two passive samplers. The frequently used solid phase adsorption toxin tracker (SPATT) with HP20 resin was tested alongside a novel passive sampler, Composite Integrated Passive Samplers (CIPS). First, the two types of samplers were co-deployed in coastal or estuarine waters of nine states (Hawaii, Washington, California, Texas, Louisiana, Florida, Virginia, Maryland, Rhode Island) to investigate their ability to sorb a range of toxins within varying aquatic environments. Secondly, the samplers were co-deployed at three sites and collected daily for one week to determine the rate of toxin uptake on both samplers, and the loss of infused standards from CIPS. Liquid-chromatography/mass spectrometry was used to quantify 25+ toxins (dinophysistoxins, brevetoxins, azaspiracids, yessotoxins, anatoxins, microcystins, cylindrospermopsin, pectenotoxins, domoic acid, karlotoxins, nodularin, anabaenopeptin, spirolide, pinnatoxin-G, and goniodomin-A) on both samplers and infused standards lost from CIPS. 13 of the 25 quantified toxins were detected throughout the entire study. We found two states where both freshwater and marine toxins were present, California (anatoxin and 7 marine toxins) and Louisiana (microcystin-LR and 3 marine toxins). Co-occurrence of toxins was common (76% of sites) and 88% of sites had at least one toxin. Okadaic acid was the most frequently detected followed by pectenotoxin-2 and 13-desmethylspirolideC. Results demonstrate that specific toxins are better retained on one sampler than the other and these exceptions should be considered when utilizing these tools in monitoring programs.

Ocular Symptoms Associated with Estimated Aerosolized Brevetoxin Exposure During *Karenia Brevis* Blooms

Garcia ME[1], *Aldrich GJ*[1], *Ortiz C*[1], *Ferguson S*[1], *Helgager D*[1], *Kirkpatrick B*[2], *Eric Milbrandt*[3], *Paris D*[1], *Crawford F*[1], *Mullan M*[1] *Abdullah L*[1],

1) Roskamp Institute, Sarasota, FL, USA,
2) Gulf of America Coastal Ocean Observation System, College, Station, Texas, USA
3) Sanibel-Captiva Conservation Foundation, Sanibel, FL, USA

Background: Blooms of the marine dinoflagellate *Karenia brevis* (*K. brevis*) occur recurrently along Florida's Gulf Coast, resulting in repeated environmental exposure of coastal populations to aerosolized brevetoxins (PbTx). Although the respiratory effects of inhaled PbTx are well established, previous lifeguard occupational health studies and analyses of electronic medical records have also documented ocular symptoms associated with *K. brevis* bloom exposure. However, the ocular effects of brevetoxin exposure remain poorly characterized.

Objective: To evaluate participant-reported ocular symptoms associated with estimated exposure to aerosolized PbTx during *K. brevis* blooms.

Methods: A community-based cohort of 158 participants was recruited from counties in Southwest Florida, as well as Gulf and Bay counties in Florida's Panhandle. A surrogate brevetoxin exposure for the air (SBE_{air}) was derived from *K. brevis* cell counts and their established relationship with PbTx concentrations in the water and subsequent aerosolized PbTx concentrations. Each participant was classified as SBE_{air}-negative (n = 120) or SBE_{air}-positive (n = 38) according to the maximum estimated aerosolized PbTx concentration during the 14 days preceding the participant's study visit. Demographic characteristics and participant-reported symptoms were compared by exposure status using Pearson's chi-square test or Student's t-test, as appropriate.

Results: Eye irritation was reported more frequently by SBE_{air}-positive than SBE_{air}-negative participants (26.3% vs. 5.8%, respectively; $p < 0.05$), as was eye redness (15.8% vs. 1.7%; $p < 0.05$). Eye dryness, pain, double or blurred vision, and vision loss did not differ significantly between exposure groups. In addition to these ocular findings, consistent with prior work, participant reported a higher prevalence of upper respiratory symptoms during bloom: sore throat (21.0% in SBE_{air} positive versus 7.5% SBE_{air}-negative and coughing (SBE_{air}-positive 57.9% vs SBE_{air}-negative 15.0%).

Conclusion: Estimated exposure to aerosolized PbTx during *K. brevis* blooms was associated with a higher prevalence of participant-reported eye irritation and redness, suggesting a potential relationship between aerosolized PbTx exposure and ocular symptoms. Further analyses incorporating relevant confounding factors, including age, are needed to assess the robustness of this association and to characterize potential exposure-response relationships.

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Impact of Nutrients on Algal Growth and Toxin Production in Skaneateles Lake

***Emily Garlock*[1], *Zac Triumph*[1], *Dominique Derminio*[2], *Stephan B Shaw*[2], *Gregory L. Boyer*[1]**

[1]Department of Chemistry, State University of New York College of Environmental Science and Forestry (SUNY ESF), Syracuse, NY, United States

[2]Department of Environmental Resources and Engineering, State University of New York College of Environmental Science and Forestry (SUNY ESF), Syracuse, NY, United States

Cyanobacterial harmful algal blooms (cHABs) can impact water quality and can affect recreational activity around the lake. Generally, cHABS are observed in eutrophic lakes, however there are increasing reports of cyanobacteria blooms in oligotrophic lakes. Skaneateles Lake is an oligotrophic lake (average TP < 5 ug/L) in the Finger Lakes region of New York and is an important source of drinking water. Over the past decade, Skaneateles Lake has experienced an increasing number of cHABs dominated by a single genus *Microcystis*. The lake is phosphorus-limited and has implemented a 9-element plan focusing on phosphorus reduction. However, there is increasing evidence that nitrogen may also play a role in oligotrophic lakes. Here we conducted nutrient addition experiments over the summer to determine the effects of added nitrogen, phosphorus and nitrogen + phosphorus on algal productivity. Bottles were incubated both *in situ* and in the laboratory. Each treatment was analyzed after 3, 7 and 14 days using the bbe FluoroProbe and for microcystin production. Early in the season, the lake was strongly phosphorus limited and dominated by green algae and diatoms. As the season progressed into August (the cyanobacteria growth season), the cyanobacteria did respond to added phosphorus alone but were stimulated by added phosphorus and nitrogen. Toxin formation per cyanobacteria chlorophyll did not change with nutrient addition, suggesting that the increase in toxin concentrates observed with N&P addition were due to increased cyanobacteria biomass and not a change in the cellular toxin production rate. This work suggests that a dual nutrient limitation management approach may have significant advantages for oligotrophic lakes as well as for eutrophic lakes.

Periphyton Response to Nutrient Enrichment Experiments in the Illinois River

Jessica D. Garrett

U.S. Geological Survey, Iowa City, Iowa, USA

Experimental nutrient diffusing substrates were deployed in the Illinois River during the summers of 2022 and 2023 to assess the effects of nutrient additions on periphyton productivity, community composition, and cyanotoxin production. The Illinois River is heavily utilized for industry, agriculture, navigation, and recreation and has widespread sources of anthropogenic nitrogen and phosphorus inputs. These nutrients are linked to harmful algal blooms, though this connection is not well understood in riverine systems. Nutrient diffusing substrates were deployed in the Illinois River near Starved Rock Marina, Ottawa, Illinois. Three separate field deployments included a control group and five treatment groups amended with combinations of nitrogen (nitrate or ammonium) and phosphorus (phosphate). The deployment location was selected based on ease of access, good connection with the main river channel, protection from hazards such as boat traffic and recreators, and in proximity to an area where cyanobacterial blooms are known to occur on the Illinois River. Productivity was assessed using several metrics including measurements of chlorophyll *a*, pheophytin *a*, biomass, and in-field primary production and respiration determined by rate of change of dissolved oxygen in light and dark bottles. Community composition was described by microscopic particle taxa classification with flow imaging microscopy. Cyanotoxins were analyzed by enzyme-linked immunosorbent assay (ELISA) for microcystins, cylindrospermopsins, anatoxins, and saxitoxins.

Toxicity of Freshwater Cyanobacterial Blooms on Human Small Airway Epithelial Cells

***Maria Garzon-Ramirez*[1]*, Tamas Jilling*[1]*, Claire Fisher*[1]*, Kevin Kroll*[2]*, Sarah Bisesi*[2]*, Maria Carolina Ferreira*[3]*, Jessica Moretto*[3]*, David Berthold*[3]*, Dail Laughinghouse*[3]*, Nancy Denslow*[2]*, Tara Sabo-Attwood*[1]

[1]University of South Carolina, Columbia, South Carolina, United States
[2]University of Florida, Gainesville, Florida, United States
[3]University of Florida, IFAS, Davie, Florida, United States

Freshwater HABs are commonly composed of cyanobacteria, which produce cyanotoxins—diverse secondary metabolites associated with significant health effects. Microcystin-LR (MC-LR) is a toxic congener known for causing hepatotoxicity upon ingestion. Despite evidence of MC-LR aerosolization from water bodies, respiratory effects from inhalation remain unknown. This gap led us to investigate the toxicity of cyanobacteria-containing MC-LR to human lung cells.

Microcystis aeruginosa (MA) with high levels of MC-LR (2.4 ng/ug biomass) and *Floridanema aerugineum* (FA) with non-detectable MC-LR, were isolated from freshwater bodies in Florida and maintained in culture. MC-LR was quantified by Liquid Chromatography Mass Spectrometry. Lysed cyanobacterial aliquots were added to growth media of cultured small airway epithelial cells (SAECs) at increasing concentrations (120, 240 and 480 ng MC-LR/mL media). As a toxin-only control, one group received purified MC-LR (200 µg/mL). After 48-hours, cell viability was characterized by flow cytometry and transcriptomic changes analyzed by RNA sequencing (RNA-seq).

SAECs exposed to MA showed a dose-dependent decrease in viability with increased apoptotic and dead cells. Purified MC-LR caused similar effects, while FA caused no significant cellular changes compared to controls. Despite disparate cytotoxicity, RNA-seq revealed both MA and FA induced significant transcriptomic changes. Of 1191 gene changes, 222 were common between FA and MA, with most modifications unique to each. Exposures to FA and MA share TNF and IL-17 signaling; FA enriches NF-kappa B, NOD-like receptor and ER processing, while MA enriches JAK-STAT and cytokine-cytokine receptor interactions.

This work reveals some of the first data supporting unique toxicity to lung cells, dependent on both strain and toxin. These observations support that the lung may be a site of toxicity of inhaled HABs. Future work is aimed at better understanding the mechanism behind such toxicity.

Ciguatera Poisoning Incident Investigations: Lessons from Five Years of Data Collection

***Kirk Gaston**, Karl Klontz, Ron Benner, Karen Swajian*

FDA, Dauphin Island, AL, USA

Ciguatera poisoning (CP) is endemic to many tropical and subtropical coral reef regions of the world. Different suites of ciguatoxins have been identified in the Pacific (P), Indian (I), and Caribbean (C) oceans, which has given rise to three CTX-group toxins. Because of differences in toxin profiles in these regions, symptom patterns in humans have differed such that, in the Caribbean, gastrointestinal symptoms and signs are often prominent early in illness outbreaks and followed largely by peripheral neurologic symptoms thereafter. In contrast, in Pacific and Indian Ocean regions, neurologic and cardiovascular signs and symptoms are pronounced in the acute phase of illness. Pacific ciguatoxin-1 (P-CTX-1) is the principal and most potent ciguatoxin found in fish in the Pacific, while Caribbean ciguatoxin-1 (C-CTX-1) is less toxic than P-CTX-1 and is the main ciguatoxin in the Caribbean. P-CTX-1 is generally considered to be 10 times more toxic than C-CTX-1.

Advisory levels advanced by the U.S. Food and Drug Administration (FDA) based on a review of 109 outbreaks of CP in the U.S. from 1998 – 2008 and CONTAM Panel conclusions, FDA concluded these studies served as a basis for industry and consumer advisory levels of 0.10 µg C-CTX-1 eq./kg fish from the tropical Atlantic, Gulf of Mexico, and Caribbean and 0.01 µg P-CTX-1 eq./kg fish from Pacific regions.

Here, we present findings from a recent five-year series of CP cases in the United States and Puerto Rico. In addition to describing epidemiologic and clinical features of illness, we provide quantitative estimates of ciguatoxin ingested by a subset of 21 cases. Noting that some ill individuals consumed estimated amounts of ciguatoxin from fish found to contain <0.1 µg C-CTX-1 eq./kg and yet experienced illnesses significant enough to seek medical care, we believe these observations could be relevant to existing public health guidance regarding concentrations of ciguatoxin present in fish which cause human illness.

Genetic Diagnostics for Rapid Detection of Toxic Pseudo-nitzschia Species

Taylor Gibson, *Camden Conte[2], Alex DeSmidt[2], Yida Gao[3], Sydney Greenlee[4], Robin Sleith[4], Kate Hubbard[2], Pete Countway[4], Shelly Wanamaker[5], Matthew Harke[1]*

[1]Gloucester Marine Genomics Institute, Gloucester, MA, USA
[2]Florida Fish and Wildlife Conservation Commission, St. Petersburg, FL, USA
[3]Woods Hole Oceanographic Institute, Woods Hole, MA, USA
[4]Bigelow Laboratory for Ocean Sciences/University of Maine, East Boothbay, ME, USA
[5]University of Washington, Seattle, WA, USA

The pennate diatom *Pseudo-nitzschia* occurs globally and is known to produce the neurotoxin domoic acid (DA), causing Amnesic Shellfish Poisoning (ASP), which can have detrimental effects on both marine life and humans. Current monitoring efforts primarily use light microscopy to identify *Pseudo-nitzschia* threat potential but are unable to distinguish between toxic and non-toxic species. In addition, as blooms of *Pseudo-nitzschia* progress, there can be fluctuation in toxin levels driven by both biotic and abiotic factors, creating a need for rapid detection of domoic acid threat. Existing toxin detection tests require lab expertise, can be expensive, and have long turn-around time for results. Genetic methods offer rapid, sensitive assays that can be run in the lab, as well as be field deployable. Here, we have developed quantitative PCR (qPCR) and isothermal amplification (LAMP) + CRISPR assays to detect if dabA, the first gene in the domoic acid biosynthesis operon, is present and/or being expressed in two known toxic *Pseudo-nitzschia* species, *P. australis* and *P. multiseries*. These assays have been tested across synthetic material, cultured isolates, and field samples and are able to detect both DNA and RNA in less than an hour. With these molecular tools, the time to detect toxin threat is reduced, allowing for quicker decision making by state managers to be able to protect public health.

Shifting Nutrient Sources and Shifting Baselines Contribute to More Sustained *Karenia brevis* Blooms

Patricia M. Glibert[1], *Cynthia Heil*[2], *Ming Li*[1], *Joaquín Martínez Martínez*[1], *Emily Hall*[2], *Amanda Muni-Morgan*[3], *So Hyun Ahn*[1,4], *Yuren Chen*[1], *Bruna Sobrinho*[1], *Nayani Vidyarathna*[1]

[1]University of Maryland Center for Environmental Science, Horn Point Laboratory, Cambridge, MD, USA
[2]Mote Marine Laboratory, Sarasota, FL, USA
[3]Ecosystem Insights LLC, St. Petersburg, FL, USA
[4] Korea Institute of Science & Technology, Geoje, South Korea

Karenia brevis blooms, increasing in frequency and duration in recent years on the West Florida Shelf (WFS), are initiated and sustained by a range of nutrient sources. In this talk, these nutrient sources will be reviewed, bringing new data to bear and placing different nutrient sources in the context of bloom stage and changing environments. Blooms are generally initiated offshore in association with nitrogen released from co-occurring *Trichodesmium* blooms and have been thought to be maintained in oligotrophic waters through recycling. It is now known that land-based nutrient sources are helping sustain these blooms inshore for up to 4 to 5 months longer than in previous decades, a trend related to increased flow from the Caloosahatchee River and its total nitrogen load. Warming waters are also contributing to faster rates of nitrogen regeneration. Another source of nutrients is submarine groundwater discharge, and the blue holes that dot the Florida coast are active sites of nitrogen processing related to river flow. The role of mixotrophy is also better understood, with grazer rates dependent on temperature and relative prey availability (picoplankton). Mixotrophy, as shown by recently modeling, is most important at the offshore front for the bloom, where the importance of land-based nutrients is less. The frequent hurricanes of recent years also enhance nutrient and dissolved organic (humic) material inputs. Such humic inputs (brownification) amplify respiratory metabolism while warming enhances dissolved organic matter (DOM) degradation, shifting the system toward net heterotrophy; high respiration rates of the dinoflagellates may lead to oxygen depletion. Viral interactions also increase under warming conditions leading to potential cell demise but also further release of nutrients. Seasonally, nutrients from river discharge are important in early bloom stages, with increasing dependence on regeneration and mixotrophy/microbial interactions in later stages.

Needle in a Haystack: Using Satellites in Concert with Other Tools to Predict Low Biomass, Vertically Migrating, and Near-shore HABs

Christopher J. Gobler

School of Marine and Atmospheric Sciences, Stony Brook University, Southampton, NY

Since its inception, Harmful Algal Bloom (HAB) monitoring has encountered a "space-time" problem. Single-point time-series analyses document bloom evolution but may not be representative beyond a single locale. Conversely, synoptic surveys provide detailed spatial resolution but fail to capture the time course of bloom development. Satellites offer incredible promise as a tool to overcome these shortcomings by providing broad spatial coverage and a daily refresh rate. From a managerial perspective, this represents a highly desirable outcome; indeed, modeling breakthroughs by NOAA and others have provided excellent predictive tools for HABs from Lake Erie to the Gulf of Mexico. Still, not all HABs leave behind signatures optimized for satellite detection. In New York, a multitude of marine and freshwater HABs occur annually, creating a need for managers to protect public health while concurrently safeguarding aquaculture and shellfisheries. Until recently, HABs in New York were dominated by *Aureococcus anophagefferens* and *Margalefidinium polykrikoides*, whose high-biomass signatures made them relatively easy to detect via satellite. More recently, however, blooms caused by *Alexandrium catenella* and *Dinophysis acuminata* have become more common. Beyond their propensity to synthesize biotoxins, these HABs often arise as part of a consortium of other phytoplankton and may form subsurface thin layers—attributes that may cause them to evade satellite detection. A second complexity regarding these events is their tendency to initiate in enclosed, nearshore water bodies. Ultimately, the implementation of a multi-technology suite will likely be required to overcome the grand challenges of detecting HABs that are low-biomass, vertically migrate, or develop nearshore.

Solving the Mystery of Brown Tide: Co-evolution of Watersheds, Fisheries, HABs, and HAB Science

Christopher J. Gobler

School of Marine and Atmospheric Sciences, Stony Brook University, Southampton, NY

In 1985, a novel HAB deemed "brown tide" occurred simultaneously in estuaries across NY, NJ, and RI. It caused mass devastation of habitats (e.g., seagrass meadows) and fisheries; the collapse of the bay scallop fishery in NY alone represented more than a $100M cumulative loss. The causative organism was identified as *Aureococcus anophagefferens*, a picoplanktonic pelagophyte that was previously unknown, making it both a scientific mystery and an enormous managerial challenge. Initial, locally supported studies yielded slow scientific progress. In 1996, NOAA's ECOHAB program was launched, with the Brown Tide Research Initiative being among its first activities. This initial program funded eight investigations into the biological, chemical, and physical processes that promoted brown tides; more than 10 ECOHAB projects exploring brown tides followed. These projects led to a series of discoveries that evolved alongside the science of HABs and facilitated a deep understanding of the initiation, peak, and demise of these events. Interestingly, many of the discoveries that have been made are coherent with changes occurring in NY during the past 50 years. For example, ECOHAB studies evolved from culture-based to field-based and eventually genome-based approaches to identify the key role that elevated dissolved organic nitrogen (N) plays in promoting brown tides. Concurrently, watershed-wide analyses revealed that the installation of nearly 400,000 onsite septic systems had progressively enriched N levels in groundwater entering bloom-prone estuaries. ECOHAB research also identified the importance of filter-feeding bivalves in controlling or allowing brown tides. The onset of brown tides in the 1980s in NY coincided with the depletion of hard clam populations, which allowed for the unfettered proliferation of this HAB. Critically, the findings of these ECOHAB studies facilitated local initiatives to restore bivalve populations and upgrade septic systems. In happy news, brown tides have been absent following these managerial changes.

Development of RPA–CRISPR/Cas12a Platform for Rapid In Situ Detection of Harmful Algal-Forming Cyanobacteria

Seung Ho Chung, Alyxandra S Cicerrella, Anna Antrim and ***Ping Gong***
U.S. Army Engineer Research and Development Center, Vicksburg, MS, U.S.A.

Harmful algal blooms (HABs) are caused by toxin-producing cyanobacteria, posing significant risks to public health, aquatic ecosystem functions, and water quality. Timely and accurate monitoring of these cyanobacteria is essentially important for effective management and prevention of HABs. Although various technologies, such as microscopy, ELISA, and qPCR, have been employed for HABs-forming cyanobacteria detection, they are often time-consuming, require specialized laboratory equipment, and are not practical for rapid, on-site applications in the field. To address these limitations, we developed a fast and simple on-site detection system utilizing recombinase polymerase amplification (RPA)-CRISPR/Cas12a technology to monitor cyanobacteria of interest or concern. In this study, we designed and validated RPA primers and guide RNAs (gRNAs) targeting the 16S rRNA gene for specific detection of *Microcystis aeruginosa*, one of the cyanotoxin-producing cyanobacteria. We optimized key reaction parameters, including incubation temperature and time, and the concentrations of Cas12a, gRNAs, and signal probes to enhance the assay performance. Additionally, we prepared and optimized lyophilized RPA–Cas12a reagents, eliminating the need for cold-chain logistics for field deployment. The RPA-CRISPR/Cas12a assay demonstrated high specificity for *M. aeruginosa* and enabled qualitative and quantitative detection that were achieved by using a lateral flow strip and a fluorescence reader, respectively. Therefore, the RPA-CRISPR/Cas12a assay offers a simple, rapid and field-deployable solution for detection of HABs causing cyanobacteria in the field. This innovative detection system will provide a practical tool for early warning and proactive management of HABs.

Genetic Engineering of Cyanophages for Harmful Algal Bloom Mitigation: Current Status and Future Perspectives

Erin Peters, Anna Antrim, Alyx Cicerrella, Natalie Barker, Xiao Luo, ***Ping Gong***

Environmental Laboratory, US Army Engineer Research and Development Center, Vicksburg, MS, USA

Harmful algal blooms (HABs) occur when microscopic photosynthetic algae grow rapidly. HABs have become a global environmental problem as they can disrupt ecosystem functions and cause deterioration of water quality and harmful effects on human beings, grazing zooplankton and wildlife through nutrient shifting, hypoxia, and release of toxins. A novel treatment utilizing cyanophages, viruses that specifically infect cyanobacteria, has gained traction due to their natural availability and high host specificity. However, cyanophages have two main limitations preventing them from being a viable treatment option: (a) some cyanophages have a lysogenic phage in which their genome is incorporated into the host genome instead of proceeding with replication and lysis, and (b) many cyanophages are extremely host-specific, some infecting only a single strain of cyanobacteria, which has limited efficacy as a treatment for HABs containing multiple species of cyanobacteria. Genetic engineering methods could provide a solution to addressing both these limitations through generating genetically modified cyanophages without a lysogenic cycle and with a broadened host range. Current research supports the possibility of utilizing established gene editing techniques from bacteriophage models, but additional verification and optimization experiments must be done to advance the field.

Molecular Tools for Detecting and Monitoring Harmful Algal Blooms

***Ping Gong**, Seung Ho Chung, Anna Antrim, Alyx Cicerrella, Erin Peters, Natalie Barker, Xiao Luo*

Environmental Laboratory, US Army Engineer Research and Development Center, Vicksburg, MS, USA

Harmful algal blooms or HABs occur when microscopic photosynthetic algae grow out of control. HBAs have become a global environmental problem. Early, rapid and accurate detection of HABs may enable preventative strategies and facilitate informed decision-making and targeted mitigation actions. There are many methods available for HABs monitoring, including microscopic identification and enumeration (e.g., light microscopy and automated FlowCam imaging and analysis), hyperspectral imagery, biosensing, spectrophotometry, fluorometry, biochemical assays (ELISA, chlorophyll and phycocyanin), and molecular techniques. In this presentation we will introduce some of the existing and widely used molecular techniques as well as emerging ones, including PCR (polymerase chain reaction), qPCR (quantitative PCR), SHA (sandwich hybridization assay), RPA- Cas12a (recombinase polymerase amplification coupled with CRISPR associated protein 12a), 16S/18S ribosomal RNA amplicon sequencing, and metagenomic sequencing. We will use case studies to illustrate their applications, discuss their individual pros and cons, and demonstrate their respective advantages, such as high sensitivity and specificity of amplification-based PCR, qPCR and RPA-Cas12a, cell culturing-independence, community-wide profiling of amplicon and metagenomic sequencing, and portability and field deployability of RPA-Cas12a-based assays. Compared with the currently employed routine monitoring methods that are often slow, labor intensive and non-specific (i.e., measuring the total phytoplankton biomass), molecular tools generally have a quicker turnaround and higher accuracy, and produce more taxonomically specific data. Many of these powerful molecular tools have been accepted for HABs application and are poised to substitute for or supplement current methods, especially in addressing the growing demands for rapid, in situ and species-specific HABs monitoring under field settings.

Modeling Changes in Habitat Suitability of Emerging Harmful Algal Taxa on the Texas Coast

***Susana M. Gonzalez**, Michael S. Wetz*

Harte Research Institute, Texas A&M University-Corpus Christi, Corpus Christi, Texas, USA

Environmental modeling has become pivotal in efforts to predict the occurrence of harmful algal blooms (HABs) and to mitigate their impacts. Co-occurring species abundance and environmental data are necessary for this, but historical data for many HAB species can be limited, especially for emerging or understudied taxa. On the Texas coast, there is a growing repository of presence-absence data collected for these less common HAB species, in conjunction with relevant environmental data that can be utilized to better understand environmental drivers of HABs. This presentation describes the construction of habitat suitability models for some of these emerging HAB taxa, including *Prorocentrum cordatum*, *Akashiwo sanguinea*, and *Pseudonitzschia spp.*, using presence-absence observations from several bays along the Texas coast. These models will be projected onto Texas estuaries under present day and expected future environmental conditions. Collective use of data from these bays resulted in models that most often identified salinity and orthophosphate as key predictors of presence. However, the relative importance of different water quality variables changed when bays were isolated in the model building process. The most significant model was found when observations from Baffin Bay were used in isolation for training and testing, and in this case, temperature and ammonium were found to be the most important predictors (*Prorocentrum cordatum* model statistics: Accuracy = 0.737, No Information Rate = 0.602, p-value = 0.001, Area Under Curve = 0.709). Baffin Bay is known to be a unique ecosystem because of regular low inflow and hypersaline conditions, and these findings suggest that habitat suitability modeling for individual species may need to be done at local and regional scales to better identify drivers and inform models and mitigation efforts.

Recreational Responses to Cyanobacterial Harmful Algal Blooms in U.S. National Parks: Evidence from Monthly Visitation and Satellite Data

Tony Good[1]***,*** *Keith Loftin*[2]

[1]US Geological Survey, Science and Decision Center, 12201 Sunrise Valley Drive, Reston, VA 20192, USA
[2] US Geological Survey, Central Plains Water Science Center, Algal and Other Environmental Toxins Laboratory, 1217 Biltmore Drive, Lawrence, KS 66049, USA

Cyanobacterial harmful algal blooms are an increasing environmental and public health concern, with documented impacts on drinking water, ecosystems, and outdoor recreation. Blooms are stimulated by nutrient enrichment, warming temperatures, and altered hydrology, and they can produce toxins that threaten both human and animal health. Despite the well-documented ecological and health impacts of these events, little is known about whether cyanobacterial harmful algal blooms influence recreation on federally managed lands. This study addresses this gap by linking satellite-derived cyanobacteria indices from the Cyanobacteria Assessment Network with aggregate monthly visitation data from the National Park Service Visitor Use Statistics Program across 64 National Park Service units from 2018 to 2024. The Cyanobacteria Assessment Network produces harmonized, long-term measures of cyanobacterial abundance across lakes and reservoirs based on satellite imagery from the Sentinel-3 Ocean and Land Colour Instrument. Recreational exposure is defined using standardized World Health Organization recreational guidance thresholds for cyanobacteria-dominated waters to ensure comparability across parks. We estimate the relationship between bloom conditions and visitation using panel models with high-dimensional fixed effects that control for park-specific seasonality, time-varying shocks at the park level, and weather conditions. Identification comes from within-park variation in visitation associated with fluctuations in bloom conditions relative to each park's typical seasonal pattern and annual trend. By integrating satellite-derived environmental indicators with observed visitation behavior, this study provides the first national-scale empirical framework for assessing the recreational implications of cyanobacterial harmful algal blooms on federally managed lands.

Microcystin Congeners and Relations to Water Quality in New York State Lakes

Benjamin J. Kramer[1], James H. Larson[2], Gregory L. Boyer[3], Matthew Kraft[4], Brian Duffy[4], Jennifer L. Graham[5], ***Rebecca M. Gorney***[5]

[1]U.S. Geological Survey, Ann Arbor, MI, USA
[2]U.S. Geological Survey, La Crosse, WI, USA
[3]State University of New York, College of Environmental Science and Forestry, Syracuse, NY, USA
[4]New York State Department of Environmental Conservation, Albany, NY, USA
[5] U.S. Geological Survey, Troy, NY, USA

Cyanobacterial harmful algal blooms can pose health risks to humans, pets, and wildlife through the production of cyanotoxins including microcystins. Risk assessment and health guidance development are complicated by the diversity of microcystin congeners, variability in toxicity, and unclear drivers of congener relative abundance. To characterize environmental drivers of microcystin congener occurrence and abundance, we analyzed a multi-year dataset (2014 – 2021; n=538 samples) of microcystin congener concentrations from 36 lakes in New York (USA). The dataset represents considerable variability in lake size (0.05–50 km^2) and trophic status (oligotrophic to hypereutrophic). Our objectives were: (1) evaluate spatial and temporal patterns in congener prevalence; (2) evaluate relations between abiotic factors (nitrogen, phosphorus, and specific conductance) and congener abundance; (3) determine whether cyanobacteria community composition is related to congener occurrence; and (4) develop and apply a congener-specific toxicity-weighted index to assess trends in relative toxicity. Microcystin concentrations varied considerably (range of <3 to >1,000,000 µg/L, median=103 µg/L). More than 20 microcystin congeners were detected across the dataset and among these, eight congeners exhibited the highest concentration in at least one sample. The most frequently detected congeners were -LR, -LA, and -YR. In pairwise correlation analyses, congeners varied in their relation to water quality parameters. *Microcystis*, *Woronichinia*, and *Aphanizomenon* were the most common taxa and co-occurred with nearly every congener. In a global linear model, no single environmental parameter or group of parameters (water quality, trophic state, mean depth, etc.) predicted toxicity; among the parameters, specific conductance was the strongest predictor ($p<0.1$). Findings from this work will support more robust microcystin risk frameworks and inform monitoring strategies across trophic conditions.

50 Years of Riverine Harmful Algal Bloom Modeling: Approaches, Challenges, and Opportunities

Jennifer L. Graham[1]*, Jennifer C. Murphy*[2]*, Rebecca M. Gorney*[1]*, Lisa A. Lucas*[3]*, Jacob A. Zwart*[4]

[1]U.S. Geological Survey, Troy, New York
[2]U.S. Geological Survey, DeKalb, Illinois
[3]U.S. Geological Survey, Moffett Field, California
[4]U.S. Geological Survey, San Francisco, California

We conducted a systematic literature review of harmful algal bloom modeling in riverine systems to identify persistent gaps, clarify emerging challenges, and highlight opportunities to advance future modeling efforts. Across 162 articles representing 80 rivers worldwide, most studies focused on large, eutrophic systems with flow modifications. Approaches were dominated by process-based models, though use of data-driven methods increased over time. Nutrients, light, streamflow, physiological processes, and temperature were key predictors, though algal processes were rarely included in data-driven models. Endpoints varied and some studies included multiple measures; chlorophyll and algal abundance or biovolume were most common, but few models addressed toxins. While all articles described at least one harm that motivated the modeling effort, most only implicitly linked the modeling endpoint to the stated motivation. The weak linkage between modeled endpoints and actual harms highlights an important challenge for the field. Five other challenges emerged: 1) available datasets may be missing important processes; 2) key environments are underrepresented; 3) modeling efforts are geographically clustered and are not necessarily occurring in areas with the highest occurrence or risk; 4) insufficient documentation of river features limited cross-study synthesis and 5) disparate skill metrics and endpoints limited model comparability. Opportunities include leveraging estuarine modeling advances to better characterize riverine complexities, developing benchmark datasets to allow focus on model improvement, improving contextual reporting to facilitate cross-system and model-performance comparisons, and expanding community-driven tools to promote rapid advances. Addressing these challenges and opportunities will enhance model transparency, transferability, and ultimately support operational riverine harmful algal bloom forecasting for management and public health applications.

Overview of Economic Research on HABs: Uses and Research Needs

Gretchen Greene[1], *Sabine Postma*[2],*Miles Bukowsk*[2]

[1]Greene Economics, Ridgefield, WA, USA
[2] Greene Economics, Seattle, WA, USA

The economic impact of Harmful Algal Blooms has raised concern since at least the 1970s - - when note was taken of the economic stimulus associated with spending on cleanup and scientific analyses to understand the blooms! Since then much work has been completed to understand that the economic damage from a bloom is a function of the biophysical characteristics of the bloom itself, the size and nature of the exposed economy, and the response system that mediates between these two features. This presentation will cover the highlights of economic research to date on HABs, focusing on pathways between the bloom and the impact, and also the different economic approaches used to measure impacts. Each of the approaches will be described using actual research examples from Florida and other regions, emphasizing how different economic approaches may be appropriate depending on the purpose of the research. The presentation will address the importance of quantifying impacts to the economy and how decision-makers can use the information to make better choices about control and management of HABs. Outstanding issues of measurement will be identified, and an assessment of research needs will conclude the presentation.

Do Nitrogen and Acidification Make a 'Perfect Storm' for Harmful Algal Blooms?

Dianne I. Greenfield*[1,2]*, *Penny Vlahos*[3]*, Julia Sandke*[2,1]*, Rachel Spera*[3]*, Emma Rosser*[1]

[1]Advanced Science Research Center, City University of New York, New York, NY, USA
[2]Queens College, City University of New York, Flushing, NY, USA
[3]Marine Sciences Department, University of Connecticut, Groton, CT, USA

The combined ecosystem stressors of elevated nitrogen (N), ocean acidification (OA), and harmful algal blooms (HABs) characterize many urban estuaries, but they are particularly acute in the Long Island Sound (LIS) and nearby New York (NY) and Connecticut (CT) embayments encompassing the NYC metropolitan area. These systems receive N inputs from wastewater, runoff, and other sources, making them epicenters for numerous HAB taxa and their impacts. N and OA have been shown to independently affect HAB development and toxicity, but their synergistic impacts are not well understood. This new ECOHAB project tests the hypothesis that HAB and OA dynamics are inextricably linked through their associations with N-form and concentration through field studies and experimentation, in order to provide stakeholders with new tools that assess HAB risk. Using the LIS region, here we describe initial (Y1) field efforts, emphasizing phytoplankton genera (*Alexandrium*, *Dinophysis*, *Pseudo-nitzschia*) identified by NY/CT water quality and shellfish managers as priorities. Monthly surveys were conducted in the LIS mid-channel year-round, as well as bi-weekly (shore and mid-channel) spring-early fall to measure water quality, nutrients, HABs (cell abundances, toxin) and OA (full carbonate system) beginning July, 2025. Sample locations spanned areas of both varying aragonite saturations and active shellfish harvesting, with sampling frequency increasing following reports of a HAB. To augment routine surveys, local communities and shellfish commissions participated in two full-day 'HAB-blitzes' across LIS (late spring, early fall) to assess large-scale HAB species distributions.

Gene-Environment Interactions Pertaining to Saxitoxin

***Matthew O. Gribble**, Baylin Bennett*

University of California, San Francisco, San Francisco, CA, USA

Although the primary toxicity noted for saxitoxin and related compounds is sodium channel binding, there are other toxicity targets, and may be biological impacts beyond the acute toxidrome known as paralytic shellfish poisoning. This literature review leveraged the Comparative Toxicogenomics Database (CTDbase) to identify genes that have been noted as interacting with "saxitoxin" (a chemical name in the database that also covers some related compounds); there might be congener-specific interactions not reflected in the results of this search. As of May 14, 2026, there were 4,443 results for gene-environment interactions reported for saxitoxin. The gene-environment interaction results indexed in CTDbase were from six toxicological models: zebrafish embryos (PMC11645194); bovine adrenal chromaffin cells (PMID 19486905); equine macrophages (PMC7345530); murine hippocampal neuronal cells [cell line HT-22] (PMID 29128272), murine macrophage-like immune cells [cell line RAW 264.7] (PMC7345530), and murine neuroblastoma cells [cell line N2A] (PMID 29228856). No CTDbase-indexed results on saxitoxin gene-environment interactions came from studies of human-derived cells or human populations (e.g., genetic epidemiology). We entered these gene lists into the Database for Annotation, Visualization, and Integrated Discovery (DAVID) and did pathway enrichment analysis for those gene lists using the Kyoto Encyclopedia of Genes and Genomes (KEGG). In a *Danio rerio* (zebrafish) model, there were 122 significantly enriched pathways. The 5 gene pathways that were significantly enriched for a *Homo sapiens* model were: coronavirus disease/ COVID-19, basal cell carcinoma, metabolic pathways, Fanconi anemia, and the Hippo signaling pathway**.** We suspect that several of the documented gene-environment interactions may be downstream consequences resulting from sodium channel binding, for example sodium intake has been shown to impact Hippo signaling (PMC11900413, PMC3749438). Further research is warranted to evaluate the potential for other biological effects of saxitoxins than acute emergency poisoning events, including research on chronic, lower-level exposures and cancers associated with these gene pathways.

HAB Control Technologies & Regulatory Logistics (HAB CTRL) Webpage: A resource for Researchers and Managers

Amy E. Grogan*, C. Taylor Armstrong, Allen R. Place*

University of Maryland Center for Environmental Sciences, Institute of Marine and Environmental Science, Maryland, USA

Harmful algal blooms are a ubiquitous issue in fresh and marine waters. Several mitigation strategies are used to combat HABs, but preventative actions often fall short in tackling the nation's largest issues. Recurring HAB events, such as those caused by *Karenia brevis, Pseudo-nitzschia, Alexandrium, Margalefidinium, Aureococcus,* and a suite of harmful Cyanobacteria, damage economies, natural resources, and environmental functions, and pose risks to public health. With climate change and anthropogenic activity exacerbating the severity of HABs, the "wait it out" strategy is no longer a viable option. However, the current selection of HAB treatments is limited or non-existent for most marine HABs. New control technologies with limited indirect impact are needed, but to date, well-meaning regulations have stifled innovation. The EPA's Federal Insecticide, Fungicide, and Rodenticide Act (FIFRA) permits algaecide products in the US. FIFRA approval is costly and time-intensive, requires exhaustive data submission, and a stringent review process. In an effort to streamline the regulatory process for new HAB control products, the Harmful Algal Bloom Control Technologies and Regulatory Logistics Webpage (HAB CTRL), a product of the US Harmful Algal Bloom Control Technologies Incubator (HAB CTI), provides step-by-step guidance from development through deployment. HAB CTRL is a multifaceted resource highlighting FIFRA and state-specific approval procedures, HAB management efforts and needs, current and emerging HAB issues and control technologies, and information on additional regulatory acts governing algaecide deployment. This website will be an invaluable tool for HAB researchers, control product developers, stakeholders, and algaecide end users.

A Hyperspectral Perspective of Phytoplankton Pigment Variability: From Diagnostic Pigments to Physiology and Phenology

Brice Grunert[1], *Audrey Ciochetto*[1,2], *Kelly Hondula*[3], *Emily Hyland*[1], *Kendra Herweck*[1], *Anshula Dhiman*[1], *Greg Asner*[3]

[1]Cleveland State University, Cleveland, OH, USA
[2]University of Rhode Island, Narragansett, RI, USA
[3]Arizona State University, Hilo, HI, USA

Phytoplankton community structure, and the emergence of blooms both harmful and not, are one of the most dynamic components of aquatic ecosystems. Driven by spatiotemporally diverse processes, the development and evolution of algal blooms represents a balance between environmental state, such as light and nutrient availability, and phytoplankton community response to these conditions. Satellite datasets offer a means of observing whole ecosystem dynamics, but to date, our perspective of phytoplankton communities has been largely tied to bulk properties of biomass and general community partitioning based on size or specific, harmful phytoplankton groups through diagnostic pigments. Hyperspectral imagers, such as NASA's PACE Ocean Color Instrument and Planet's Tanager, offer spectrally dense, spatially resolved datasets that respond to individual phytoplankton pigments. What these datasets offer, particularly our ability to observe phytoplankton pigment variability and relate to phenology, physiology, and the evolution of harmful algal blooms, is still being discovered. Here, we provide an overview of past multi- and hyperspectral capabilities and how these have translated to hyperspectral imagers. Then, we introduce current and planned hyperspectral capabilities for observing phytoplankton pigment variability. Through the use of in situ data, we demonstrate how variable pigment profiles inform phytoplankton phenology and physiological response to changing environmental conditions. We then link this perspective to targeted validation of NASA's PACE Ocean Color Instrument and Planet's Tanager, including strengths and limitations of hyperspectral tools, to frame how phytoplankton community dynamics, including harmful algal blooms and emergent, event-driven aquatic features, can be observed and characterized through pigment variability and hyperspectral imagers.

Automated Retrieval of Phycocyanin Concentrations Using Sentinel-2 MSI and Machine Learning With Independent Validation

***Natalie C. Hall**, Kendall C. Wnuk, Leah E. Staub, Tristan G. Mohs, Laura J. Wortman*

U.S. Geological Survey, MD-DE-DC Water Science Center, Catonsville, MD, USA

While chlorophyll-*a* is traditionally used to develop remote-sensing-based predictive models for the monitoring of harmful algal blooms (HABs), other pigments can also be used. Phycocyanin, a pigment unique to cyanobacteria, can be used as an indicator of potentially toxic blooms, although the ability to distinguish phycocyanin from other HAB-related pigments using satellite data has not been intensively researched. Existing models are local or regional, trained on individual lakes and rivers, or focused on limited monitoring stations. A larger-scale machine-learning model to predict phycocyanin concentrations could augment spatial and temporal areas that lack in-situ water quality instrumentation and data related to HABs monitoring efforts. Using historical multispectral data, we have developed a machine-learning model trained to predict phycocyanin concentrations as an essential step towards the distinction of cyanobacterial taxa from other phytoplankton and chlorophyll-*a* containing organisms. A training dataset, composed of sonde-based, in-situ phycocyanin data from continuous monitoring stations across the contiguous United States (CONUS), was matched with spatially and temporally coincident Sentinel-2 surface reflectance data from 2015-2024 to train a Random Forest model. Model performance on a CONUS-wide scale was assessed using spatial cross-validation and fully independent validation data. Model performance on the independent validation dataset demonstrated moderate predictive skill, achieving an R^2 of 0.52 across 9,386 paired observations and an RMSE of 0.79 Relative Fluorescence Units. Overall results indicate that, despite limitations of validation data sourced from spatially continuous boat surveys, the model still performs reasonably well in reproducing observed spatial and temporal patterns of phycocyanin. This study emphasized the use of remotely sensed data to distinguish between phycocyanin and other optically active constituents, with results producing a model with the ability to independently identify phycocyanin concentrations across varying concentrations of turbidity, dissolved organic matter, and chlorophyll-*a*.

Class-level Phytoplankton Net Growth Rates Defy Expectations Based on Intrinsic Growth in a River-dominated Estuary

Nathan S. Hall

UNC Chapel Hill Institute of Marine Sciences, Morehead City, NC, UNC

Maximum growth rates and temperature optima are often used to predict impacts of changes in residence time and water temperatures on phytoplankton community composition. This reasoning implicitly assumes that intrinsic growth (rate of cell division) is the dominant factor controlling phytoplankton populations, and that loss factors play weaker roles. The assumption of the dominance of intrinsic growth in controlling class-level community composition was tested by comparing the net growth of phytoplankton class-level biomass during downstream transport in a river-dominated, microtidal estuary. Class-level net growth rates were calculated as the regression slopes of freshwater age on log-transformed HPLC-derived class-level biomass for the first ten days after freshwater had entered the estuary. Net growth was then compared across phytoplankton classes and under different temperature conditions. Dinoflagellates, which are known to have slow intrinsic growth rates, had net population growth rates that were 60-70% higher than diatoms, which are known to have much faster intrinsic growth. Additionally, temperature played only a minor role in governing net growth rates despite its well-established first-order control on intrinsic growth. Results provide a reminder that intrinsic growth is not always the dominant factor determining population growth rates. Environmental influences on population losses can strongly shape phytoplankton communities in ways that defy expectations based only on intrinsic growth, and, in ways that may be hard to explore with small scale experiments.

As We Drink, Bathe, and Breathe: Preclinical Models of Multi-Organ Cyanotoxin Injury in the Great Lakes

Steven Haller

University of Toledo College of Medicine and Life Sciences, Toledo, OH, USA

Human exposure to cyanobacterial harmful algal blooms can occur through drinking water, recreational contact, and inhalation of aerosolized bloom material, yet the comparative health impacts of these exposure routes remain incompletely understood. This presentation will summarize preclinical approaches used to model cyanotoxin injury across multiple organ systems relevant to Great Lakes communities. We will discuss experimental designs that examine ingestion, dermal, and inhalational exposure to cyanobacterial toxins and bloom-associated mixtures, with attention to dose, exposure duration, and susceptibility factors. Emphasis will be placed on organ systems that may be affected after environmentally relevant exposures, including the lung, liver, kidney, cardiovascular system, and immune system. The talk will highlight evidence for inflammation, oxidative stress, tissue injury, and impaired repair responses as convergent outcomes across models. We will also describe how preclinical studies can complement field monitoring and human health observations by providing mechanistic insight, identifying biomarkers of exposure and effect, and informing risk assessment for vulnerable populations. Together, these models provide a framework for understanding how Great Lakes bloom exposures may contribute to multi-organ injury.

Cyanobacteria – From Biomass to Toxins

Sophia Feuerhake, ***Julie Hambrook Berkman***

Association to Preserve Cape Cod, Dennis, Massachusetts, US

The Cyanobacteria Monitoring Program, initiated by the Association to Preserve Cape Cod (APCC) in 2017, monitors harmful cyanobacteria blooms (HCBs) across Cape Cod's freshwater ponds in partnership with towns and volunteer groups. Since 2019, it has produced a standardized dataset spanning ~140 ponds and 160 monitoring sites (2025). Insights from biweekly biomass monitoring, including regional bloom dynamics and fluctuations across the years will be presented. In addition, the evolution of APCC's toxin monitoring, from laboratory-based ELISA analyses for microcystin (2022) to expanded anatoxin sampling and rapid strip testing (2025) will be summarized. Comparison of strip test results and ELISA to assess strip test reliability showed that in ~59% of paired microcystin samples and ~13% of paired anatoxin samples, strip tests did not detect toxin concentrations that were measured above the 0.4 ppb detection limit by ELISA. In contrast, only one anatoxin strip test detection at ~0.4 ppb was not detected by ELISA; all other anatoxin and microcystin strip test detections were confirmed by ELISA, suggesting that false positives from strip tests are relatively uncommon. Our key takeaway is that strip tests can serve as an early warning tool for health officials, while confirmatory ELISA testing should continue for a subset of non-detects in visibly cyanobacteria-impacted ponds to further assess agreement between methods. Relationships between biomass and the toxin microcystin are examined, showing general alignment during Microcystis-dominated blooms but substantial variability that limits predictive use. Methods used to communicate risks will be highlighted, including pet-focused cyanobacteria outreach brochures for veterinarians developed in collaboration with the Woods Hole Oceanographic Institution.

Efficacy and Scale-Up of Engineered Phages Against Microcystin Producing *Microcystis aeruginosa* Blooms

Scott D. Hamilton-Brehm[1]*, Lahiru N. Jayakody*[1]*, Charlotte Narr*[1]*, Marjorie L. Brooks*[1]*, Sandhya Jayasekara*[1]*, Bhagya Jayantha*[1]*,* and *Hannah Phillips*[1]

[1]Southern Illinois University, Carbondale, USA.

Harmful algal blooms are increasing in frequency and severity in freshwater systems throughout the united states and globally. A major concern is the proliferation of *Microcystis aeruginosa*, a dominant bloom-forming cyanobacterium that, like other cyanobacteria, produces microcystins, including microcystin-LR, a potent hepatotoxin and potential human carcinogen. Microcystins are often cell-associated and can be released into surrounding water upon cell lysis, creating challenges for conventional bloom-control strategies such as algicides, mechanical disruption, or other approaches that may unintentionally increase toxin release. Because microcystins are difficult to remove once released, new mitigation strategies are needed that suppress toxin production while minimizing ecological disturbance.

We are developing an engineered phage-based platform to selectively target *M. aeruginosa* and reduce microcystin production. Our approach uses a modified bacterial phage as a molecular delivery vehicle for antisense oligonucleotides designed to interfere with microcystin biosynthesis within cyanobacterial cells. Initial work has demonstrated the feasibility of engineering a phage to recognize *M. aeruginosa* through tail-fiber replacement that targets the prokaryote. Building from this proof-of-concept, current efforts focus on improving toxin suppression efficiency, expanding strain coverage through engineered phage 'cocktails' that recognize different strains of *M. aeruginosa*, and evaluating performance under increasingly realistic bloom conditions.

To support eventual scale-up, we are testing engineered phage formulations in larger aquarium-based systems that better approximate environmental complexity and provide data for techno-economic assessment. In parallel, we are developing a two-tiered mitigation strategy that combines intracellular suppression of microcystin biosynthesis with potential incorporation of microcystin-degrading functions. Environmental compatibility is being evaluated through off-target testing using representative aquatic organisms, including eukaryotic algae and Daphnia. Together, this work advances a scalable, targeted, and potentially sustainable strategy for mitigating microcystin-producing harmful algal blooms.

If a HAB Occurs in a Remote Glacial Fjord, Is It Still Harmful?

John Harley[1]*, Tania Lewis*[2]*, Alexandra Gulick*[2]*, Matteo Masotti*[3]*, Shannon Cellan*[3]

[1]Alaska Coastal Rainforest Center, University of Alaska Southeast, Juneau, AK, USA
[2]Glacier Bay National Park and Preserve, National Park Service, Gustavus, AK, USA
[3]Environmental Research Lab, Sitka Tribe of Alaska, Sitka, AK, USA

Glacier Bay National Park (*Sit' Eeti Geiyí*), the traditional homeland of the Huna Kaawu and UNESCO World Heritage Site, is a dramatic mountainous landscape in Southeast Alaska roughly the size of Connecticut. This region has undergone drastic changes over the recent past, where glacial retreat has opened more than 65 miles of coastal fjords and estuaries, fostering a thriving and interconnected environment of marine and terrestrial ecosystems. While there is knowledge of HABs occurring in Southeast Alaska through traditional knowledge and modern monitoring programs, the occurrence and impact of HABs in the park is largely unknown. Using an ecosystem approach, we describe preliminary data from field efforts to capture the extent and magnitude of paralytic shellfish poisoning (PSP) producing HABs in Glacier Bay. Extremely high concentrations of PSP toxins were observed in clams collected during 2025 in multiple areas of the park. Congeners of PSP were also detected in tissues of stranded sea otters as well as in the scat of terrestrial predators known to forage on sea otters and in the intertidal. Concentrations of PSP congeners measured in forage fish known to be vectors for toxins in seabird die-offs were generally very low. While we have strong evidence of a significant bloom occurring as well as the trophic transfer of toxins to other species, the broad scale impacts of these toxins on the fauna and ecosystem is largely unknown and an area of ongoing research.

Evaluating Satellite Indices for Harmful Algal Bloom Detection in the Ohio River Using PlanetScope Imagery

***Brealynn Harper**, Geneve Brady, John Moccio, Mindy Yeager-Armstead*

Marshall University, Huntington, West Virginia, USA

Large river systems are difficult to monitor because their size, depth, and flow create strong spatial variability, while field sampling is costly and limited. In the Ohio River Greenup Pool, a remote sensing workflow using PlanetScope 8-band surface reflectance imagery (PSB.SD platform; 3 m spatial resolution, daily revisit) was developed to support harmful algal bloom (HAB) monitoring in turbid, regulated rivers. Imagery was processed using Usable Data Masks (UDM) to filter images with 95-100% area coverage and less than 30% cloud coverage to reduce skewed pixels. ArcGIS Pro's Band Arithmetic was applied to images to calculate indices for turbidity, chlorophyll-a, and cyanobacteria (phycocyanin). These indices were extracted from fixed main channel sites and paired with EXO sonde measurements collected at Greenup Dam and the USGS gage at Ironton, OH, and field samples analyzed with BenthoTorch fluorescence readings and laboratory phytoplankton counts. Results show that turbidity was the strongest and most consistent remotely sensed parameter, with the Normalized Difference Turbidity Index (NDTI) producing the strongest correlation, particularly with USGS turbidity data. Chlorophyll-a and cyanobacteria proxies were weaker and more variable, indicating that pigment-based metrics require further refinement in this turbid river environment. Overall, this workflow improves field efficiency and provides a transferable framework for future bloom monitoring and predictive development in large river systems.

Automated vs Manual ELISA Testing

***Deann Harreld**, Jonnie Gibbs , Haley Martin*

Kansas Department of Health and Environmental Laboratories, Topeka, KS, United States

The Kansas Health and Environmental Laboratories have been testing toxins in surface and drinking water for several years. We will discuss the topic of what instrumentation we use in our lab and make a comparison between each. We use both automated and manual instrumentation intermittently throughout the season. We have had the opportunity to discuss with other labs about what instruments they use to run their tests. Most have mentioned only using the manual ELISA but have been curious on rather an automated option is worth having in the lab. The reason why we decided to compare the different findings between automated, manual with plate washer and manual is to figure out which may save the most time and money yearly. For our findings we are making a comparison of failed and passing plates as well as cost and time consumption for each of the instruments. We like having both automated and manual options to run tests because this allows for flexibility to get test results in a timely manner. We wanted to put together these findings so we could provide other labs with helpful information on options they could look into for their own HAB testing.

Multi-Barrier Phosphorus Control: Integrating Lanthanum-Modified Bentonite, Coagulants, and Peroxides for Durable Cyanobacteria Suppression

Bush Heathman[2] *, Andrew Skibo, PHD CLM*[1]*, Anja Brey*[3]*, Eli Kersh CLM*[2]

[1]Phoslock Environmental Technologies, Wyoming, USA
[2]Amaruq Environmental Services, Montana, USA
[3]East Bay Regional Park District, California, USA
LakeTech, California, USA

Lanthanum-modified bentonite (LMB) can permanently bind dissolved and sediment-released phosphorus, and when used alongside oxidative algaecides such as Peracetic Acid (PAA) and peroxides, and coagulants like aluminum chloralhydrate (ACH), the combined treatment can enhance cyanobacteria suppression and reduce bioavailable phosphorus more effectively than any single product alone. Lanthanum-modified bentonite (LMB) is a phosphorus-inactivation agent in which lanthanum is exchanged onto a bentonite matrix, forming highly insoluble lanthanum–phosphate minerals, stripping orthophosphate from the water column and intercepting internal loading from sediments. This process targets the low-concentration dissolved phosphorus pool that sustains cyanobacterial blooms and can maintain reductions in bioavailable phosphorus for many years in eutrophic systems.

Polymeric aluminum coagulants such as aluminum chloralhydrate (ACH) similarly bind and precipitate phosphorus, forming metal–phosphate flocs that settle to the benthic zone, thereby reducing water-column phosphorus and turbidity and directly improving light climate.

Peroxides such as Peracetic Acid (PAA) and hydrogen peroxide selectively damage cyanobacteria because these taxa are more sensitive to reactive oxygen species than many eukaryotic algae, so appropriately dosed treatments can rapidly reduce cyanobacterial biomass and associated toxins while minimizing non-target impacts.

When applied in a coordinated strategy, peroxides first selectively lyse cyanobacterial cells and release intracellular phosphorus while preserving beneficial phytoplankton communities. Independently, aluminum chloralhydrate captures and settles the particulate and dissolved phosphorus and consumes less alkalinity, which means less pH depression, fewer buffering chemicals, and more reliable performance in low alkalinity or variable pH lakes and ponds.

Applied as a top layer to these treatments, Lanthanum-modified bentonite (LMB) on or near the sediment binds released phosphate and ongoing internal loads, creating a multi-barrier approach that permanently binds bioavailable phosphorus, limits bloom regrowth, and extends treatment longevity beyond that achievable with algaecides or coagulants alone.

Metabolomics-Driven Pipeline for Cyanopeptide Compound Identification

Sierra Hefferan

University of Michigan, Ann Arbor, MI, USA

Metabolomics-Driven Pipeline for Cyanopeptide Compound Identification
Cyanobacteria occupy diverse ecological niches and possess extensive biosynthetic gene clusters that drive production of structurally diverse and biologically potent secondary metabolites. Rapid, accurate metabolite identification is critical for environmental monitoring and drug discovery. However, structural diversity, adduct variability, isomerism, and limited cyanobacteria-specific reference libraries constrain current LC-MS/MS annotation workflows. Existing platforms rely heavily on spectral libraries, while CyanoMetDB provides MS1-level annotations but requires time-intensive manual interpretation. To address these limitations, we developed CyanoPeptideMatching (CPM), a metabolomics-driven pipeline for rapid identification and classification of cyanobacterial secondary metabolites directly from LC-MS/MS data. Available as both a web interface and Python workflow, CPM employs a diagnostic-ion-guided strategy that bypasses preprocessing tools by filtering mass spectrometry files for cyanobacteria-specific fragmentation patterns and precursor ions.

CPM maps precursor ions to CyanoMetDB entries within diagnostic ion-inferred compound classes, reducing false positives while maintaining sensitivity to diverse congeners. Features lacking database matches but containing class-consistent diagnostic ions are flagged as candidate novel cyanopeptides. The Python implementation further enables semi-quantitative analysis through extraction of ion chromatograms. Utilizing a four-year time series dataset, we analyzed that CPM-calculated abundances preserve compound-class-specific covariance structure and resolve differing degrees of temporal organization across cyanopeptide classes, capturing both directional interannual shifts and substantial bloom-scale heterogeneity.

CPM provides a rapid, scalable, and cyanobacteria-centric platform compatible with standard mass spectrometry workflows, accelerating both environmental toxin detection and natural product discovery.

NOAA's HAB Programs: A Critical Driver of *Karenia* Research in the Gulf of Mexico

Cynthia Heil

Mote Marine Laboratory, Sarasota, Florida USA

Although *Karenia brevis* blooms in the Gulf of Mexico are among the most predictable of harmful algal blooms (HABs), they also exemplify the challenges of conducting HAB research on physiological complex organisms in the diverse biological, chemical and physical environments that characterize bloom phenomena. NOAA's HAB programs have played a critical role in advancing *Karenia brevis* science and management through peer reviewed research for 28 of the last 78 years since *K. brevis* was identified as the cause of Florida Red Tide. The 46 NOAA funded projects focused on *Karenia* in the Gulf of Mexico from 1997 to 2025 cover a broad spectrum ranging from those projects directly and immediately applicable to management (e.g. validation and implementation of detection and monitoring technologies, 18 projects) to those in development for potential management applications (e.g. new technology (4), modeling (4), mitigation (2) and socioeconomic research (4)) to those focused directly on understanding the organism, its blooms and its environment (15). These have included three regional, multi-investigator, collaborative grants (1997, 2006 and 2019) which have involved laboratory and field efforts, modeling studies, and diverse PI expertise, and have demonstrated: 1) the unique nature of the west Florida shelf environment, 2) the critical role of the physical environment in bloom dynamics, 3) the complex nutritional, photosynthetic and behavioral physiology of the organism, 4) the diverse nutrient sources available for HABS in an oligotrophic environment, 5) a complex interdependence with other organisms (e.g. marine cyanobacteria), 6) the dynamic role of brevetoxins in the marine environment, and 7) *Karenia's* unique responses to a local, regional and globally changing environment. These projects have advanced basic *K. brevis* science while simultaneously making this research available and applicable to management and stakeholder needs to protect human and environmental health.

Beyond Heatwaves: Discovery of Warming Metrics that Control *Microcystis* Bloom Biomass and Colony Size Distributions

***Ronojoy Hem**, Christopher Gobler*

School of Marine and Atmospheric Sciences, Stony Brook University, Stony Brook, NY, USA

Cyanobacterial blooms dominated by *Microcystis* are intensifying globally, yet factors linking environmental conditions to bloom development and colony size structure remain poorly resolved. Increasing heatwave frequency and intensity under climate change may amplify bloom dynamics through sustained thermal loading and enhanced stratification. We employed a novel automated three-dimensional imaging approach to quantify *Microcystis* colony biovolume and size distributions across three consecutive bloom seasons (2023–2025) at Lake Agawam, a shallow eutrophic lake on Long Island, New York. By coupling high-resolution continuous environmental records with discrete field measurements, we derived a suite of environmental metrics to examine what shapes bloom biomass and colony size structure. Our results revealed that cumulative warming and within-day thermal fluctuations were both associated with greater *Microcystis* colony biomass and larger mean colony sizes. Diel temperature difference, a measure of within-day thermal amplitude, was a dominant predictor of colony size diversity and mean colony size, with greater diel thermal fluctuation associated with larger mean colony sizes and shifts in size distribution. Heatwaves, as previously defined, was not a useful predictor of bloom dynamics. Instead, cumulative positive warming over a 14-day window was the dominant thermal predictor of *Microcystis* bloom dynamics, significantly predicting total biovolume, mean colony size, median colony size, and the relative abundance of smaller colonies. Additionally, water clarity, measured as the light extinction coefficient, emerged as a robust predictor of total biovolume, consistent with light limitation and bloom-driven self-shading dynamics. Together, these results demonstrate that continuous thermal exposure dynamics, rather than discrete heat events, may significantly shape *Microcystis* colony size structure and bloom biomass. Monitoring these metrics may therefore improve short-term bloom forecasting under intensifying climate warming.

Sorption and Desorption of Marine Phycotoxins to Microplastics and Bioavailability to Aquatic Wildlife

***O.S. Hernandez**, M.E Seeley, R.J. Latour, J.L. Smith*

Virginia Institute of Marine Science, William & Mary's Batten School of Coastal and Marine Sciences, Gloucester Point, VA, USA

Microplastics are ubiquitous in the aquatic environment, causing global concern due to their persistence and ability to harm marine life. They have gained attention as possible vectors of organic contaminants to marine food webs and therefore, humans. Several studies have shown that certain phycotoxins produced by harmful algae blooms (HABs), such as microcystins and okadaic acid, sorb to microplastics. However, data are absent for other phycotoxins, and studies are lacking focus on the potential of microplastics to function as a vector for phycotoxins if desorption occurs in the gut of a consumer. As HABs are worsening due to climate change and microplastic pollution is global, this issue is a research priority. In this study, three types of microplastics (polypropylene, polyethylene, and polyester), both pristine and UV weathered, were exposed to marine phycotoxins (okadaic acid, domoic acid, and brevetoxin-3) in artificial seawater for 96 hours. Sorption capacity was evaluated by measuring the mass balance between the microplastics and the water. Microplastics that sorbed phycotoxins were placed in artificial gut and intestinal fluid to replicate digestion and evaluate bioavailability. Concentrations of phycotoxins sorbed to microplastics and in seawater were determined via liquid chromatography tandem mass spectrometry (LC-MS/MS). This study determines whether a) phycotoxins sorb to microplastics, b) they subsequently desorb under simulated digestive conditions, c) if UV weathering has an effect on the amount of phycotoxin able to be sorbed and desorbed, and therefore d) if microplastics are a vector for exposing aquatic organisms to high doses of phycotoxins in a concentrated manner, or a sink for those phycotoxins. This can help to inform risk assessments and better predict the fate of phycotoxins in aquatic food webs.

HAB Response to Modeled Residence Time of Tributary Inputs in Lake Erie: A Lagrangian Perspective

Kendra Herweck[1]*, Forough Naali*[1]*, Daniel Whitt*[2]*, Kait Reinl*[3]*, Ruchi Bhattacharya*[1]*, Brice Grunert*[1]

[1]Cleveland State University, Cleveland, OH, USA
[2]NASA Ames Research Center, Mountain View, CA, USA
[3]Rensselaer Polytechnic Institute, Troy, NY, USA

Earth's biogeochemical processes are inextricably linked across aquatic, terrestrial, atmospheric, and anthropogenic systems. The terrestrial-aquatic linkage is widely influenced and pushed beyond its natural balance due to climate-induced shifts in hydrologic regimes and accelerated warming events, coupled with the legacy of anthropogenic watershed disturbances. Consequently, how shifts in timing, quantity, and composition of riverine material influx to coastal systems influences phytoplankton dynamics such as seasonal succession and bloom timing, extent and intensity is limited. In the Great Lakes, harmful algal blooms (HABs) severity has been well linked to Maumee River discharge in western Lake Erie. However, the spatiotemporal variability of HABs to the integration timescales of tributary inputs – how long it takes for river-transported organic matter and nutrients to be incorporated into lake and coastal ecosystems – has not been well quantified. We present our initial findings of quantifying river influence on phytoplankton bloom progression and HABs in the Great Lakes by considering the integration of riverine material into these lake systems from a Lagrangian parcel tracking perspective. We relate spatial patterns and timescales of riverine transport with satellite-observed HAB dynamics in eutrophic Lake Erie, and consider the potential to explore similar relationships between transport and emerging blooms in oligotrophic Lake Superior. Across these systems, we explore the extent to which spatial trajectories of tributary loads relate to satellite-observed changes in algal biomass and indicators of cyanobacteria presence. Finally, we offer perspectives on next steps when biogeochemical timescales are explicitly incorporated into our analysis.

Current Status of Golden Algae (*Prymnesium parvum*) in Arizona

Joann Hill

Arizona Game and Fish Department, Phoenix, AZ, USA

Golden Algae (*Prymnesium parvum*) was first confirmed in Arizona in 2005 in a small 5-acre urban pond. Since then, it has spread throughout the Phoenix metro urban ponds and surrounding reservoirs. Most urban ponds are fed by infested water as the only water source while others use highly saline well water that is susceptible to Golden Algae invasion. Blooms occur frequently during winter months. As new urban ponds are built in the Phoenix area, some are inoculated with Golden Algae almost immediately as many of them use the same infested source water. Small urban ponds can be treated with algaecides however large reservoirs are not practical to treat. Arizona Game and Fish Department staff have tried new methods of preventing these harmful blooms, so far without success. Detection is done by microscopy to determine if cells are present. There are currently no toxin detection tests as no lab standard for prymnesin toxin exist and no field tests have been invented yet. Outside of new Phoenix area urban ponds, Golden Algae spread seems to have stopped naturally and we are still guessing as to why. After 20 years in Arizona, we still have a limited understanding of bloom and toxicity triggers.

Brevetoxin Biosynthesis in *Karenia brevis* in Relation to Light, Growth Phase, and the Cell Cycle

*Charles L. Tilney[1], **Alicia E. Hoeglund**[1,2], Eric Muhlbach[1], Leanne Flewelling[1], Maria Célia Villac[1], Dana M. Nieuwkerk[2], Sugandha Shankar[1], John H. Paul[2], Katherine A. Hubbard[1]*

[1]Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, St. Petersburg, Florida, USA
[2]College of Marine Science, University of South Florida, St. Petersburg, Florida, USA

Karenia brevis synthesizes picograms of brevetoxins per cell and regularly produces extensive blooms with cell concentrations exceeding 1 million cells L^{-1}. Biological population growth requires repeated cellular biosynthesis and cell cycling, however, it is not yet known how molecular biosynthesis of brevetoxins might be tied to cellular biosynthesis and the cell cycle. Here, using laboratory cultures of *K. brevis,* we report two complementary experiments exploring how brevetoxin biosynthesis is linked to cellular biosynthesis (proxied through cell biovolume, growth rates, DNA, and chlorophyll-*a*). The first experiment assessed brevetoxin quotas, cell physiology, and the cell cycle over 27 h. The second assessed brevetoxin quotas and RuBisCO transcript expression (*rbcL*) in response to growth phase and light limitation/supersaturation. Multiple lines of evidence revealed relatively synchronous (~55–60% of the population) mitotic cell division which occurred within a 4.5 h period before 'dawn'. Following division, cell biovolume increased throughout the day, reaching maximum at 'dusk'. Different from biovolume, brevetoxin quotas slightly increased late in the daytime coinciding with entry into S-phase, and reached a maximum during the night before division. Brevetoxin quotas returned to G1 phase levels following cytokinesis. In the second experiment, only growth phase, not light level, affected cellular brevetoxin quotas, showing that decreased growth rates do not necessitate increased brevetoxin quotas. Coherent with the diel cell cycle experiment, it is suggested that brevetoxin quotas are regulated by processes also tied to cell cycle progression. Interestingly, a positive relationship between brevetoxin quotas and *rbcL* expression hinted at a link between the pyrenoid and brevetoxin production.

Searching for Genetic Signatures of *Karenia brevis* in Sediments from Southwest Florida Estuaries

Alicia Hoeglund[12]*, Julie Koester*[1]*, Cary Lopez*[1]*, Rebecca Rash*[1]*, Chloe Mikus*[1]*, Mya Breitbart*[2]*, Katherine Hubbard*[1]

[1]Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, St. Petersburg, Florida, USA
[2]University of South Florida, College of Marine Science, St. Petersburg, Florida, USA

Florida's Gulf Coast has a long history of harmful algal blooms, largely due to the toxic dinoflagellate, *Karenia brevis*. Despite extensive research, the entirety of the *K. brevis* lifecycle, especially as it pertains to bloom dynamics and the initiation and termination stages of a bloom, is not known. One hypothesis is that a resting stage for *K. brevis* that resides in sediment may provide a missing link. This study investigated genetic and toxin signatures of *K. brevis* in sediment and water column samples collected from three prominent estuaries along the southwest Florida coastline where *K. brevis* blooms often occur. Triplicate samples were collected in summer 2024 from nine sites, three from each estuary, selected based on the detection of >100,000 cells/L during the 2022-2023 *K. brevis* bloom. An additional "control" site where *K. brevis* blooms do not occur was included. Both metabarcoding targeting the V9 region of the 18S rRNA gene to evaluate phytoplankton community diversity and a sensitive SYBR Green *K. brevis* qPCR assay targeting the *rbcL* gene were conducted in triplicate technical replicates on resulting DNA extracts. Initial results indicate low, but detectable, *K. brevis* signal in two of the three estuaries via qPCR, whereas *K. brevis* was present at very low abundances in each estuary via metabarcoding. Analyses to compare phytoplankton assemblages in sediment across sites and estuaries relative to each other, to *K. brevis*, to sediment brevetoxin concentrations and to sediment grain composition are ongoing. These results suggest *K. brevis* DNA is broadly distributed in estuarine sediments, even more than a year after a bloom event, and highlight the value of using sensitive molecular detection approaches given the observed patchiness. To further explore the *K. brevis* lifecycle, we collected additional estuarine subsamples for paired microscopy and genetic single-cell analysis and continue to conduct parallel work offshore.

Satellite-Estimated Sediment Resuspension and Associated Phosphorus Inventories for Improved HAB Forecasting

Trevor Holm[1*], *Anshula Dhiman*[1], *Forough Naali*[1], *Kendra Herweck*[1], *Audrey Ciochetto*[1,2], *Brice Grunert*[1]

[1]Cleveland State University
[2]University of Rhode Island

The Great Lakes continue receiving substantial anthropogenic nutrient inputs, primarily from agriculture, which have profound immediate and legacy impacts on water quality. Harmful algal blooms (HABs) in the Western Basin of Lake Erie have been historically predicted using ongoing and legacy nutrient loads from the Maumee River; however, predictions have yet to incorporate spatiotemporal knowledge of the internal cycling of legacy phosphorus despite the frequent resuspension of this material in the quite shallow system (7.4m average depth). Utilizing the life history of Sentinel-3 OLCI satellite imagery, we have built a decadal perspective of sediment resuspension characteristics in Lake Erie's West Basin. During resuspension, we have observed in situ increases of total dissolved phosphorus by 450% and total suspended particulate matter (SPM) loads increase by 1200%. By analyzing annual SPM loading characteristics, we disentangled the basin-scale water column increases in benthic sediment concentrations during resuspension and internal nutrient loading across an annual timeframe, through linkage with our in situ measurements. In this study, we present a decadal perspective of HAB development in the West Basin of Lake Erie as related to these internal phosphorus cycling dynamics, examined through the lens of satellite imaging. We validated a suite of chlorophyll-detection algorithms for phytoplankton retrievals in the optically complex waters of the West Basin, and scrutinized annual HAB development trends across a nine year time-series of satellite imagery. Employing this time-series in tandem with our resuspended sediment loading time-series, we have developed a long-term perspective of HAB evolution patterns in the basin as they pertain to internal nutrient cycling. Herein, we discuss how our findings can assist in explaining algal bloom development in the basin, shortcomings in current prediction capabilities, and how our work can further our understanding and HAB forecasting capacity in the future.

Developing a Mechanistic Model to Predict Changes in Cyanobacterial Bloom Intensity in Western Lake Erie

Alexandria Hounshell[1]*, Erik Davenport*[2]*, Caroline Owens*[3]*, Timothy Wynne*[2]*, Richard Stumpf*[2]

[1]National Centers for Coastal Ocean Science (NCCOS), National Oceanic and Atmospheric Administration (NOAA), Seattle, WA, USA

[2] National Centers for Coastal Ocean Science (NCCOS), National Oceanic and Atmospheric Administration (NOAA), Silver Spring, MD, USA

[3]RPI under contract to National Centers for Coastal Ocean Science (NCCOS), National Oceanic and Atmospheric Administration (NOAA), Santa Barbara, CA, USA

Since 2012, NOAA's National Centers for Coastal Ocean Science (NCCOS) has produced seasonal forecasts of summer cyanobacterial bloom severity for western Lake Erie. These forecasts provide advanced warning of potential bloom intensity and impacts to end-users and stakeholders, including drinking water treatment managers, lake resource managers, and public health officials. Current forecasts rely on an ensemble of statistical models developed by NOAA and partners, which use empirical relationships between historical Maumee River phosphorus loading and cyanobacterial bloom severity from satellite observations. However, this historical relationship will likely be altered due to various stressors, including changes in water temperature, river discharge, and nutrient management strategies in the watershed. Mechanistic models, which rely on our understanding of biogeochemical cycles, are an important technique that take into account how blooms may respond to changing environmental and ecological conditions. Thus, we developed a mechanistic model to better constrain and forecast the relationship of cyanobacterial bloom biomass to watershed loading, lake nutrient cycling, and water quality parameters in western Lake Erie. The resulting mechanistic model will allow us to consider how climatic and anthropogenic changes may influence future cyanobacterial bloom intensity in Lake Erie and will be integrated into the ensemble of models to improve the robustness of seasonal forecasts for end-users.

Integrated Framework for Tracking Anomalous Harmful Algal Blooms on the West Florida Shelf (2025–2026)

Katherine Hubbard[1], *Chuanmin Hu*[2], *Yonggang Liu*[2], *Jennifer Cannizzaro*[2], *Yao Yao*[2], *Sebin John*[2], *Haibo Xu*[2], *Chad Lembke*[2], *Jason Law*[2], *Julie Koester*[1], *Eric Muhlbach*[1], *Matthew Garrett*[1], *Alexa Iorillo*[1], *Savannah Barnard*[1], *Meredith Zahara*[1], *Jay Abbott*[1], *Kelly Bickley*[1], *Molly Joseph*[1], *Sugandha Shankar*[1], *Alexandra DeSmidt*[1], *Cary Lopez*[1], *Camden Conte*[1], *Christine Tran*[1], *Alicia Hoeglund*[1], *Ariannie Gomez*[1], *Georgia Skipper*[1], *Shelby Mahank*[1], *Stephanie Keller Abbe*[1], *Laura Markley*[1], *Karen Henschen*[1], *Celia Villac*[1], *Yida Gao*[3]

[1]Florida Fish and Wildlife Conservation Commission-Fish and Wildlife Research Institute, St. Petersburg, FL, USA
[2]University of South Florida-College of Marine Science, St. Petersburg, FL, USA
[3]Woods Hole Oceanographic Institution, Woods Hole, MA, USA

From summer 2025 through spring 2026, a series of harmful algal blooms caused by *Pyrodinium bahamense, Karenia brevis,* and *Pseudo-nitzschia* spp. occurred in the Florida Panhandle and respectively resulted in shellfish tissue exceedances of regulatory thresholds for saxitoxins and brevetoxins, and enhanced levels of domoic acid in seawater. Summer populations of *P. bahamense* were observed in Saint Joseph Bay and saxitoxins exceeded action levels in early September and then declined shortly thereafter, giving way to a highly localized *K. brevis* bloom and elevated brevetoxin concentrations that endured from late September through March. A large offshore feature of elevated chlorophyll, extending from west of Florida along the shelfbreak to offshore of the greater Tampa Bay area, was observed throughout the *K. brevis* bloom, however, integration of shipboard Imaging FlowCytobots onto cruises of opportunity indicated that other taxa were present, not *K. brevis*. Interestingly, diatoms including *Pseudo-nitzschia* spp. were instead prevalent, and as the *K. brevis* bloom declined nearshore, a *Pseudo-nitzschia* bloom transpired along with increased particulate domoic acid concentrations. We implemented a highly collaborative framework for tracking this unprecedented succession of HAB events in northwest Florida, and efforts are underway to understand bloom drivers in this area relative to southwest Florida, as well as factors that may have led to these anomalous events.

Biogeochemical Impacts Driven by *Sargassum* Inundation in a Tropical Marine Reserve: Addressing Management Challenges

Julio Morell, Luis Rodríguez, Keviin Martínez, Julián Morell, and ***Raymond Infante***
CARICOOS, Lajas, PR, USA

La Parguera Marine Reserve (LPMR), off the western end of Puerto Rico's south coast, hosts an array of tropical coastal ecosystems, including mangrove forests, seagrass beds, coral reefs, and offshore keys. Since 2011, these have experienced seasonal arrivals of pelagic Sargassum (SSO). Three years of weekly observations of biomass influx and biogeochemical parameters at representative ecosystems in the LPMR provide evidence of biogeochemical impacts with varying intensity/persistency.

CARICOOS inundation forecasts provide a robust estimate of weekly SSO biomass accumulation along the mangrove-lined shoreline in LPMR, data that, coupled with observations, has supported the development of an empirical hypoxia forecast model for the mangrove-lined shoreline, which will become operational in the upcoming months and support management decisions.

Unlike SSO inundation of shoreline mangroves, the biogeochemical impact in the inner and mid-shelf keys is not only modulated by biomass loading, but also by the retention efficiency in keys/reefs, attributable to geomorphology, boundary elevation, and wave exposure. Ongoing efforts will enable the identification of vulnerable keys that require SSO removal, along with the physical criteria supporting that identification.

Harmful Algal BloomS Observing System (HABSOS):A Tool for Public Health and Natural Resource Managers

***Jonathan Jackson*[1], *Heather McCullough*[2]**

[1]Northern Gulf Institute, Mississippi State University, Stennis Space Center, MS, United States
[2]NOAA National Centers for Environmental Information, Boulder, CO, United States

The Harmful Algal BloomS Observation System (HABSOS) is a data collection and distribution system for harmful algal bloom (HAB) information in the Gulf of America, operated by NOAA National Centers for Environmental Information (NCEI). The goal of HABSOS is to provide environmental managers, scientists, and the public with a data resource for harmful algal bloom events. HABSOS operates as a cooperative venture with the Gulf of America state agency partners who monitor Karenia brevis blooms closely and submit their near real-time data to the HABSOS database. By leveraging multiple datasets into a single unified Gulf region dataset, users have a more comprehensive picture of current and historical bloom events. HABSOS users are able to visually access both near-real time and historical data, along with numerous other satellite derived, oceanographic, and meteorological layers. This collaboration enables comprehensive near real time data to be available for resource management response, while the long-term NCEI Archive preserves the integrity and provenance of these state-sourced records for future use.

The data are publicly available at https://data.noaa.gov/onestop/collections/details/91e34e68-bdac-4ccc-b637-b949ac1cdd6e.

Integrating FlowCam and Phytoxigene into the HAB Monitoring Toolkit of a Large Drinking Water Utility

Jennifer Jankowiak

New York City Department of Environmental Protection, Kingston, New York, USA

The New York City DEP operates the largest municipal water utility in the country, providing over 1 billion gallons of drinking water daily to 9 million residents in New York City and surrounding counties. The system is comprised of 19 reservoirs and 3 controlled lakes across a nearly 2,000 square mile watershed extending 125 miles northwest of the city. Yearly, harmful algal blooms (HABs) cause filter clogging and taste and odor issues in these sources, along with concerns for cyanotoxins, although none have been detected in the distribution system to date. The severity of these issues varies widely across the system and therefore maintaining high quality drinking water requires extensive monitoring. In 2015, the DEP expanded its HAB monitoring program to include baseline sampling for cyanotoxins in response to the EPA drinking water health advisories and upcoming UCMR4 rule. Since then, the program has grown to include a higher sampling frequency, a longer monitoring season and updated triggers for bloom classification using an integrated approach of continuous monitoring, microscopy-based abundances, and ELISA/ LC-MS cyanotoxin testing. In 2025, FlowCam and Phytoxigene were added to the HAB toolkit to further support data-driven operational and treatment decisions. Currently, the FlowCam is being used in tandem with light microscopy for phytoplankton enumeration and has reduced processing time while increasing sample volume, allowing for better detection of problematic taxa and reducing analyst variation by using image derived metrics. Phytoxigene is being used to identify toxin-producing potential of visible blooms providing a more rapid screening of multiple toxins than in house ELISA or contract LC-MS testing. The DEP is working to establish baselines and compare abundances to long term datasets generated using standard methods to develop trigger levels for these analyses and will highlight findings from the 2026 bloom season.

Seasonal Environmental Conditions and River Morphology Shape Summer Phytoplankton and Cyanobacteria Communities

Kathi Jo Jankowski, *James Larson, John Manier*

U.S. Geological Survey, La Crosse, WI, USA

Phytoplankton form the base of large river food webs but there are limited studies on the nature and drivers of communities over longer time scales. Further, climate change is projected to favor taxa associated with harmful algal blooms, but our knowledge of the timing, locations, and drivers of cyanobacteria in rivers lags that of other aquatic environments. To address these gaps, we used a summer phytoplankton community dataset collected from 2010-2020 across main channel, side channel and backwater areas in the La Grange reach of the Illinois River to assess: 1) How much do summer phytoplankton communities across diverse aquatic areas within a large river vary from year to year?, 2) What environmental and seasonal conditions are associated with that variation?, and 3) Do cyanobacteria respond differently than the full phytoplankton community? We found that phytoplankton communities differed more over time than among habitats and that their annual variation was synchronous among taxa in the same aquatic area. After accounting for this spatial variation, phytoplankton responded to river conditions across multiple seasons, responding positively to summer total phosphorus and invasive carp abundance and negatively to winter discharge and spring silica to nitrogen ratio. Annual variation in cyanobacteria was similarly distinct among habitats but best explained by the ratio of summer air temperature to discharge, representing conditions that favored growth over transport. These results show that annual variation in summer phytoplankton and cyanobacterial communities both reflected the spatial diversity of the river landscape and responded to conditions that occurred at different spatial and temporal scales. Thus, when evaluating and monitoring river phytoplankton communities, it is important to consider how their sensitivity to environmental change may vary across the river landscape and depend on how seasonal conditions unfold each year.

Evaluation of Mitigation Strategies for Harmful Algal Blooms in the West Coast Dungeness Crab Fishery

Amre Abken[1], ***Sunny L Jardine***[2]

[1]Economics Department, University of Washington, Washington, USA
[2] School of Marine and Environmental Affairs, University of Washington, Washington, USA

The Dungeness crab fishery, the most economically valuable on the U.S. West Coast, has faced repeated, climate-driven disruptions over the past decade due to harmful algal blooms (HABs). These blooms, fueled by warming ocean temperatures, lead crabs to ingest toxin-producing algae, making them unsafe for human consumption. In response, fisheries managers have traditionally shut down the fishery, triggering substantial economic losses.

To reduce these losses, some West Coast states have turned to evisceration orders, which allow crabs to be harvested during HABs if their toxin-containing intestines are removed before sale. However, the economic viability of this strategy depends on how it affects ex-vessel prices, i.e., the prices harvesters receive at the dock.

This study quantifies the impact of evisceration orders on ex-vessel prices in Washington's non-tribal fishery using quasi-experimental data from a 2021 HAB event. Employing both a difference-in-differences approach and structural demand estimation, we find that evisceration orders led to a decline in ex-vessel prices ranging between 26.5-33.5%.

These results reveal a significant economic trade-off: while evisceration orders may preserve fishing opportunities during HABs, they also substantially erode market value. Our findings offer critical insights for designing adaptive fishery management strategies that protect public health while supporting industry resilience in an era of accelerating ocean change.

Assessing the Economic Impacts of Harmful Macroalgae Blooms in US Coastal Waters

Di Jin [1], *Avery Wang* [2], *Tracey Dalton* [3]

[1]Woods Hole Oceanographic Institution, Woods Hole, MA, USA
[2]Washington University in St. Louis, St. Louis, MO, USA
[3]University of Rhode Island, Kingston, RI, USA

The frequency, intensity, and distribution of sargassum events have been rising in the Caribbean region in recent years causing social and economic disruptions. We develop estimates of the scale of annual economic impacts on local economies of sargassum events using multi-sector economic impact models for Puerto Rico, U.S. Virgin Islands, and coastal Florida. Using field observations from the Sargassum Watch database, we validate the current sargassum forecast in the region. We show that the forecast is performing well and that sargassum season has started earlier and lasted longer in recent years. The high-risk regions for sargassum inundation include Puerto Rico, U.S. Virgin Islands, and southeast coastal areas in Florida. Results of the study show that sargassum events are expected to cause significant negative economic impacts, in multimillion dollars each year, across the study regions, and the impact may be in billions of dollars along Florida's Atlantic coast. These results provide important input to the planning process in deciding the investments in future sargassum response and cleanup. They can also facilitate targeted data collection and valuation efforts to develop more accurate measures of economic losses.

A Coupled Physical-Biological Model Study of the Initiation of the 2020 *Karenia brevis* Bloom on the West Florida Coast

Sebin John[1]*, Yonggang Liu*[1]*, Katherine A. Hubbard*[2]*, Robert H. Weisberg*[1]*, Haibo Xu,*[1]*Matthew J. Garrett*[2]*, Julie A. Koester*[2]*, Chuanmin Hu*[1]*, Yao Yao*[1]

[1] College of Marine Science, University of South Florida, Saint Petersburg, FL, 33701, USA
[2]Florida Fish and Wildlife Conservation Commission – Fish and Wildlife Research Institute, Saint Petersburg, FL 33701, USA

The 2020-2021 *Karenia brevis* bloom (red tide) started in the coastal area near Sanibel Island – Ft. Myers in December, and endured from December 2020 through November 2021. Based on comparison with prior events, the onset occurred further south and later in the year than most blooms. To further investigate the initiation process of this unusual bloom, we used both a Lagrangian particle trajectory model and a coupled physical-biological model based on realistic hindcast simulations from the West Florida Coastal Ocean Model (WFCOM). Results showed that the bloom was initiated offshore in subsurface waters, but at a more southern location than previously hypothesized, thus expanding the potential source region for *K. brevis* blooms. Inclusion of the vertical behavior of *K. brevis*, i.e., active diel vertical migration (DVM) rather than passive sinking, improved model performance in simulating the progression of bloom cells towards the coast.

Exploiting the Extracellular Polymeric Substance (EPS) Layer in the Mitigation of *Microcystis Aeruginosa* Blooms

*Borui Wang[1], Pedram Azizihariri[1], **Vijay John**[1], Josh Alarcon[2], Vince Lovko[2]*

[1]Tulane University, New Orleans, Louisiana, USA
[2]Mote Marine Laboratory, Sarasota, Florida, USA.

Microcystis aeruginosa (MC) produces extensive EPS which links cells in colony formation. In planktonic cells, the EPS layer can extend to 300 nm allowing the entrapment of nanoclays such as laponite and halloysite. Such entrapment increases the effective density of the cell or cell aggregates, and results in the sinking of the cells. In the case of laponite, the entrapment is based on the collapse of a house-of-cards nanoclay morphology into the EPS layer facilitating rapid sinking. We complement this finding by demonstrating the use of extended mesh-like networks of the bio-derived tannic acid through metal coordination as a flocculation technology for the removal of MC. These systems serve as a potential alternative to conventional flocculants such as polyaluminum chloride (PAC) where the aluminum content has environmentally deleterious consequences. While tannic acid (TA) alone exhibits cell aggregation due to its bioadhesive properties and inhibits algal growth, coordination with Fe(III) and La(III) to produce metal phenolic networks (MPNs) significantly enhances flocculation, with almost total removal efficiency (~99% within 3 hours) in La(III) based systems. Through detailed electron microscopy imaging, we show that MPNs associate with the EPS layers suggesting a mechanism involving EPS-mediated adsorption, coordination-driven assembly, and interfacial bridging. Integration of nanoparticulate algaecides into the EPS layer offers the potential for targeted cell destruction. Overall, our study demonstrates that the EPS layers can be effectively exploited in designing technologies for flocculation, sinking and destruction of cyanobacterial harmful algal blooms.

Arctic Coastal CyanoHABs: Physiological Ecology in the Context of a Changing Environment

Andrew Juhl[1]*, Deni Lopez*[1]*, Alex Whiting*[2]*, Meredith Kime*[1]*, Mariam Moreno*[3]*, Heather Sutherland*[3]*, Matthew Harke*[4]*, Ed Carpenter*[3]*, Ajit Subramaniam*[1]

[1]Lamont Doherty Earth Observatory, Columbia University
[2]Native Village of Kotzebue
[3]San Francisco State University
[4]Gloucester Marine Genomics Institute

Mixed cyanobacterial blooms and associated cyanotoxins have been observed in August and September near Kotzebue, Alaska since 2008, raising concerns among the local community due to potential impacts on subsistence resources. Understanding why cyanobacterial blooms have expanded in Kotzebue Sound will help identify whether the expansion is a localized concern, or whether it represents an emerging pan-Arctic phenomenon. Many environmental conditions in the coastal Arctic are changing rapidly. In this study, we focus on the potential for increases in air and water temperatures, and declines in water transparency near Kotzebue to favor cyanobacterial growth. We quantified the growth rates and photophysiology of newly- isolated cyanobacteria and other co-occurring phytoplankton originating from surface water near Kotzebue across a range of temperatures. For comparison to the Arctic strains, parallel experiments used temperate and tropical cyanobacterial isolates. All high-latitude phytoplankton had thermal optima for growth that were at least 15-20 ˚C lower than the thermal optima of temperate cyanobacteria. Physiological adaptation to low temperatures suggests that the Kotzebue isolates represent Arctic strains that were likely present long before the blooms became apparent. Low temperature optima would allow Arctic cyanobacteria to form blooms at colder temperatures than their temperate congeners. However, the temperature sensitivity of growth rate (Q10) indicates that increases in water temperatures over recent decades would have only had a negligible effect on cyanobacterial growth rates. Photophysiological measurements (rapid PAM light curves) similarly did not indicate that decreased water transparency would particularly favor cyanobacteria over other co-occurring phytoplankton. Testing the potential importance of other environmental factors that may have changed in Kotzebue Sound, such as nutrient availability, are planned.

An Unusual *Microcystis* Bloom in the Hudson River Estuary

Andrew Juhl[1]*, Meredith Kime*[1]*, Matthew Harke*[2]*, Ajit Subramaniam*[1]

[1]Lamont Doherty Earth Observatory, Columbia University
[2]Gloucester Marine Genomics Institute

Reports of discolored water in the Hudson River Estuary near Kingston, NY began in Aug. 2025. Sampling revealed the discoloration was related to colonies of *Microcystis* sp., large enough to be seen by eye. High *Microcystis* abundance persisted from Aug – Oct, and floating colonies were observed until at least mid Nov. Fortunately, microcystin concentrations in source water for the communities that rely on the Hudson for drinking water remained below regulatory guidelines. While the Hudson River Estuary has high nutrient concentrations, phytoplankton blooms are rare in this portion of the estuary, due to high turbidity, strong vertical mixing, and low residence time. While not unprecedented, the 2025 bloom was unusually dense and persistent. The combination of low rainfall, low winds, low water levels, and long residence time in the summer and fall of 2025 likely contributed to favorable conditions for the bloom to form and persist. The bloom included lobose and spherical *Microcystis* colonies. The lobose, but not the spherical colonies, were surrounded by epiphytic, phycoerythrin-containing cyanobacteria, resulting in more complex optical properties than *Microcystis* alone.

Turning the Tide on HABs: Integrating Models, Data, and Management

Paul Julian

The Everglades Foundation, Palmetto Bay, FL USA

Harmful algal blooms (HABs) continue to pose growing risks to ecosystem health, water resources across freshwater, estuarine, and marine environments. This increased risk is driven by intersecting pressures from nutrient enrichment, climate variability, and hydrologic alteration. Effective response to HABs requires approaches that integrate monitoring data, predictive modeling, and management decision frameworks, yet these components are often applied in isolation.

This presentation synthesizes recent advances from published research and applied case studies to highlight how integrated modeling and data-driven approaches can support HAB risk assessment and management. Drawing from recent work evaluating algal bloom dynamics within managed freshwater systems, modeling frameworks are presented that link hydrology, nutrient loading, and climatic drivers to observed patterns in chlorophyll-a and bloom frequency. These approaches demonstrate how changes in water management operations and restoration infrastructure can meaningfully alter bloom potential when evaluated at appropriate spatial and temporal scales.

Complementary insights from long-term ridge-to-reef monitoring across South Florida and the Florida Keys underscore the importance of connectivity across freshwater, estuarine, and marine environments. Multi-decadal observations reveal that algal biomass and nutrient dynamics respond not only to long-term pressures such as restoration and warming but also to episodic disturbances including storms, droughts, and extreme hydrologic events. Together, these studies illustrate how HAB responses emerge from interactions among physical processes, nutrient availability, and management actions rather than from single drivers. Therefore, future management should adopt a holistic, integrated approach to reducing the risk of blooms and mitigating their impacts wherever possible.

Using a Resting Cyst Germination Model to Predict Onset of *Pyrodinium bahamense* Blooms Across Florida

***Sara G. Kaminski**, Cary Lopez, Katherine A. Hubbard, Grace Harris*

Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, St. Petersburg, FL USA

The cyst-forming and saxitoxin producing species, *Pyrodinium bahamense*, causes recurrent blooms in the summertime in central Florida estuaries. Since 2016, shellfish harvesting closures due to saxitoxins highlighted a potential expansion of toxic *P. bahamense* events into three new regions along Florida's Gulf coast, from the Panhandle to Charlotte Harbor, underscoring the need to better understand drivers of initiation. Germination of *P. bahamense* resting cysts is mediated by the annual temperature cycle, which influences the rate of germination as well as the transition between cyst quiescence and dormancy. We hypothesized that latitudinal differences in annual temperature ranges would affect the duration of quiescence (i.e., the time when cysts can germinate) and/or the timing of peak germination across the different bloom regions. We accordingly developed a germination model that captures three critical components: 1) the transition from dormancy to quiescence based on cool temperature exposure, 2) the transition from quiescence to secondary dormancy based on warm temperature exposure, and 3) the temperature dependent rate of germination of quiescent cysts. We used local temperature data to apply this simplified germination model in different regions, and compared model results against field observations, including initial detection of cells and peak cell abundance. The first date of detection and sampling efforts from the different regions over the past decade were also considered and compared. This investigation is advancing efforts to forecast appearance and persistence of *P. bahamense* in emerging and recurring regions across Florida, and to improve monitoring efforts for saxitoxins and resulting impacts.

Field Comparison of Chlorophyll Measurements by Fluorescence Sensors in the Illinois River Basin, Illinois

Colin Peake, ***Brock Kamrath***

United States Geological Survey Central Midwest Water Science Center, Urbana, IL, USA

The U.S. Geological Survey (USGS) deployed instream chlorophyll fluorescence sensors in the Illinois River to better understand the formation, dynamics, and persistence of riverine algal blooms. At five sensor locations across four USGS streamgages, YSI EXO Total Algae PC smart sensors were fitted onto YSI EXO2 multiparameter sondes and set to measure chlorophyll fluorescence (fChl) in micrograms per liter as chlorophyll at 15-minute intervals. These sensors estimate fChl from algal pigment fluorescence but do not directly measure chlorophyll *a* (Chl) concentrations or algal biomass. In this study, fChl measurements were compared to laboratory-extracted Chl concentrations obtained from water-quality samples collected at the sensor locations and analyzed using standard chromatographic-fluorometric method with acetone extraction to evaluate the reliability of using fChl as a proxy of Chl. Paired fChl and Chl observations were analyzed using Pearson's correlation and model II regression. Significant positive correlations (Pearson's correlation coefficient of 0.68–0.95) were detected at all sensor locations, indicating that fChl generally tracked with Chl. However, model II regression detected both proportional and fixed bias at three of the five locations, proportional bias only at one location, and no significant bias at the remaining location. At locations with proportional biases, model II regression slopes were less than 1, indicating that fChl increasingly underestimated Chl as concentrations increased. Substantial variability in proportional bias was also observed across sensor locations with slopes ranging from 0.43 to 0.93. Overall, the results indicated that fChl tracks with Chl in the Illinois River, but fChl may not reliably represent true Chl without adjustment. These findings underscore the importance of field validation, consistent sensor placement, and careful interpretation of fChl data, particularly when reported in micrograms per liter as chlorophyll.

Breaking Bloom: Hyperspectral Fingerprints of Cyanobacterial Cell Lysis

***Denesh Karunakaran*[1]*, Lucas Clark Burnette*[1]*, Miki Hondzo*[1]*, Leif Olmanson*[2]*, Ardeshir Ebtehaj*[1]

[1]Saint Anthony Falls Laboratory, Department of Civil, Environmental, and Geo-Engineering, University of Minnesota Twin Cities, Minneapolis, Minnesota, USA
[2]Department of Forest Resources, University of Minnesota, Saint Paul, Minnesota, USA

Cell lysis marks a critical ecological transition in harmful cyanobacterial blooms, shifting intracellular toxins into extracellular contaminants. While optical approaches successfully track biomass, monitoring toxin release remains challenging because it is driven by cellular rupture rather than biomass alone. This study investigates whether cell lysis produces distinct hyperspectral signatures in *Microcystis aeruginosa* to bridge this gap. Using freeze–thaw cycles as a controlled lysis mechanism, we employed two experimental routes to decouple physical rupture from subsequent pigment degradation. The first isolated mechanical lysis via dark freeze–thaw cycles followed by photo-oxidative degradation; the second alternated lysis and degradation to represent coupled rupture and decay during bloom collapse. Throughout these sequences, we characterized concentrations of intracellular and extracellular microcystin, chlorophyll *a*, and phycocyanin, alongside bidirectional hyperspectral reflectance measured with a custom goniometer-spectroradiometer system and hyperspectral microscopy. Our results demonstrate that lysis triggers unique optical shifts across visible and near-infrared wavelengths. Extracellular microcystin correlated strongly with the red-edge region at backscattering angles, consistent with structural changes in scattering caused by cell rupture. In contrast, forward-scattering directions were more sensitive to pigment absorption, underscoring the need to account for bidirectional reflectance. Microscopic observations validated these macroscale shifts, confirming the consistency of the signature across scales. By isolating rupture and tracking degradation, this study establishes a mechanistic baseline for interpreting optical changes during bloom senescence and advances remote sensing beyond biomass detection toward identifying critical toxin-release events.

From Images to Automated HAB Alerts: A Multi-Tiered QC Pipeline for the California IFCB Network

Kasia M. Kenitz[1,2]*, Melissa L. Carter*[1]*, Kayla Martin*[1]*, Kendra Hayashi*[3]*, Iwen Su*[4]*, Henry A. Ruhl*[5]*, Clarissa R. Anderson*[1,2]

[1] Scripps Institution of Oceanography, University of California San Diego, La Jolla, CA
[2] Southern California Coastal Ocean Observing System, Scripps Institution of Oceanography, University of California San Diego, La Jolla, CA
[3] Ocean Sciences, University of California Santa Cruz, Santa Cruz, CA
[4] Tetra Tech, Pasadena, CA
[5] Central & Northern California Ocean Observing System, Monterey Bay Aquarium Research Institute, Moss Landing, CA

The California IFCB Network has moved beyond the pilot phase into a sustained operational role, providing high-frequency data to coastal stakeholders. However, the transition from raw image acquisition to reliable automated alerting requires addressing several layers of uncertainty that are often overlooked in smaller-scale studies. This work outlines a multi-tiered quality control (QC) framework designed to ensure that the data feeding into stakeholder products accurately reflects the plankton community across diverse deployment sites. First, we examine the influence of instrument configuration on observed community composition through: (i) side-by-side comparisons of topside deployments to quantify variability between instruments calibrated using the same protocol, and (ii) concurrent topside and in situ deployments to quantify how the use of pumped system versus in-water sampling affects the observations. Second, we assess the consistency of the network by comparing IFCB abundance data to manual weekly samples from the HABMAP monitoring program to determine if the two programs capture the same community dynamics despite differing methodologies. To ensure the integrity of the data products, QC protocols are implemented at both the sample acquisition and sample processing levels. Early-stage protocols exclude low-quality samples from the pipeline, while the QC of automated classification involves rigorous classifier validation and the implementation of class-specific minimum confidence thresholds. The final data product is then used for the generation of HAB alerts to stakeholders. We investigate multiple criteria and thresholds for generating alerts to optimize for precision vs. recall on HAB events, which is critical when balancing alert fatigue for stakeholders and ensuring that significant bloom events are not missed. This multi-tiered approach ensures that the California IFCB Network provides the high-quality data necessary for effective and timely HAB early warning.

From Bloom to Bedside: Clinical Presentations and Community Health Signals in the Great Lakes Region

David Kennedy

University of Toledo College of Medicine and Life Sciences, Toledo, OH, USA

Harmful algal blooms in the Great Lakes are increasingly recognized as a public health challenge that extends beyond water quality advisories. This presentation will connect environmental bloom events with clinical and community health signals observed in impacted communities. We will summarize routes of exposure relevant to residents, workers, and recreational users, with emphasis on ingestion, dermal contact, and inhalation of aerosolized bloom material. The talk will highlight clinical presentations that may be encountered by healthcare providers, including respiratory irritation, cough, asthma-like symptoms, gastrointestinal complaints, skin and mucosal irritation, and concerns among individuals with pre-existing cardiopulmonary disease. We will also describe how community-engaged health surveillance, symptom questionnaires, spirometry, exhaled nitric oxide, and paired environmental sampling can help identify signals that warrant further investigation. By moving from bloom conditions to bedside relevance, this talk will outline practical opportunities to improve clinician awareness, community messaging, exposure prevention, and future translational research on harmful algal bloom-associated illness.

Wildfires and Harmful Algal Blooms: Identifying Vulnerable Waterbodies in the Western United States

Minseung Kim[1], *Addison Testoff*[1], *Jiyoung Lee*[1,2]

[1]Division of Environmental Health Sciences, College of Public Health, The Ohio State University, Columbus, OH, USA
[2]Department of Food Science & Technology, The Ohio State University, Columbus, OH, USA

Increasing trends in wildfire frequency and intensity have become a global concern. The western United States is among the most affected regions, with wildfires causing substantial loss of life and property damage. Wildfires can also degrade water quality through ash deposition and postfire runoff, potentially increasing the risk of cyanobacterial harmful algal blooms. However, large-scale evidence linking wildfire activity to cyanobacterial bloom dynamics remains limited. We analyzed weekly timeseries on algal bloom intensity and wildfire activity across the western US during 2007-2012 and 2016-2026. Among 447 waterbodies, 35 with less than 20% missing observations were selected for analysis. Annual cumulative fire radiative power was calculated within each watershed boundary, and Generalized Additive Models were applied to evaluate relationships between wildfire activity and algal bloom intensity while controlling for seasonality. Among the waterbodies analyzed, 14 (40.0%) showed significantly increasing trends ($p<0.05$) in algal bloom intensity, whereas only 1 (2.9%) showed a decreasing trend. Positive relationships between wildfire activity and algal bloom intensity were identified in 8 waterbodies (22.9%), while 5 (14.29%) showed significantly negative relationships ($p<0.05$). Spatial variability in wildfire influence was evident. Generally positive wildfire effects were observed along the Pacific Coast, where mild rainy winters following the wildfires may transport fire-derived nutrients into downstream waterbodies. In contrast, responses in mountainous regions (Sierra Nevada and Rocky Mountains) were inconsistent. This study provides one of the first large-scale regional assessments linking wildfire with cyanobacterial bloom dynamics and offers a framework for identifying vulnerable waterbodies and informing targeted postfire water-quality management strategies.

Progress Toward a Comprehensive, National-Scale Harmful Algal Blooms Monitoring Network

Tyler King[1], *Kyle Compare*[1], *Carl Legleiter*[2], *Jessica Garrett*[3], *Natalie Hall*[4], *Wilson Salls*[5], *Keith Bouma-Gregson*[6], *Michael F Meyer*[7], *Natalie Day*[8], *Schuyler Nardelli*[6], *Rebecca Gorney*[5], *Robert Bean*[2], *Tim Stagnitta*[5], *Mackenzie Marti*[9], *Matt Gyves*[10], *Victoria Scholl*[2], *Scott Ducar*[1]

[1]U.S. Geological Survey, Boise, Idaho, USA
[2]U.S. Geological Survey, Denver, Colorado, USA
[3]U.S. Geological Survey, Iowa City, Iowa, USA
[4]U.S. Geological Survey, Catonsivlle, MD, USA
[5]U.S. Geological Survey, Troy, NY, USA
[6]U.S. Geological Survey, Sacramento, CA, USA
[7]U.S. Geological Survey, Portland, OR, USA
[8]U.S. Geological Survey, Grand Junction, CO, USA
[9] U.S. Geological Survey, Urbana, IL, USA
[10] U.S. Geological Survey, Philadelphia, PA, USA

Monitoring is essential for characterizing Harmful Algal Blooms (HABs) and mitigating public-health impacts. Satellite remote sensing enables retrospective analyses of HAB dynamics and facilitates early detection of bloom onset, improving our ability to target field sampling, guide mitigation, and identify driving factors. Identifying and monitoring bloom formation with remote sensing is challenging, as bloom onset might be nuanced or otherwise unobservable with terrestrially corrected reflectance products. To expedite the pace of remotely sensed water quality monitoring, recent advances in operational generation of 20 m aquatic reflectance products support routine satellite monitoring of lakes, reservoirs, and rivers across the contiguous United States.

Even with this product's development, HAB monitoring includes an inherent tradeoff between measurement accuracy and spatial coverage. Combining in-situ and remote sensing observations leverages the strengths of both. In-situ measurements provide place-based process-level information not measurable by satellite data like speciation, growth stage, genetic information, and toxins. On the other hand, satellite-based monitoring provides synoptic spatial context and temporal continuity.

In this talk, we highlight recent achievements from projects that intentionally combine complementary data characteristics and modalities, integrating in-situ data collection, systemic knowledge, and remote sensing products to improve HABs detection and management. We then examine how these integrated approaches can be replicated across diverse freshwater systems using remote sensing models as foundational layers that are subsequently augmented with local in-situ data. Finally, we outline a vision for a comprehensive, national-scale HAB monitoring network that fuses satellite remote sensing and targeted field campaigns to deliver locally relevant, operationally scalable, and nationally consistent HAB assessments.

Red Tide Meets the Heart: Seven Dimensions of Bureaucratic Caring for *K. brevis* Human Health Impacts

Koszalinski, *R.[1], Wilson, C.[2], Schaefer, A.[3]*

[1]University of Central Florida, Orlando, Florida, United States
[2]Florida Atlantic University, Boca Raton, Florida, United States
[3]Apt Global, Rockville, MD, 20852

Background: Red Tide impacts arise from interactions among environmental exposures, social systems, and institutional responses. Nurses play a vital role integrating environmental science, community engagement, and policy advocacy to reduce harm and build resilience.

Design: This study applies Bureaucratic Caring Theory to examine how systemic processes and spiritual-ethical caring intersect in responses to harmful algal blooms. The theory blends spiritual ethical commitments with organizational processes to create a holographic view of care across individual, institutional, and community levels. Seven dimensions—Physical, Educational, Spiritual cultural, Technological, Economic, Legal, and Political—frame pathways by which *Karenia brevis* blooms affect health and reveal nursing leverage points.

Results: Application of the theory yields three core contributions: (1) co-creation of safer environmental and social conditions with community partners; (2) promotion of health self-awareness across the seven dimensions, unified by spiritual cultural meaning; and (3) translation of theory into actionable communication strategies that convey community needs to clinicians and policymakers.

Discussion: Grounding harmful algal bloom research in Bureaucratic Caring enhances nurses' and interprofessional teams' capacity to respond in ways that are scientifically rigorous and morally grounded. The framework informs curriculum development, community-engaged research, and policy advocacy by clarifying institutional levers and cultural values, reframing bureaucratic constraints as opportunities for compassionate, systems-level action.

Conclusion: The Bureaucratic Caring Theory's seven dimensions and central spiritual-ethical construct offer a coherent foundation for advancing research, education, and practice on harmful algal blooms, improving environmental health literacy, guiding caring interventions, and informing policy to enhance community well-being.

A Characterization of Benthic Cyanobacteria and Associated Cyanotoxins in New York State Lakes

Matthew Kraft[1]*, Keleigh Reynolds*[1]*, Rebecca Gorney*[2]*, Brian Duffy*[1]

[1]New York State Department of Environmental Conservation Monitoring and Assessment Section, Albany, New York, USA
[2] U.S. Geological Survey, Troy, NY, USA

Cyanobacteria are naturally occurring and ubiquitous in aquatic ecosystems, yet their ability to form harmful algal blooms (HABs) poses a threat to ecological integrity and public health. While the dynamics and risks associated with planktonic blooms are well-documented, a similar understanding of benthic cyanobacteria remains a critical knowledge gap in water quality management. To address this, the New York State Department of Environmental Conservation's Monitoring and Assessment Section implemented a comprehensive survey to characterize the prevalence of benthic cyanobacteria and associated cyanotoxins in New York State's lakes. From 2024 to 2025, a statewide probability-based survey was conducted to evaluate potential recreational health risks and identify environmental drivers of benthic cyanobacteria blooms. Sampling protocols included littoral zone periphyton sampling paired with a suite of chemical, biological, and physical water-quality measurements. Preliminary findings indicate that benthic cyanobacteria and cyanotoxins are widely distributed across New York lakes of varying trophic states and watershed characteristics, showing no clear statewide spatial patterns. Potentially toxigenic taxa did not consistently coincide with cyanotoxin detection. Cyanotoxins were detected more frequently and at higher concentrations in periphyton scrapes and detached floating mats than in the overlying water column. These results highlight important gaps in our knowledge of the temporal and environmental drivers of benthic cyanobacteria in lakes. The study will inform future benthic monitoring efforts to ensure statewide HAB monitoring and communication strategies are sufficient to protect public health and recreational users in nearshore lake environments.

Composite Red Tide Vulnerability Index: Assessing and Communicating Communities' Vulnerability to Red Tide in Florida

Lisa Krimsky[1]*, Christa Court*[2]*, Sandra Anderson* [3]*, Kevin Ash*[4]*, Kara Coffey*[5]*, Roberto F. Koeneke*[2]*, Mengming Li*[2]*, Angie Lindsey*[6]*, Kelsey McDaid*[2]*, Claire Mitchell*[3]*, Xiaohui Qiao*[2]*, Andrew Ropicki*[2]*, Jawata A. Saba*[4]*, Ricky Telg*[3]

[1]Institute of Food and Agricultural Sciences Extension, Florida Sea Grant, University of Florida, Ft. Pierce, FL, USA
[2]Food and Resource Economics Department, Institute of Food and Agricultural Sciences, University of Florida, Gainesville, FL, USA
[3]Center for Public Issues Education, Institute of Food and Agricultural Sciences, University of Florida, Gainesville, FL, USA
[4] Department of Geography, University of Florida, Gainesville, FL, USA
[5]Harte Research Institute, Texas A&M University–Corpus Christi, Corpus Christi, TX, USA
[6]Department of Family, Youth and Community Sciences, University of Florida, Gainesville, FL, USA

Karenia brevis red tides are a recurring phenomenon along Florida's Gulf Coast. While the impacts of individual red tide events have been documented, few studies have attempted to generalize beyond case studies to assess long-term socio-economic vulnerability for all of Florida's coastal regions. This study addresses this gap by creating a Composite Red Tide Vulnerability Index (CRTVI) to estimate the vulnerability of Florida's coastal communities to red tide events. CRTVI incorporates indicators across five domains: human health, tourism, fisheries and marine activities, socio-economic vulnerability, and red tide exposure. Through literature reviews and focus groups, relevant metrics were selected, a weighting scheme was developed within and between the domains, and a composite indicator approach was used to construct the CRTVI. Data were collected for each domain and vulnerability was assessed at the county level. The results were presented in an interactive web platform, designed for policymakers, stakeholders, and the public, offering detailed data visualizations that were usability-tested to meet user needs. The CRTVI provides a systematic framework for comparing and understanding the socio-economic impacts of red tide events across Florida. This index can significantly enhance decision-making related to red tide preparedness, mitigation, and response, offering valuable insights for reducing negative impacts on human health, local economies, and tourism.

Prevention, Mitigation and Cleanup of Sargassum Inundation Events

Mariana C. León-Pérez[1], Lisamarie Carrubba[2], Andrés Bisonó León[3], Amy Dempsey[4], Arielle Benjamin[5], David Dale[6], José Martínez-Ortiz[7], Karen Urelius[8], ***Lisa Krimsky***[9]*, Ricardo Colón[10]*

[1]Mar Caribe Consulting, San Juan, Puerto Rico, US
[2]Retired NOAA, Cabo Rojo, Puerto Rico, US
[3]SOS Carbon, Dominican Republic
[4]BioImpact, St. Croix, US Virgin Islands, US
[5]U.S. Environmental Protection Agency, New York, New York, US
[6]NOAA Fisheries, St. Petersburg, Florida, US
[7]Knauss Fellow, Washington, DC, US
[8]US Army Corps of Engineers, Seattle, Washington, US
[9]UF/IFAS Southeast District, Ft. Pierce, Florida, US
[10]Puerto Rico Department of Natural and Environmental Resources, San Juan, Puerto Rico, US

Management of Sargassum Inundation Events (SIEs) includes both in-water and on-land strategies for reducing shoreline accumulation, minimizing ecological impacts, and supporting response efforts across affected jurisdictions. In-water strategies focus on intercepting, diverting, or removing Sargassum before it reaches the shore through the use of deflection structures, harvesting systems, and experimental disposal approaches. In contrast, on-land management consists of response actions implemented after *Sargassum* has beached and remains the most widely applied approach in U.S. jurisdictions. These strategies are primarily aimed at removing accumulated biomass from beaches and coastal areas to restore beach amenity, reduce impacts on tourism and public health, and minimize environmental damage from both the seaweed and the cleanup operations. Approaches vary depending on local conditions but typically include manual collection, mechanized removal, transport to staging areas, temporary drying, and final disposal or processing. Across jurisdictions such as Puerto Rico, the U.S. Virgin Islands, and Florida, management strategies are adapted to local environmental conditions, infrastructure, and regulatory requirements, highlighting the importance of coordination among federal, territorial, and local agencies. However, not all impacted US states and territories have clear and accessible *Sargassum* management plans, hindering the ability of coastal managers to respond to SIEs. Resource limitations in the US and wider Caribbean in particular, highlight the need for management of SIEs at a broader scale. Addressing these challenges requires developing standardized best management practices, improving understanding of ecological impacts, strengthening offshore and nearshore collection technologies, optimizing logistics and disposal pathways, advancing safe and scalable valorization options, and clarifying regulatory and governance frameworks to support effective and coordinated *Sargassum* management.

Hindcasting and Forecasting Domoic Acid Events in the California Current at Days to Decades Resolution

***Raphael M. Kudela[1]**, Marco Conci[1], Aurpita Saha[1], Jerome Fiechter[1], Dale Robinson[2], and Clarissa Anderson[3]*

[1]Institute of Marine Sciences & Ocean Sciences, University of California Santa Cruz, CA
2Southwest Fisheries Science Center, Santa Cruz, CA
3Scripps Institution of Oceanography, La Jolla, CA

Identification of *Pseudo-nitzschia* and domoic acid as a significant threat in the California Current System (CCS) occurred shortly after the 1987 Prince Edward Island event that resulted in three human mortalities. Within the CCS, several decadal-scale drivers such as the El Niño Southern Oscillation and Pacific Decadal Oscillation were quickly identified but with varying influence from south to north. More recently several modeling efforts have confirmed and expanded on the importance of these oscillations, which modulate upwelling and therefore nutrient availability, key drivers of bloom dynamics and toxin production. An ongoing challenging in monitoring, predicting, and responding to these events is the sparse shore-based and shipboard sampling. To overcome these issues predictive statistical models have been developed, in particular the California Harmful Algae Risk-Mapping (C-HARM) system which predicts the presence of *Pseudo-nitzschia* and domoic acid using circulation models, satellite remote-sensing data, and statistical models, but is limited to real-time predictions, and is deliberately restricted to California. While very successful, the research and management communities would benefit from consistent historical forecasts, forward decadal-scale projections of risk, and expansion to the northern CCS. Towards that end we have been working on two updated analyses. First, using Random Forest models, we have developed statistical models based on remotely-sensed data for both the Pacific Northwest and California as a proof-of-concept of what an updated domoic acid risk model might look like. In parallel, we have generated statistical models of domoic acid probability using a large in situ dataset and a biogeochemical model for 1995-2020. Current efforts are using this model to forward project domoic acid risk within California to the end of the century. This talk will provide an overview of these modeling approaches and lay out a roadmap for future application.

Making Satellite Data Useful for End-Users Tracking HABs in Estuarine and Inland Waters

Raphael M. Kudela [1], *Aurpita Saha*[1], *Lindsey Sim*[2] *and David A. Senn*[2]

[1]Institute of Marine Sciences & Ocean Sciences, University of California Santa Cruz, CA
[2]San Francisco Estuary Institute, Richmond, CA

Since the introduction of ocean color satellite sensors almost 50 years ago, the Harmful Algal Bloom (HAB) community has embraced the use of remote sensing as a powerful tool for monitoring, modeling, and predicting HAB events, complementing but not replacing in situ data collection. The steady progression of sensor development has gradually increased spatial and spectral resolution available from open-source (non-commercial) data providers such as NASA, ESA, and USGS, while standardization of products such as chlorophyll across multiple sensors makes it easier than ever to seamlessly integrate these data into existing programs. Despite these advances, coastal, estuarine and inland remote sensing is still technically challenging. The coarse spatial resolution (typically 300-1000 m) for global ocean color sensors such as PACE, MODIS, and OLCI and the coarse temporal resolution (8-16 days) and limited spectral bands for high spatial resolution (10-60 m) sensors such as Landsat and Sentinel-2 are less than ideal for these environments. Additionally, coastal, estuarine, and inland waters are optically challenging compared to the open ocean, introducing interference from colored dissolved organic matter, suspended sediments, and atmospheric correction issues. This leads to a fundamental challenge for end-users: which product(s) do I use, and should I trust them? Here we use San Francisco Bay and Delta, California inland lakes, and adjacent central California coastal waters to explore some examples of successful remote sensing methods that have, or on their way to, moving from research to operational tools, and the promises and challenges associated with application of next-generation sensors such as the hyperspectral data available from the PACE satellite.

What Have 30+ Years of Research in California Taught Us About Domoic Acid?

Raphael M. Kudela[1], *Aubrey J. Trapp[2], Julia McGrath[1], Aurpita Saha[1], and Clarissa Anderson[3]*

[1]Institute of Marine Sciences & Ocean Sciences, University of California Santa Cruz, CA
[2]Northwest Indian College, Bellingham, WA
[3]Scripps Institution of Oceanography, La Jolla, CA

Pseudo-nitzschia and domoic acid (DA) leapt to prominence in 1987 after the intoxication and subsequent mortality of three people in Prince Edward Island, Canada, although we now know that DA has been associated with marine mortality events in California since at least the 1960s. Today DA is considered one of the most significant and common algal toxins impacting coastal marine bird and mammal populations on the west coast with collateral damage to coastal fisheries and ongoing risks to human health. Continued investment from NOAA has greatly improved our understanding of *Pseudo-nitzschia*, domoic acid, and the interactions of both with food webs and climate, but many aspects of its ecophysiology and even the underlying basis for toxin production remain a mystery, or at least there often seems like there are as many possible answers as questions for when and why toxic blooms proliferate. Our understanding has gradually increased from a narrow view of these events, presumed to be dominated by *P. australis* driven into nutrient limitation in coastal "hotspots" where retentive circulation and upwelling overlapped with transfer of DA primarily into shellfish. Today we know that while this view is not incorrect, species matter—as do potential vectors for trophic transfer. We now have a solid understanding of bloom dynamics and drivers at the mesoscale. Exciting new findings suggest, amongst other things, that climate-driven changes may move us into a new paradigm (understandable by looking at the molecular ecology of *Pseudo-nitzschia*), understudied vectors such as squid are emerging as a serious risk, and we should be paying attention to both particulate and dissolved forms of DA. This talk will highlight some of the exciting new discoveries that have started to unravel the enigma of what drives these blooms and where we may be headed in the next 30 years.

Microplastics Negatively Affect Copepod Grazing on *Alexandrium* and Have Effects on Plankton Community Grazing Dynamics

Megan Ladds[1,2]*, Christopher Gobler*[2]

[1]Old Dominion University, Norfolk, VA, USA
[2]Stony Brook University, Southampton, NY, USA

Microplastics are one of the most prevalent and concerning pollutants that are affecting coastal ecosystems especially within the plankton since the most abundant microplastic particles overlap in size with key members of microbial food webs. In this study, the effects of polystyrene microplastics at varying sizes (4 - 10 µm) and concentrations (250, 500, 1000, 10000 microplastics mL^{-1}) on *Acartia tonsa* grazing of differing densities of *Alexandrium catenella* (250, 500, 1000) and *Gymnodinium aureolum* (500, 1000) as well as a mixture of the two algae were tested. Additionally, a 10 µm (1000 mL^{-1}) and 4um (10000 mL^{-1}) microplastic mixture was tested with 1000 cells mL^{-1} *A. catanella*. It was shown that high levels (10000 microplastics mL^{-1}) of 10 µm microplastics significantly reduced grazing of *A. catanella* by *A. tonsa* copepods. The inclusion of 4 µm microplastics with the 10 µm microplastics seemed to mitigate this effect. Additionally, high densities of 10 µm microplastics enhanced grazing on *G. aureolum*. In a further study where high densities of 10 µm microplastics were added to natural water incubations, with and without *A. tonsa* additions, there were differing effects based on the types of plankton that were present. Overall there was a decrease in grazing on the dinoflagellates, especially when they were dominant and an increase in grazing on diatoms which was significant when diatoms were dominant. These studies collectively indicate that there is a potential for microplastics to interact and become co-stressors on copepods during *A. catanella* and other dinoflagellate blooms, and may lead to initiation or prolong these types of HABs.

Implementing Receptor Binding Assay for Screening Shellfish in Washington State

*Alex Moseley, Daniel Chavez[1], **Jeff Lahti**, Morgan Langis, Brittany Jones, Reanna Martinez, Gabe Santana, Shelley Lankford*

Washington State Department of Health Public Health Lab, Shoreline, WA, King

The National Shellfish Sanitation Program (NSSP) lists the Receptor Binding Assay (RBA) as an approved method for testing Paralytic Shellfish Poisoning (PSP) in mussels for the control of shellfish produced and sold for human consumption. Washington State (WA) has the largest commercial and recreational shellfish harvesting surveillance in the United States. On average the WA Public Health Lab (WAPHL) tests over 3200 surveillance samples per year on a variety of shellfish species and since the inception of the program in the 1950's all samples have been tested for PSP using the mouse bioassay (MBA). Aside from ethical reasons for using an animal model, recent cost increases and the increasing difficulty to acquire and care for mice led WAPHL to investigate alternative methods for screening samples. From the list of NSSP methods, RBA offered rapid same-day turnaround time, similar extraction method, and uses sodium ion channels which closely model MBA detection and quantitative analysis of PSP. This work describes the validation WAPHL performed for RBA to allow for the screening of PSP on the six most common shellfish species harvested in WA: mussels, oysters, razor clams, hard clams, cockles and geoducks. The validation consisted of blank matrix from each of the six species that was spiked with known saxitoxin (STX) concentrations at quarter the action limit (20 µg of STX), half the action limit (40 µg of STX), at the action limit (80 µg of STX), twice the action limit (160 µg of STX) and four times the action limit (320 µg of STX) along with naturally incurred samples to compare against MBA. WAPHL conducted analysis for quantitative accuracy, reproducibility, matrix interference, limit of detection and limit of quantitation. Testing was performed as outlined in the official AOAC method, using MicroBeta2 Liquid Scintillation counter 12-detector.

Physical, Chemical, and Biological Drivers of *Sargassum* Inundation Events

Lapointe, B.E.[1]*, Cox, D.* [2]*, Morton, P.*[3]*, McGillicudy, D. Jr.*[4]

[1]Florida Atlantic University, Fort Pierce, FL, USA
[2]Bermuda Institute of Ocean Science, Bermuda
[3]Texas A&M University, College Station, TX, USA
[4]Woods Hole Oceanographic Institution, Woods Hole, MA, USA

Sargassum growth is substantially influenced by nutrient availability, with studies from the late 1980s demonstrating elevated photosynthetic and growth rates that correlate with increased tissue nitrogen (N) and phosphorus (P) levels. Long-term nutrient analyses of *Sargassum* tissues since the 1980s reveal an increase in tissue N (55% overall) and a slight decrease (-6%) in tissue P, resulting in a 50% increase in the N:P ratio over the past ~40 years. In addition to nutritional status, tissue nutrient concentrations and stable nitrogen isotopic composition ($\delta^{15}N$) can be used to identify potential nutrient sources such as riverine inputs, atmospheric deposition, coastal upwelling, nitrogen fixation, and vertical mixing. Of particular interest is the influence of atmospheric deposition, with the potential to contribute N, P and trace nutrients (e.g., Fe and Zn) to remote regions of the North Atlantic, with seasonal varying concentrations, relative ratios, and solubility (bioavailability). The cycling of nutrients in *Sargassum* is also influenced by the microbiome, a diverse consortium of viruses, bacteria, archaea, cyanobacteria, and microeukaryotes. The composition of this microbial community varies with location, collection conditions, and host health, and includes active heterotrophs, diazotrophs, and phosphonate degraders that can convert inert (e.g., N_2 gas) and organic forms of nutrients (e.g., DOP) to more bioavailable forms accessible by *Sargassum*. Despite ongoing advances in *Sargassum* research, several key information gaps hinder a comprehensive understanding of the physical, chemical, and biological drivers. These include:1) surface water nutrient and tissue N and P data for the eastern and central tropical Atlantic regions, 2) photosynthetic and growth rates for the entire tropical Atlantic, 3) the seasonality of vertical nutrient transfer to the surface mixed layer from nutrient-rich subsurface waters, and 4) the impacts of El Niño/La Niña on winds, current/mixing intensities, and drought/flood cycles that affect land-based nutrient runoff.

A Meta-analysis of Growth and Toxicity Responses in Naturally Occurring Algal Communities

James H Larson

U.S. Geological Survey, Upper Midwest Environmental Sciences Center, La Crosse, WI, USA

Harmful algal blooms (HABs), often dominated by cyanobacteria, are a growing global concern due to their ecological and economic impacts. Many cyanobacteria produce microcystin (MC), a potent hepatotoxin, but the environmental triggers of MC production in natural communities remain poorly understood. This study synthesizes experimental evidence from naturally occurring phytoplankton communities to evaluate three hypotheses for MC production: nitrogen overflow, oxidative stress response, and intracellular metal management. A literature review identified 23 studies (102 experiments) that manipulated environmental conditions and measured both phytoplankton biomass (chlorophyll a) and MC concentration in naturally occurring communities. Effect sizes were standardized using log response ratios (RR) for chlorophyll a, MC, and MC per chlorophyll a. Meta-analyses tested predictions from the three hypotheses, and machine-learning models (XGBoost with SHAP values) explored additional drivers of MC variability. Biomass and MC concentration responded similarly to treatments (Pearson's r = 0.37), but MC per biomass generally declined when growth was stimulated (r = - 0.40). Evidence from these studies indicated that alleviating P or N+P limitation reduced MC per biomass, while controls under nutrient limitation showed increased MC content. Machine-learning analysis highlighted initial chlorophyll a, MC concentration, TN:TP ratio, and cyanobacterial proportion as key predictors of MC response. MC production in natural communities is only loosely coupled to biomass and appears most strongly influenced by nutrient limitation and associated physiological stress, rather than by simple nutrient surpluses.

Lessons Learned from CyanoHAB Monitoring and Prediction in Iowa Lakes

Jaejin Lee

Iowa State University, Ames, IA, USA

Cyanobacterial harmful algal bloom monitoring and prediction increasingly draw on diverse environmental observations, molecular measurements, and machine-learning approaches. Yet advances in these technologies do not by themselves determine what should be measured, predicted, or interpreted. Based on four years of monitoring and prediction research in Iowa lakes, this presentation will reflect on several fundamental questions that arise before and alongside model development: What exactly are we trying to predict? How well do our observations represent the processes or risks we care about? And do we have enough of the right data to answer those questions? Rather than focusing on a single modeling study, the presentation will consider how scientific questions, operational definitions, monitoring design, and long-term data collection shape the meaning and usefulness of environmental prediction.

Marine Mammals: Sentinels for Increasing Algal Toxin Presence in Arctic Ecosystems Due to Warming Oceans

Kathi A. Lefebvre[1]*, Patrick Charapata*[2]*, Emily K. Bowers*[3]*, Raphaela Stimmelmayr*[3]*, Peigen Lin*[4]*, Robert S. Pickart*[5]*, Katherine A. Hubbard*[6]*, Brian D. Bill*[1]*, Gay Sheffield*[7]*, Donald M. Anderson*[8]*, Evangeline Fachon*[5,9]*, Rick Thoman*[10]*, Chelsea M. Campbell*[11]

[1]NOAA/Northwest Fisheries Science Center/Environmental and Fisheries Science Division/WARRN-West, Seattle, WA, USA
[2]Center for Species Survival, Georgia Aquarium, Atlanta, GA, USA
[3]North Slope Borough, Dept. of Wildlife Management, Utqiagvik, AK, USA
[4]School of Oceanography, Shanghai Jiao Tong University, Shangai, China
[5]Physical Oceanography Dept., Woods Hole Oceanographic Institution, Woods Hole, MA, USA
[6]Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Institute, St. Petersburg, FL, USA
[7]Alaska Sea Grant/Marine Advisory Program, University of Alaska Fairbanks, Nome, AK, USA
[8]Biology Dept., Woods Hole Oceanographic Institution, Woods Hole Oceanographic Institution, Woods Hole, MA, USA
[9]Dept. of Earth Atmospheric and Planetary Sciences, Massachusetts Institute of Technology, Cambridge, MA, USA
[10]International Arctic Research Center, University of Alaska Fairbanks, Fairbanks, AK, USA
[11]Ecosystem Conservation Office, Aleut Community of St. Paul, AK, USA

Over the last two decades, ocean warming and rapid loss of sea ice have dramatically changed the Pacific Arctic marine environment. These changes are predicted to increase harmful algal bloom prevalence and toxicity, as rising temperatures and larger open water areas are more favorable for growth of some toxic algal species. It is well known that algal toxins are transferred through food webs during blooms and can have negative impacts on wildlife and human health. Yet, there are no long-term quantitative reports on algal toxin presence in Arctic food webs to evaluate increasing exposure risks. In the present study, algal toxins were quantified in bowel samples collected from 205 bowhead whales harvested for subsistence purposes over 19 years. These filter-feeding whales served as integrated food web samplers for algal toxin presence in the Beaufort Sea as it relates to changing environmental conditions over two decades. Algal toxin prevalences and concentrations were significantly correlated with ocean heat flux, open water area, wind velocity, and atmospheric pressure. These results provide confirmative oceanic, atmospheric, and biological evidence for increasing algal toxin concentrations in Arctic food webs due to warming ocean conditions. This novel approach elucidates breakthrough mechanistic connections between warming oceans and increasing algal toxin exposure risks to Arctic wildlife, which threatens food-security for Native Alaskan Communities that have been reliant on marine resources for subsistence for 5,000 years. Recent algal toxin-related mortality events involving other important marine mammal species utilized for subsistence purposes will also be discussed.

Backyard Blooms: Residential Stormwater Ponds Are Hotspots for CyanoHABs, Sometimes…

Forrest W. Lefler[1]*, Shuo Chen*[2]*, Jéssica A.S. Moretto*[1]*, David E. Berthold*[1]*, Alexander J. Reisinger*[2]*, H. Dail Laughinghouse IV*[1]

[1]Agronomy Department, Fort Lauderdale Research and Education Center, University of Florida / IFAS, Davie, FL, USA.
[2]Department of Soil, Water and Ecosystem Sciences, University of Florida / IFAS, Gainesville, USA

Stormwater ponds (SWPs) are engineered aquatic ecosystems in (sub)urban communities. In Florida, there are an estimated 76,000 urban SWPs covering > 600 km^2 of land. Designed to retain stormwater runoff and mitigate downstream flooding, SWPs also receive high loads of nutrients (e.g., nitrogen, phosphorus) from surrounding developments and are assumed to sequester these nutrients before discharging to naturally occurring aquatic ecosystems (e.g., rivers, wetlands). Despite the cultural eutrophication, SWPs are capable of high rates of nutrient processing, and are considered "hotspots" for nutrient cycling. However, the connection between the microbial community and their roles in biogeochemical cycling within SWPs remain unexplored. We sampled 19 ponds across Florida during wet and dry seasons to characterize water chemistry along with microbial community structure and function using metagenomic sequencing. Trophic state and community structure of these SWPs varied greatly both between and within communities, with some SWPs experiencing *Microcystis*-dominated cyanoHABs. However, despite their proximity, <100 m in some cases, not all SWPs would experience cyanoHABs. Furthermore, cyanoHABs were more common in Gainesville, especially in the hot, wet season; potentially due to differences in management practices (e.g., fertilizer regulations) contributing to nutrient runoff. By comparing community structure and function across trophic states, residential communities, and time, we identify key microbial taxa and assemblages which contribute to the microbially mediated biogeochemical cycling in these widespread manmade ecosystems. These data can help strengthen science-based management practices for nutrient mitigation which can inform policy and design guidelines for SWPs globally.

Identification and Confirmation of the First Aaerophytic Saxitoxin-producing Cyanobacterium from a Residential Home

Forrest W. Lefler[1], *David E. Berthold*[1], *Jing Hu*[1], *Jéssica A.S. Moretto*[1], *Zacharias J Smith*[2], *Cathleen Chapman*[2], *H. Dail Laughinghouse IV*[1]

[1] Agronomy Department, Fort Lauderdale Research and Education Center, University of Florida / IFAS, 3205 College Avenue, Davie, FL 33314, USA

[2] USDA-ARS, Hydrology and Remote Sensing Laboratory 10300 Baltimore Avenue, BARC-West, B-001. Beltsville, Maryland 20705

Paralytic shellfish poisoning (PSP) toxins (PSPTs), or "saxitoxins", are a class of more than 84 highly lethal neurotoxins produced by cyanobacteria in freshwater systems and dinoflagellates in marine systems. PSPT cause illness when ingested and can present as: nausea and vomiting, diarrhea, numbness and tingling of the extremities, difficulty breathing and speaking, paralysis, cardiac arrest, and even death; with deaths attributed to PSP occurring across the globe. Until recently, PSPTs were considered to be confined to aquatic systems. However, recent findings have identified trace amounts of PSPTs or sxtA fragments from terrestrial cyanobacterial biofilms in Antarctica and the Arctic. *Brasilonema brancoi* BLCC-T110 was isolated from pavement in subtropical suburban neighborhood in Miami, Florida. PSPT production from *B. brancoi* BLCC-T110 was confirmed utilizing ELISA and LC-MS/MS, with the latter identifying 11 total congeners, and genomic analyses confirmed the presence of the complete biosynthetic gene cluster, and qPCR confirmed amplification of sxtA. *Brasilonema brancoi* BLCC-T110 is only the second strain of this species, which was recently described from subaerial growth on a stone in tropical rainforest from Costa Rica. Terrestrial and aerophytic cyanobacteria have historically received less attention for identification and monitoring of cyanotoxins, especially PSPT, due to their perceived lower threat to human and animal health. Currently, PSPTs and related genes have been identified from polar to subtropical climates, potentially indicating a wide distribution. With more data, we suspect these are not isolated phenomena and there are more PSPT producers occurring in unexpected places across the globe. Finally, this finding highlights a previously unrecognized source of PSPTs, and the toxicity of aerophytic mats should be given more careful consideration as new data arise.

SoundToxins Phytoplankton Monitoring Program - 20 Years of Monitoring HABs in Washington Marine Waters

Michelle Lepori-Bui, *Melissa Petrich*
Washington Sea Grant, Seattle, WA, USA

The SoundToxins Phytoplankton Monitoring Program is a diverse partnership of tribes, shellfish growers, environmental centers, health agencies, colleges, and community science volunteers. The primary goal is to provide early warning of harmful algal blooms (HABs) to minimize human health risks and economic losses through strategic monitoring at 37 sites throughout Washington's marine waters. Over the past 20 years, the program has grown to include 9 target genera including human health concerns (*Alexandrium*, *Dinophysis*, *Pseudo-nitzschia*, *Azadinium*, *Karenia*) and threats to finfish and shellfish populations (*Heterosigma*, *Akashiwo*, *Protoceratium*, *Phaeocystis*). Data collected by monitors are entered into an online database that can be accessed in real time by health officials to make timely decisions such as which harvest sites require additional shellfish samples or should be closed to harvesting. These data also ensure confidence to reopen areas, maximizing harvest opportunity and reducing testing costs. SoundToxins also provides outreach and education opportunities for volunteers and the greater community. This includes annual training for monitors, tabling at community events, and sharing results with the scientific community. Individual sites and partners conduct their own community events, greatly expanding the reach of the program. In addition to these core functions, SoundToxins contributes to and supports research efforts. In the past few years, this has included a socioeconomic analysis of HAB monitoring in Washington, research shellfish-killing HABs, and the connections between ocean acidification and HABs. Washington Sea Grant manages this program, including providing equipment, training, and technical support for monitors, coordinating collaborative research studies, and supporting a database also used by regional partner programs including Olympic Region Harmful Algal Bloom Partnership (ORHAB), Oregon Department of Fish and Wildlife.

I Want to See Your Peacock Grouper: Novel Detection of M-seco-ciguatoxin-4A/B in Previously Undetected Species

Schaeffer Lersch[1], *Sarah May* [2], *Edward Ianuzzi*[2], *Kirk Gaston*[2]

[1]VSG Contracting: Cognizance Technologies , LLC, Gulf Coast Seafood Laboratory, Dauphin Island, AL, USA
[2]US Food and Drug Administration, Gulf Coast Seafood Laboratory, Dauphin Island, AL, USA

Ciguatera poisoning is an international public health threat, impacting tens of thousands every year. The disease is linked to the contamination of seafood with ciguatoxins, a class of potent sodium channel-activating neurotoxins, which induce an array of symptoms including paralysis, numbness, and thermal dysesthesia, as well as cardiovascular and gastrointestinal issues. Currently, there is no clinical test for diagnosis in a potential ciguatera illness case. Confirmation of ciguatera poisoning relies on analysis of recent dietary history, symptomatology, and testing of meal remnants for ciguatoxin contamination. The analytical workflow involves screening extracts via a mouse neuroblastoma (N2a) cell assay followed by confirmation of ciguatoxins using liquid chromatography tandem mass spectrometry (LC-MS/MS). Over 40 structural congeners of ciguatoxins have been identified, causing a major impediment to the analytical confirmation of ciguatera poisoning. Currently, the various congeners are classified based on geographic region of origin, including the Atlantic Ocean and Caribbean Sea, Pacific Ocean, and Indian Ocean types. The Pacific ciguatoxins are the most well studied, with some commercial standards available. In this study, four archived samples of *Cephalopholis argus* (peacock grouper or roi) from previous ciguatera poisoning cases confirmed to contain Pacific ciguatoxin-1B were re-analyzed using updated LC-MS/MS methods to screen for additional Pacific congeners. The expanded screens demonstrated similar profiles across samples, reconfirmed the presence of Pacific ciguatoxin-1B, and identified 52-epi-54-deoxy-ciguatoxin-1B and 54-deoxy-ciguatoxin-1B. Interestingly, this is the first report identifying M-Seco-ciguatoxin-4A/B in peacock grouper, which has significant implications for ciguatera poisoning diagnosis in the region. Additional details regarding the geographic origin and potential emergence of ciguatoxins into new areas will be discussed.

Hydrographic Changes in the Gulf of Maine and Their Influence on Gulf of Maine Harmful Algal Blooms: 2018-present

Yizhen Li[1]*, Richard Stumpf*[2]*, Steve Kibler*[2]*, Caroline Owens*[3]*, Michelle Tomlinson*[2]*, Kari St. Laurent*[2]

[1]CSS Inc. under contract to NOAA National Centers for Coastal Ocean Science (NCCOS)
[2]NOAA National Centers for Coastal Ocean Science
[3]RPI Inc. Under Contract to NOAA NCCOS

NOAA NCCOS has issued the annual Gulf of Maine (GOM) Harmful Algal Bloom forecast (focusing on *Alexandrium catenella*) since 2008, based on fall or winter ship-survey data of cyst seed abundance and realistic atmospheric forcing and hydrodynamic conditions. We report the lessons learned in combining modeling effort and retrospective data analyses of *in situ* observations. In the last decade, *Alexandrium* blooms in the GOM have been mild, due to lower abundances of the overwintering cyst seed population, yet changes in timing of local blooms have become increasingly challenging to understand. We examined the variability in hydrodynamics and harmful algal blooms since 2018 (including *Alexandrium, Pseudo-nitzschia, and Tripos muelleri)*, leading to several conclusions. 1) Overall, the interannual variability of *Alexandrium* in the western GOM correlates with number of quiet spring wind days, suggesting that wind-induced mixing influences *Alexandrium* blooms between years with comparable cyst seed population. 2) An anomalous *Pseudo-nitzschia* bloom in winter 2019-early summer 2020 coincided with significant freshening in the GOM deep basins. 3) Anomalous hydrodynamics may affect plankton composition and timing of the bloom. For example, the unusual spring 2023 blooms of *Tripos muelleri* were associated with a late April river plume, supported by simultaneous downwelling-favorable wind events. *Tripos* may have outcompeted *Alexandrium* for that year.2024 was completely absent of *Alexandrium* blooms, with a historically high preceding snow melt and river discharge events during the prior winter; 4) In 2025, the *Alexandrium* bloom returned to the typical phenology of the years up to 2018; namely, the bloom initiated in early April through May, peaking in late May to early JuneOur work demonstrates the rising challenges in forecasting coastal ecosystems under a rapidly changing climate at various temporal and spatial scales, and highlights the value of combining observations and models to understand and address anomalies in ecological forecasting.

The Transition of Lake Erie Hypoxia Forecast System from Research into Operations: A Collaborative Paradigm

Yizhen Li[1]*, Richard Stumpf*[2]*, Mark Rowe*[3]*, Peter Alsip*[3]*, Caroline Owens*[1]*, Alexandria Hounshell*[2]*, and Kari St. Laurent*[2]

[1]CSS Inc. under contract to NOAA National Centers for Coastal Ocean Science (NCCOS)
[2]NOAA National Centers for Coastal Ocean Science
[3]NOAA GLERL

We highlight the collaborative effort to transition the Lake Erie Hypoxia Forecast System (LEHFS) from research to operations. The LEHFS was developed by NOAA's Great Lakes Environmental Research Laboratory, in partnership with regional public water systems and resource managers and was successfully transitioned to full operations by NOAA's National Centers for Coastal Ocean Science in 2024. The LEHFS is a 3-D physical-dissolved oxygen (DO) model that provides early warnings for decision makers of coastal upwelling events in Lake. Lake Erie is a drinking water source to more than 2 million people along the Ohio coast. In summer, the central basin stratifies, creating a distinction between warm water at the top and cold, dense, deep water down below. Stratification combined with consumption of oxygen via decomposition of organic matter leads to depletion of oxygen in the deep water. By mid-summer the deep water often becomes hypoxic (DO ≤ 2 mg/L). Easterly wind events then push surface water away from the Ohio coast, leading to upwelling events in which cold, hypoxic bottom water comes up to the surface close to shore. This hypoxic water occasionally causes fish mortality along beaches. The low DO water also has different chemistry from oxygenated water, characterized by low pH and elevated levels of iron and manganese, which requires public water suppliers to make significant changes to water treatment processes to avoid a sudden degradation of drinking water quality. As these upwelling events largely occur with an irregular frequency, local decision makers need timely warnings of the conditions that may cause them. We will highlight the success story of an early warning event from the operational LEHFS which helped stakeholders prepare for hypoxic events during the first two years of operations.

Domoic Acid and Microcystins Occurrence Across Freshwater-Coastal Connections in Southern California Coastal Waterbodies

***Alle AY Lie**, Jayme Smith*

Southern California Coastal Water Research Project, Costa Mesa, California, USA

Harmful algal bloom (HAB) toxins are increasingly recognized as a concern in coastal environments, where both marine and freshwater toxin-producing organisms may contribute to ecological and human health risks. This regional assessment evaluated the occurrence and distribution of domoic acid (DA) and microcystins (MCY) across coastal waterbodies in Ventura and Los Angeles counties through monthly monitoring in 2024 to investigate potential connections between coastal HAB dynamics and freshwater inputs. A multifaceted monitoring approach was used, incorporating Solid Phase Adsorption Toxin Tracking (SPATT), mussel tissue sampling, discrete water sampling, and DNA metabarcoding at coastal sites and selected hydrologically connected freshwater sites. Both DA and MCY were frequently observed in SPATT and mussel samples but were infrequently detected in particulate water samples. DA was detected in more than 80% of mussel samples collected from northern coastal sites throughout the study period. Co-occurrence of DA and MCY was also common, particularly in mussel tissues, where both toxins were detected in approximately 50% of samples. DNA metabarcoding further revealed a diverse assemblage of potentially toxigenic cyanobacteria, diatoms, and dinoflagellates, including taxa associated with toxins beyond DA and MCY. Overall, the findings highlight the complexity of HAB toxin occurrence in southern California coastal waterbodies and the potential importance of considering both marine and freshwater influences when evaluating HAB risk. The study also demonstrates the value of integrating multiple monitoring approaches to characterize toxin occurrence and potentially toxigenic communities across connected aquatic environments.

Assessing the Impact of Storing Water Samples at Ambient Temperature on Plankton Metabarcoding

Stephanie N. Lievano*, John Kristoffer Q. Andres, Ashley M. Reaume, Mousumi A. Mary, Michelle R. Gaither*
University of Central Florida, Orlando, FL, USA

Increasing water temperatures and nutrient loads can create conditions favorable for harmful algal blooms (HABs), which have been linked to economic impacts, fish kills, and health hazards. The Florida Fish and Wildlife Conservation Commission Fish and Wildlife Research Institute (FWC-FWRI) monitors HABs by collecting water samples and conducting cell counts. In collaboration with community scientists, they receive samples from across the state. These samples are stored at ambient temperature for up to 24 hours during transport. To ensure the efficacy of their protocol, FWC-FWRI, in partnership with the University of Central Florida, is investigating whether storage at ambient temperature impacts the plankton community composition of samples. In this study, we collected water samples from a single location in the Indian River Lagoon and processed them across six time points (0, 3, 6, 12, 24, and 48 hours). Four replicate samples, along with one negative control, were filtered at each time point. The 0-hour time point was filtered on-site to represent community structure at the time of collection. DNA metabarcoding was employed using 18S V9 and 16S V3-V4 primer sets to characterize plankton communities. Analysis of Similarities (using Bray–Curtis dissimilarities) revealed significant differences in community composition among time points ($P < 0.05$) in both the 18S and 16S datasets. However, other comparisons did not indicate significant differences. Here we discuss the data and its implications on statewide monitoring programs.

Optimizing a Molecular Toolkit for the Accurate and Efficient Detection of HABs Across Florida

Mousumi Akter Mary[1], Katherine Hubbard[2], Julie A. Koester[3], John Kristoffer Andres[1], Alicia E. Hoeglund[2], Michelle R. Gaither[1] *Presented by:* ***Stephanie N. Lievano***

[1]Department of Biology, Genomics and Bioinformatics Cluster, University of Central Florida, Orlando, FL 32816, USA

[2]Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, St. Petersburg, FL, 33701, USA

Harmful algal blooms (HABs) cost the state of Florida millions of dollars each year in lost revenue. These events affect human health, ecosystem function, and coastal economies through toxin production, habitat degradation, and the creation of hypoxic conditions. The state investment in monitoring and mitigation is substantial; however, effective response depends on accurate taxonomic identification of HAB species, which is challenging due to emerging taxa, expanding species distributions, and coincident bloom events. Traditional monitoring approaches based on morphological identification via light microscopy remain the standard but are limited by the need for taxonomic expertise and the difficulty of distinguishing closely related species. To overcome these limitations, we are working to develop an optimized molecular toolkit to improve the detection and monitoring of HAB species, while concurrently characterizing shifts in the broader plankton community during HAB events. Using metabarcoding approaches, we evaluated seven published primer sets, including those from the Earth Microbiome Project. These primer sets target eukaryotic (18S rRNA) and prokaryotic (16S rRNA) gene regions. First, primer sets were tested on cultures representing 11 known HAB taxa to assess specificity and taxonomic resolution. Based on the results, two sets of each 18S and 16S primers were selected for further testing on a limited set of field samples. Comparative analyses revealed variation among primer sets in taxonomic coverage and community composition profiles. Finally, one of each 18S and 16S primer sets were selected based on reliable detection of target HAB taxa, broad taxonomic coverage, and reproducibility across culture and field samples. The selected primer sets were then applied to large scale field sampling for HAB detection and community composition analysis. This work will help to establish a reliable set of molecular tools for large scale monitoring and improved early detection and management of harmful algal blooms in U.S. waters.

Bacterioplankton Communities of *Karenia brevis* Harmful Algal Blooms in Southwest Florida and *Karenia* spp. Cultures

Shen Jean Lim[1]*, Julie Koester*[2]*, Rachel Stein-Plog*[2]*, Alexandra Rogers*[1]*, Katherine Hubbard*[2]*, Mya Breitbart*[1]

[1]University of South Florida, St Petersburg, Florida, USA
[2]Fish and Wildlife Research Institute, St. Petersburg, Florida, USA

The dinoflagellate *Karenia brevis* causes harmful algal blooms (HABs) in the eastern Gulf of Mexico, affecting the region's environment, public health, and economy. Intermicrobial interactions between *K. brevis* and other microorganisms can influence bloom dynamics, but are poorly understood at the community scale. We sequenced the prokaryotic 16S rRNA gene and eukaryotic 18S rRNA gene content from the 0.45 µm size-fraction of 54 field samples collected from Southwest Florida, USA between 2021-2023 and 59 cell culture samples obtained from 17 *Karenia* spp. strains grown in the laboratory. Bacterioplankton diversity showed significant associations with *K. brevis* cell counts, sample type, and spatiotemporal variables. In field samples, eukaryotic alpha diversity inversely correlated with *K. brevis* cell counts. Bacterial alpha diversity positively correlated with *K. brevis* cell counts, peaking at medium cell densities before declining at high densities. Although Alphaproteobacteria and Gammaproteobacteria were common in field and culture samples, no consistent core microbiome was resolved below the class level. Nevertheless, many bacterial pathways predicted by PICRUSt2 were shared between field and culture samples. Core pathways were related to central carbon metabolism, photosynthesis, photorespiration, fermentation, as well as the biosynthesis and degradation/utilization/assimilation of amino acids, carbohydrates, aromatic compounds, secondary metabolites, and other compounds. At the genus level, *Karenia* was the most abundant eukaryotic genus and positively correlated with *K. brevis* cell counts in field samples. The parasitic dinoflagellate *Dino-Group-I-Clade-1_X* was the second most abundant genus and detected in all field samples, suggesting widespread infection during blooms. The bacterial genus *Tenacibaculum*, an opportunistic fish pathogen, was enriched in samples with high *K. brevis* counts and showed direct network associations with *Karenia*, suggesting a potential role in bloom-associated fish mortality. Future investigations on nutrient exchange in the phycosphere and the effects of intermicrobial associations on bloom dynamics could elucidate biological drivers of *K. brevis* blooms.

Phytoplankton Functional Groups and Harmful Algal Blooms in Gulf Waters Using PACE and EMIT Hyperspectral Observations

Bingqing Liu [1], *Eurico J. D'Sa* [2], *Melissa M. Baustian* [3], *S. Morgaine McKibben* [4 5], *Inia Soto Ramos* [6 7], *Katherine K. Harrison* [8]

[1] Department of Earth, Ocean and Atmospheric Science, Florida State University, Tallahassee, FL 32304, USA
[2] Department of Oceanography and Coastal Sciences, Louisiana State University, Baton Rouge, LA 70803, USA
[3] Wetland and Aquatic Research Center, U.S. Geological Survey, Baton Rouge, LA 70808, USA
[4] NASA Goddard Space Flight Center, Greenbelt, MD 20771, USA
[5] Science Systems and Applications Inc, Lanham, MD 20706, USA
[6] GESTAR II, Morgan State University, Baltimore, MD, USA
[7] Ocean Ecology Laboratory, NASA Goddard Space Flight Center, Greenbelt, MD, USA
[8] Gulf of America Alliance, Ocean Springs, MS 39564, USA

Satellite remote sensing excels at capturing the surface ocean biosphere with high spatiotemporal resolution. Over the past two decades, significant international efforts have advanced ocean color algorithms to retrieve not only chlorophyll-a but also phytoplankton functional types (PFG), most of which have been developed and validated primarily in open ocean waters using multispectral satellite data. As satellite sensors evolve from multispectral to hyperspectral imaging, such as the recent NASA PACE and EMIT missions, the increased number of wavebands, narrower bandwidths, and full visible-spectrum coverage provide more detailed bio-optical information about aquatic environments.

Satellite-derived phytoplankton functional group (PFG) products are critically needed in coastal and inland waters, where physical–biological dynamics are more transient and difficult to interpret, and harmful algal blooms (HABs) pose significant environmental and public health risks. The hyperspectral capabilities of EMIT and PACE enable full spectral exploitation of remote sensing reflectance (R_{rs}), its derivatives, and improved retrieval of phytoplankton absorption (a_{phy}) to derive PFG through spectral unmixing.
In this study, we introduce two AI-based hyperspectral unmixing algorithms to investigate phytoplankton community dynamics in estuarine and coastal waters of the Gulf of America. Two case studies are presented: one using EMIT to examine a cyanobacterial bloom dominated by Dolichospermum and Oscillatoria in an inland lake, and another using PACE to study a red tide (Karenia brevis) outbreak following Hurricane Milton in 2024 on the West Florida Shelf.

While both missions are individually transformative, they serve complementary roles: PACE is well suited for open coastal systems, whereas EMIT demonstrates strong capability in resolving features in inland and estuarine environments. The development of globally applicable, cross-mission algorithms holds strong promise for future hyperspectral satellite missions.

Transferability and Scalability of Water Quality Remote Sensing Models and Hot Spot Analysis of HABs

Hongxing Liu[1], *Jilin Men*[1], *Yuehan Lu*[1], *Ekaterina Miliutin*[1], *Amanjit Premsagar*[1], *Anindya Palaparthi*[1], *Haibin Su*[2], *Naveenkumar Purushothaman*[1]

[1]University of Alabama, Tuscaloosa, Alabama, USA
[2]Texas A&M University – Kingsville, Kingsville, Texas, USA

Harmful algal blooms (HABs) pose growing risks to drinking-water security, aquatic ecosystems, fisheries, recreation, and public health. Remote sensing provides an effective capability for detecting, mapping, and tracking HAB dynamics across broad spatial extents. However, many traditional water-quality remote sensing models remain constrained by limited spatial transferability and scalability. These limitations reduce their operational value for regional-to-continental HAB monitoring.

This research reviews recent advances in transferable and scalable water-quality remote sensing models for HAB monitoring. It first examines random forest and multi-predictor ensemble machine-learning models that integrate multiple predictors for varying optical and environmental conditions to improve model robustness across different water bodies and observation seasonal periods. Compared with traditional empirical approaches, these models demonstrate stronger spatial transferability and temporal repeatability by capturing nonlinear relationships between satellite observations and HAB-related water-quality variables. This research further highlights emerging opportunities from physics-informed deep learning models, which incorporate optical-process constraints into data-driven learning, and from deep learning foundation models such as NASA Prithvi-EO, which are promising for scalable, transferable, and sensor-flexible water-quality retrieval.

In addition, this research demonstrates hot spot analysis for characterizing remotely sensed spatiotemporal variability of HABs. Using Sentinel-3 observations for the African Great Lakes, hot spot analysis is applied to identify persistent and emerging HAB-prone areas and evaluate seasonal and interannual patterns. Together, these modeling and spatial-analysis advances provide a pathway toward more operational, scalable, and transferable remote sensing systems for HAB monitoring and early warning across diverse inland water environments.

Modeling HABs Transport to Inform Monitoring Strategies

Qianqian Liu[1], *Carter Beaulieu*[1,2]

[1]University of North Carolina Wilmington, Wilmington, NC, USA
[2]University of Rhode Island, Narragansett, RI, USA

Cyanobacteria Harmful Algal Blooms (CHABs) are recurrent in the Chowan River. However, the physical processes governing their movement remain insufficiently understood. Using an active Lagrangian particle tracking model driven by hydrodynamic model output and in situ observations, we investigated bloom transport and connectivity between the Chowan River and its adjacent Albemarle Sound. Our simulations reveal that CHABs can be transported both upstream and downstream, with directions strongly controlled by the combined effects of wind forcing and river discharge. During low-discharge periods, wind-driven circulation enabled upstream intrusions and cross-channel redistribution, while higher discharge accelerated downstream export. Notably, blooms required measurable transport time, > 10 days, to reach western Albemarle Sound, even during high discharge periods, revealing that local observations cannot immediately reflect upstream bloom origin. Furthermore, under certain wind-discharge combinations, HABs can be advected toward the northern part of the western Albemarle Sound, an area that is not routinely monitored, suggesting a potential blind spot in current surveillance efforts. These findings demonstrate that transport pathways and residence times can diverge substantially from assumptions based solely on local bloom observations. By identifying unmonitored regions susceptible to transported blooms and clarifying conditions that promote upstream vs. downstream movement, this modeling framework provides actionable guidance for designing more effective and proactive HAB monitoring strategies across the Chowan-Albemarle system.

Coastal Ocean Circulation Monitoring Improves the Seasonal Prediction of Florida Red Tide

***Yonggang Liu*[1]**, *Logan Dudney*[1], *Jing Shi*[1], *Robert H. Weisberg*[1], *Jason A. Law*[1], *Matthew J. Garrett*[2], *Katherine A. Hubbard*[2]

[1]College of Marine Science, University of South Florida, Saint Petersburg, FL, 33701, USA
[2]Florida Fish and Wildlife Conservation Commission – Fish and Wildlife Research Institute, Saint Petersburg, FL 33701, USA

The central portion of the west Florida continental shelf is the epicenter for blooms of the harmful alga *Karenia brevis*, which is hypothesized to form at mid-shelf under nutrient depleted, or oligotrophic, conditions. Whether or not the shelf is conducive to such bloom formation in any given year may be related to when and where the Loop Current interacts with the shelf slope. If this occurs in the southwest corner, where shallow isobaths wrap around the Florida Keys at the Dry Tortugas, then the shelf may be set into a protracted upwelling circulation that can both reset water properties and transport mid-shelf materials to the shoreline within the bottom Ekman layer. To test this hypothesis, we examine the 28 years (1998-2025) of observations from a moored array, which include water column velocity recorded by Acoustic Doppler Current Profilers (ADCPs) and water temperature at selected depths. Upwelling events are identified from these velocity data through progressive vector diagrams (PVDs), as well as the subsurface temperature anomaly time series. These are further linked to the red tide events in the past. We find that the ocean circulation data can provide essential information in improving the previous seasonal forecast of red tide that is based merely on satellite altimetry-derived offshore forcing upwelling index. By combing real time mooring array observations with the satellite altimetry product, we can develop an improved seasonal prediction of the Florida red tide.

Suspended Sediment, CDOM, and Nutrient Interactions Affecting Cyanobacteria Harmful Algal Blooms in Mississippi Agricultural Watersheds

***Richard Lizotte**, Matthew Moore*

USDA-ARS National Sedimentation Laboratory, Oxford, MS, USA

The objective of this study was to assess interactions between suspended sediment (TSS) and colored dissolved organic matter (CDOM) light limitation and nitrogen (N) and phosphorus (P) nutrient relationships for cyanobacteria harmful algal blooms (cyanoHABs) in two case-study Mississippi agricultural watersheds. Intensive agricultural activity can transport eroded materials such as sediment, CDOM, N, and P that influence the timing, intensity, and duration of cyanoHABs. Both Mississippi watersheds were assessed from 2017-2023 (excluding pandemic years 2020-2021). Roundaway Lake is a conventionally row crop farmed impounded bayou and Beasley Lake is an oxbow lake farmed with multiple integrated conservation practices. Surface water samples were collected biweekly and measured for TSS, CDOM (as $SUVA_{254}$), total N, total P, and phycocyanin (representing cyanoHABs). To ascertain effects of TSS and CDOM on phycocyanin, moving median data smoothing followed by polynomial regressions were conducted. To determine the influence of TSS and CDOM on phycocyanin N and P relationships, a moving window correlation analysis was conducted followed by linear or log-linear regressions to obtain target N or P concentrations for mesotrophic phycocyanin levels. Within Roundaway, TSS (>28-192 mg TSS/L) and CDOM $SUVA_{254}$ (>2.96-4.98 L/mg C/m) decreased cyanoHABs due to light limitation. Highest phycocyanin-nutrient correlations occurred across TSS but more narrowly with CDOM $SUVA_{254}$ (< 4.00 L/mg C/m). Roundaway target nutrients were 0.548-0.984 mg TN/L and 0.031-0.087 mg TP/L. For Beasley, TSS (>64-90 mg TSS/L) and CDOM $SUVA_{254}$ (>5.61-8.74 L/mg C/m) decreased cyanoHABs due to light limitation. Highest phycocyanin-nutrient correlations within TSS were <50 mg/L within CDOM $SUVA_{254}$ between 2.00-3.00 L/mg C/m. Beasley target nutrients were 0.388-0.491 mg TN/L and 0.019-0.027 mg TP/L. This information is useful to farmers and land managers implementing conservation to reduce HABs.

Assessment of Phytoplankton and Cyanotoxins in the Nearshore Environment of Lake Tahoe, June – October 2024

Keith A. Loftin[1], *Ramon Naranjo*[2], *Gwendolyn E. Davies*[2], *Viviana Mazzei*[3], *H. Dail Laughinghouse, IV*[4], *Forest W. Lefler*[4], *Jessica Moretto*[4], *David Berthold*[4], *Zachary Laughrey*[1], *Olivia Jenks*[1], *David Lutin*[1]

[1] US Geological Survey, Central Plains Water Science Center, Algal and other Environmental Toxins Laboratory, Lawrence, KS 66049, USA

[2] US Geological Survey, Nevada Water Science Center

[3] US Geological Survey, Florida-Caribbean Water Science Center, Orlando, FL

[4] University of Florida, IFAS, Davie, FL 33314, USA

Lake Tahoe, a deep, natural, and oligotrophic lake that shares a border with California and Nevada (USA), has been experiencing declining water clarity, nuisance algal blooms, and reports of cyanotoxin occurrence in its nearshore environments, especially in the Tahoe Keys area. Monthly surveys were conducted along tangential transects at multiple depths around the perimeter of the lake between June and October 2024. Water quality variables (chlorophyll-a, phycocyanin, DO, pH, etc.) were measured in the field. Chlorophyll-a did not exceed 1.1 relative fluorescence units in any of the samples. Phycocyanin fluorescence was elevated in the Tahoe Keys consistently and occasionally at several other sites. Enzyme-linked immunosorbent assay was used to measure cyanotoxins. Anatoxin-a was measured in separate months at Tahoe City and Incline Creek sites at concentrations of 0.18 µg/L or less. Cylindrospermopsins and saxitoxins were not detected at any locations, and microcystins at 0.24 µg/L or less were detected 3 times in the Tahoe Keys. Concentrations were below the World Health Organization and Environmental Protection Agency recreational thresholds. Morphologic evidence and corresponding metagenomic analysis confirmed the presence of known toxin-producing cyanobacteria in the Tahoe Keys area in August 2024 and the potential for cyanopeptide production of unknown toxicity according to measured biosynthetic gene clusters. High-resolution mass spectrometry analysis is being conducted to confirm corresponding cyanopeptide production.

Occurrence of Nearshore Cyanotoxins in Select US National Wildlife Refuge System Waterbodies

*Dominic A. Libera[1], Lee C. Jones[2], **Keith A. Loftin[3]**, Zachary R. Laughrey[3], Amelia Wyndrum[3], Viviana Mazzei[4]*

[1] U.S. Fish and Wildlife Service, Natural Resource Program Center, Raleigh, NC
[2] U.S. Fish and Wildlife Service - Wildlife Health, Natural Resource Program Center, Bozeman, MT
[3] U.S Geological Survey Central Plains Water Science Center, Algal and Other Environmental Toxins Laboratory, Lawrence, KS
[4] U.S. Geological Survey Florida-Caribbean Water Science Center, Orlando, FL

Cyanotoxins potentially threaten the health of fish, wildlife and humans at United States Fish and Wildlife Refuges, but prevalence is largely unknown. A baseline cyanotoxin assessment was conducted every two weeks between June and October 2023 at 25 sites on 17 waterbodies across 16 National Wildlife Refuge System units with a known or suspected history of cyanotoxin occurrence. Cyanotoxins were quantified by liquid chromatography high resolution mass spectrometry and evaluated against thresholds of health concern. Anatoxin-a (ANAA), cylindrospermopsin (CYLS), and summed microcystins (MCs) were detected in 5.4, 8.3, and 36% of samples, respectively. Maximum concentrations were detected up to 0.32, 1.5, and 13,800 µg/L for ANAA, CYLS, and MCs, respectively. CYLS was detected persistently at Lake Mattamuskeet (North Carolina, USA) and nodularin-R was not detected in any tested locations. MCs exceeded World Health Organization (WHO) Alert Level 2 for recreational contact in 5.4% of the 240 samples collected. ANAA, CYLS, and MCs exceeded WHO Alert Level 1 in 5.4, 8.3, and 30.8% of samples. MCs exceeded the Environmental Protection Agency (EPA) Recreational Advisory Threshold in 9.2% of samples. Only 3 of the 25 sampled sites had no cyanotoxin detections at any time throughout the study season. Microcystin-LR (MCLR) was the most frequently detected congener (35%) followed by MCHtYR (15%), MCRR (10%), MCYR (8.8%), and MCLY (6.7%). The other five measured microcystin congeners were each detected at 5.8% or less of the sites. Cyanotoxin class mixtures were measured in 1.7% of samples where ANAA was mixed with MCs. A subset of sites was sampled for phytoplankton and multiple potentially toxic cyanobacteria were identified. This study documents frequent cyanotoxin occurrence across multiple US National Wildlife Refuge System units, and in some cases at concentrations that potentially threaten wildlife health and recreational access.

Practical HAB Mitigation: Logistical Considerations for *In Situ* Mitigation Deployments

Lizabeth Longstreet[1]*, Kevin Claridge*[1]*, Cynthia Heil*[1]*, Emily R. Hall*[1]*, Jennifer Toyoda*[1]*, Cameron Morris*[2]*, Andy Eggebrecht*[3]

[1]Mote Marine Laboratory, Sarasota, Florida, USA
[2]Simeon Global Consulting LLC, Tallahassee, Florida, USA
[3] Emerge Marine, Sarasota, Florida, USA

The Red Tide Mitigation and Technology Development Initiative was established in 2019 as a partnership between Mote Marine Laboratory (Mote) and the State of Florida to advance prevention, control, and mitigation technologies aimed at reducing the impacts of Florida red tide (*Karenia brevis*). Over the past seven years, Mote and its partners have conducted laboratory testing on hundreds of mitigation products, resulting in several candidates now ready for pilot-scale field testing in coastal waters. However, a comprehensive logistical framework, including best practices for marine harmful algal bloom (HAB) mitigation testing *in situ,* have not been established in the United States. Recently, Mote has focused significant effort on identifying, addressing and validating the logistical considerations required for *in situ* HAB mitigation deployments. These efforts include navigating state and federal permitting processes, evaluating site selection criteria based on product characteristics and natural resource sensitivities, conducting public outreach, coordinating multiple groups including scientists, deployment and ship staff and contractors for product application, and defining appropriate sampling and monitoring protocols and parameters. Building on this foundation, Mote has conducted several mitigation 'test' deployments along Florida's west coast in 2025-2026. Each product and deployment scenario have required unique logistical considerations, which are being systematically documented in the *Harmful Algal Bloom Mitigation Standard Operating Procedure and Deployment Playbook*. Developed in collaboration with Simeon Global Consulting LLC, this resource is intended to serve as a comprehensive guide for marine HAB mitigation practices.

Key Factors in *Pyrodinium bahamense* Bloom Absence in Tampa Bay after 17 Years of Blooms

***Cary Lopez**, Colin Shea, Sugandha Shankar, Sara Kaminski, Katherine Hubbard, Grace Harris*

Florida Fish and Wildlife Conservation Commission, Fish and Wildlife Research Institute, Saint Petersburg, Florida, USA

In recent years, blooms of *Pyrodinium bahamense* in Tampa Bay have posed challenges for management due to repeated failed attainment of chlorophyll *a* regulatory criteria and sustained loss of seagrass coverage. However, after 17 years of recurring summer blooms in Tampa Bay's northern segment, *P. bahamense* blooms were absent in the bay in 2024 and 2025. We investigated the cause of this decline as well as drivers of bloom probability and biomass severity using a 13-year time series of routine monitoring data. Statistical models of bloom probability showed support for multiple environmental drivers, but scenarios with a substantial source of cells (i.e., high cyst abundance or existing bloom) and high rainfall events resulted in the highest bloom probabilities. Model predictions compared to observations suggested rainfall conditions had the most influence in springtime or early summer. Similarly, variability in derived annual severity indices for *P. bahamense* and chlorophyll *a* was partially explained by rainfall and bay-wide nutrient loadings in spring (the pre-bloom period), but not by rainfall or loadings in summer (the period of bloom peak). Notably, a significant decline in resting cysts in the vicinity of Tampa Bay *P. bahamense* "hotspots" coincided with the bloom absences, and ongoing efforts are investigating different causes of the decline. Results from Tampa Bay will be compared to other regions of Florida that continue to experience high biomass *P. bahamense* blooms or are emerging areas of concern.

Biochar-Based Flocculation Strategies for Removal of HAB Cells and Toxins

Vincent Lovko[1]*, Toufiq Reza*[2]*, Robert Cheatham*[2]

[1]Mote Marine Laboratory, Sarasota, FL, USA
[2]Florida Tech, Melbourne, FL, USA

Flocculation and sedimentation are promising strategies for the control and mitigation of harmful algal blooms (HABs). Previous work using polyaluminum chloride (PAC)-modified kaolinite clay demonstrated high efficacy for *Karenia brevis* cell removal; however, brevetoxin removal was limited. Biochar, produced from pyrolyzed organic waste material, has shown high adsorption capacity for several HAB toxins and also functions effectively in the flocculation and sedimentation of HAB cells when combined with an inorganic polymer coagulant such as PAC.

In our US HAB CTI-funded projects, we conducted multi-tier laboratory studies to evaluate the efficacy of PAC-modified biochar in reducing cell abundance and toxin concentrations in three marine dinoflagellates: *Alexandrium tamarense*, *K. brevis*, and *Pyrodinium bahamense*. In experiments conducted in 80-L vertical tanks, PAC-modified biochar effectively removed cells and toxins in all tested species, achieving cell removal efficiencies of 60% for *A. tamarense*, >80% for *K. brevis*, and >95% for *P. bahamense* at 3 h post-treatment. By 24 h post-treatment, cell removal reached 95–100% for all three species. Brevetoxin removal reached approximately 60% by 24 h, compared with ~30% removal at 72 h using PAC-modified clay. Results for saxitoxin removal in *A. tamarense* and *P. bahamense* are pending.

Despite these promising results, PAC is not included on the EPA minimum-risk pesticide list and is therefore unlikely to receive permitting for near-term in situ application in coastal waters. Consequently, through two EPA-funded projects, we are investigating alternative flocculants, including organic compounds such as tannic acid and chitosan, as well as combinations of biochar, flocculants, algaecides, and calcined oyster shell (COS) to provide additional ballast and promote nutrient sequestration. Results from these ongoing studies will be presented.

Cyanotoxin Risks in Agricultural Catchments: Full-Profile Analyses of Four Inland Lakes with Varying Trophic Status

Chiqian Zhang[1], Ian Struewing[2], Kyle D. McIntosh[3], Nathan Sienkiewicz[4], Laura Webb[5], Steven Baker[6], Amy Shields[7], Eric Villegas[2] ***Jingrang Lu****[2*]*

[1]Civil Engineering Program, College of Engineering & Computer Science, Arkansas State University, Arkansas 72467
[2]U.S. Environmental Protection Agency (USEPA), Office of Applied Science and Environmental Solutions, Cincinnati, Ohio
[3]Ohio Dept. of Agriculture, Canal Winchester, Ohio
[4]Left USEPA Office of Water on a personal sabbatical
[5]Retired from USEPA Region 7
[6]Federal Acquisition Service, Kansas City, Missouri/Kansas
[7]USEPA Region 7, Kansas City, Kansas/Missouri

Eutrophication-driven phytoplankton blooms threaten ecological integrity, economic sustainability, and public health. Agriculture is widely regarded as a major driver of eutrophication, but direct, quantitative, and source-specific evidence attributing eutrophication to agriculture remains limited. To address this gap, we integrated environmental and molecular profiling across four historically understudied yet important freshwater lakes with different trophic statuses in the Central United States. Through weekly sampling for an entire growth season, we assessed environmental variables, trophic status, and anthropogenic tracers (agricultural pesticides and metals) to explain the dynamics in phytoplankton abundance, community structure, and cyanotoxin production. Our preliminary data showed that synthetic pesticides could serve as a tracer of agriculture with metals as a secondary indicator of anthropogenic influence. The distinct trophic statuses effectively account for the differences in phytoplankton abundance, community structure, and cyanotoxin production across the four lakes. Specifically, Smithville and Perry Lakes were hypertrophic, Bethany Lake was eutrophic, and Nine Eagles Lake was mesotrophic. Consequently, the four lakes formed two contrasting groups: high-algal abundance systems (Smithville and Perry) and low-algal abundance systems (Nine Eagles and Bethany). The high-abundance systems had distinct phytoplankton community structures and higher cyanotoxin (mainly microcystin) risks than the low-abundance systems. Anthropogenic activities were a major driver of the distinct trophic statuses. Importantly, pesticides show strong positive correlations with trophic status (adjusted R-squared = 0.87), phytoplankton abundance (adjusted R-squared = 0.94), transcript level of the 16S rRNA gene of *Microcystis* (adjusted R-squared = 0.98), and microcystins. Our preliminary analysis shows that crop farming could be a dominant driver of eutrophication and downstream phytoplankton blooms. The significant positive linear correlation between metals and trophic status further reinforces the role of anthropogenic influence. Overall, our preliminary data support that this tracer passed framework may link agriculture to eutrophication-driven phytoplankton blooms and cyanotoxin risks, offering actionable insights for freshwater rehabilitation.

Drone-Based Hyperspectral Remote Sensing of Dissolved Organic Matter Source Dynamics in a River-Reservoir System

Amanjit Premsagar[1], Jilin Men[2], Hongxing Liu[2], Ekaterina Miliutina[2], Tantu Mandal[2], ***Yuehan Lu[1]***

[1]Molecular Eco-Geochemistry (Meg) Laboratory, Department of Geological Sciences, Tuscaloosa, AL, USA
[2]Department of Geography and the Environment, Tuscaloosa, AL, USA

Discriminating autochthonous (algal and microbial) from allochthonous (terrestrial) dissolved organic matter (DOM) is critical for understanding carbon cycling and its implications for harmful algal blooms (HABs). Autochthonous DOM, particularly protein-rich fractions from microbial turnover, can fuel cyanobacterial growth and exacerbate bloom severity. Despite the efficiency of remote sensing in reducing labor, cost, and time for water quality monitoring, its application in resolving DOM sources remains limited. Here, we collected drone-based hyperspectral data concurrently with water sampling from a river–reservoir system in Alabama, and analyzed DOM using absorbance and fluorescence spectroscopy to characterize DOM source composition dynamics. We developed and validated hyperspectral reflectance–based proxies (400–720 nm) for DOM source discrimination. Systematic optimization of >8,000 spectral band ratio combinations identified a green-to-red reflectance ratio [Rrs(525)/Rrs(655)] as the strongest predictor of DOM provenance, exhibiting a robust correlation with the biological index. A multivariate Random Forest model integrating five optimized spectral features predicted the protein-to-humic fluorescence ratio—a proxy for bloom-supporting labile DOM—with strong cross-validated performance. Feature importance analysis indicated that the green-to-red ratio accounted for the majority of predictive contribution. Seasonal evaluation demonstrated that our model captured shifts from humic-dominated post-bloom conditions to protein-enriched turnover conditions that favor cyanobacterial blooms, confirming temporal robustness. These results demonstrate that hyperspectral reflectance can quantitatively resolve DOM source dynamics in freshwaters, offering a promising pathway for early warning and monitoring of HAB-prone conditions in drinking water reservoirs.

Evaluating Innovative Treatment Strategies to Control Near-Shore HABs

Fred S. Lubnow

U.S. Princeton Hydro, LLC, 35 Clark Street, Suite 200 Trenton, NJ, USA

Addressing the watershed-based, external nutrient load is the absolute foundation of long-term, effective, and consistent HAB control in aquatic ecosystems. In addition, in the case of large, deep lakes and reservoirs, particularly those that exhibit some degree of thermal stratification and associated depletion of deep-water dissolved oxygen, internal nutrient control measures may be required. However, it has also been recognized that the shallow, near-shore sections of a waterbody can serve as a source of cyanobacteria that can then expand into other sections of the lake and result in HABs. These shallow, nutrient-rich sediments can receive a sufficient amount of light to stimulate the growth of overwintering cyanobacteria early in the spring. Thus, by not addressing this source of HABs, lake management efforts may be hampered in producing the expected water quality improvements. This presentation will address the ecology of these shallow near-shore habitats relative to the development of HABs. Additionally, the presentation will review innovative techniques that can be considered to either proactively or reactively address these HABs.

Evaluation of the Prevention and Management of Nearshore HABs in Lake Hopatcong, NJ

Fred S. Lubnow, *Pat Rose[1], Paul Cooper*

U.S. Princeton Hydro, LLC, 35 Clark Street, Suite 200 Trenton, NJ, USA

A wide variety of watershed-based management measures have been implemented over the last 20 years to reduce the external nutrient loads entering Lake Hopatcong, Morris and Sussex Counties, New Jersey. Additionally, the internal phosphorus load has been addressed with an alum treatment in October 2024. However, it is recognized that overwintering cyanobacteria in the nearshore sediments can still contribute toward HABs in the lake. Given these conditions, a set of innovative treatments were conducted and evaluated over the 2025 growing season in select nearshore bays and coves of Lake Hopatcong. Two of the treatments involved spring applications of approved algicides, a chelated copper product and an oxidizer, over the sediments in April. Four additional treatments utilizing various combinations of peroxide-based algicides, natural coagulants, and clay products were conducted later in the season. Pre- and post-treatment incubation studies were conducted in an environmental chamber with sediment and water samples collected from each location to quantify the cyanobacteria that may bloom from the overwintering cells present. Additional field data were collected before and after the treatments at immediate (one week), short-term (one month), and long-term (one year) intervals. Multiple lines of evidence were used to assess the effectiveness of the treatments spatially and temporally and a cost-benefit analysis was developed for each treatment. This presentation will provide an update on this project and an analysis of the collected data. The ultimate goal is to determine the feasibility and cost effectiveness of these innovative treatments to prevent or control nearshore HABs.

Rethinking Genome Streamlining in Toxic Microcoleus from Freshwater Cyanobacterial Blooms

Kabilan Mani *[1], Abeer Sohrab[1], Sydney Stubler[2], Rosalina Stancheva[2], Robert Shriver[3], Joanna Blaszczak[3], Ramesh Goel[1]*

[1]University of Utah, Salt Lake City, UT, USA
[2]George Mason University, Fairfax, VA, USA
[3]University of Nevada, Reno, NV, USA

Anatoxin-producing strains of Microcoleus, key contributors to harmful benthic cyanobacterial blooms (cyanoHABs)usually coexist with non-toxic strains, other cyanobacteria, and diverse heterotrophic bacteria. Previous studies have suggested that toxic Microcoleus strains underwent genome streamlining, resulting in the loss of essential biosynthetic pathways, including genes involved in thiamine (vitamin B1) synthesis. This study evaluates the validity of this hypothesis using both culture-dependent and culture-independent approaches. The samples were collected during a cyanoHAB event in a Virgin River tributary within Zion National Park, Utah, in 2023. Shotgun metagenomic reads were quality-filtered and assembled using metaSPAdes v3.13.0, and metagenome-assembled genomes (MAGs) were reconstructed with MetaBAT v2.12. Taxonomic profiling revealed the dominance of Microcoleus, with an average relative abundance of ~70%. Phylogenetic analysis showed that the recovered MAGs were highly similar (ANI > 99.9%) to a known toxic strain, Microcoleus anatoxicus, previously isolated from the same site. Contrary to expectations from the genome streamlining hypothesis, pathway analysis identified the presence of thiamine biosynthesis genes, including thiD, and associated pathways for thiamine diphosphate production in the MAGs. The toxin-producing potential of these genomes was confirmed through detection of type I polyketide synthase (T1PKS) gene clusters using antiSMASH. To further validate these findings, whole-genome sequencing was performed on non-axenic toxic Microcoleus strains isolated from the same benthic mats, collected a month earlier. These genomes also retained thiamine biosynthesis genes. Together, these results challenge the assumption that toxic Microcoleus lack key biosynthetic functions, showing retained thiamine pathways and metabolic autonomy. This indicates greater ecological versatility, shaping their adaptation and interactions in freshwater cyanoHABs.

Single-Cell Quantification of rLSU D1–D2 Gene Copy Number in *Alexandrium monilatum* Using Digital PCR

Savannah A. Mapes[1]*, Wayne Litaker*[2]*, Kimberly S. Reece*[1]

[1]Virginia Institute of Marine Science, Gloucester Point, VA, USA
[2]University of North Carolina at Chapel Hill, Chapel Hill, NC, USA

Accurate PCR-based quantification requires knowing the per-cell target copy number of the cell types in a sample. PCR cell concentrations, however, are typically calibrated with standard curves built from vegetative (1N) cells. Across a dinoflagellate life cycle, per-cell DNA content, and therefore rDNA copy number, varies from haploid vegetative cells and gametes (1N, 1C) to the replicated diploid resting cyst (2N, ~4C). When a population contains these higher-copy-number stages, calibration on vegetative cells alone can bias cell estimates. *Alexandrium monilatum* life cycle stages were documented, and digital PCR (dPCR) was used to quantify rLSU D1–D2 gene copy number in individual cells of each stage. Vegetative cells, gametes, fusing gametes, planozygotes, and hypnozygotes were observed in field samples, a mixture of stages with differing DNA content that illustrates the challenge of PCR-based quantification. Individual cells were isolated from cultures for single-cell dPCR. Vegetative cells and gametes (1N) averaged 77,924 copies/cell. Fusing gametes (two 1N gametes) and single planozygotes (2N) were comparable, averaging 170,594 and 172,946 copies/cell. Hypnozygotes averaged 286,734 copies/cell (~4C; replicated diploid prior to meiosis). Copy numbers differed significantly among stages (Kruskal–Wallis, $p < 0.0001$); pairwise comparisons (Mann–Whitney, Bonferroni-corrected) separated all groups except fusing gametes and planozygotes. This is the first single-cell quantification of rDNA copy number across *A. monilatum* life stages. Accounting for stage-specific copy-number variation could improve PCR-based quantification.
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LC-MS/MS Caribbean Ciguatoxin Profile of Puerto Rican Fish

Marco Marotta [1], *Sarah May*[2] *and Kirk Gaston*[2]

[1]VSG Contracting Company: Pure Talent Consulting LLC, Gulf Coast Seafood Laboratory, Dauphin Island, AL, USA
[2]US Food and Drug Administration, Gulf Coast Seafood Laboratory FDA, Dauphin Island, AL

Ciguatera poisoning is an affliction caused by consuming fish contaminated with ciguatoxins (CTX). Fish can become contaminated with ciguatoxins by ingesting epiphytic algae *Gambierdiscus* or *Fukuyoa* associated with coral reefs upon which the fishes graze. Ciguatoxins can bioaccumulate through the food web in larger carnivorous fish, which humans then consume. This poses a significant public health concern, as ciguatera poisoning affects between 10,000 and 50,000 people globally each year with some estimates as high as 500,000 when considering unreported cases. This study analyzes confirmed ciguatera poisoning cases in Puerto Rico to characterize the distribution of Caribbean ciguatoxin congeners across fish species in the coral reef food web. Liquid chromatography–mass spectrometry (LC-MS/MS) was employed to screen for the toxin congeners present in collected samples. African pompano and hogfish were tested and congeners found included Caribbean ciguatoxins C-CTX-1, C-CTX-3 and C-CTX-1157, among other congeners. Establishing detailed toxin profiles across species enhances our understanding of ciguatoxin biotransformation patterns and supports the development of predictive frameworks such as information campaigns with more concrete details of toxicity. Currently, the Food and Drug Administration has guidance levels only for Caribbean ciguatoxin-1 (C-CTX-1: 0.1 ppb in finfish) and there are few fish that have established profiles regarding which ciguatoxin congeners are present such as amberjack and moray eels; here African pompano and hogfish are two of the novel fish profiles being developed. As profiles become established, novel congeners could be further categorized and isolated for reference materials for more accurate composite toxicity results and even quantitation. Understanding how different congeners contribute to fish toxicity could help take steps to make risk assessment and monitoring strategies more robust for ciguatera poisoning in the Caribbean.

Cyanobacterial Response to Kaolinite and Laponite Treatments as a Bloom Control Strategy

Becca Marston[1]*, Cody Sheik*[2]*, Chris Filstrup*[2]

[1]University of Minnesota Duluth Large Lakes Observatory and University of Minnesota Natural Resources Research Institute, Duluth, MN, United States
[2] University of Minnesota Duluth Large Lakes Observatory, Duluth, MN, United States
[3] University of Minnesota Natural Resources Research Institute, Duluth, MN, United States

Cyanobacteria Harmful Algal Blooms are a recurring threat to water bodies worldwide, and treatment options can be difficult to implement, especially after a bloom has developed. Our study focuses on the efficacy of a potential cHAB treatment method—the aggregation of cells with clays kaolinite and laponite. We ask: Does clay aggregation trigger cyanobacteria to initiate or alter the expression of genes involved in nutrient acquisition and/or cyanotoxin production during and after treatment? In the lab, kaolinite and laponite can effectively remove algal cells, but how does this upscale to mesocosms? To test these questions, Lake Erie water in mesocosms was treated with five doses of either kaolinite or laponite (control, low, optimal, high, and optimal with mixing), and samples were collected from the surface and bottom of each mesocosm at 0, 3, and 24 hours. Using a metatranscriptomic (RNA) and 16S amplicon (DNA) approaches, we seek to understand differences in species abundance and gene expression in response to treatment. If cyanobacteria respond to treatment by upregulating nutrient uptake or cyanotoxin production genes, this treatment may be counterproductive. Initial results suggest a trend of decreasing cyanobacterial abundance between hour 0 and hour 3 for surface laponite samples in the optimal, high, and optimal + mixing samples, but not in low or control samples. Similarly, cyanobacterial abundance in kaolinite surface samples initially decreased in hour 3 samples but rebounded to pre-treatment values at hour 24 in low, optimal, and high treatments. Kaolinite and Laponite applications reduced cyanobacterial abundance in surface mesocosm samples while minimally affecting other microbial biota, suggesting clay aggregation is a promising mitigation technique.

Contrasting Markers of Nutrient Limitation: Lipids vs. Gene Expression in Lake Erie *Microcystis* microcosms

Robbie M. Martin[1]*, Kelly E. Joyce*[2]*, David J. Niknejad*[3]*, Malcolm A. Barnard*[4]*, Justin D. Chaffin*[5]*, Katarina A. Jones*[6]*, Shawn R. Campagna*[6]*, Hans W. Paerl*[7]*, Steven W. Wilhelm*[1]

[1]Department of Microbiology, University of Tennessee at Knoxville, Knoxville, TN, USA
[2]UT-ORNL Graduate School of Genome Science and Technology, University of Tennessee at Knoxville, Knoxville, TN, USA
[3]Department of Biological Sciences, University of Southern California, Los Angeles, CA, USA
[4]Department of Chemistry, University of Texas at Austin, Austin, TX, USA
[5]F.T. Stone Laboratory, Ohio Sea Grant, and The Ohio State University, Put-In-Bay, OH, USA
[6]Department of Chemistry, University of Tennessee at Knoxville, Knoxville, TN, USA
[7]Institute of Marine Sciences, University of North Carolina at Chapel Hill, Morehead City, NC, USA

Phosphorus (P) availability is a driver of phytoplankton dynamics in freshwater ecosystems. Scarcity of P limits primary productivity, while excess stimulates harmful algal blooms. Previous work showed that *Microcystis* increases sulfolipid content during P limitation and proposed that the lipid ratio of sulfoquinovosyl diacylglycerol (SQDG) to phosphatidylglycerol (PG) could serve as an indicator of P availability in cyanobacterial blooms. We further tested this hypothesis with microcosm experiments conducted during high ambient nutrient concentrations in Lake Erie (196 µM dissolved nitrogen (N), 1.3 µM dissolved P). Lake water was diluted to 40% ambient nutrient concentration using lab water supplemented with major ion solution matching historic concentrations. Treatments consisted of amendment series of N (10-µM increments), P (0.1-µM increments), and N+P. Cubitainers were incubated *in situ* for 48 hr. Undiluted, amended Cubitainers served as controls. SQDG:PG for the undiluted controls was ~6 and did not change across the series. In diluted treatments, N additions caused an increase in the lipid ratio from 9.6 to 13.4 ($P = 0.0013$). P additions to diluted treatments caused a strong decreasing trend in the lipid ratio from 14.7 to 9.3, but narrowly missed significance ($P = 0.06$) due to one outlier. No differences were detected in expression of *sqdB* or *sqdX*, the genes responsible for SQDG biosynthesis. Follow up lab studies using continuous cultures and 24-hr sampling demonstrated rapid changes in lipid ratios and differences in *sqdB* expression (but not *sqdX*), suggesting that 48-hr sampling in Lake Erie captured lipid changes but not the underlying transcriptional response. Collectively, these findings reinforce the idea that sulfolipid ratios can serve as a sensitive and rapid indicator of P availability with likely applicability across diverse lake systems.

Kodiak HAB Monitoring and Toxin Testing: Mid-Project Update

***Julie A. Matweyou*[1]*, Isaiah Dela Cruz*[2]*, Andie A. Wall*[2]*, Jennifer R. McCall*[3]*, Leanne M. Poussard*[4]*, Mark W. Vandersea*[4]*, Steven R. Kibler*[4]

[1]Alaska Sea Grant Marine Advisory Program, University of Alaska Fairbanks, Kodiak, AK, USA
[2]Kodiak Area Native Association, Kodiak, AK, USA
[3]SeaTox Research Inc., Wilmington, NC, USA
[4]NOAA National Centers for Coastal Ocean Science, Beaufort Lab, Beaufort, NC, USA

Paralytic shellfish toxins (PSTs) are recurring and well-documented in the Kodiak Archipelago. Produced by the marine dinoflagellate *Alexandrium catenella*, these neurotoxins accumulate in filter-feeding shellfish, transfer through the food web, and can cause human illness ranging from mild neurological symptoms to respiratory paralysis. PST variability reflects patchy *Alexandrium* distribution, making bloom monitoring and prediction difficult. This project integrates research, monitoring and outreach to build community awareness of PST risks, support informed subsistence harvesting decisions, and advance harmful algal bloom (HAB) forecast development.

Frequent monitoring with timely data turnaround is critical for informing the public and reducing PSP risk. This project establishes multi-year HAB surveys in Chiniak Bay and combines shore-based phytoplankton and shellfish toxin monitoring with complementary methods to improve data quality, timeliness, and cost-effectiveness of HAB surveillance.

Phytoplankton are monitored weekly in summer and biweekly in winter at three primary Kodiak Road system sites using two approaches. Net tow samples are analyzed microscopically the day of collection, providing rapid relative cell abundance estimates. In parallel, whole seawater samples are collected, concentrated, and filtered for qPCR analysis, which provides higher-accuracy data but is retrospective and requires analysis off-site. The Chiniak Bay HAB surveys also employ qPCR protocols, enabling high-throughput analysis.

Shellfish toxins are assessed biweekly in blue mussels using the receptor binding assay (RBA), with results typically available within 6–10 days. The newly developed SeaTox PSP ELISA is being implemented as a faster screening tool at the Kodiak Seafood and Marine Science Center, with additional samples from primary and secondary sites analyzed in-house. With validation against HPLC–FLD, the ELISA has demonstrated reproducible performance in inter-laboratory comparisons.

Together, these approaches enhance monitoring capacity by balancing rapid field-based assessments with higher-resolution and screening-based laboratory methods. Results from the first three years of the project will be shared.

Emerging HABs in Lake Superior: A Multi-Disciplinary Approach to Identify Drivers, and Risks

Julie Maurer[1]*, Tom Hollenhorst*[2]*, Aabir Banerji*[2]*, Meghan Klasic*[2]*, Terri Jicha*[2]

[1]Oak Ridge Institute of Science and Education Fellow, Great Lakes Coastal Science Branch, Duluth, MN
[2]USEPA Office of Applied Sciences and Environmental Solutions, Great Lakes Coastal Science Branch, Duluth, MN

Harmful algal blooms (HABs) are a nationwide concern in lakes and rivers, including the Laurentian Great Lakes. For many years, HAB events have been frequently reported in eutrophic nearshore areas of the Great Lakes. However, sporadic HAB outbreaks have recently been recorded in the oligotrophic waters of Lake Superior, which contradicts the typical HAB paradigm that has been observed across the Great Lakes and other freshwater systems. Extreme weather, ongoing human activity, and environmental change are expected to enhance the frequency and severity of HABs in Lake Superior over time. The priorities of this work are twofold. The first is to better understand, quantify, and predict HABs in nearshore areas of Lake Superior, particularly southwestern Lake Superior and the St. Louis River Estuary. The second priority is to contrast similarities and differences between algal bloom drivers and seasonality in Lake Superior and Lake Erie through mathematical models, observational and experimental data. An existing hydrodynamic-ecological model for Lake Erie is being leveraged to develop a similar model for Lake Superior. Long-term monitoring data, nutrient stoichiometry experiments, and genomics studies are being used to assess relationships between HAB occurrences and environmental drivers in both lakes, and to validate model output. Altogether, this multi-disciplinary project is advancing understanding of the drivers and risks of HABs in under-studied oligotrophic systems like Lake Superior through mathematical modeling and observational data. Ultimately, this work is facilitating the development of predictive tools for a bloom forecasting system in the Great Lakes Region.

Small Cells, Big Toxins: Toxin Profiling of Gambierdiscus and Fukuyoa

Sarah May [1], *Clayton Bennett* [2], *Kirk Gaston* [1]

[1]US Food and Drug Administration, Gulf Coast Seafood Laboratory, Dauphin Island, AL, USA
[2]VSG Contracting: Nitya, LLC, Gulf Coast Seafood Laboratory, Dauphin Island, AL, USA

Ciguatoxins are marine biotoxins produced by benthic dinoflagellates of the genera *Gambierdiscus* and *Fukuyoa*. While ciguatoxins are the most well-known toxin class, species from these genera have also been found to produce other classes of marine biotoxins, including maitotoxins, gambierones, and gambieric acids. These toxins may bioaccumulate and undergo biotransformation as they move through marine food webs to fish consumed by humans. Consumption of seafood—usually finfish from tropical and subtropical regions—contaminated with ciguatoxins can cause ciguatera poisoning, the most frequently reported phycotoxin-related seafood illness in the world. Here, we assess the cytotoxicity and spectrum of toxin profiles produced by algal cultures encompassing various strains and species of the genera *Gambierdiscus* and *Fukuyoa*. Profiles generated include both known toxic strains and strains for which no toxicity data currently exist. To date, all strains tested for cytotoxicity using the mouse neuroblastoma (N2a) assay have been positive for either voltage-gated sodium channel-specific toxicity, non-specific toxicity, or both. Targeted LC-MS (MRM) analyses of the extracts reveal the presence of gambierones/gambieric acids, maitotoxin (MTXs), and/or ciguatoxins produced by the algae. By determining which toxins are produced by specific algal strains, we can isolate and purify reference materials.

Saxitoxin Modulates Immune Responses and Impairs Lipopolysaccharide-Sensing in Monocytes/Macrophages

Jennifer R. McCall[1,2]*, Kathryn T. Sausman*[1]*, Samuel H. McCall IV*[2]

[1]School of Nursing, University of North Carolina Wilmington, Wilmington, NC, USA
[2]SeaTox Research Inc, Wilmington, NC, USA

Saxitoxin (STX) and its analogs, the causative agents of Paralytic Shellfish Poisoning, are potent neurotoxins that bind voltage-gated sodium channels (VGSCs). While their neurological pathologies are well-characterized, the impact of STX on immune sentinel cells, such as macrophages, remains poorly understood. Macrophages express VGSCs and rely on precise membrane dynamics to coordinate responses to inflammatory stimuli. We investigated the effects of sub-toxic STX exposure on macrophage polarization and effector function. Macrophages were treated with STX with or without lipopolysaccharide (LPS) co-stimulation. Surface marker expression (CD14, TLR4, CD80, CD206, and IL4Ra) was assessed via flow cytometry, and cytokine secretion (IL-6, TNF, and IL-10) was measured by ELISA. Exposure to STX alone significantly reduced the expression of the anti-inflammatory marker IL4Ra without inducing a basal pro-inflammatory state. However, during LPS challenge, STX induced a profound disruption of the LPS-sensing machinery: surface expression of the co-receptor CD14 significantly decreased, while TLR4 expression paradoxically increased. This reciprocal shift suggests a trapping of TLR4 on the cell surface due to the loss of the CD14-mediated internalization shuttle. Functionally, this receptor dysregulation led to a concomitant reduction in the secretion of both pro-inflammatory (TNF) and anti-inflammatory (IL-10) cytokines. These results indicate that sub-toxic doses of STX may induce a state of "immune paralysis," rendering macrophages functionally deaf to infectious stimuli. By disrupting the stoichiometry of the TLR4-CD14 complex, likely through VGSC-mediated interference with membrane trafficking, STX impairs the cell's ability to initiate critical signaling cascades. This study highlights a novel immunotoxicological mechanism for STX and suggests that low-level exposure may increase susceptibility to infection by quieting the innate immune response.

Progress and Future Directions for Biotoxin Certified Reference Materials

Pearse McCarron

National Research Council Canada, Biotoxin Metrology, Halifax, Canada, B3H 3Z1

The National Research Council of Canada (NRC) has an established research program dedicated to enhancing toxin measurement capabilities, with a core focus on development and distribution of certified reference materials (CRMs). Initially these efforts produced CRMs for individual toxins in response to the domoic acid poisoning crisis in the late 1980s. Subsequent work addressed the limited availability of CRMs for toxins of concern in North America and globally including saxitoxins, okadaic acid and dinophysistoxins, pectenotoxins, yessotoxins, cyclic imines and azaspiracids. These materials have played a critical role in the development of commonly used methods for toxin analysis, including chemical and biochemical techniques, which in turn have impacted regulations. As research objectives and regulations evolve to study and measure additional toxins classes, or multiple toxins simultaneously, requirements for CRMs have increased. This presentation will provide an overview of ongoing efforts and future objectives to meet these needs. Shellfish matrix CRMs have been produced and certified to cover all the primary polar and non-polar regulated toxin groups. In addition to the certified analytes, complex profiles of additional toxins present in these materials have been extensively characterized using liquid chromatography with high-resolution mass spectrometry. Novel applications of these multi-component seafood matrix reference materials in support of emerging non-target analysis processes will be described. Development of materials for freshwater toxins will also be summarized, including progress on providing a broader range of calibration solution and cyanobacterial matrix CRMs. Finally, the discussion will highlight collaborative efforts aimed at making critically needed reference materials available for ichthyotoxins and ciguatoxins.

Effects of Coastal Acidification and Low Dissolved Oxygen on the Growth of *Margalefidinium polykrikoides*

Sarah McCready, *Christopher J. Gobler*

School of Marine and Atmospheric Sciences Stony Brook University, Southampton, NY, USA

Within coastal zones, increased nutrient loading promotes algal productivity and can result in the formation of harmful algal blooms (HABs). *Margalefidinium polykrikoides* is an ichthyotoxic dinoflagellate that forms HABs across the globe and causes hundreds of millions of dollars in fisheries losses annually; therefore, it is imperative to understand how environmental stressors will affect the growth of this harmful alga. Specifically, increased microbial respiration that follows enhanced algal productivity, consumes oxygen and decreases seawater pH, which promotes low dissolved oxygen (DO) and coastal acidification, respectively. It is hypothesized that dinoflagellates may experience enhanced growth under elevated carbon dioxide conditions due to them containing Form II ribulose-1,5-bisphosphate-carboxylase/oxygenase. However, low pH and low DO conditions occur at the same time due to their metabolic connection, and few studies have evaluated their combined effects on marine organisms, including HABs. This study examined how low pH, both individually and in combination with low DO, affected the growth rate of *Margalefidinium polykrikoides*. *Margalefidinium polykrikoides* (CPSB-1G) cultures were exposed to a range of pH levels (7.0 – 8.0) and growth rates were found to be inhibited at pH<7.2 and lower. Exposure of cultures to combinations of moderately lower pH and DO (pH~7.4; DO=4 milligrams per liter) significantly increased the growth rate of *Margalefidinium*. An additional experiment found that when *Margalefidinium* was exposed to low pH and low DO separately and collectively, only the combination of moderately lower pH and DO enhanced growth. This study suggests that low pH may not enhance the growth rate of *Margalefidinium* except when in combination with low DO; however, further research is needed. Research examining the combined effects of low pH, low DO, and *Margalefidinium polykrikoides* on the survival of larval fish will also be presented.

Harmful Algal Bloom Monitoring and Management Applications with NASA's PACE Mission

Morgaine McKibben

[1]Science Systems & Applications, Inc., Lanham, MD, USA
[2]Ocean Ecology Laboratory, NASA Goddard Space Flight Center, Greenbelt, MD

Launched in 2024 Plankton, Aerosol, Cloud, and Ocean Ecosystem (PACE) mission is continuing NASA's legacy of over forty years of satellite ocean color measurements. PACE is innovating Earth-observing and monitoring capabilities through global, daily hyperspectral imaging and multi-angle polarimetric observations of open ocean, coastal, estuarine, and large inland water bodies. This technology provides an unprecedented view of our home planet and is supporting user-driven water resources management needs through research and applied science to address societal challenges and inform decision-making. We will highlight PACE's capabilities to advance space-based tools in support of societal needs in water management relevant to harmful algal blooms (HABs). Hyperspectral and polarimetric PACE data provide water resource managers and decision-makers with highly accurate, novel ocean color observations capable of improving operational products and applied technologies. We will outline projects utilizing PACE data to better identify HABs in large lakes, coastal/estuarine systems, as well as applications in support of relevant topics such as waterborne pathogen monitoring, aquaculture, and best-management practices for estuary and watershed health. We will also present on the PACE Applications program and provide opportunities to connect. This program advances the applied science of PACE and connections between science and decision-making through efforts such as the Early Adopters program, workshops and focus sessions, and information-sharing and co-production activities.

Partitioning of Cyanotoxin Production, Taste-and-Odor Compounds, and Cyanophage Diversity During a Mixed Cyanobacterial Bloom

Joann Jacobs[1,2], *Hunter Adams*[3], ***Katelyn McKindles***[1,2]

[1] Department of Biology, Baylor University, Waco, Texas, USA
[2] Center for Reservoir and Aquatic Systems Research, Baylor University, Waco, Texas, USA
[3] City of Wichita Falls - Water Source & Purification Divisions, Wichita Falls, Texas, USA

Cyanobacterial harmful algal blooms (cHABs) present overlapping water quality concerns, yet these hazards are often treated independently despite occurring simultaneously within mixed cyanobacterial assemblages. To better understand how distinct cyanobacterial populations contribute to bloom-associated risks, we characterized cyanobacterial community composition, toxin-associated taxa, taste-and-odor producers, and *Microcystis*-associated cyanophages during a July 2025 bloom in Lake Kickapoo, Texas. Long-read 16S rRNA gene sequencing revealed a cyanobacteria-dominated community with heterotrophic bacteria commonly associated with freshwater blooms. Dominant cyanobacterial genera included *Dolichospermum*, *Planktothricoides*, and *Microcystis*. Molecular characterization linked methylisoborneol (MIB)-associated sequences primarily to *Planktothricoides*, while taxa-specific microcystin marker analyses identified *Microcystis* as the primary cyanotoxin producer. We also quantified *Microcystis*-associated cyanophages and characterized viral diversity using marker gene sequencing. Cyanophage abundances were six orders of magnitude lower than *Microcystis* host abundances, suggesting low infection pressure during sampling. Cyanophage marker genes were most closely related to freshwater cyanophages Ma-LMM01 and MVGF-J_19. Long-read sequencing identified a dominant capsid sequence closely related to J_19 and a less abundant Ma-LMM01-like sequence, indicating co-occurrence of at least two cyanophage genotypes. Together, these results demonstrate that mixed cyanobacterial blooms contain distinct populations associated with cyanotoxin production, taste-and-odor generation, and virus-host interactions, highlighting the importance of integrating community structure, functional marker analyses, and viral ecology to better understand bloom-associated water quality hazards.

Application of Large-scale Genomic and Phylogenomic Methods Resolves Microcystin Inheritance and Evolutionary Patterns Across Cyanobacteria

***Christopher J McLimans**, Jessica E. Beyer, K. David Hambright*

University of Oklahoma, Norman, OK, USA

The gene cluster encoding production of the cyanotoxin microcystin is well described within many cyanobacterial genera, however the gene cluster's overall evolutionary history and distribution across all cyanobacteria remains unsatisfactorily resolved. Monitoring efforts focus on limiting human exposure to microcystins, yet predicting toxin production of cyanobacterial harmful algal blooms (cyanoHABs) is made difficult because toxigenicity can be clouded by cryptic morphological diversity and the inconsistent presence of microcystin gene cluster (*mcy*) even within a species. As global climate change may shift conditions towards those that favor toxigenic cyanoHABs, threatening freshwater integrity and safe drinking water access worldwide, understanding the taxonomic distribution and evolution of the microcystin gene cluster will be essential to studying the ecology of microcystin and developing taxon-specific risk assessments. Through a survey of more than 8,000 cyanobacterial genomes with robust genomic taxonomic classification, this work revealed the presence of the *mcy* gene cluster across many genera spanning three common cyanobacterial orders. BLAST-based approaches were applied to resolve *mcy* gene presence, recovering more high-quality genes than previous protein-annotation approaches. Recovered gene sequences were used in a large-scale phylogenetic analysis to examine the presence and absence, sequence diversity, and recombination across *mcy* genes among all cyanobacterial genera. Phylogenetic analyses of *mcy* genes were consistent with a cyanobacterial species tree, reflecting the ancestral state of *mcy* to cyanobacteria. Sequence diversity was constrained to species boundaries, suggesting limited gene flow or recombination between species. By resolving the distribution of *mcy* genes and toxigenicity across all cyanobacteria and employing a phylogenetic framework to support studies on *mcy* evolution, these results are supportive of an improved taxon-specific understanding of freshwater risk.

Operational Phosphorus Sequestering Program Limits HAB in the Western United States

Terry McNabb

Aquatechnex, LLC, Bellingham Washington, USA

In the past decade HAB conditions have dramatically increased in western US Waters. One of the most effective tools to reduce the impacts of HAB is in-lake phosphorus sequestration. Aquatechnex biologists have developed and implemented several successful projects utilizing lanthanum modified clay applications. This paper will highlight the adaptive management planning process and present case studies on lakes ranging from 200 acres to over 6,000 acres.

Informing Scalable Management of Benthic HABs in Lake St. Clair

***Andrew McQueen**, Alyssa Calomeni-Eck, Justin Wilkens, Caroline Mastria, Molly Reif, Denise Lindsay, Madeleine Malmfeldt*

U.S. Army Engineer Research and Development Center, Vicksburg, MS, USA

Benthic harmful algal blooms (HABs) caused by *Microseira wollei* (formerly *Lyngbya wollei*) have expanded across Lake St. Clair, MI (USA) for decades, posing risks to fisheries, recreation, and drinking water. Management remains limited due to challenges quantifying spatial and temporal variability across large, heterogeneous systems. In 2023, the U.S. Army Corps of Engineers (USACE) partnered with stakeholders and state agencies to monitor a ~80 km^2 region along the western shoreline and develop a science-based adaptive management framework. A multi-platform, data-integrated approach combined satellite and fixed-wing aerial imagery with high-resolution autonomous underwater vehicle (AUV) surveys to map benthic conditions across depth and distance gradients. AUV imagery confirmed *M. wollei* within mixed cyanobacterial and submerged aquatic vegetation assemblages from nearshore to ~2.2 km offshore. Aerial imagery resolved benthic coverage in shallow waters (<1 m depth) up to ~900 m from shore, enabling spatially explicit estimates of percent cover. Environmental DNA (eDNA) analyses supported taxonomic identification and complemented microscopy. These datasets informed an adaptive management framework to support decision-making under uncertainty and enabled allocation of state funding for pilot-scale treatment planning. This study demonstrates how coordinated sensing technologies and molecular tools can bridge monitoring gaps and provide a scalable foundation for managing benthic HABs. Building on this foundation, the future advancements of remote sensing platforms, rapid molecular tools for HAB detection, real-time data assimilation, and data integration into predictive models could greatly expand the operational decision-support system for large-scale HAB impacts, enabling more proactive and resource efficient management solutions.

Fish Abundance and Diversity in Nearshore Sargassum in St. Thomas

Jessica Michael[1]*, Helen Holt*[1]*, Avery Coble*[2]

[1]Coral World Ocean and Reef Initiative, St. Thomas, Virgin Islands, US
[2]University of the Virgin Islands, St. Thomas, Virgin Islands, US

Pelagic Sargassum is considered an Essential Fish Habitat (EFH) for several species across the Atlantic, Caribbean and Gulf. Regionally across Puerto Rico and the U.S. Virgin Islands (USVI), Sargassum is classified as an EFH for Dolphinfish and Wahoo. The Puerto Rican fisheries management plan also lists gray triggerfish, great barracuda, tripletail, pompano dolphin, little tunny, blackfin tuna, king and cero mackerel for Sargassum as an EFH, all of which are also present in the USVI, though not listed in the fisheries management plan. These species can be found at varying life stages utilizing Sargassum rafts for spawning, larvae development, and foraging. This study aimed to determine which species were utilizing nearshore rafts around the USVI and if there was a point at which they were no longer present. Our sampling efforts were focused to the east end of St. Thomas since this where Sargassum enters the region and eastern beaches on this island experience higher levels of inundation. Drop cameras were deployed in the center of rafts opportunistically found in nearshore areas to determine species abundance and diversity. We visualized the community composition of fish within the Sargassum using a Non-Metric Multidimensional Scaling and analyzed potential differences between depth, proximity to shore, and an isolation index with Permutational Multivariate Analysis of Variances (PERMANOVAs). Initial results indicate that fish community structure was not significantly different across any measured environmental gradients, depth, distance from shore, or isolation index, though visually there appeared to be a trend in the data. More samples are being collected and will be included in the final analysis. These data provide a baseline for identifying what species are associated with nearshore Sargassum within the USVI region and could provide deeper insight into when fish begin to abandon Sargassum rafts.

Arsenate toxicity dynamics in brown tide-forming *Aureococcus anophagefferens*

Maverick Shiflett, Shannon Ashby, Owen Crumpler, ***Camryn Micket****, Louie Wurch*
James Madison university, Harrisonburg, VA, USA

Blooms of the ecosystem destructive alga, *Aureococcus anophagefferens,* thrive in coastal ecosystems that are heavily impacted by human activity, including areas that have high concentrations of heavy metals like arsenate. Arsenate is an analog of phosphate, with inadvertent incorporation leading to toxicity. In natural populations of *A. anophagefferens*, an arsenite translocating ATPase shows expression patterns that mirror a high-affinity phosphate transporter, suggesting a need for arsenate detoxification during low phosphate conditions. Here we grew axenic cultures of *A. anophagefferens* CCMP1984 at 0, 2, 6, 12, and 36 µM arsenate concentrations to determine the dose-response relationship between *A. anophagefferens* growth/physiology and arsenate toxicity under environmentally relevant phosphate conditions. Growth was monitored via cell counts and fluorescence. Photosynthetic efficiency was monitored using the Fv/Fm method. Results suggest there is an initial increased toxicity effect of arsenate under phosphate limitation, followed by swift recovery. The employment of an arsenate detoxification pathway during increased phosphate uptake may give *A. anophagefferens* a competitive advantage over other phytoplankton during low phosphate conditions, particularly in anthropogenically contaminated coastal ecosystems.

SHARC in Action: Autonomous Reporting of Algal Toxin Concentrations in the Great Lakes and Beyond!

Christina Mikulski[1]*, Zachary Gold*[2]*, James Birch*[3]*, Louise Lingerfelt*[4]*, William Ussler*[3]*, Christina Preston*[3]*, Nadia Allaf*[3]*, Chloe Weinstock*[3]*, Kyle Beadle*[5]*, Benjamin Downing*[5]*, Shelby Brunner*[6]*, Reagan Errera*[5]

[1]NOAA/NOS/National Centers for Coastal Ocean Science, Charleston, SC, USA
[2]NOAA/OAR/Pacific Marine Environmental Laboratory, Seattle, Washington, USA
[3]Monterey Bay Aquarium Research Institute, Moss Landing, CA, USA
[4]RPI contractor to NOAA/NOS/National Centers for Coastal Ocean Science, Charleston, SC, USA
[5]NOAA/OAR/Great Lakes Environmental Research Laboratory, Ann Arbor, MI, USA
[6]Great Lakes Observing Systems, Ann Arbor, MI, USA

Field deployment of the Surface Harmful Algal Research Craft (SHARC) in Lake Erie during the summers of 2023 and 2024 demonstrated the feasibility of autonomous, near real-time cyanotoxin detection in a shallow-water system. Lessons learned from previous deployments indicated that regeneration conditions, chip surface longevity, and reproducibility over the deployment period required further optimization for sustained operation. Building on these insights, we present surface plasmon resonance (SPR)-based microcystin results from the summer 2026 deployment in Lake Huron (Saginaw Bay), along with an evaluation of the improvements to SPR performance. The SHARC integrates a compact, field-deployable SPR sensor with a third-generation Environmental Sample Processor (3G-ESP) aboard a SeaTrac uncrewed surface vehicle capable of collecting samples in less than 1 meter in depth. This paired system autonomously collects and lyses water samples, followed by antibody-based detection of particle-associated microcystins via reusable, functionalized SPR chips. The 2026 deployment marks the inaugural field trial of the SHARC system in Lake Huron and serves as a pilot evaluation of its effectiveness as an event-response platform, designed to provide stakeholders with near-real-time toxin concentrations as cyanobacteria blooms expand and disperse through the ecosystem. In parallel, we describe the initial development of an SPR-based paralytic shellfish poisoning (PSP) assay targeting saxitoxin for use with the SPR-ESP system, with planned deployments on the SHARC off the coast of Nome in 2027 and 2028, where PSP toxins pose a threat to coastal and subsistence communities. Together, these results highlight the applicability of SPR-based assays for robust, in situ biotoxin quantification and expand the validation of SHARC in both freshwater and marine systems.

Ecological Sorting of Cyanobacterial Genotypes and Toxins Along a Connecting Waterway to the Nation's Largest Freshwater Estuary

Todd Miller[1]*, Ryan Newton*[2]*, Sarah Bartlett*[3]*, and Christopher Houghton*[4]

[1]Zilber College of Public Health, University of Wisconsin – Milwaukee
[2]School of Freshwater Sciences, University of Wisconsin – Milwaukee
[3]NEW Water Green Bay Metropolitan Sewerage District
[4]Biodiversity, Conservation and Management, University of Wisconsin – Green Bay

Southern Green Bay, Lake Michigan, is a designated Area of Concern by the United States Environmental Protection Agency due in part to seasonal occurrences of intense cyanobacterial harmful algal blooms (cyanoHABs). The Fox River is the largest hydrologic input to southern Green Bay carrying water 39 miles northward from Lake Winnebago. Lake Winnebago itself is a hypereutrophic environment that also experiences intense cyanoHABs. This suggests that there are strong ecological connections between cyanoHABs in Lake Winnebago and Green Bay, however, these connections have been largely unexplored. Here, we describe the genetic cyanobacterial community composition and toxin variability along the Winnebago-to-Green Bay continuum. Water was sampled over the course of the open water season on two dozen dates along this continuum. Cyanobacterial toxins were measured using tandem mass spectrometry and cyanobacterial genetic community composition was assessed using tag sequencing of the 16S to 23S intertranscribed spacer region. We found that the abundance of genotypes of major bloom forming cyanobacterial genera gradually transitions along this continuum. Furthermore, bioinformatic sequence analyses of the most abundant cyanobacteria in Green Bay show near exact matches to major genotypes in the Western basin of Lake Erie. Cyanobacterial toxin congener profiles also displayed gradual transitions along this continuum with highest concentrations within the Fox River upstream of dammed sites. These data show important sorting processes for algal toxins and cyanobacterial genotype composition along a major connecting waterway to a Great Lakes coastal environment.

Algal Bloom Phenology in the Chesapeake Bay Using an Improved Satellite-derived chlorophyll-*a* Product

Sachidananda Mishra[1]*, Michelle C. Tomlinson*[2]*, Richard P. Stumpf*[2]*, Catherine Wazniak*[3]*, Kari Stlaurent*[2]*, Andrew Meredith*[1]

[1]CSS Inc., Fairfax, VA, USA
[2]NOAA, National Centers for Coastal Ocean Science, Silver Spring, MD, USA
[3]MD Department of Natural Resources, Annapolis, MD, USA

Harmful algal blooms (HABs) in Chesapeake Bay are a significant water quality issue that negatively impact human health through toxin production, as well as the economy by affecting the fisheries and aquaculture industries. Water quality managers often rely on satellite-based monitoring of HABs in the bay to provide synoptic observations at a finer spatial and temporal scale. However, accurate satellite-based detection of chlorophyll a (chl-*a*) is challenging in optically complex case-2 waters in most rivers and major tributaries in the Chesapeake Bay. The Harmful Algal Bloom Forecasting Branch at the National Centers for Coastal Ocean Science (NOAA) has been utilizing a chlorophyll-switch product that employs two algorithms: OCx for waters with chl-*a* concentrations less than 10 µg L^{-1}, and Red-edge-10 for waters with chl-*a* concentrations greater than 10 µg L^{-1}. This approach is applied to spaceborne, multispectral data from the Ocean and Land Colour Imager (OLCI) sensor on the Sentinel-3 satellites, enabling real-time monitoring of algal blooms in the Bay. This study evaluated the chlorophyll-switch product from OLCI in the Chesapeake Bay, and compared it with *in situ* chl-*a* data. Algorithmic bias was corrected using a simple temporal baseline correction to improve the accuracy of the chl-*a* in optically complex waters. Additionally, we used data from the Sentinel-3 mission (2016-present) to develop a phenological time series of the algal blooms, representing unique spatial segments spanning the entire Bay, enabling us to document the changes in algal bloom phenology.

Identifying Cyanobacteria Species with Spaceborne Hyperspectral Sensing

Sachidananda Mishra[1]*, Kaytee Pokrzywinski*[2]*, Richard P. Stumpf*[3]*, Michelle C. Tomlinson*[3]*, Andrew Meredith*[1]

[1]CSS Inc., Fairfax, VA, USA
[2]NOAA, National Centers for Coastal Ocean Science, Beaufort, NC, USA
[3]NOAA, National Centers for Coastal Ocean Science, Silver Spring, MD, USA

Cyanobacterial harmful algal blooms (cyanoHABs) are recurring water-quality issues in the U.S. Great Lakes region and other freshwater lakes across the country, posing significant risks to public health and local economies. Spaceborne multispectral sensors, including the Ocean Land Colour Imager (OLCI) on Sentinel-3, are commonly used to monitor freshwater cyanoHABs by exploiting the optical features of chlorophyll fluorescence and phycocyanin absorption. However, identifying cyanobacteria species has been challenging due to the lack of continuous spectral signatures required for species-level discrimination. Recently, a cyanobacteria species classifier was developed in a deep learning framework using a laboratory-generated hyperspectral library of 15 cyanobacteria species. The classifier was independently tested in the Milford Gathering Pond south of the Milford Lake Dam, Kansas, using hyperspectral reflectance data collected from an unmanned aerial platform. The classifier accurately predicted the top three genera of cyanobacteria - *Dolichospermum*, *Microcystis*, and *Pseudanabaena* - with F1-scores ranging from 0.94 to 1, demonstrating the method's potential for identifying cyanobacterial genera. The classifier was then extended to the spaceborne Ocean Color Instrument (OCI) onboard NASA's Plankton, Aerosol, Cloud, ocean Ecosystem (PACE) satellite to produce cyanobacteria species distribution maps in Lake Erie and Sandusky Bay, providing an additional layer of crucial information on species composition to complement the cyanobacteria concentrations obtained by the higher resolution OLCI. This study further demonstrates the accuracy of the cyanobacteria species composition products from PACE-OCI in Lake Erie by comparing them with field data. While hyperspectral sensors can monitor cyanoHABs at the species level through machine learning and optimal feature selection, its effectiveness is limited by factors like signal-to-noise ratio and spatial resolution.

Using Choice Experiments to Estimate the Economic Benefits of Red Tide Mitigation Along the Florida Gulf Coast

*Vincent J. Lovko[1], **Klaus Moeltner[2]**, Michael L. Parsons[3], Seth Peery[2], Florian Zach[2]*

[1]Mote Marine Laboratory, Sarasota, Florida, USA
[2]Virginia Tech, Blacksburg, Virginia, USA
[3]Florida Gulf Coast University, Ft. Myers, Florida, USA

Florida Red Tide (Karenia brevis) is one of the most notorious examples of Harmful Algal Blooms in the United States. It has impacted the South Florida Gulf Coast almost annually since systematic record taking started in the 1950s. Blooms can last for months and stretch over 100+ miles of coastline, causing widespread mortality to marine life and respiratory irritation in humans via airborne toxins. The economic consequences to this region, which represents about one fifth of the state economy, are profound and widespread. To determine the best response to this natural hazard, policy makers need to have an understanding of the expected net benefits of specific interventions to underlying stakeholders. Survey-based choice experiments are well-suited to elicit estimates of household-specific, dollar-valued benefits before actual policy selection. In this presentation we show examples of these tools, along with parallel innovations in survey methodology and data analytics. We first illustrate the use of choice experiments in the context of refined (hypothetical but realistic) forecasting systems for impaired air quality caused by Red Tide to facilitate adaptation. In a different, but related project, we introduce choice experiments designed to capture benefits associated with (hypothetical but realistic) large-scale use of emerging control and mitigation technologies, such as clay dispersal. We will discuss results for the air quality / forecasting project and expect to be able to share preliminary findings for the control and mitigation project by the time of the symposium.

Predicting Karenia brevis Bloom Severity Using Long-Term Observations and Subregional Machine Learning Models

Mohammad Mohsin[1,2]*, Xiuming Sun*[1,2]*, Ebrahim Ahmadisharaf*[1,2]*, Isabella Simoncelli*[1,2]*, Vicky Gao*[3]

[1]Department of Civil and Environmental Engineering, Florida A&M University-Florida State University, Tallahassee, Florida, USA
[2]Resilient Infrastructure & Disaster Response Center, Florida A&M University-Florida State University, Tallahassee, Florida, USA
[3]Economics and Environmental Science Department, Belmont University, Nashville, TN, USA

Karenia brevis (K. brevis) blooms occur recurrently along the Florida Gulf of Mexico and pose significant ecological, public health, and coastal management challenges. Despite their frequent occurrence, predicting bloom severity remains difficult because *K. brevis* dynamics are influenced by complex interactions among environmental conditions, hydroclimatic variability, seasonal patterns, and regional coastal characteristics. Therefore, a modeling framework that integrates long-term bloom observations with relevant environmental predictors is needed to better characterize and predict bloom severity across spatially diverse coastal regions. In this study, long-term in situ *K. brevis* cell-count records from the HABSOS database were used to analyze historical spatial and temporal bloom patterns along the South Florida coast. This analysis focused on major bloom-prone regions, including the Tampa–Sarasota region, the Fort Myers–Naples coast, and the lower Florida Keys, where bloom behavior may differ because of regional environmental variability. To represent the conditions associated with bloom development, environmental and hydroclimatic predictors, including sea surface temperature, sea surface temperature anomaly, salinity, precipitation, wind, storm tide, and lagged antecedent conditions, were incorporated into a severity-classification framework. Random Forest, XGBoost, Support Vector Machine (SVM), and Artificial Neural Network (ANN) models were then developed to predict K. brevis bloom severity classes. To examine the effects of spatial heterogeneity on model performance, predictive skill was evaluated using both an all-station model and separate subregional models. The results indicate that tree-based ensemble models generally provide stronger predictive performance than SVM and ANN, while subregional models helped capture the representation of localized bloom–environment relationships. Overall, this study demonstrates that combining long-term in situ K. brevis observations with environmental and hydroclimatic predictors can support more regionally adaptive harmful algal bloom monitoring and early warning efforts.

Decades of Discovery: The Evolution of Research and Management of *Pseudo-nitzschia* HABs in the Pacific Northwest

Stephanie K. Moore[2]*, Vera L. Trainer*[3]*, Ryan M. McCabe*[2]

[1]NOAA Fisheries, Northwest Fisheries Science Center, Seattle, WA, USA
[2]University of Washington, Olympic Natural Resources Center, Forks, WA, USA
[3]NOAA Research, Pacific Marine Environmental Laboratory, Seattle, WA, USA

Domoic acid was first detected in Pacific Northwest (PNW) shellfish in October 1991, following initial U.S. reports in California. Resulting marine mammal deaths and purported human illnesses starkly highlighted the urgent need to manage the risks associated with domoic acid. This talk showcases how NOAA's National Competitive HAB Program has advanced research and management of *Pseudo-nitzschia* HABs in the PNW. Early federal funding bolstered the grassroots Olympic Region Harmful Algal Bloom (ORHAB) Partnership in Washington State, establishing optimized phytoplankton monitoring at coastal beaches to track *Pseudo-nitzschia* dynamics and provide HAB early warning. ORHAB inspired the development of Monitoring Oregon's Coastal Harmful Algae Program; both initiatives successfully transitioned from federal funding to state support. Subsequent multi-disciplinary research investigated the origins of toxic blooms and the environmental conditions that promote toxicity. These projects provided the mechanistic basis for forecasting domoic acid risk via the PNW HAB Bulletin. They also identified the need for real-time observations at offshore domoic acid "hot spots" to improve forecasts, provided by autonomous sensor platforms such as the Environmental Sample Processor. The most recent projects evaluate the social and economic value of HAB forecasts and mitigation strategies, providing a data-driven justification for public investment and more flexible management practices that minimize the financial loss caused by shellfish harvest closures. The iterative knowledge generation from over a dozen funded projects over almost three decades transformed HAB management in the PNW, and set the stage for the next wave of innovation to address remaining gaps.

Bacterial-derived Prodigiosin Controls Bloom-Forming Benthic Cyanobacteria

***Jéssica A.S. Moretto*[1]**, *Forrest W. Lefler[1], Meng B. Lin[1], Maximiliano Barbosa[1], David E. Berthold[1], Sofia Iliakopoulou[2], Alina Gialleli[2], Triantafyllos Kaloudis[2], Israel Urcuyo[1], Kaytee Pokrzywinski[3], H. Dail Laughinghouse IV[1]*

[1] Agronomy Department, Fort Lauderdale Research and Education Center, University of Florida / IFAS, Davie, FL, USA.
[2] Athens Water Supply and Sewerage Company - EYDAP SA, AquOmixLab - Laboratory of Organic Micropollutants, Water Quality Control Department, Menidi, Greece
[3] NOAA National Centers for Coastal Ocean Science, Beaufort, NC, USA

Heterotrophic bacteria in the phycosphere engage in diverse ecological interactions with associated cyanobacteria, ranging from mutualism and commensalism to antagonism. Harnessing cyanobacteria-associated bacteria and their cyanocidal potential offers a promising yet underexplored strategy for mitigating benthic cyanobacterial harmful algal blooms (cyanoHABs). This study aimed to characterize the cyanocidal potential of bacteria associated with benthic cyanoHABs, evaluate their potential as biocontrol agents, and elucidate cyanocidal mechanisms through cell-to-cell contact and compound-to-cell interaction experiments. Of the 30 bacteria screened, crude extracts from *Serratia nematodiphila* (BLCC-B138) demonstrated cyanocidal activity comparable to or greater than copper sulfate-based algaecides against various benthic cyanobacteria (i.e., *Floridanema*, *Heteroscytonema*, and *Iningainema*). Genomic analyses of *S. nematodiphila* (BLCC-B138) revealed the presence of biosynthetic gene clusters associated with the production of viobactin, yersinopine, prodigiosin, and chrysobactin, suggesting potential cyanocidal agents responsible for its antagonistic activity. Further metabolomic analyses, utilizing LC-qTOF, confirmed production of prodigiosin. Subsequently, tests using prodigiosin to assess cyanobacterial inhibition were also conducted. Prodigiosin is known to exhibit antibacterial activity through quorum sensing inhibition. In addition, transcriptomic analyses were performed to elucidate the cellular responses of benthic cyanobacteria to prodigiosin, providing mechanistic insights into its mode of action and informing the development of ecologically sustainable strategies for mitigating benthic cyanoHABs in freshwater ecosystems. Overall, this study provides a foundational framework for leveraging cyanobacteria-associated bacteria as sustainable biocontrol agents to mitigate toxic benthic cyanoHABs.

Interrogating Electroactive Bacteria as Living Soft Sensors for Harmful Algal Bloom Monitoring

Jesús Morón-López[1,2]*; *Juan F Ortiz-Medina*[1], *Maria Gomez-Mingot*[3], *Kenneth Flores*[1], *Carlos M. Sánchez-Sánchez*[4], *Abraham Esteve-Núñez*[2], *Sergi Garcia-Segura*[1]

[1] School of Sustainable Engineering and the Built Environment, Arizona State University, Tempe, AZ 85287-3005, USA.
[2] IMDEA Water Institute, Avenida Punto Com, 2, Parque Científico Tecnológico de la Universidad de Alcalá, Alcalá de Henares, 28805, Spain.
[3] Laboratoire de Chimie des Processus Biologiques, Collegè de France, UMR 8229 CNRS, Sorbonne Université, PSL Research University, 75005 Paris, France.
[4] Sorbonne Université, CNRS, Laboratoire Interfaces et Systèmes Electrochimiques (LISE), 75005 Paris, France.

Harmful algal blooms (HABs) are increasingly recurrent in freshwater systems, where they compromise water quality, ecosystem health, recreation, and drinking-water security. Current monitoring approaches rely largely on optical and physicochemical sensors that track chlorophyll-a, phycocyanin, turbidity, dissolved oxygen, pH, and conductivity. These variables are essential for HAB surveillance, but they provide limited insight into the microbial activity that drives bloom development, persistence, and decline. During blooms, cyanobacteria release organic matter, modify oxygen and nutrient gradients, and stimulate bacterial communities involved in carbon, nitrogen, and phosphorus cycling. These conditions may create microbial hotspots where biodegradable substrates, redox gradients, electron donors, electron acceptors, and shuttling compounds favor bacteria with electroactive potential. Although electroactive bacteria have been widely studied in microbial fuel cells, their use as living biosensing elements for HAB monitoring remains largely unexplored. In this study, we evaluate whether graphite-based electrodes can be engineered to favor bacterial colonization while improving electrochemical communication between bacteria and the electrode. Graphite electrodes were modified with conductive polymer coatings, including polypyrrole, polyaniline, and PEDOT, and compared with unmodified graphite using complementary electrochemical, surface, and biofilm analyses. The objective was not only to identify the most conductive coating, but to select the interface that best supports bacterial attachment, early biofilm formation, and signal generation. This is relevant because, while biofouling often deteriorates conventional water-quality sensors, microbial electrochemical biosensors deliberately use the developing biofilm as the active sensing layer. By transforming bloom-associated bacterial activity into usable electrochemical information, these biosensors could operate as low-cost soft sensors for HAB-relevant variables, reducing reliance on expensive sensor packages that require frequent maintenance. This approach supports the development of smarter monitoring strategies and biologically informed early-warning systems for HABs.

Spatiotemporal Variations in Microbial Community Structure During Toxic *Karenia brevis* Blooms in Southwest Florida

***Eric Muhlbach*[1]**, *Yida Gao[2], Julie Koester[1], Matthew Garrett[1], Kelsey Marvin[1], Savannah Barnard[1], Alexa Iorillo[1], Alex Clark[1], Enrique Montes[3], Nicole Millette[4], Maisie Grogan[4], Ian Smith[3], Rachel Cohn[3], Katherine Hubbard[1]*

[1]Florida Fish and Wildlife Conservation Commission – Fish and Wildlife Research Institute, St. Petersburg, FL, USA
[2]Woods Hole Oceanographic Institution, Woods Hole, MA, USA
[3]University of Miami – Cooperative Institute for Marine and Atmospheric Studies, Miami, FL, USA
[4]William & Mary – Virginia Institute of Marine Science, Gloucester Point, VA, USA

Blooms of the toxic dinoflagellate *Karenia brevis* occur nearly annually on the West Florida Shelf and impact both coastal and estuarine systems, requiring extensive monitoring. While harmful algal bloom monitoring typically focuses on target species rather than the entire microbial assemblage, less is known about how broader microbial and phytoplankton communities shift during blooms or how these communities may interact with *K. brevis*. Here, we combine high-resolution observations from shipboard and submerged in situ Imaging FlowCytobot deployments, traditional flow cytometry, light microscopy, and concurrent environmental measurements to begin to evaluate how microbial community diversity changes relative to *K. brevis* blooms. We focused primarily on a series of inshore-to-offshore transects, sampled bimonthly as part of South Florida Ecosystem Restoration surveys, to capture a range of bloom and non-bloom conditions across multiple events. We hypothesized that phytoplankton diversity would be negatively related to *K. brevis* bloom presence and abundance, and preliminary analyses indicate reduced phytoplankton community diversity and evenness during bloom events. We also observed marked cross-shelf shifts in diversity and *K. brevis* distribution patterns over the course of a bloom. We are continuing to process additional survey samples to help address spatiotemporal structure in West Florida Shelf phytoplankton assemblages, including examining the size distributions of dominant taxa, bacterial abundance, and the habitat associations of *K. brevis* and other taxa based on satellite-derived seascape classifications for the region.

Chesapeake Bay HABs: Niche Differentiation Across Time and Space from Marine to Fresh Waters

Margaret R. Mulholland[1]*, Megan Ladds*[1]*, Jessica Kellner*[1]*, Chyna Law*[1]*, Ava Guercio*[1]*, Katherine McCormick*[1]*, Michael Lane*[1]*, Michelle C. Tomlinson*[2]*, Todd Egerton*[3]*, Debbie McKay*[4]*, Cathy Wazniak*[4]*, Emily Brownlee*[5]*, Greg Silsbe*[6]*, and Jennifer Wolny*[7]

[1]Old Dominion University, Norfolk, VA, USA
[2]National Centers for Coastal Ocean Science, NOAA, Silver Spring, Maryland, USA
[3]Virginia Department of Health, Norfolk, VA, USA
[4]Maryland Department of Natural Resources, Annapolis, Maryland, USA
[5] St Mary's College of Maryland, St Mary's City, MD, USA
[6]University of Maryland Center for Environmental Science, Cambridge, Maryland, USA
[7]US Food and Drug Administration, College Park, MD, USA

The Chesapeake Bay Program (CBP) monitoring formally began in 1984. As part of this program, phytoplankton species have been identified and enumerated using microscopy alongside concomitant hydrographic and biogeochemical observations. Long term trends have shown that many HAB species occur in the Bay and its major tributaries, however interannual variability in blooms is profound. In addition, over the CBP monitoring program's history, blooms of new dinoflagellate HAB species have been observed, while blooms of others have waned, suggesting that long term changes in climate and water quality and hydrographic conditions in the Bay and connected coastal systems, are selecting or allowing for their emergence or disappearance. The Chesapeake Bay represents a continuum of salinity, and to some extent temperature, that is seasonally variable. It has been observed that the lower Chesapeake Bay is warming at a rate twice that of the upper bay largely due to its connectivity to the Atlantic Ocean. Here we examine long term patterns in phytoplankton communities with respect to hydrographic and biogeochemical observations with a particular focus on HAB species to determine potential drivers of these blooms and their phenology in the Chesapeake Bay. Of particular interest are the emergence and disappearance of blooms of *Alexandrium monilatum*, *Margalefidinium polykrikoides*, and *Karlodinium veneficum*; the now bi-modal blooms of *Prorocentrum minimum* in early winter and late spring; the emergence of *Karenia papilionacea* in the lower Bay; the sporadic but now routine occurrences of *Dinophysis* spp. and *Pseudo-nitzchia* spp.; and the emerging cyanobacteria blooms in the freshwater end-members of the Bay.

Developing Networks to Co-develop HAB Forecasts for the Chesapeake Bay Region: Combining Citizen Science, Low-cost Observations, Models, and Satellite Observations

Margaret R. Mulholland[1]*, Eileen Hofmann*[1]*, Megan Ladds*[1]*, Jessica Kellner*[1]*, Chyna Law*[1]*, Peter Bernhardt*[1]*, Marjorie Friedrichs*[2]*, Pierre St-Laurent*[2]*, Dante Horemans*[2]*, Kim Reece*[2]*, Willy Reay*[2]*, Susanna Musick*[2]*, Kirstin Wakefield*[3]*, Sheri Schwartz*[4]*, and Michelle C. Tomlinson*[5]

[1]Old Dominion University, Norfolk, VA, USA
[2]Virginia Institute of Marine Science, Gloucester Point, VA, USA
[3]MARACOOS, Washington DC, USA
[4]Tetratech, South Kingstown, Rhode Island, USA
[5]National Centers for Coastal Ocean Science, NOAA, Silver Spring, Maryland, USA

Destructive blooms of the ichthyotoxic harmful algal bloom (HAB) species *Margalefidinium polykrikoides*, have occurred nearly annually in late summer in the lower Chesapeake Bay and mid-Atlantic coastal waters for decades. Since 2007, *M. polykrikoides* blooms have been succeeded by blooms of *Alexandrium monilatum*. Blooms have been linked to eutrophication and warming temperatures and contribute to regional hypoxia/anoxia, and finfish and shellfish mortality. Through previous research, bloom initiation hotspots were identified, transport pathways from initiation sites established, and models for bloom development and transport implemented. Networks for bloom detection and monitoring that include fixed station sampling, underway "DataFlow" sampling from boats, and satellite surveillance are in place, and we are implementing enhanced surveillance systems through deployment of low-cost, high throughput, phytoplankton imaging PlanktoScopes. Results are advising state-of-the-art estuarine forecast models, that are being leveraged to build an operational forecast system for *M. polykrikoides* and *A. monilatum* blooms in the mid-Atlantic region and that will be accessible to stakeholder groups in near real time through the Chesapeake Bay Environmental Forecasting System (CBEFS) and MARACOOS' OceansMap portal. This presentation will describe this project, our collaboration with NCCOS, its evolution, and a pathway forward for building instrument agnostic monitoring and observational networks to support the national HAB observing network (NHABON). It will also describe the many challenges and opportunities of using multiple imaging tools and platforms, and community scientists to create a unified delivery system for images and forecasts with some minimum metadata.

Development of an Infrared Microspectroscopy Technique to Measure Real-Time Physiological Changes of Living Individual Algal Cells

Justin Murdock, *Samantha Satterfield*

Center for the Management, Utilization, and Protection of Water Resources, Tennessee Tech University, Cookeville, Tennessee, USA

Methods for predicting algal responses to environmental changes are quickly progressing across subcellular to ecosystem spatial scales. Each scale and technique, e.g., quantifying gene expression to satellite imaging of blooms, provides distinct but corroborating evidence towards a more holistic understanding of algal bloom dynamics. Our project is focused on understanding the response of individual cells and colonies to changes in nutrients, light, and temperature to better identify threshold exposure levels and timing for bloom development and toxin production. We are advancing an established infrared microspectroscopy-based technique to now measure environmentally induced physiological responses of living algal cells and cyanobacteria colonies in real-time. This technique measures relative lipid, protein, carbohydrate, and other macromolecule concentrations in cells. This data is used to detect shifting macromolecule proportions, such as increasing energy storage lipids when stressed, or increasing protein production prior to cell division. This presentation will demonstrate method capabilities and limitations, and current data of time-lapse cellular macromolecular changes in cyanobacteria. This technique can fill a niche between molecular studies and laboratory incubations to identify the timing of cellular level responses, and it can also be used with natural, mixed-species communities to assess real-time competition among species.

Beyond the Mainstem: Spatiotemporal Patterns of Chlorophyll Across Aquatic Habitats of a Large Floodplain River

Mackenzie Marti[1], ***Jennifer Murphy***[2]

[1]U.S. Geological Survey, Urbana, Illinois, USA
[2]U.S. Geological Survey, DeKalb, Illinois, USA

Harmful algal blooms (HABs) are increasingly documented in large U.S. rivers, yet their spatial and temporal dynamics remain poorly resolved. Using chlorophyll *a* (chl-a) in relative fluorescence units (RFU) modeled from satellite imagery (Sentinel-2A, -2B, -2C), we characterized longitudinal, seasonal, and annual patterns across aquatic areas of the Illinois River, Illinois from 2019-2024. The three aquatic areas are the main navigation channel, connected floodplain lakes, and intermittently connected floodplain lakes. Modeled chl-a values were extracted from rasters for 273 polygons, each representing an individual lake or a 2-mile river segment. For each polygon, we computed median RFUs and exceedance rates relative to a threshold, used as a bloom proxy. Across 557 image dates, chl-a varied longitudinally and by aquatic area. Period-of-record median chl-a was lowest in the main channel, while floodplain lakes exhibited the highest RFUs and exceedance rates. Peoria Lake, a large connected floodplain lake, divided the river into an upstream reach with longitudinally increasing chl-a and a downstream reach with elevated and spatially variable chl-a. Despite its lentic and eutrophic setting, Peoria Lake showed unexpectedly low chl-a. The depression of chl-a RFUs in Peoria Lake was apparent only in the summer and fall, times of year when chl-a RFU rose in the upstream and downstream reaches from low winter values. Annual median chl-a of individual polygons showed substantial interannual variability, particularly downstream of Peoria Lake, yet longitudinal patterns remained consistent. Together, the results show strong spatial patterns and notable differences between the mainstem and floodplain lakes in this regulated, eutrophic river system. These variations highlight specific river segments, lakes, years, and seasons with historical HAB risk. Remotely sensed chl-a helps resolve patterns in chl-a and HAB vulnerability at scales hard to capture with field data alone.

Developing the Pacific Ciguatera Network to Collaboratively Understand Ciguatera in the Pacific Islands

Eileen Nalley[1]*, Matt Iachhei*[2]*, Mia Comeros*[3]*, Talofa Fe'a*[4]*, Kelsie Kuniyoshi*[5]*, Benedict Yamamura*[6]*, Alison Robertson*[7]*, Mindy Richlen*[8]*, Deana Erdner*[9]

[1]Hawai'i Sea Grant, Honolulu, Hawai'i USA
[2] Hawai'i Pacific University, Honolulu, Hawai'i USA
[3] Pacific Islands Ocean Observing Systems, Honolulu, Hawai'i USA
[4] Emory University, Atlanta, Georgia USA
[5] University of Hawai'i at Mānoa, Honolulu, Hawai'i USA
[6] Marshall Islands Marine Resources Authority, Majuro, Marshall Islands
[7] University of South Alabama, Mobile, Alabama USA
[8] Woods Hole Oceanographic Institute, Woods Hole, Massachusetts USA
[9] University of Texas, Austin, Texas USA

Ciguatera poisoning is the most common form of seafood poisoning in the Pacific Islands, yet it is understudied in much of the region. The physical, social, and economic impacts of ciguatera can affect access to fisheries and intergenerational knowledge transfer that supports sustainable management. Ciguatera is caused by the consumption of seafood that has accumulated ciguatoxins produced by epiphytic dinoflagellates (typically *Gambierdiscus* spp.) and can cause a range of acute or chronic symptoms. The Pacific Ciguatera Network was developed through a partnership between Hawai'i Sea Grant and the Pacific Islands Ocean Observing Systems at the University of Hawai'i in collaboration with other Universities and more than 30 organizations representing managers, communities, and fishers across the Pacific. The Network was established to address long-standing questions about ciguatera poisoning and aims to support standardized data collection to improve regional comparisons and analyses, while also promoting collaboration and capacity building. Online surveys and targeted interviews were conducted in Hawai'i (n = 106 and 20, respectively) and American Samoa (n = 102 and 12) to characterize the impacts of ciguatera in these locations, and standardized dinoflagellate sampling was conducted in partnership with local agencies and organizations in Hawai'i (n = 20 sites), American Samoa (n = 6), and the Marshall Islands to determine the abundance and distribution of *Gambierdiscus* spp. Additional studies have been initiated that explore links between environmental variables with measured *Gambierdiscus* abundances to better understand potential drivers and improve predictive capacity in the region. In addition to generating critical fisheries data, building connectivity, and addressing urgent questions about seafood safety in the Pacific, this Network is strengthening partnerships and offering technical training through workshops and student engagement.

Effects of Antecedent Conditions on Harmful and Beneficial Algal Blooms in Upper San Francisco Estuary

Schuyler Nardelli[1]*, Sarah Perry*[2]*, Ryan Hankins*[3]*, Alex Berk*[3]*, Kyle Leathers*[1]*, Shaela Noble*[3]*, Keith Bouma-Gregson*[1]*, Ellen Preece*[2]*, Laura Twardochleb*[3]

[1]U.S. Geological Survey California Water Science Center, Sacramento, CA, USA
[2]California Department of Water Resources, Sacramento, CA, USA
[3]California State Water Resources Control Board, Sacramento, CA, USA

Upper San Francisco estuary (USFE; Sacramento-San Joaquin Delta and Suisun Bay), California, has low productivity compared to other estuaries yet serves as rearing habitat for numerous native fish species. In the late 1980s, chlorophyll *a* (chl-*a*) concentrations declined by more than half in brackish waters, contributing to declines of endangered fish species. The chl-*a* decline is hypothesized to result from combined effects of invasive clams, wastewater contamination, and reduced managed river flows. Additionally, cyanobacterial harmful algal blooms (CHABs) have become common each summer in recent decades. Resource managers are interested in understanding how flow and nutrient management could promote phytoplankton blooms beneficial to the food web while reducing CHABs. Most studies in USFE have focused on the effects of contemporary environmental conditions, but emerging evidence suggests antecedent conditions – flows and nutrients in seasons preceding blooms – may play an important role. Our study sought to identify the major drivers of phytoplankton blooms and community composition across seasons and regions of USFE. We synthesized water quality, flow, grazer, chl-*a*, and phytoplankton community data collected from 1979-present. We then applied generalized additive models and piecewise structural equation models to identify drivers of blooms over the entire timeseries and harmful versus beneficial blooms from 2008-present. Preliminary results show that across regions and seasons, high temperatures and high dissolved ammonium concentrations drive blooms. Sacramento River inflow during the previous season was also an important predictor of chl-*a*. Under low-flow conditions, chl-*a* increased with increasing outflow. Under high-flow conditions, chl-*a* declined with increasing outflow. Chl-*a* was highest in the south Sacramento-San Joaquin Delta where CHABs are prevalent and lowest in the brackish water regions where diatom blooms dominate. These results improve our understanding of how antecedent environmental drivers and water management impact phytoplankton bloom dynamics and food webs supporting native fish species within USFE.

Can Satellite-Derived Soil Moisture Aid in Harmful Algal Blooms Predictions: A Machine Learning Approach

Jyoti Neupane[1]*, Debabrata Sahoo*[2]*, Narendra Das* [3]*, Sarah Waickowski*[4]*, Stefanie L Whitmire*[5]*, Hemanth Dakshinamurthy*[6]*, Jodi L Ryder*[7]

Harmful algal blooms (HABs) are indicated by excessive growth of algae in water bodies, which results from excessive accumulation of nutrients, especially phosphorus and nitrogen, along with other environmental factors. Excessive accumulation of nutrients is a product of runoff that enters rivers and lakes from diffuse sources, such as agricultural and urban areas, and point sources such as wastewater treatment plant outfalls. Soil moisture plays a critical role in the runoff process; when soil is saturated or poorly drained, excess water carries dissolved nutrients into nearby waterways, increasing the potential for HABs to occur. On the contrary, well-drained and well-managed soil can reduce nutrient losses, thereby lowering the risk of HABs. Because of soil moisture's likely critical role in the nutrient-HAB relationship, its influence on HABs needs attention. Although numerous studies have focused on predicting HABs using various water quality parameters, satellite-derived (SAMP) soil moisture data have not been incorporated into predictive frameworks. To explore the missing link, the objective of the study aims to integrate satellite-derived soil moisture data with in-situ water quality measurements to evaluate their relationship with HABs' occurrences. Multiple machine learning models such as decision tree, random forest, support vector machine, extreme gradient boosting, and artificial neural networks will be explored to develop predictive models based on key variables identified through correlation analysis. The findings from this study will aid in establishing machine learning based relationships among soil moisture, water quality parameters, and HABs occurrences. Since satellite derived data is available at a global scale, the results from this study may assist in the development of decision support tools for water bodies lacking comprehensive water quality information with broader implications globally.

Fly-Over Surveillance of Select New Jersey Lakes – Incorporating Fixed Wing Aircraft into Cyanobacteria Harmful Algal Bloom Monitoring

Robert Newby[1], *Christopher Kunz*[2], *Emily Mayer*[2], *Mike Kusmiesz*[3], *Briana Morgan*[4], *Sheri Shifren*[5], *Victor Poretti*[3]

[1]Division of Science and Research, New Jersey Department of Environmental Protection, 428 East State Street, Trenton NJ, USA
[2]Bureau of Freshwater and Biological Monitoring, New Jersey Department of Environmental Protection, 35 Arctic Parkway, Ewing NJ, UDSA
[3]Directors Office, Division of Water Monitoring and Standards, 401 East State Street, Trenton NJ, USA
[4]Bureau of Marine Water Monitoring, New Jersey Department of Environmental Protection, 929 E. Stoney Hill Road, Leeds Point NJ, USA
[5]Bureau of Environmental Analysis and Restoration, 401 East State Street, Trenton NJ, USA

Cyanobacteria harmful algal blooms (cHAB) represent a growing public health and ecological concern across New Jersey's surface waters. Traditional ground-based monitoring methods, while foundational, are inherently limited in spatial coverage and temporal resolution, often failing to capture the true dynamic nature of bloom development and expansiveness. Remote sensing platforms offer a promising complement to conventional surveillance, yet satellite-based approaches are constrained by revisit frequency, cloud cover interference, and spatial resolution limitations that may obscure bloom features at smaller water bodies common throughout the state.

To combat this limitation, the New Jersey Department of Environmental Protection (NJDEP) has incorporated fixed-wing aircraft monitoring with a hyper spectral camera over select bodies of water during our bloom season (May-October). This represents a cost-effective, flexible, and high-resolution tool, capable of complimenting traditional monitoring techniques. Aerial observations were cross-validated against concurrent ground-truth sampling including phycocyanin fluorometry, cell enumeration, and cyanotoxin analysis, enabling assessment of detection sensitivity and the utility of aerial imagery for triggering targeted field response.

Results from the last nine years of integration demonstrate that the fixed-wing aircraft provide actionable spatial and spectral data at resolutions suitable for bloom delineation on water bodies where satellite imagery currently underperforms. Aerial overflights successfully identified bloom features, consistent with field sampling or buoy monitoring. These findings help support the use of multiple monitoring approaches when conducting HAB surveillance and tracking bloom progress and allow for more rapid response and allocation of resources when bloom conditions may be changing.

Spatially Balanced Surveys Characterizing Potential Risk from Benthic Cyanotoxins in Four Rivers of the USA

***Christopher Nietch**, Nathan Smucker, Jingrang Lu*

U.S. EPA, Office of Applied Sciences and Environmental Solutions, Cincinnati, OH, USA

Toxin producing benthic cyanobacteria in rivers and streams present unique risk characterization and management challenges. To help address these, US EPA set out to evaluate different field sampling and laboratory methods by conducting studies at seven pilot sites in rivers across six states in 2023. The lessons learned were then used to design four spatially balanced probability surveys that were completed in 2024 and 2025. Systems assessed included 415 km of the Virgin River, UT; 587 km of the North Fork of the Shenandoah River (NFSR), VA; 85 km (centerline distance) of the Columbia River in the Tri-Cities area of western WA; and 521 km of the banks of the Ohio River, near Cincinnati, OH. The benthic biomass sampled in each had unique risk characteristics in terms of the relative abundance of toxigenes and concentrations of different cyanotoxins. To demonstrate potential impacts, study-specific levels for dog ingestion of toxins in benthic biomass were used based on extrapolations from water recreation values and assumptions about body weight and potential ingestion rate. The preliminary results suggest that potential impact probabilities for kilometers assessed were 34% from anatoxin in the Virgin River; 25% and 45% from anatoxin and saxitoxin, respectively in the NFSR; 18% and 32% from microcystin and anatoxin, respectively in the Columbia River; and 10%, 34%, and 54% from anatoxin, saxitoxin, and microcystin, respectively in the sections of the Ohio River sampled. Visual assessments of benthic cyanobacteria cover were not reliable indicators of toxin levels in benthic biomass in this study.

A Collaborative Approach to Investigating Harmful Algal Bloom-Associated Illnesses in California Waters

*Karen Odkins [1], **Carly Nilson**[2], Marisa Van Dyke[2], Thomas Hayashi[3], Shannon Murphy[4], and Beckye Stanton[4]*

[1]California Department of Fish and Wildlife, Sacramento, CA, USA
[2]California State Water Resources Control Board, Sacramento, CA, USA
[3]California Department of Public Health, Richmond, CA, USA
[4]California Office of Environmental Health Hazard Assessment, Sacramento, CA, USA

Harmful algal blooms (HABs) can produce potent toxins, cyanotoxins, and other compounds that can cause illness or death in fish, wildlife, domestic animals, and humans. Adverse health effects associated with freshwater and estuarine cyanobacterial HABs may result from ingestion or contact with cyanobacteria, cyanotoxin-contaminated water, or algal mats. Tracking HAB-associated illnesses at the state and national level can be used to elucidate patterns of occurrence and scale of impact, enact communication with the public to prevent future illnesses, and prioritize management efforts to reduce risk of adverse effects in high HAB impacted areas. The US Centers for Disease Control and Prevention's guidance promotes consistency in illness investigations and encourages reporting to the One Health Harmful Algal Bloom System (OHHABS). This paper provides a thorough overview of California's standardized response system to receive, triage, investigate, and make determinations on freshwater and estuarine HAB-associated illness cases for state and national reporting. A primary strength of California's standardized system is the collaboration and coordination of an interdisciplinary team of experts within the California Interagency HAB-related Illness Workgroup (Illness Workgroup). Illness tracking and subsequent reporting to OHHABS has bolstered California's understanding of the spatial and temporal occurrences of HABs and associated illnesses, and helped the State identify, document, and communicate the negative health impacts of HABs. These findings have been instrumental in prioritizing resource allocation, investigation efforts, event reporting, and communications to the public.

Using Microbiomes as Microsensors to Forecast Toxic Algae Blooms: A Proteomic Approach

Brook L. Nunn *[1], Miranda C. Mudge [1], Claire E. Elbon [1], Emma Timmins-Schiffman [1], Gabriella Chebli [2], Michael Riffle[1], William S. Noble[1], Mark D. Scheuerell[3], Tatiana Rynearson[4], Julia Kubanek[2]*

[1]Department of Genome Sciences, University of Washington, Seattle, USA
[2]School of Biological Sciences and School of Chemistry & Biochemistry, Georgia Institute of Technology, Atlanta, GA, USA
[3]U.S. Geological Survey Washington Cooperative Fish and Wildlife Research Unit, School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA, USA
[4]School of Oceanography, University of Rhode Island, Narragansett, Rhode Island, USA

Harmful algal blooms (HABs) are increasing in frequency and severity, yet reliable early-warning indicators remain limited. We applied high-resolution metaproteomics to the free-living marine microbiome to identify bacterial peptide biomarkers that reproducibly shift prior to bloom onset in the San Juan Islands, Washington, USA. Surface waters were sampled every four hours across two pre-bloom periods associated with harmful *Chaetoceros socialis* events (maximum chlorophyll *a* ~94 μg L^{-1}). Using Hidden Markov Models (HMM), we identified non-reverting bacterial peptide state changes occurring at least 24 hours before algal bloom onset. Validated biomarkers were identified to be produced by bacterial classes Gammaproteobacteria, Flavobacteriia, and Verrucomicrobiae, and included TonB-dependent receptors and proteins involved in translation and membrane restructuring, consistent with rapid changes in resource acquisition and cellular physiology. Independent validation on a second pre-bloom sample set confirmed a subset of peptides as reproducible early bloom indicators across contrasting nutrient regimes. To contextualize these predictive biomarkers within broader community dynamics, we expanded our analysis using metagenomics data collected every 4 hours and spanning 22 days, which captured the bloom initiation, peak, decline, and a secondary growth pulse. Dynamic factor analysis of 102 bacterial classes and corresponding KEGG Ortholog (KO) profiles revealed coherent, low-dimensional temporal structure underlying community change. Empirical dynamic modeling (EDM) is being applied to the metagenomic time series to infer causal relationships among microbial taxa, functional genes, and environmental drivers. A complementary EDM analysis is also being conducted on the metaproteomic protein functions across the full time series to evaluate whether protein-level dynamics provide stronger or earlier predictors of bloom initiation than genomic signals alone.

Together, integrated metaproteomic and metagenomic time-series analyses reveal coordinated microbial restructuring that precedes and accompanies HAB formation, advancing a predictive and mechanistic framework for understanding bacterial–phytoplankton interactions in coastal bloom systems.

Phosphorus Forms in the Maumee River and Western Lake Erie During HAB Phenology

Teige O'Brien[1], *Casey M. Godwin*[1], *E. Riley Peterson*[1], *Rima Upchurch*[1], *Jim Hood*[2], *and Reagan Errera*[3]

1University of Michigan, Ann Arbor, MI, USA
2The Ohio State University, Columbus, OH, USA
3National Oceanic and Atmospheric Administration, Ann Arbor, MI, USA

Western Lake Erie harmful algal blooms (HABs) are strongly influenced by spring Maumee River phosphorus (P) loads, but bloom development also depends on how P is partitioned, transformed, and recycled in the western basin. We conducted synoptic sampling from the upper Maumee River into western Lake Erie across 2 years to assess the roles of riverine P inputs. Water samples collected before, during, and after summertime HABs were analyzed for P speciation, including soluble reactive, mineral-associated, labile, and recalcitrant fractions, and for biological allocation to growth-associated DNA/RNA-P versus storage-associated polyphosphate. In the river, total P changed little while dissolved P declined relative to total P, without a corresponding increase in exchangeable particulate P, suggesting incorporation of dissolved P into stable particulate forms and biomass during transport. In the lake, dissolved P was highest in early spring, declined in early summer as biological P fractions increased, and rose again in late summer. DNA/RNA-P represented a major fraction of total P during peak phytoplankton biomass, indicating strong biological incorporation during bloom development. Exchangeable and acid-hydrolysable P varied proportionally with total particulate P, suggesting limited seasonal change in sorption to seston. Together these results help explain the seasonal changes in apparent yield – the conversion of dissolved forms from the landscape into bloom biomass. Incorporating P partitioning and transformation into HAB models may improve predictions for western Lake Erie.

Brevetoxin Dynamics and Bioavailability from Floc Following PAC-Modified Clay Treatment of *Karenia brevis* Cultures

Nicholas R. Ohnikian[1]*, Christopher D. Sibley*[1]*, R. Ben Freiberger*[2]*, Kristen N. Buck*[2]*, Alyssa Meyers*[1]*, Samantha Harlow*[1]*, Donald M. Anderson*[3]*, Richard Pierce*[1] *and Jennifer H. Toyoda*[1]

[1]Ecotoxicology Research Program, Mote Marine Laboratory, Sarasota, FL, U.S.A.
[2]College of Earth, Ocean, and Atmospheric Sciences, Oregon State University, Corvallis, OR U.S.A.
[3]Woods Hole Oceanographic Institution, Woods Hole, MA, U.S.A.

Harmful algal blooms (HABs) caused by the dinoflagellate Karenia brevis present serious ecological and public health concerns due to the production of brevetoxins (BTX). Clay flocculation and sedimentation of cells, particularly with polyaluminum chloride (PAC)-modified clays, is a promising HAB mitigation approach. This study evaluated the efficacy of Modified Clay-II (MCII), a PAC-modified kaolinite clay, in reducing K. brevis cell abundance in mesocosm experiments and examined the bioavailability of BTX potentially released from settled floc back into the water column and sediment over the first 72 h after treatment. Additionally, we quantified trace metals in benthic clams (Mercenaria mercenaria) exposed to the floc post-treatment to assess metal accumulation and potential toxicological effects from MCII application. MCII treatment (0.2 g/L) resulted in a 91% reduction in K. brevis cell density and a 50% decrease in waterborne brevetoxins after 5 h. Brevetoxins accumulated in sediment post-flocculation, with BTX-B5 emerging as the dominant congener. Clams exposed to MCII-treated floc showed comparable tissue BTX levels to controls and significantly elevated aluminum concentrations, though without mortality. The aluminum accumulations in this study do not raise concerns for the health of the clams or the humans who eat them, given other dietary exposures. These findings, as reported in Ohnikian et al. (2025), support the potential of MCII for HAB mitigation while underscoring the need for further evaluation of exposure risks to all benthic species. This work was funded by the National Oceanic and Atmospheric Administration (NOAA) Prevention, Control, and Mitigation of Harmful Algal Blooms (PCMHAB) program through NOAA Grant NA21NOS4780156.

Relative Influence of Limnological Factors on Cyanobacterial Biovolume and Toxin Variability in U.S. Lakes

Yusuf O. Olaleye [1,2], *Stephen M. Powers* [3], *Katelyn M. McKindles* [1,2]

[1]Department of Biology, Baylor University, Waco, Texas, USA
[2]Center for Reservoir and Aquatic Systems Research, Baylor University, Waco, Texas, USA
[3]Water Resources Research Institute, University of Idaho, Boise, Idaho, USA

Harmful cyanobacterial blooms are increasingly endangering freshwater ecosystems, water security, and recreational lake use across the U.S. Lake condition assessments have often relied on phytoplankton indicators, including chlorophyll-a (chl-a) and total cyanobacterial abundance. However, these indicators often fail to reliably predict cyanotoxin concentrations due to variability in toxin production across taxa and environmental conditions. Using nationwide datasets from the U.S. EPA's National Lakes Assessment (NLA; 2012 - 2022), we examined whether the physicochemical predictors of biomass indicators, such as (chl-a) and total cyanobacterial biovolume, differ from those influencing the biovolumes of key toxin-producing taxa, including *Microcystis* and *Cylindrospermopsis*. We further assessed what limnological factors are most strongly associated with microcystins (MICX) and cylindrospermopsins (CYLSPER). We used statistical models to quantify relationships and rank predictor importance across (chl-a), total cyanobacterial biovolume, and the biovolumes of dominant toxin-producing taxa, and main factors driving the two major toxins. Results showed all biomass-based indicators, including toxin-producing taxa, were influenced by nutrients, turbidity, and lake elevation. The two major toxins (MICX and CYLSPER) showed an inverse relationship across lakes. Nitrogen was the most important predictor of toxin-producing taxa and MICX levels, with pH also identified as a significant predictor of MICX. Temperature and lake area (HA) were among the significant predictors of CYLSPER. Phytoplankton community indices and mineral elements also showed significant influence on both toxins. Our findings therefore demonstrate that factors influencing bulk biomass differ in their relative influence on toxin-producing taxa, and that distinct factors influence different toxin types at nation-wide scale.

Urea Reshapes Growth and Photophysiology in *Raphidiopsis raciborskii*

JL Olavesen[1], *S Eckl*[1], *RM Martin*[1], *KM Yoshimura*[1,2], *DJ Weston*[3], *D Talmy*[1] *and SW Wilhelm*[1]

[1] Department of Microbiology, The University of Tennessee
[2] Department of Biology, James Madison University
[3] Biosciences Division, Oak Ridge National Laboratory, Oak Ridge, TN, USA

Recent agricultural shifts toward urea-based fertilizers have raised pressing questions about how nitrogen form influences cyanobacterial competitive dynamics and photophysiology during harmful bloom events. The increasingly important yet understudied filamentous bloom former *Raphidiopsis raciborskii* provides an effective model for addressing these knowledge gaps. The effects of different nitrogen species on the phenotype, growth, and photophysiology of *R. raciborskii* were evaluated in batch culture. Comparative transcriptomic analyses were integrated with PAM fluorometry, in vivo fluorescence, pigment measurements, and flow-cytometric quantification. Under bloom-relevant conditions of elevated pH and low inorganic carbon availability, urea supported higher growth rates than nitrate and other nitrogen forms. This advantage was accompanied by pronounced phenotypic divergence, increased phycobiliprotein production, depressed photosynthetic efficiency, and transcriptional downregulation of photosystem II. By clarifying how *R. raciborskii* exploits urea, tolerates environmental stress, and gains a competitive advantage, this work has implications for improved forecasting of bloom onset and severity. More broadly, it advances understanding of cyanobacterial metabolic flexibility, with implications for freshwater management and emerging biotechnologies.

Cardinal Flow: Broadening Community Participation Through Multidisciplinary Red Tide Data Sonification

Heather O'Leary
University of South Florida

What if HAB decision-makers could smell a Red Tide? What if community stakeholders could articulate the gaps and misunderstandings in complex multi-variate data? This common ground is pivotal to the mutual understanding, science diplomacy, and civil discourse necessary to solving HABs. It is also embodied. By applying social science's embodied techniques to innovative data-driven arts (sonification and visualization), stakeholders can surmount their differences to collaborate on creating sustainable solutions to HABs.

The United Nation's Sustainable Development Goals foreground the "triple bottom line," championing a fusion of people, planet, and prosperity in sustainable modeling and design. However, in practice, scientists who merge datasets across disciplines and communities face tremendous difficulties. Not only are timescales, metrics, and analyses different, but so is communicating across disciplinary expertise. Likewise, scientific communication—and increasingly science diplomacy—is ever more crucial to enriching sustainable modeling that includes the invisiblized perspectives of everyday water experts. Communicating Research Expansively through Sonification and Community-Engaged Neuroaesthetic Data-literacy Opportunities (CRESCENDO) translates triple bottom line data about Florida's coastal water challenges to engage the public and scholarly communities alike. It uses open-access data repositories and cutting-edge scientific data through the mediums of music and art to address coastal risk regardless of data literacy. This presentation will showcase the process of sonification and neuroaesthetics using social, economic, and environmental data about Florida's harmful algae blooms.

Local Knowledge as a Community-Embedded Early Warning and Governance Signal for Harmful Algal Blooms

***Horace Owiti Onyango*[1,2]*, Julia Akinyi Obuya*[2,3]*, Peter B. McIntyre*[1]*, John Hoddinott*[1]*, Kathryn Fiorella*[1]

[1]Cornell university, Ithaca, NY, USA
[2]Kenya Marine and Fisheries Research Institute, Kisumu, Kenya
[3]Bowling Green State University, Ohio, USA

Harmful algal blooms (HABs) are intensifying in freshwater systems worldwide, posing escalating risks to ecosystems, public health, and livelihoods. In Lake Victoria, riparian communities experience these blooms directly, yet formal early warning policies remain largely technocratic—centered on satellite monitoring, laboratory diagnostics, and institutional reporting chains. This paper examines how Indigenous and local ecological knowledge can inform and reshape early warning policy design for HABs' hazard response and governance.

Drawing on eleven Focus Group Discussions conducted with fishing communities and institutional stakeholders along the Kenyan shore of Lake Victoria, the study applies a hybrid inductive–deductive thematic analysis structured around the UNDRR Sendai Early Warning Framework. Findings reveal that communities possess detailed taxonomies of blooms, shoreline-based monitoring practices, seasonal forecasting indicators, and trusted communication networks that function as an embedded early warning infrastructure. Despite this, such knowledge is rarely institutionalized within formal policy processes.

We argue that engaging Indigenous and local knowledge in policy making requires moving beyond consultation toward structural integration within risk assessment, monitoring protocols, communication pathways, and preparedness planning. By demonstrating how community-derived indicators can strengthen early detection, contextual interpretation, and response legitimacy, this study contributes to broader debates on co-production, environmental governance, and the democratization of early warning systems.

Using Statistical Tools and Model Outputs to Advance Harmful Algal Bloom Forecasts in Lake Erie

Caroline Owens[1,2], *Andrew Meredith*[1,3], *Yizhen Li*[1,3], *Alex Hounshell*[1], *Rick Stumpf*[1]

[1]NOAA National Centers for Coastal Ocean Science, Harmful Algal Bloom Forecasting Branch
[2]Research Planning, Inc.
[3]Consolidated Safety Services

Recurring summer cyanobacterial harmful algal blooms (cyanoHABs) in western Lake Erie have severe negative impacts on human and ecological health. Since 2009, NOAA has been delivering a suite of cyanoHAB monitoring products and ecological forecasts for western Lake Erie which now include a seasonal cyanoHAB forecast, daily hypoxia forecast, and a daily cyanoHAB nowcast/forecast. This daily cyanoHAB product provides water resource managers, recreational fishers, and public health officials with near-real time information on bloom location and short-term (3-5 days) forecasts of bloom movement. In this work, we 1) developed evaluation metrics for forecasts of cyanoHABs in Lake Erie by applying statistical and software tools (METplus) adapted from numerical weather forecasting and 2) applied one of these metrics, the mean Pratt's Figure of Merit, to assess how incorporating total predicted cyanobacterial biomass as a model input could improve forecast performance when recent satellite imagery is not available. We examined forecast performance relative to a persistence forecast both with and without the addition of total biomass inputs. While cyanoHAB forecast products provide value to a wide range of stakeholders, we are continually seeking to address limitations and increase stakeholder usability of forecast products. This validation framework provides a promising avenue to evaluate many aspects of our product such as future model improvements, forecast sensitivity to varying weather conditions, and variation in forecast uncertainty. Results from this study will allow us to advance our broader understanding of HAB and ecological forecast performance, and deliver more relevant information to stakeholders around Lake Erie and other HAB-affected regions.

Assessing and Improving the Scalability of a Physical HAB Removal Process

Martin Page*[1]*, *Marissa Campobasso[1], Catherine Thomas[2], Kathryn Gunderson[1], Bruce MacAllister[1], Al Kennedy[2], and Andy Hur[1]*

[1] US Army ERDC Construction Engineering Research Laboratory, Champaign, IL, USA
[2] US Army ERDC Environmental Laboratory, Vicksburg, MS, USA

The mitigation of harmful algal blooms (HAB) via physical removal processes can provide potential additional environmental benefits by removing the intracellular nutrients and degradable biomass that typically remain in the water after destructive mitigation approaches. However, the scalability of physical HAB removal processes remains a challenge. The Harmful Algal Bloom Interception, Treatment, and Transformation System (HABITATS) was a research project that demonstrated a potentially scalable capability to quickly separate algae from water and rapidly process the resulting biomass while recovering resources. The core technologies demonstrated in field settings, in collaboration with industry, academic, and federal partners, included floating weir skimmers, dissolved air flotation, biomass dewatering presses, and hydrothermal liquefaction. This presentation will summarize physical and economic scalability analyses of HABITATS with a focus on lessons learned and opportunities for improvement. Results from recent experimentation aimed at improving economic scalability will also be presented, including a novel in-situ flotation method, integration of membrane separation systems, and future design concepts that could leverage existing spillway infrastructure.

What Investment is Needed for Effective Harmful Algal Bloom Management: Insights from Ciguatera Poisoning

Michael L. Parsons[1], *Alison Robertson*[2,3]

[1]Florida Gulf Coast University, Fort Myers, FL, USA
[2]Dauphin Island Sea Lab, Dauphin Island, AL, USA
[3]University of South Alabama, Mobile, AL, USA

Ciguatera poisoning (CP) is the most prevalent form of phycotoxin-associated seafood poisoning maladies globally, afflicting tens of thousands of people on an annual basis. In addition to its prevalence, CP has received much interest from the research community of late because of a lag in progress in addressing common (classic) HAB challenges that have hindered management efforts to protect people from this risk/threat, including: 1) identification and characterization of the toxins (and/or precursors) responsible for CP and the organisms that produce them; 2) tools to quickly (and cheaply) identify and quantify these compounds and organisms; 3) standardized tools and methodologies to monitor for the dinoflagellates and toxins ultimately responsible for ciguatera outbreaks; and 4) forecasting and predictive tools to transition from reactive to proactive management responses. Here, we provide an overview of progress made by researchers in the field towards these challenges, highlighting the return on investments made through federally funded programs addressing CP and other HAB phenomena. Some highlights of these funded efforts include: 1) identification of algal "superstrains" responsible for toxin production; 2) identification of novel toxins being produced by the primary culprit behind CP (*Gambierdiscus*); 3) identification of novel piscine metabolites in fish and their corresponding contribution to toxicity; 4) improved understanding of toxin uptake and clearance in fish vectors; 5) improved knowledge of fish CTX metabolites and CTX-induced biomarkers; 5) improved field, molecular, and chemical methods for detection of algal species and their toxins; and 6) initiation of predictive models. Collectively, these outputs provide a foundation for the development of future management strategies.

Toxicity Screening and Gene Characterization of *Microcystis aeruginosa* Strains Using a Brine Shrimp Bioassay

Kaveen Patel[1], *Katelyn McKindles*[1,2]

[1] Department of Biology, Baylor University, Waco, Texas, USA
[2] Center for Reservoir and Aquatic Systems Research, Baylor University, Waco, Texas, USA

Heterotrophic bacteria within the *Microcystis aeruginosa* phycosphere may influence bloom growth, persistence, and toxin dynamics. We investigated how bacterial additions affected *Microcystis* growth and whether introduced bacteria could persist within the phycosphere. Initial screening experiments inoculated a non-toxic *Microcystis* strain with *Variovorax*, *Sphingopyxis*, *Runella*, or a mixed bacterial assemblage. These treatments produced isolate-specific effects, with *Variovorax* showing a dose-dependent increase in pigment-based growth, *Sphingopyxis* showing limited effects, and *Runella* producing variable growth responses. A follow-up experiment inoculated a distinct *Variovorax* isolate into both toxin-producing and non-toxin-producing *Microcystis* strains. This isolate did not significantly alter chlorophyll or phycocyanin-based growth in either host strain. However, 16S rRNA gene sequencing showed that the introduced bacterium persisted over 30 days in the toxin-producing strain but not in the non-toxin-producing strain. These results suggest that phycosphere bacterial establishment may depend on host strain identity, even when host growth responses are minimal.

A Multimetric Approach to Quantifying Freshwater HAB Occurrence and Intensity at the National Scale

Brenna Friday, Megan Coffer, and ***Michael Paul***

United States Environmental Protection Agency, Office of Water, Washington, DC, USA

Freshwater harmful algal bloom (HAB) monitoring is an integral part in protecting environmental and public health from adverse effects of cyanotoxins. In recent decades, statewide and national scale monitoring efforts have expanded across the US to collect cyanotoxin and cyanobacteria data from drinking water treatment facilities, lakes, rivers, streams, and wetlands. The information collected from these projects may reveal trends in HAB occurrence and intensity across large spatial scales for recreational and drinking water exposures. Here we introduce a quantitative framework to combine data on HAB occurrence, frequency, magnitude, and toxicity from a variety of sources: the Unregulated Contaminant Monitoring Rule (UCMR) surveys, National Aquatic Resources Surveys (NARS), Cyanobacteria Assessment Network (CyAN), state HAB advisories, and reports shared on the Water Quality Exchange (WQX). Our goal for this evaluation is to illustrate patterns and trends in HAB occurrence and intensity using multiple lines of evidence from distinct monitoring efforts. With geospatial analyses and weighted index development, we are able to aggregate information from these datasets and illustrate spatial trends and gaps in HAB measurements. These results could inform risk communication and resource investment in HAB programs at the federal, state, and local levels.

A Statutory View of Harmful Algal Blooms in Freshwaters

***M.J. Paul**, B. Friday, J.B. Walsh, J. Alers-Garcia, M. Coffer, J. Oliver*

United States Environmental Protection Agency, Office of Water, Washington, DC, USA

There are a wide range of statutes and regulations applicable to HAB management in the United States, and the US EPA National HAB Program is responsible for coordinating HAB activity across the agency under all of these. It is valuable for managers and researchers to understand these so they can better understand the legal constructs affecting their work and where science can make contributions in the future. This talk provides a brief review and instruction on the relationship of regulations to laws and statutes and the major statutes and regulations applicable to HAB management programs including the Harmful Algal Bloom and Hypoxia Research and Control Act (HABHRCA), Clean Water Act (CWA), Safe Drinking Water Act (SDWA), Federal Insecticide, Fungicide and Rodenticide Act (FIFRA), and the Federal Food, Drug, and Cosmetic Act (FFDCA). Attendees should expect to come away with a better understanding of these laws and their attending regulations and where they can go for more information.

Salish Sea Harmful Algal Bloom Research and Management: Sustaining Shellfish Harvest for Decades

Misty B. Peacock[1], *Teri King*[2], *Cheryl Greengrove*[3], *Stephanie K. Moore*[4], *and Vera L. Trainer*[5]

[1]Salish Sea Research Center, Northwest Indian College, Bellingham, WA, USA
[2]West Coast Regional Office, NOAA, Shelton, WA, USA
[3]University of Washington - Tacoma, Tacoma, WA, USA
[4]Northwest Fisheries Science Center, NOAA, Seattle, WA, USA
[5]Olympic Natural Resources Center, University of Washington, Forks, WA, USA

Washington State is the largest producer of farmed shellfish in the United States, supporting thousands of jobs and generating more than $240 million annually. Washington shellfish growers provide significant economic contributions to regional economies, supporting with more than 300 companies permitted to grow, harvest, or wholesale shellfish for domestic and world markets. However, these commercial growers, together with recreational and tribal subsistence harvesters, are severely impacted by several species of HABs and their toxins that impact human and shellfish health. Over the past three decades, projects funded through NOAA's National Competitive HAB Program have transformed HAB research in the Pacific Northwest into a nationally recognized model for HAB science, focused on advanced research, monitoring, and management, the establishment of long-lasting partnerships such as SoundToxins, and partnerships with the Washington State Department of Health for early-warning systems. Collaboration has been a key to understanding: 1. the spread of PSP toxins throughout Puget Sound, 2. the relationship of *Alexandrium* cyst populations to the severity of PSP outbreaks, 3. the appearance and impact of massive blooms, such as *Protoceratium reticulatum*, that impact shellfish health, 4. the conditions that provide an early warning of *Heterosigma akashiwo* blooms to fish farmers, 5. the appearance of new HABs of importance in the region, such as *Azadinium* and *Dinophysis*, and 6. the impacts of changing ocean conditions, such as reduced pH and increased temperature, on the severity and success of HAB species. Together these projects have helped to sustain shellfish harvest throughout the Salish Sea region by providing accurate HAB risk assessment, optimized early warning programs, and an assessment of the economic benefit of HAB forecasts to decision-makers across the Nation.

Improving HAB Event Communications: Best Practices and Potential Pitfalls

Sarah K. D. Pease

National Oceanic and Atmospheric Administration, Silver Spring, MD, USA

This presentation will synthesize concepts introduced throughout the session, alongside additional lessons from recent harmful algal bloom (HAB) events across the U.S., to outline best practices, potential challenges, and other essential considerations for HAB event communications. The objective of this presentation is to provide those involved in HAB event communication and response, including researchers, resource managers, public health and response professionals, and others, with actionable information to enhance their communication strategies for both recurrent and emerging HAB events. Topics to be addressed include internal (responder to responder) versus external (responder to stakeholder) communications and management, conveying potential HAB event impacts, mitigating the risks of misinformation, accessing existing response and communications resources, and developing targeted messaging and materials. Despite the regional and species-specific nature of HABs and their impacts, coordinating communication strategies and materials across the HAB community could greatly benefit HAB response efforts nationally.

Physical Lake Dynamics Shape Cyanotoxin Detectability in Mountain Lakes

Samantha Peña[1], *Sarah Collins*[1], *Annika Walters*[1], *Michael Wachtendonk*[2], *Raphael Kudela*[3], *Kevin Gauthier*[1]

[1]Department of Zoology and Physiology, University of Wyoming, Laramie, Wyoming, USA
[2]Wyoming Department of Environmental Quality, Cheyenne, Wyoming, USA
[3]Department of Ocean Sciences, University of California Santa Cruz, Santa Cruz, California, USA

High-elevation lakes in the Intermountain West are increasingly vulnerable to harmful cyanobacterial blooms (HCBs), yet the physical processes influencing cyanotoxin distribution in these systems remain poorly understood. This study examines how stratification, wind-driven mixing, and spatial variability influence cyanotoxin detectability in the Brooks Lake watershed, a group of subalpine lakes in northwestern Wyoming that exhibit differing bloom and toxin dynamics despite similar regional climate conditions. High-frequency buoy data, including temperature and dissolved oxygen measurements, were collected alongside meteorological data such as wind speed and direction. Cyanotoxin monitoring was conducted using biweekly grab samples and passive Solid Phase Adsorption Toxin Tracking (SPATT) samplers deployed in littoral zones and at both surface and depth in pelagic waters. Nutrients and phytoplankton community composition were also evaluated throughout the summer season. Preliminary results suggest cyanotoxin patterns are highly dynamic and spatially heterogeneous. Surface grab samples generally showed more frequent toxin detections than deep samples throughout the summer; however, during a late-season bloom event, toxin concentrations increased substantially at depth relative to surface waters. Littoral sites also exhibited consistently higher toxin concentrations than pelagic sites, with northern shoreline locations frequently showing greater toxin detectability than southern sites currently used in routine state monitoring. SPATT samplers detected cyanotoxins more frequently than discrete grab samples, highlighting the episodic and spatially patchy nature of toxin occurrence. These findings suggest physical lake structure and wind-driven transport processes strongly influence where and when cyanotoxins are detectable in mountain lakes and support development of improved monitoring strategies for remote and understudied systems.

Interactive Molecular Network for Natural Toxin Discovery and Statistics

Judy Westrick, ***Nicholas Peraino***
Wayne State University, Detroit, MI, USA

The congener diversity of natural toxins from mold and cyanobacteria combined with their low concentrations makes broad targeted analysis cost prohibitive. We present a combined untargeted liquid chromatography–mass spectrometry method and software platform for screening sample extracts for these toxins. Automated feature extraction, combined with molecular networking against a provided cyanotoxin and mycotoxin library and retention-time model, enables putative identification of unknowns and sample-level statistical analysis. In the workspace, users can explore multiple clustering techniques to visualize related features by retention time, accurate mass, and fragmentation pattern, or using principal component analysis and partial least squares discriminant analysis. Clicking a data-point displays feature metadata and enables top-down in silico fragmentation and retention-time matching generated from a library of chemical structures. Interactive statistical and clustering views allow iterative exploration (e.g. lassoing clusters) to link molecular and statistical networks and identify up or down regulated conditions or previously uncharacterized toxins. Users can create custom libraries to re-train the retention-time model and molecular network for specific substrate classes. This combined integrated analytical workflow and computational platform establishes a scalable framework for the discovery, visualization, and comparative analysis of known and unknown cyanotoxins and mycotoxins across complex environmental and biological samples.

Herbicide-Tolerant Aquatic Macrophytes That Inhibit HAB Growth in the U.S.

Ian Pfingsten[1]*, Arden Williams*[2]*, and Keith Loftin*[3]

[1]USGS, Gainesville, FL, USA
[2]Cherokee Nation System Solutions, Contractor to USGS, Gainesville, FL, USA
[3]USGS, Lawrence, KS, USA

Harmful algal blooms (HABs) pose significant risks to both human health and aquatic ecosystems. Numerous aquatic plants and algae possess allelopathic compounds that promote their own growth while inhibiting competing photosynthetic species. A widely adopted adaptive management strategy involves multi-year plant population control, followed by restoration actions such as reseeding and transplanting macrophytes. By occupying ecological niches and utilizing available resources, these restoration efforts aim to prevent the resurgence of introduced species and reduce the need for repeated biomass reduction treatments. Restoration treatments may contribute to the decline or prevention of HAB-causing algae by creating competitive environments that limit algal proliferation through allelopathy and resource limitation. Selecting appropriate plant species for restoration is crucial; species chosen must efficiently utilize resources after substantial biomass loss due to control measures. Furthermore, managers must determine the optimal timing to reduce or discontinue control treatments, balancing management objectives and minimizing unintended impacts on non-target species utilized in restoration. Notably, aquatic macrophytes with documented herbicide tolerance are infrequently studied in restoration contexts, despite evidence that their resilience can decrease the frequency of retreatments. We conducted a comprehensive literature review to identify native U.S. aquatic plants with allelopathic effects on HABs, subsequently evaluating their herbicide tolerance. Emphasis was placed on natural settings, such as protected lands and parks, which typically lack anthropogenic nutrient inputs. Our review identified 93 plant species with allelopathic interactions with HABs, of which 11 demonstrate confirmed herbicide tolerance. These findings support adaptive management strategies that incorporate restoration and inform future research on the role of non-target plants in excluding HABs. Integrating herbicide-tolerant, allelopathic native macrophytes into restoration efforts offers a promising pathway for sustainable HAB management in natural aquatic ecosystems. Future directions include experimentally testing select macrophytes for herbicide efficacy and HAB reduction.

Competitive Exclusion with Beneficial Phytoplankton for Lake Productivity and HAB Prevention

Ryan Philipsborn

Hydralife Solutions Inc., Denver, Colorado, United States

Live beneficial phytoplankton offers a natural, practical way to prevent harmful algae blooms and improve lake productivity in nutrient-rich waters. Hydralife Solutions provides live, concentrated beneficial freshwater phytoplankton in bulk. The phytoplankton consumes phosphate, ammonia, and nitrate throughout the growing seasons and, through competitive exclusion, replaces problematic cyanobacteria, filamentous algae, and nuisance algae with multi-species, nutrient-consuming, nutritional microalgae. The phytoplankton feeds zooplankton, fish fry, and the aquatic food web, while utilizing carbon dioxide to increase dissolved oxygen, which builds a healthier ecosystem. In waters used for irrigation, phytoplankton acts as an excellent soil biostimulant. Hydralife has reduced nutrients from elevated levels to low or barely detectable levels through entire warm seasons, eliminated a posted cyanobacteria advisory on a public pond, and delivered healthier, more attractive, and more productive waters. Managers report less nuisance algae, no new harmful algae blooms, less labor, and a reduction in water management costs. Hydralife delivers live concentrated phytoplankton direct to site. The phytoplankton complements aeration, beneficial bacteria, and existing water management programs. Hydralife Solutions is a developing company with encouraging field results, offering a biological option with positive ecological outcomes for limnologists to consider. Hydralife Solutions welcomes conversations about at-risk waters, trial sites, or collaboration with current water management programs.

Nature's Alien Covenant: The Little Algae That Eats Its Brother & Is Host to Its Parasite

Allen R. Place

UMCES@IMET, Baltimore, MD, USA

Nature is stranger than fiction, even science fiction. In the waters of Baltimore Harbor, a small single-cell plant that eats other algae, produces a toxin that makes holes in its prey, as well as any unlucky fish that would try to eat it. Nature's revenge on this single-cell plant is a parasite that burrows into the cell and eats its brain (nucleus) while producing 40 copies of itself. At the correct time, the parasite and its brethren burst out to find another host. This single-cell plant is *Karlodinium veneficum,* responsible for the 1997 fish kill attributed to *Pfiesteria piscicida,* which hosts its parasite *Amoebophrya sp.* ex *Karlodinium veneficum* (Syndiniales). For decades, high densities of the dinoflagellate *Karlodinium veneficum* have been associated with aquatic faunal mortalities worldwide. This small (~8–12 µm) athecate phytoplankton, common in coastal aquatic ecosystems, has a mixed nutritional mode, relying on both photosynthesis and phagotrophy for growth (mixotrophy). It is frequently present in relatively low cell abundance (10^{2}–10^{3} cells·mL$^{-1)}$ but is capable of forming intense blooms of (10^{4}–10^{5}cells·mL$^{-1)}$that are often associated with fish kills. A suite of toxic compounds (karlotoxins) have been characterized, both in the laboratory and in the field, with hemolytic, ichthyotoxic, and cytotoxic properties. These toxins have been shown to generate pores in membranes with desmethyl sterols and to increase ionic permeability, resulting in membrane depolarization, disruption of motor function, osmotic cell swelling, and lysis. The biological raison d'etre for karlotoxin production appears to be prey capture, but grazing deterrence is an additional advantage. This "cell from hell" has disappeared from Baltimore Harbor for the last 7 years and forces responsible for this will be addressed.

Reading the Rainbow: What Hyperspectral Signatures Reveal About Algal Identity and Health

Kaytee Pokrzywinski[1], *Chris Holland*[1], *Rance Hardison*[1], *Sachidananda Mishra*[2], *Dail Laughinghouse*[3], *Michelle Tomlinson*[4], *Richard Stumpf*[4]

[1]National Oceanic and Atmospheric Administration, National Centers for Coastal Ocean Science, Beaufort, NC, USA
[2]Consolidated Safety Services Inc., contracted to National Oceanic and Atmospheric Administration, National Centers for Coastal Ocean Science, Fairfax, VA, USA
[3]University of Florida, Institute for Food and Agricultural Sciences, Fort Lauderdale, FL, USA
[4] National Oceanic and Atmospheric Administration, National Centers for Coastal Ocean Science, Silver Spring, MD, USA

Harmful algal blooms threaten freshwater and marine resources, yet conventional multispectral sensors lack the resolution needed to distinguish community composition. Hyperspectral imagers (HSIs) capture subtle reflectance differences across hundreds of contiguous bands, offering the potential to differentiate key phytoplankton groups at high taxonomic levels and assess physiological status. A comprehensive laboratory-based spectral reference library will be presented, along with the capabilities and limitations of hyperspectral discrimination for HAB monitoring *in situ*. Using Resonon Pika visible-near-infrared HSIs, cultures spanning freshwater and marine phytoplankton taxa were imaged to assess class-level discrimination. Intra-class resolution was then evaluated within cyanobacteria and dinoflagellates, demonstrating that genus-level separation is achievable based on pigment-driven spectral features. To understand how environmental and management conditions alter these signatures, cultures were subjected to natural nutrient stressors and algicidal agents. Spectral shifts were paired with toxin analyses, revealing that nitrate limitation produced wavelength shifts while phosphate limitation drove reflectance intensity changes, both of which correlated with changes in toxin concentration in cyanobacteria. Additionally, non-algal particle spectra were characterized to identify potentially confounding spectral bands that may impact field applications for HABs. These results demonstrate HSI's capacity for taxonomic discrimination, health assessment, and evaluation of natural interference, which can be extrapolated to airborne, in-water, and spaceborne sensors for field-scale monitoring. This work advances HSI technology toward timely, actionable HAB intelligence for resource managers. Potential applications include UAS and satellite monitoring to assess HAB control efficacy, bloom status changes and associated toxin risks, and to identify species succession events.

Small Screens Tracking Big Blooms: How BloomSCOPE Can Redefine HAB Monitoring

Kaytee Pokrzywinski[1]*, Chris Holland*[1]*, Rance Hardison*[1]*, Richard Stumpf*[2]

[1]National Oceanic and Atmospheric Administration, National Centers for Coastal Ocean Science, Beaufort, NC, USA
[2]National Oceanic and Atmospheric Administration, National Centers for Coastal Ocean Science, Silver Spring, MD, USA

Harmful algal blooms threaten coastal ecosystems, public health, and regional economies, yet monitoring is constrained by the cost, expertise, and logistics of traditional microscopy. HABscope currently demonstrates a viable, low-cost mobile microscopy detection approach for *Karenia brevis*. While HABscope is providing data to inform the NCCOS Respiratory Irritation Forecast (RIF), it is limited to a single hardware platform (iPod Touch 6) that has been discontinued. BloomSCOPE extends this concept to modern smartphones through custom 3D-printed adapters paired with a computer vision model for the automated detection of *K. brevis* processed via cloud computing. BloomSCOPE separates data collection from analysis through a streamlined citizen science workflow. Volunteers capture standardized videos through a browser acquisition page and submit collected data via a Google Form, which triggers automatic ingestion into Microsoft Azure where the detection pipeline runs. A hybrid tracker links frame-by-frame detections to enumerate cells moving in and out of focus. Maximum tracked cells per frame are converted to densities using a Coulter Counter calibration curve and assigned a risk category consistent with HABscope. An administrative interface allows experts to review results before future public distribution and use in the NCCOS RIF. The model was trained on annotated culture and field samples spanning a range of cell densities. The model performed well with mAP50 of 92%, Precision and Recall scores of 94% and 85% respectively, and per-video enumeration correlations (R^2) between AI results and manual counts ≥0.89. Combined with its modular hardware and software architecture, the success of BloomSCOPE for *K. brevis*, positions it well for expansion to any phone model and HAB species across coastal and Great Lakes environments, with future models targeting *Pseudo-nitzschia*, *Alexandrium monilatum*, *Margalefidinium polykrikoides*, *Microcystis aeruginosa*, and *Dolichospermum* sp.

Calcined Oyster Shell (COS) and Tannic Acid as Alternative Flocculants for HAB Control

Anna Giulia Polli[1]*, Alana Espinosa*[2]*, Vincent Lovko*[2]

[1]Stony Brook University, Stony Brook, NY, USA
[2]Mote Marine Laboratory, Sarasota, FL, USA

Harmful algal blooms (HABs) caused by *Karenia brevis* are a recurring problem along Florida's Gulf coast. Flocculation and sedimentation, using coagulants or flocculants to bind and sink algal cells, is an effective strategy for removing HAB cells from the water column. However, a major obstacle to implementation of this technology is lack of EPA approval for the highly effective flocculant, polyaluminum chloride (PAC), as a minimum risk pesticide ingredient under FIFRA. Thus, we aimed to identify natural alternative flocculants that would effectively remove HAB cells and more readily gain EPA approval. We evaluated curcumin (C), tannic acid (T), biochar (B), and calcined oyster shell (O) for their ability to form flocs and remove *K. brevis* cells and toxins. Initial screening demonstrated that all compounds except biochar were able to form flocs, with treatments containing either tannic acid or calcined oyster shell most readily forming flocs. Application of TBC, TOC, and TOBC treatments effectively inactivated and removed cells, but flocculation results were obfuscated by curcumin's algaecidal properties and a lack of statistically significant differences between treatments. In a second study with applied treatments of O, TO, and TB, (all at 1:1 ratios and all @ 0.2g/L) all treatments significantly removed cells and decreased photosynthetic efficiency, but O and TB were significantly more effective than TO, suggesting that interaction between tannic acid and calcined oyster shell inhibited each other's individual flocculation ability and/or algaecidal properties. Sampling of pH during the second study revealed that TO and O raised pH, while TB lowered it. Further investigation is needed to determine the extent to which pH change explains the observed outcomes. Although change in pH is a limitation of tannic acid and calcined oyster shells, both are still promising as natural alternatives to PAC due to their effectiveness in cell removal and inactivation.

Assessing Inhalation Exposure Pathways for Microcystins: A Community Engagement Approach in Florida's DISPEL Cohort

Maizel D.[1], Casamassina A. B.[1], Smith L.[2], Cunill Flores J.[3], Swanson E.[4], Klatt N.[4], Gaston C. J.[5], Solo-Gabriele H.M.[6], Schaefer Solle N.[2,7], Caban-Martinez A.J.[2], ***Popendorf K.J.***[1]

[1] Department of Ocean Sciences, Rosenstiel School of Marine, Atmospheric and Earth Science, University of Miami
[2] Department of Public Health Sciences, Leonard M. Miller School of Medicine, University of Miami
[3] Abess Center for Ecosystem Science and Policy. Rosenstiel School of Marine, Atmospheric and Earth Science. University of Miami
[4] Medical School, University of Minnesota
[5] Department of Atmospheric Science, Rosenstiel School of Marine, Atmospheric and Earth Science, University of Miami
[6] Department of Chemical, Environmental, and Materials Engineering, University of Miami
[7] Department of Medicine, Leonard M. Miller School of Medicine, University of Miami

Cyanobacterial Harmful Algal Blooms (cyanoHABs) are an escalating public health concern in Florida, particularly near water bodies including Lake Okeechobee. While ingestion risks are well-documented, significant knowledge gaps remain regarding the health impacts of inhalation exposure to microcystins (MCs).

Within the framework of the Diversity and Innovation in Screening and Prevention of Exposure over the Long-term (DISPEL) to HABs project, a community engagement study based in a cohort of participants living and working near Florida's waterways, we analyzed environmental water samples provided by participants, alongside nasal swabs. Analysis was conducted via high-sensitivity mass spectrometry to characterize total MCs and specific congeners. We also extended our environmental monitoring to the participants' immediate surroundings by utilizing Ghostwipes to detect the presence of MC on solid surface surrounding waterbodies.

We measured the concentration of MC congeners in outdoor water samples (approximately 173) and nasal swabs (approximately 133) collected during the most recent three years of the ongoing study, from summer 2023 to summer 2026. Our findings confirm the presence of specific microcystin congeners in outdoor water (predominated by MC-LR) and nasal swabs (dominated by MC-LA), validating the existence of aerosolization processes leading to human inhalation exposure. This updates findings from our prior three years of the study (summer 2020 to summer 2023), which also found MC in both water and nasal swabs from adjacent geographic areas though not occurring within water and nasal samples from the same participants. Furthermore, from sampling with Ghostwipes, the detection of MCs on outdoor surfaces near waterbodies provides further utility for monitoring potential routes of exposure.

Monitoring Human Exposure To Aerosolized Microcystins From Harmful Algal Blooms Using Silicone Wristbands

*Casamassina A. B.[1], Smith L.E.[2], Chenail R.[1], Maizel D.[1], Cunill Flores J.M.[3], Christie J.[4], Gaston C. J.[4], Solo-Gabriele H.M.[5], Schaefer Solle N.[2,6], Caban-Martinez A.J.[2], **Popendorf K.J.[1]***

[1] Department of Ocean Sciences, Rosenstiel School of Marine, Atmospheric and Earth Science, University of Miami, Miami, FL, USA

[2] *Department of Public Health Sciences, Leonard M. Miller School of Medicine, University of Miami,* Miami, FL, USA

[3] *Abess Center for Ecosystem Science and Policy Rosenstiel School of Marine, Atmospheric, and Earth Science, University of Miami,* Miami, FL, USA

[4] *Department of Atmospheric Science, Rosenstiel School of Marine, Atmospheric and Earth Science, University of Miami,* Miami, FL, USA

[5] *Department of Chemical, Environmental, and Materials Engineering, University of Miami,* Miami, FL, USA

[6]*Department of Medicine, Leonard M. Miller School of Medicine, University of Miami,* Miami, FL, USA

Freshwater harmful algal blooms (HABs) of cyanobacterial phytoplankton communities release a host of congeners within the microcystin (MC) family which cause skin irritation as well as hepatotoxic and neurotoxic effects. Current monitoring methods for aerosolized MC are limited in duration and scale as they rely on powered air samplers run in the field and/or individuals' nasal swabs. Silicone wristbands evaluated in this study are low in cost and are user friendly. They expand monitoring through passive sampling of aerosolized MC for longer, continuous monitoring, which would result in a better representation of an individual's exposure to HAB MC from typical daily activities. Laboratory experiments were conducted to evaluate the efficacy of the wristbands regarding the limits of sensitivity and potential for quantitative analysis of aerosolized MC exposure. A culture of *Microcystis aeruginosa* was diluted to a gradient of concentrations and introduced to a bubbler system, which generated aerosolized MC toxins. The specific congeners identified in MC toxins captured on wristbands were similar to those captured on air filters, which were different from the primary congeners present in the water, as has previously been reported for aerosolized MC. These preliminary findings support the potential use of silicone wristbands as passive samplers for assessment of aerosolized MC exposure across a range of concentrations.

Congener Dependent Aerosolization of Cyanotoxins Determined by Their Structure and Aqueous Environment

Carlie Poworoznek[1], *Grace A. Young*[1], *Sharmila I. Thenuwara*[2], *Kelli Hummel*[2], *Jeremy J. Kodanko*[2], *Judy A. Westrick*[2], *Andrew P. Ault*[1]

[1]Univeristy of Michigan, Ann Arbor, MI, USA
[2]Wayne State University, Detroit, MI, USA

Cyanobacterial harmful algal blooms (cHABs) produce many toxins, including microcystins (MCs) and anabaenopeptins (ABPs). Over a hundred ABP congeners and several hundred MC congeners have been identified in cHABs, with toxicity varying based on the molecular structure of the congener. The metabolites pose risks not only through ingestion or dermal contact, but also through inhalation. They are emitted into the atmosphere within lake spray aerosol (LSA), which can travel and impact the health of the nearby community. Since inhalation often requires significantly less mass to be toxic, it is critical to understand toxin aerosolization at a fundamental physicochemical level. Prior work has shown the concentration in water of congeners is significantly different than the aerosol concentration. The likely cause is the selective partitioning to the air-water interface of rising bubbles as well as inter-congener interactions. However, the direct relationship between aerosolization efficiency, congener structure, and water conditions has not yet been systematically studied. Freshwater varies significantly more than seawater in ion concentration and pH, and thus, different water conditions must be considered to understand freshwater cHAB derived LSA. Herein, we examine how the structure and protonation state of MC and ABP congeners impact their ability to aerosolize in several different freshwater conditions. We also look at how the presence of other congeners, toxins, and organics impact the congeners' ability aerosolize, as well as the profile of the total aerosol produced. An aerosol generator was used to produce aerosol which was then studied with size-number instruments and collected on impactors. Water and aerosol samples were analyzed using liquid chromatography coupled to a triple quadrupole mass spectrometer. This work highlights the importance of studying cyanobacterial toxins on a per-congener basis in realistic water conditions to accurately predict the aerosolization potential and resulting health risks.

Co-occurrence of Freshwater and Marine Algal Toxins Across the Freshwater-marine Continuum of the San Francisco Estuary

***Ellen Preece*[1]*, Keith Bouma-Gregson*[2]*, Crystal Sturgeon*[2]*, Zoë Siman-Tov*[2]*, Leslie Troutman*[2]*, Tim Otten*[3]*, Raphael Kudela*[4]

[1]California Department of Water Resources, Sacramento, CA, USA
[2]U.S. Geological Survey, Sacramento, CA, USA
[3]Bend Genetics, Sacramento, CA, USA
[4]University of California, Santa Cruz, CA, USA

The transition zone between freshwater and marine environments in estuaries represents an understudied area where multiple harmful algal bloom (HAB) toxins can co-occur. In the San Francisco Estuary (CA) both freshwater cyanotoxins from upstream river systems and marine biotoxins can be transported and potentially accumulate along the freshwater-to-marine continuum. This study investigated spatial and temporal patterns of potentially toxic HAB genera and toxins between the Carquinez Strait and the confluence of the Sacramento and San Joaquin Rivers to understand toxin transport throughout this critical transition zone and assess risks to shellfish consumed by subsistence harvesters. We used three sampling methods: baited minnow traps for invertebrates from shoreline sites, discrete water grab samples, and passive solid phase adsorption toxin tracking (SPATT) samplers. Microcystins, domoic acid, and saxitoxins were analyzed in invertebrate tissue, water filters, and SPATT samplers. Water samples were analyzed for toxin biosynthesis genes using qPCR. Sampling occurred approximately monthly in winter (November-April) and bimonthly in summer (May-October) during 2024-2025 at four shoreline sites. Preliminary results found fewer detections of marine toxin producers *Alexandrium* and *Pseudo-nitzschia* occurred moving up-estuary into freshwater areas, while fewer detections of the freshwater toxin producer *Microcystis* occurred moving down-estuary towards marine waters. Toxins were detected more often in SPATT samples and invertebrate tissue than in discrete water samples, suggesting time-integrated sampling approaches capture toxin presence more reliably than water grab samples. Multiple invertebrate species including shrimp, crab, and crayfish accumulated toxins across the salinity gradient. Domoic acid concentrations remained below safe consumption thresholds while microcystin concentrations sometimes exceeded recommended levels. This research demonstrates connectivity between different estuary regions and potential transport processes that expand algal toxin impacts spatially. These findings highlight the importance of monitoring multiple toxin types in understudied estuarine transition zones.

From Monitoring to Management: Preparing to Dredge a Cyanobacteria Hotspot in the Delta

Ellen P Preece[1]*, Tim Otten*[2]*, Paul Bedore*[3]*, Jeff Wingfield*[4]*,Janis Cooke*[5]*, Marc Beutel*[6]*, Katherine Cook*[2]

[1]Department of Water Resources, Sacramento, CA, USA
[2]Bend Genetics, LLC, Sacramento, CA, USA
[3]Robertson-Bryan, Inc, Rancho Cordova, CA, USA
[4]Port of Stockton, Stockton, CA, USA
[3]Central Valley Water Quality Control Board, Rancho Cordova, CA, USA
[3]UC Merced, Merced, CA, USA

Cyanobacteria harmful algal blooms (CHABs), often comprised of *Microcystis*, are a major water quality issue in the hydrologically complex Sacramento-San Joaquin Delta, California. To inform an innovative sediment dredging approach for CHAB management, this study established baseline conditions by comparing proposed dredge sites with non-dredge reference sites and a previously dredged location prior to planned dredging operations in October-November 2026. Comprehensive site characterization was conducted using water, sediment, and SPATT samples collected monthly during 2025 across dredge and non-dredge zones. Samples were analyzed for *Microcystis* and total cyanobacteria seed stock, microcystins, nutrients, and molecular markers using qPCR and DNA sequencing. Sediment flux experiments quantified nutrient release under varying oxygen conditions, and sediment cores revealed vertical distribution patterns of cyanobacteria and toxins. Water column *Microcystis* exhibited seasonal variability with peak abundances in July-August across all site categories. Proposed dredge zones showed consistent *Microcystis* seed stock presence with no non-detects, while other sites had variable detection rates including 36% non-detects at non-dredge sites. Sediment flux experiments revealed that a previously dredged site had consistently lower phosphate and ammonia flux rates from sediments to overlying water compared to undredged shallow sites, indicating dredging decreased potential for internal nutrient loading. Sediment cores from undredged areas showed surface enrichment of microcystins with concentrations declining with depth. Baseline characterization revealed spatial differences in *Microcystis* seed stock persistence and nutrient flux between dredge and non-dredge zones. The consistently detectable seed stock in proposed dredge areas and the previously dredged site's significantly lower nutrient release rates provide supporting evidence that targeted sediment removal may effectively reduce factors promoting CHAB development, informing this innovative management approach.

Building Tennessee's Harmful Algal Bloom Response Program

***Jessica Rader**, Andrea Jaegge*

Tennessee Department of Environment and Conservation, Nashville, TN, USA

Harmful Algal Blooms (HABs) are an emerging public and animal health concern in Tennessee, requiring coordinated, science-based strategies to improve detection, response, and risk communication. This presentation outlines the development of Tennessee's HABs Response Program, an interdisciplinary initiative designed to strengthen statewide preparedness through enhanced awareness, cross-sector collaboration, and applied research. The program brings together the state's public health agency, environmental agency, academic institutions, veterinary experts, public water suppliers and other key stakeholders to address the complex ecological and health challenges posed by HAB events. Core efforts include increasing public awareness of HAB risks, establishing communication pathways among agencies, improving surveillance and response capacity, and fostering research partnerships to better understand impacts on human and animal health. By integrating expertise across sectors, Tennessee's approach aims to create a proactive framework for managing HAB incidents, supporting informed decision-making, and reducing health risks associated with exposure. This case study highlights both the opportunities and challenges of building a coordinated HAB response infrastructure in a state with diverse freshwater resources and growing environmental pressures. Tennessee's evolving model may offer practical insights for other states seeking to strengthen HAB preparedness and response through collaboration, education, and evidence-based management.

Western Lake Superior Cyanobacterial Blooms: A Review and Synthesis of the Science

Sam R. Blackburn[1], ***Kaitlin L. Reinl***[2], *Hilary Dugan*[1]

[1]Center for Limnology, University of Wisconsin-Madison, Madison, WI, USA
[2]Rensselaer Polytechnic Institute, Department of Biology, Troy, NY, USA

Cyanobacterial blooms are an emerging concern in Lake Superior. To date, most blooms have been clustered in the southwestern arm of the lake and have been non-toxic. These blooms are typically localized and ephemeral, making it very difficult to identify causes; however, various monitoring efforts as well as discrete studies have produced data that can be leveraged to identify drivers of blooms and typical primary productivity in Lake Superior's nearshore. To support managers and researchers in their efforts to identify the primary drivers of blooms in Lake Superior, we have harmonized data from Western Lake Superior, inflowing tributaries, and the St. Louis River Estuary across multiple agencies. We combine analysis of this dataset with evidence from peer-reviewed literature and agency reports to identify external forces influencing bloom development and nearshore productivity (i.e., chlorophyll-a), including water temperature changes, nutrient dynamics, large discharge events, and in-lake hydrodynamics. We also highlight future research needs to expand the knowledge of cyanobacterial blooms in Lake Superior.

Cyanobacterial Harmful Algal Blooms and Cyanotoxins in Freshwater Systems in North Carolina, US

***Ling Ren*[1], *Colleen Dongarra*[2], *Elizabeth Fensin*[1], *Mark Vander Borgh*[1], *and Tammy Hill*[1]**

[1]Division of Water Resources, North Carolina Department of Environmental Quality, Raleigh, NC, USA
[2]Department of Environmental Sciences & Engineering, Gillings School of Global Public Health, University of North Carolina at Chapel Hill, Chapel Hill, NC, USA

Recurring cyanobacterial blooms have been increasingly documented in freshwater lakes, reservoirs, and rivers across North Carolina (NC), with the bloom season appearing to start earlier and last longer. In response to growing scientific, public, and media attention surrounding harmful algal blooms (HABs), the NC Department of Environmental Quality Division of Water Resources implemented a statewide report-and-track system, known as the algal bloom dashboard. The dashboard plays an important role in timely reporting, investigation, and documentation of HAB events statewide. It also serves as a public interface for submitting questions and concerns related to HABs, most of which are related to potential health impacts associated with cyanotoxins. This presentation will provide data-driven analysis that include: 1) characterization of spatial and temporal distributions of cyanobacterial HABs based on dashboard records from 2020-2025; 2) assessment in distributions of cyanotoxins, primarily microcystins, in major NC freshwaters from 2017-2025; 3) evaluation of correlations between cyanobacteria presence and cyanotoxins; and 4) identification of physical and chemical conditions associated with toxin production. We will also discuss the key challenges encountered in statewide HAB monitoring and responses and outline the future directions to strengthen management strategies concerning cyanobacterial blooms and associated toxins.

Phytoplankton Community Assemblage Surrounding a *Heterosigma akashiwo* Bloom According to Multi-channel Fluorometry, Enumeration, and Metabarcoding

Emily Richardson[1], *Silvia Angles*[1], *Dan Killam*[2], *Katy O'Donnell*[3], *Ariella Chelsky*[2], *David Senn*[2], *Daphne Gille*[1], *Brian A. Bergamaschi*[3]

[1]California Department of Water Resources, West Sacramento, California, USA
[2]San Francisco Estuary Institute, Richmond, California, USA
[3]US Geological Survey, Sacramento, California, USA

To document phytoplankton community assemblages, researchers and managers across the globe use a variety of methods that may produce conflicting results. Common sampling methods include (i) phytoplankton enumeration, (ii) 18S and 16S ribosomal RNA metabarcoding, and (iii) in situ multi-channel fluorescence measurement. Each of these three sampling techniques has advantages and disadvantages. Phytoplankton enumeration can provide taxonomic identifications down to the species level for many organisms within the sample; however, the method is costly, prone to human error and sample degradation, and results may be biased towards certain size classes based on technique. Metabarcoding is a more sensitive detection method, but it can only provide relative phytoplankton abundance and identification to the species level is highly dependent on reference database completeness. Many in situ multichannel fluorometers can quantify chlorophyll pigmentation (a common proxy for phytoplankton biomass) along with that of accessory pigments, the relative abundance of which can permit, allowing users to estimate the broad composition of phytoplankton groups. Multi-channel fluorometry is cost effective and provides rapid results, however, as with all optical instruments, calibration protocols and certain environmental conditions can impact data quality. As phytoplankton monitoring programs work to improve sampling methods used to characterize community composition in addition to abundance, comparisons between the methods are important for the hindcasting of data quality and understanding the suitability of newer techniques. Here, we describe phytoplankton community composition in the San Francisco Bay before, during, and after the *Heterosigma akashiwo* bloom of 2022 using these three methods. We then compare how results may differ depending on the chosen method, identifying possible causations. This analysis may help researchers understand the validity of their historical community composition data, as well as inform phytoplankton monitoring strategies, aiding the selection of one or more sampling techniques to best suit their study questions.

Communicating the Socioeconomic Impacts of Harmful Algal Blooms: Enhancing an Interactive StoryMap Resource

Mindy Richlen[1], *Kali Horn*[1], *Stephanie Moore*[2], *Brittany King*[3], *Quay Dortch*[3], *Donald Anderson*[1], *Marc Suddleson*[3]

[1]Woods Hole Oceanographic Institution, Woods Hole, MA, USA
[2]NOAA Northwest Fisheries Science Center, Seattle, WA, USA
[3]NOAA National Centers for Coastal Ocean Science, Silver Spring, MD, USA

Millions of dollars are spent annually to address harmful algal bloom (HAB) impacts across public health, fisheries, tourism, and bloom management, with public health impacts representing the largest economic burden. However, the full socio-economic cost of HABs remains difficult to quantify due to incomplete data, different methodologies, and limited representation of indirect and community-level effects. Ongoing investments in socio-economic research are helping to address this gap, but an alternative approach was needed to convey the profound impacts that HABs have on our nation. To improve the accessibility and integration of existing information, in 2020 NOAA developed the interactive StoryMap *"Hitting Us Where It Hurts: The Untold Story of Harmful Algal Blooms,"* which compiles documented economic and social impacts from HAB events. Since the map was first developed we have expanded and refined this StoryMap to improve its value for diverse audiences. The platform enables users to explore these impacts by location and filter case studies by harmful algal group (e.g., *Alexandrium*, *Karenia*, CyanoHABs) as well as community impact category (e.g., fisheries, tourism, property values). Each mapped entry provides a concise summary based on peer-reviewed literature or reports, with links to original sources for further information. We will highlight core functionalities, describe efforts to improve consistency and coverage, and identify gaps in available data and impact representation. The session will be interactive, with a focus on soliciting audience input on additional case studies, data sources, and features to enhance the platform's scope and usability. Community contributions will guide ongoing development of this resource. By strengthening this tool, we aim to support the integration of HAB socio-economic impacts into research and management, and communicate the societal importance of sustained support for HAB science, mitigation, and control programs.

Characterizing Phytoplankton Dynamics Within Cyanobacteria-Dominated Lake Mattamuskeet, NC

Mary Kate E. Rinderle*, Mingying Chuo, Hans W. Paerl, Nathan S. Hall*

Department of Earth, Marine and Environmental Sciences, Institute of Marine Sciences, University of North Carolina at Chapel Hill, Morehead City, North Carolina, USA

Located in the Lake Mattamuskeet National Wildlife Refuge on the Albemarle-Pamlico Peninsula, Lake Mattamuskeet is the largest natural lake in North Carolina at over 40,000 acres. Historically, this shallow lake (average depth of 1.2 m) was dominated by submerged aquatic vegetation (SAVs) and was an important feeding ground for migratory birds along the Atlantic Flyway. Today, the lake is devoid of SAVs and is instead dominated year-round by small, filamentous cyanobacteria. High phytoplankton biomass (~100 μg chl a L^{-1}) creates steep light attenuation that prevents re-establishment of SAVs. During summer months, cyanobacterial biomass consistently exceeds 200 μg chl a L^{-1} and is dominated *Raphidiopsis raciborskii* and *Umezakia ovalisporum*. Consequently, Lake Mattamuskeet has experienced some of the nation's highest concentrations of the cyanotoxin cylindrospermopsin (6.6 μg L^{-1}). Our research group monitored the lake over a 2.5-year period to characterize phytoplankton community dynamics and identify factors promoting cyanobacterial proliferation. Although the relative abundance of phytoplankton classes shifted seasonally, cyanobacteria remained dominant throughout the year. Nutrient availability also shifted seasonally, highlighted by an early spring ammonium pulse (up to 105 μM NH_4^+). Together, temperature and nitrogen form and availability strongly influenced community structure and cyanobacterial abundance. Ongoing research utilizes microscopy and metagenomics to further characterize genus-specific shifts in community composition. Beginning this summer, additional work will investigate the role of diazotrophy in nitrogen cycling and the impact of nutrient stoichiometry on toxin concentrations within the lake.

The Fate of *Karenia brevis* Cells in PAC-modified Kaolinite Clay and PAC-modified Biochar

Grace Robinson*, Vincent Lovko*

Mote Marine Laboratory, Phytoplankton Ecology Research Program, Sarasota, FL, USA

Blooms of Karenia brevis (red tide) cause numerous ecological, health, and economic impacts in the state of Florida, spurring the development of numerous mitigation technologies. One well-studied method for mitigating K. brevis is with application of a polyaluminum chloride (PAC) modified kaolinite clay (MCll) that captures cells in a floc network and sinks them to the sediment. Although MCII shows high efficacy for cell removal (>90% within hours), our previous work demonstrates that many cells may remain alive in the settled floc. Additionally, MCII does not sufficiently adsorb brevetoxins. In other work, we are evaluating the efficacy of PAC-modified biochar for K. brevis mitigation. Our results suggest that modified biochar removes cells equally as well as MCII, but with the added advantage of toxin adsorption. However, preliminary tests also indicate that live cells remain in the modified biochar floc, though less than in MCII. Thus it is important to examine the fate of cells in the floc to fully understand the capabilities of each product. Live, viable cells remaining in the settled floc could potentially act as a seed population for subsequent blooms if the material becomes resuspended and the cells are able to escape the floc. The goal of this study is to determine the fate of cells in both MCll and modified biochar flocs by assessing live vs dead cells using a novel differential staining method combining neutral red and SYTOX green. In preliminary studies, we found that at least 92% of cells in MCll clay were still alive at both T5 and T48, while at least 86% of cells in modified biochar were alive at the same timepoints. In this presentation, data from ongoing studies with both MCll and modified biochar examining the fate of cells in floc will be presented.

The Ability of Microplastics to Disrupt Zooplankton (*Daphnia pulex*) Grazing on the Toxic Cyanobacterium, *Microcystis*

Ian Robinson*, Christopher J. Gobler*

School of Marine and Atmospheric Sciences, Stony Brook University, Southampton, NY, USA

Plastic pollution is an increasing concern in freshwater ecosystems, where microplastic particles (< 5 mm) are now ubiquitous and have the potential to interfere with key trophic interactions. Studies have demonstrated that microplastics can impair zooplankton grazing, yet their effects on grazer-mediated control of cyanobacterial harmful algal blooms (CHABS) remain poorly constrained. In particular, it is unclear whether microplastic exposure alters the ability of zooplankton to consume bloom-forming cyanobacteria across the range of algal densities that characterize pre-bloom and bloom conditions. *Daphnia pulex*, a small-bodied Daphnid, can play a central role in regulating phytoplankton communities and has been shown to suppress cyanobacterial harmful algal blooms formed by *Microcystis*, a genus responsible for toxic blooms and drinking water disruptions worldwide. This study investigated how microplastic exposure influences the clearance rate of *Daphnia pulex* using both cultured and bloom populations of *Microcystis*. By manipulating algal concentrations to reflect pre-bloom and bloom scenarios, this study assessed how algal abundance modifies the extent to which polystyrene microplastics (10,000 beads L^{-1}) may interfere with *Daphnia pulex* grazing. During the experiments, microplastics consistently and significantly reduced *D. pulex* clearance rates on *Microcystis* at low algal density (12.5 µg cyanobacterial chlorophyll *a* L^{-1}), while no significant effect on grazing was observed at higher algal densities ($\geq$25 µg L^{-1}). Given these findings microplastic interference at low algal densities may weaken early grazer control, potentially allowing cyanobacterial populations to escape suppression and develop into CHABs.

Effect of Increasing Water Temperature on Mixotrophs' Ingestion Rate and Toxin Content

Zabdiel Roldan Ayala*, Marta Sanderson, Juliette Smith, Nicole Millette*

Virginia Institute of Marine Sciences, William & Mary, Gloucester Point, VA, USA

Most harmful agal blooms (HAB) in United States's coastal waters are mixotrophic protists that acquire nutrients using photosynthesis and phagotrophy. Previous studies have suggested that photosynthetic activity may be positively tied with production of toxins. A potential reason for this is that mixotrophs can acquire more energy through photosynthesis to produce toxins in contrast to phagotrophy. Yet, recent research regarding mixotrophs and climate change has observed that mixotrophic plankton become more phagotrophic as temperature increases. However, there is a lack of literature on how phagotrophic ability can affect toxin content in toxin producing mixotrophs. Increasing temperature can cause for a mixotroph to be more phagotrophic which could potentially affect its toxin content. Here we looked at how increasing temperature affects both ingestion rates and toxin content in two toxin producing mixotrophs. We hypothesized that toxin producing mixotrophs will decrease their toxin content as their ingestion rate increase because previous research has suggested that photosynthesis may be necessary for toxin production. We measured the ingestion rates of *Alexandrium monilatum* and *Karenia brevis* on bacteria under three different temperatures using modified prey removal experiments. In addition, we collected samples for extracellular and intracellular toxins on day 0 and day 7 for analysis. We observed a general increase in ingestion rates with temperature for both species. *K. brevis* and *A. monilatum* showed different responses in terms of toxin content. *K. brevis*' toxin content increased with temperature while temperature had no relationship with *A. monilatium*'s toxin production. This suggests that phagotrophic activity may not be related to the content in HABs.

Process Based Modeling of HABs. Old Fashioned or Timely Tools?

Jodi L. Ryder[1], *Todd E. Steissberg[1], Emily J. Summers[2], Kunal K. Rathore[3], Hailey P. Suk[4], and Isaac J. Mudge[5]*

[1]US Army Engineer Research and Development Center Environmental Lab, Vicksburg, MS, USA
[2]US Army Engineer Research and Development Center Coastal and Hydraulics Lab, Vicksburg, MS, USA
[3]Oregon State University Environmental Sciences, Corvalis, OR, USA
[4]US Army Engineer Research and Development Center Cold Regions Research Lab, Hanover, NH, USA
[2]US Army Corps of Engineers New Orleans District, New Orleans, LA, USA

In the age of data driven modeling, is there still a place for process based environmental models in water management? The answer is an overwhelming yes. Process based models offer incredible capability to characterize algal dynamics in the context of complex meteorological and hydrological trends. Moreover, they allow us to probe relationships between algal parameters and human influences on water resources such as land use, operating, or engineered changes. In this talk we will discuss lessons learned from several applications of the numerical model CE-QUAL-W2 to inland HABs that offer insight into the benefits of utilizing a modular suite of parameterized biogeochemical processes when modeling HABs themselves or their impacts on water quality. Through these examples, we will discuss recent updates to CE-QUAL-W2 to better represent specific features of cyanobacterial blooms versus the classic high productivity eutrophication condition. We will discuss specific study objectives well suited for the complexity and effort involved in deploying a process based approach and identify some examples where data driven models might excel. Finally, we will demonstrate how they can be used in a hybrid approach to leverage the benefits of both approaches.

Inferring Nearshore Cyanobacteria Presence in Sentinel-2 Imagery Using offshore Sentinel-3 Observations in Lake Champlain

Wilson Salls[1]*, Leslie DeSimone*[2]*, Tyler King*[3]

[1]USGS New York Water Science Center, Troy, NY, USA
[2]USGS New England Water Science Center, Northborough, MA, USA
[3]USGS Water Mission Area, Boise, ID, USA

As satellite remote sensing products mature, adoption into cyanobacteria monitoring and forecasting programs continues to progress, but key limitations persist. The Ocean and Land Colour Instrument (OLCI) aboard the Sentinel-3 satellite platform effectively monitors large inland waterbodies and can distinguish cyanobacteria from other phytoplankton. However, its coarse spatial resolution (300 meters) limits nearshore observations, which are key in assessing risks to human health from cyanotoxin exposure during recreation. While the MultiSpectral Instrument (MSI) aboard the Sentinel-2 platform offers finer spatial resolution (20 meters) capable of nearshore observation, it cannot discern cyanobacteria from other phytoplankton, offering only measurement of chlorophyll-a. Thus, neither platform alone supports nearshore cyanobacterial detection.

This study presents a method to infer nearshore cyanobacteria presence. The method leverages both Sentinel-3 OLCI and Sentinel-2 MSI to infer the presence of cyanobacteria near shore, potentially filling this critical data gap. The method assumes that, if cyanobacteria are observed offshore with OLCI, chlorophyll-a observed by MSI in the adjacent nearshore area likely indicates cyanobacteria presence. Since OLCI provides daily observations, any MSI observation (occurring every five days) is accompanied by a same-day OLCI observation. Offshore cyanobacteria presence was determined using the OLCI-derived Cyanobacteria Index (CI) and nearshore chlorophyll-a magnitude was assessed using the Maximum Chlorophyll Index derived from same-day MSI imagery. To assess method performance, nearshore cyanobacteria inferred from satellite imagery will be compared to an existing field survey dataset indicating presence or absence of cyanobacteria blooms at roughly 200 beach sites along Lake Champlain. If successful, this method could be explored for other OLCI-resolvable waterbodies to produce a broader nearshore cyanobacteria indicator.

Sentinel-2 Satellite Detection of Elevated Chlorophyll-a as an Early Indicator Proxy for Freshwater Algal Blooms

*Megan Coffer[1], Blake Schaeffer[2], **Wilson Salls**[3], Tyler King[4], Scott Ducar[5], Daniel Wiltsie[2] and Michael Paul[1]*

[1]U.S. Environmental Protection Agency Office of Water, Durham, NC
[2]U.S. Environmental Protection Agency Office of Applied Science and Environmental Solutions, Durham, NC
[3]U.S. Geological Survey New York Water Science Center, Troy, NY
[4]U.S. Geological Survey Water Resources Mission Area, Boise, ID
[5]U.S. Geological Survey Idaho Water Science Center, Boise, ID

Monitoring harmful algal blooms (HABs) is critical, yet field campaigns are sparse. To augment these efforts, we assessed whether satellite remote sensing can deliver water quality information that aligns with field benchmarks. We compared chlorophyll-a estimates from the Sentinel-2 satellite series with in situ measurements from the U.S. EPA's National Lakes Assessment (NLA), a statistically robust survey of lakes, ponds, and reservoirs across the contiguous United States that samples near the surface and lake centers where satellite retrievals are most reliable. Although chlorophyll-a is not a direct HAB metric, elevated biomass serves as an early indicator of potential HABs and a triage tool for prioritizing field resources. For waterbodies coincident with the 2017 and 2022 NLA surveys, we extracted Sentinel-2 observations and estimated chlorophyll-a using six algorithms prioritized in a recent literature review. All NLA and Sentinel-2 data are publicly available, and the algorithm code will be uploaded to GitHub for replicability. We first compared Sentinel-2 and NLA chlorophyll-a distributions to evaluate whether satellites indicated similar waterbody condition as the NLA with multiplicative mean absolute error of 1.93 and bias of 0.94. A critical assumption in satellite validation studies is that field measurements represent truth; however, both models and field measurements contain errors and neither provides a perfect result. We then assigned satellite-derived Good, Fair, or Poor categories following NLA methods and contrasted category counts between 2017 and 2022. Results demonstrate that satellite observations approximate NLA patterns at national and ecoregional scales and can reproduce NLA-style condition categories. While our focus on chlorophyll-a reflects current Sentinel-2 limitations and the absence of a specific HAB metric, future efforts can extend to more diagnostic indicators. Collectively, these findings support integrating Sentinel-2 into HAB monitoring frameworks as an early biomass indicator. This approach can inform routine assessments for targeted sampling and mitigation planning.

Microbial Dynamics & Microcystin Biodegradation Across CyanoHAB Conditions in Lake Okeechobee, Florida

Paisley S. Samuel*, Jose V. Lopez*

Department of Biological Sciences, Nova Southeastern University, Fort Lauderdale, FL, USA

Toxin-producing cyanobacterial harmful algal blooms (cyanoHABs) have been recorded in Floridian freshwater systems for decades. However, these cyanoHABs appear to be increasing in frequency and intensity in recent years. Lake Okeechobee (Lake O) is one such watershed ecosystem suffering by this rise in cyanoHAB events—especially in blooms dominated by the cyanobacterium *Microcystis aeruginosa*. There is also a diverse microbial community within Lake O and heterotrophic bacteria are suggested to play a role in the development and persistence of cyanoHABs, while some photosynthetic picoplankton (e.g. *Cyanobium sp.*) may stabilize non-bloom periods. Still, there remains a lack of detailed understanding in the functional interactions between *Microcystis sp.* and heterotrophic bacteria in Lake O, particularly in the biodegradation of the microcystins produced during these cyanoHABs. This study serves as a preliminary profile of the microbial community composition and toxin-biodegradation potential in response to cyanoHAB conditions in Lake O. A subset of previously collected and processed DNA samples was used to generate extensive metagenomic libraries which were then sequenced using next-generation shot-gun metagenomic sequencing technologies. The samples were categorized based on bloom condition (pre-bloom, peak bloom, no bloom, and post bloom) then taxonomically and functionally analyzed based on this categorization using a combination of bioinformatic tools including R, KBASE, and Unix/Linux-based tools. Understanding these interactions can help provide valuable insights into how the microcystins of these toxic blooms are naturally broken down, which could, in turn, aid in potentially mitigating and managing the harmful effects of these cyanoHABs in Lake O.

Negative Impacts to Shellfish Aquaculture Industry from Oxidized Byproducts of Phytoplankton

Marta P. Sanderson[1]*, Samantha Glover*[2]*, Amy Menegay*[3]*, Bethanie Edwards*[4]*, Ryan B. Carnegie*[1]*, and Juliette L. Smith*[1]

[1]Virginia Institute of Marine Science, William & Mary, Gloucester Point, VA, USA
[2]Oyster Seed Holdings, Inc., Hudgins, VA, USA
[3]Lamont-Doherty Earth Observatory of Columbia University, Palisades, NY, USA
[4]Department of Earth and Planetary Science, University of California, Berkeley, Berkeley, CA, USA

The sustainability of shellfish aquaculture production on the US East Coast is highly dependent on successful hatchery production. In 2020, a troublesome new syndrome was presented in young oyster larvae at a hatchery in Maine, resulting in production failures which decreased seed output. Affected larvae were delayed in development and exhibited signs of digestive obstruction. Preliminary in-hatchery experiments, coupled with lipidomic analyses, demonstrated a link between the pathology and oxidized phytoplankton byproducts, i.e., oxylipins and polyunsaturated aldehydes (PUAs), in hatchery water. Similar symptoms have since been observed in hatcheries across the East Coast and are reoccurring yearly, demonstrating the syndrome's persistence. Phytoplankton are rich in polyunsaturated fatty acids (PUFAs), which make them a high-quality food source for oyster larvae. However, some phytoplankton activate an oxidative cascade, transforming PUFAs into smaller compounds in response to stress, such as grazing. The resulting bioactive PUAs and oxylipins have the potential to impact larvae through direct consumption or aqueous exposure. New research on the effects of one PUA, decadienal (DDA), and two oxylipins, hydroxy eicosapentaenoic acid (HEPE) and hydroperoxy hexadecatrienoic acid (HpHTrE), on oyster larval fertilization and development will be presented along with results of mitigation and removal experiments. Through partnerships between industry and academia, this research strives to characterize and increase awareness on this new but persistent hatchery production issue and to identify effective mitigation technology with the goal of enhancing overall hatchery production.

Assessing Nitrogen-Acidification Multi-Stressor Influences on *Pseudo-nitzschia* Distribution in Long Island Sound (NY/CT)

***Julia M. Sandke*[1,3]**, *Rachel Spera*[2], *Georgie E. Humphries*[1,3,4], *Emma Rosser*[3], *Penny Vlahos*[2], *Julie Granger*[2], *Craig Tobias*[2], *Dianne I. Greenfield*[1,3]

[1]School of Earth and Environmental Sciences, Queens College, City University of New York, Flushing, NY, USA
[2]Department of Marine Sciences, UCONN Avery Point, University of Connecticut, Groton, CT, USA
[3]Advanced Science Research Center at the Graduate Center, City University of New York, New York, NY1, USA
[4]Earth and Environmental Sciences, Graduate Center, City University of New York, New York, NY, USA

The Long Island Sound (LIS) estuary receives excess nitrogen (N) inputs from urbanization (waste and stormwater outfalls), groundwater and riverine discharge, atmospheric deposition, and runoff. N-loading influences the development, distribution, and persistence of harmful algal blooms (HABs), and multiple HAB-forming genera have been reported in LIS and surrounding embayments, particularly toxigenic dinoflagellates. N-enrichment also accentuates regional ocean and coastal acidification (OA). Yet, little is known regarding how and if combined excessive N loads and acidification interact to influence HABs in LIS. Reports of the domoic-acid producing diatom *Pseudo-nitzschia* along the U.S. east coast have occurred since 2016, with recent sightings including Narragansett Bay (Rhode Island) and LIS (New York and Connecticut). Water sampling during 2025 confirmed a broad distribution of *Pseudo-nitzschia* within LIS. This study emphasizes *Pseudo-nitzschia* distribution and its connection with co-occurring N and OA conditions. Sampling sites (2025) ranged in distance from wastewater and stormwater inputs, as well as (2026) areas near recreational shellfish harvesting and fishing access points. Field data spans LIS shorelines from NYC to eastern CT, as well as mid-channel data collected by the Connecticut Department of Energy and Environmental Protection. This presentation highlights 2025 and 2026 field observations in LIS, including water quality, phytoplankton community composition (microscopy and molecular techniques, emphasizing *Pseudo-nitzschia*), chlorophyll *a*, nutrients, carbonate measurements, and toxin analysis. Results will inform regional stakeholders and managers on shellfish safety and water quality, and the development of HAB risk maps for LIS.

Evaluating Sources of Uncertainty in Domoic Acid Bloom Simulations Across California Coastal Waters

Marco Sandoval-Belmar[1], *Fayçal Kessouri*[1,2], *Raphael M. Kudela*[3], *Martha Sutula*[2], *Jayme Smith*[2], *Clarissa Anderson*[4], *Daniele Bianchi*[1]

[1]Department of Atmospheric and Oceanic Sciences, University of California, Los Angeles, Los Angeles, California, USA
[2]Southern California Coastal Water Research Project, Costa Mesa, California, USA
[3]Ocean Sciences Department, University of California Santa Cruz, Santa Cruz, California, USA
[4]Scripps Institution of Oceanography, University of California, San Diego, La Jolla, CA, USA

Domoic acid-producing harmful algal blooms (HABs) caused by *Pseudo-nitzschia* are a recurring threat to coastal ecosystems, marine mammals, fisheries, aquaculture, and public health along the U.S. West Coast. Observations indicate that upwelling, climate variability, nutrient ratios, and terrestrial nutrient inputs can influence bloom development and toxin production, but their relative importance remains difficult to separate using observations alone. Here, we use mechanistic modeling to investigate the physical and biogeochemical drivers of domoic acid (DA) bloom risk in California waters. Building on a three-dimensional (3D) regional ocean biogeochemical model with a mechanistic DA module developed for the Southern California Bight, we use 3D model output to force a reduced box model and test how key sources of uncertainty in physiological parameters and DA-production formulations influence bloom dynamics and toxin production. Together, extended simulations across a broader California coastal domain and a reduced box model will allow us to examine DA responses along the wider California coast while isolating key mechanisms and parameter sensitivities that are difficult to diagnose from 3D simulations alone. Analyses focus on identifying where the model captures observed spatial toxin patterns and which parameter assumptions most strongly affect estimates of bloom frequency, severity, and duration above risk thresholds. By linking high-resolution regional simulations with targeted sensitivity experiments, this work advances the interpretability of regional HAB models and lays the groundwork for DA risk assessment along the California coast under changing climate and nutrient-loading conditions.

Ozone Nanobubbles Outperform Hydrogen Peroxide Through Rapid Cell Disruption and Photosynthetic Dysfunction in *Microcystis aeruginosa*

Asma Sattar*[1,2]*, Diego Sánchez*[1]*, Andre Luna-Magdaleno* [1]*, Bruce E. Rittmann*[2]*, Sergi Garcia-Segura*[1]*, Jesús Morón-López*[1]*

[1] Nanosystems Engineering Research Center for Nanotechnology-Enabled Water Treatment, School of Sustainable Engineering and the Built Environment Arizona State University Tempe, AZ, USA

[2] Biodesign Swette Center for Environmental Biotechnology, Arizona State University, Tempe, AZ, USA

Cyanobacterial harmful algal blooms (HABs) pose escalating threats to freshwater ecosystems, drinking water supplies, and public health, demanding rapid and scalable mitigation solutions. Conventional oxidants such as hydrogen peroxide (H_2O_2) are commonly explored for bloom control but are constrained by slow reaction kinetics and diminished performance in complex aquatic environments. This study evaluates ozone nanobubbles (O_3-NBs) as an emerging advanced oxidation approach for cyanobacterial mitigation, with emphasis on improving oxidant stability, delivery efficiency, and reactivity in freshwater matrices. Nanobubble generation in synthetic freshwater produced stable concentrations of approximately 10^8 particles per milliliter, providing a high surface-area-to-volume ratio that improves oxidant-cell contact. Under equivalent treatment conditions, O_3-NBs achieved approximately 50% reduction in *Microcystis aeruginosa* abundance within 1-3 hours at low ozone concentrations (≤1.5 ppm), substantially outperforming H_2O_2, which required 6-9 hours and approximately fourfold higher concentrations (~6 ppm) to achieve comparable inhibition. Mechanistic investigation revealed that O_3-NBs treatment induced extensive cellular disruption, as evidenced by the release of intracellular organic matter and pronounced changes in cell size distributions. Elevated antioxidant enzyme activity further confirmed intensified oxidative stress at the cellular level. By contrast, H_2O_2 produced a markedly milder cellular response, suggesting a less efficient mode of action for cyanobacterial inactivation. Collectively, these findings indicate that O_3-NBs provide a more efficient oxidative treatment than H_2O_2 under the tested conditions, combining rapid cyanobacterial inactivation with controlled ozone delivery at comparatively low doses. This technology represents a promising, scalable intervention for HABs mitigation in drinking water sources and recreational water bodies affected by increasingly severe and frequent bloom events.

Using Short-Lived Radium Isotopes to Investigate Vertical Transport in Captiva Blue Hole

Kelly Sauter[1]*, Elisa Prodhomme*[2]*, Emma J. Bullock, Ph.D.*[3]*, Emily R. Hall, Ph.D.*[3]

[1]University of Connecticut, Groton, CT, USA
[2]Nova Southeastern University, Fort Lauderdale, FL, USA
[3]Mote Marine Laboratory, Sarasota, FL, USA

Karenia brevis blooms form offshore and are hypothesized to develop at depth, making offshore benthic inputs a potential nutrient source during early bloom development. One potential hotspot for such inputs is submerged sinkholes, where fractures in subsurface confining layers may provide pathways for submarine groundwater discharge (SDG) to supply dissolved constituents to these environments. Captiva Blue Hole is a sinkhole on the West Florida Shelf whose geomorphology partially isolates the deeper water column from the fluid dynamics above. Higher nutrient concentrations have been observed within the hole than in surrounding shelf waters. Whether these nutrients remain isolated at depth or are transported upward determines their influence on algal species like *K. brevis* in overlying waters. This study collected vertical profiles of temperature, dissolved oxygen (DO), short-lived radium isotopes, and nutrients from Captiva Blue Hole in March, May, and July 2026. In May and July, a distinct boundary layer formed between approximately 35 and 47 m depth. Higher radium and nutrient concentrations were observed with increasing depth, along with decreasing temperature and DO. A 1-D diffusion model using the vertical radium gradients from May and July produced eddy diffusivity coefficients (k_z) of 1.35 m^2/day and 0.317 m^2/day, respectively. Applying k_z to nutrient gradients produced upward NH_4^+ and PO_4^{3-} flux estimates, with greater fluxes in May than in July. A steady-state mass balance of the bottom layer (47-50 m) identified an unknown ^{223}Ra source in May and July of 1.07×10^5 DPM/day and 1.30×10^5 DPM/day, respectively, potentially indicative of SDG inputs. These results suggest additional benthic inputs beyond sediment diffusion and indicate that vertical eddy diffusion may transport dissolved constituents introduced at the bottom of Captiva Blue Hole toward overlying coastal waters.

Tracking Cyanobacterial Bloom Dynamics in New York City Public Parks using rRNA-based Methodologies

Erin Schneider[1,2], Christopher Ward[3,4], Riley Ralph[3], Emma Rosser[2], Georgie Humphries[1,2,5], Dianne I. Greenfield[1,2]
[1]School of Earth and Environmental Sciences, Queens College, City University of New York, Flushing, NY, USA
[2]Advanced Science Research Center at the Graduate Center, City University of New York, New York, NY,USA
[3] Department of Biological Sciences, Bowling Green State University, Bowling Green, OH 43403, USA
[4] Department of Estuarine and Ocean Sciences, University of Massachusetts Dartmouth, New Bedford, MA, USA
[5] Earth and Environmental Sciences, Graduate Center, City University of New York, NY, USA

New York City's (NYC) green spaces, including the public park system, span over 30,000 acres (14% of the city). NYC parks draw millions of visitors annually, with the majority of visits occurring between May and September, which coincides with summer conditions that promote cyanobacterial blooms in freshwater lakes and ponds. Cyanobacteria harmful algal bloom (cHAB) genera, including *Microcystis* and members of the Nostocales clade, have been detected in The Lake (Central Park, Manhattan) and Prospect Lake (Prospect Park, Brooklyn). The popularity of NYC parks, combined with the susceptibility of their lakes to cyanobacterial blooms, makes it essential to efficiently characterize cHABs in these areas to identify potential public health hazards. Here, we assess the bloom dynamics of a variety of cHAB species in some of NYC's most high-traffic freshwater systems using taxa-specific ribosomal RNA (rRNA)-based methodologies. Cell quantification data are paired with corresponding nutrient (nitrogen, phosphorus) and physical water quality conditions. Summer (2026) sampling in Central Park, Prospect Park, and Flushing Meadows Park (Queens) evaluates water temperature, pH, light, dissolved oxygen, nutrients, and relevant cHAB toxin levels (microcystins and anatoxins). Multiple rRNA techniques, including fluorescence *in situ* hybridization (FISH) and two 96-well plate sandwich hybridization assay (SHA) protocols, are applied and evaluated for cHAB cell detection and quantification. Ultimately, this research will enhance our ability to expedite alerts for cHAB events and improve public safety and awareness for NYC park guests.

How Will Projected Ocean Acidification Affect Growth and Toxigenicity of *Protoceratium reticulatum*, a Yessotoxin Producer?

Megan Schulz[1,2]*, Misty B. Peacock*[1]*, Vera L. Trainer*[2]*, William P. Cochlan*[1,3]

[1]Salish Sea Research Center: Northwest Indian College, Bellingham, Washington, USA
[2]Olympic Natural Resources Center: University of Washington, Forks, Washington, USA
[3]Estuary and Ocean Science Center: San Francisco State University, San Francisco, California, USA

Ocean acidification is anticipated to have effects throughout marine ecosystems, including phytoplankton's growth rates and toxigenicity. A harmful dinoflagellate commonly found in coastal waters, Protoceratium reticulatum, produces yessotoxin, a lipophilic phycotoxin. While yessotoxin is not known to impact human health, it has been identified as a factor contributing factor to 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. To investigate the effect of ocean acidification on this dinoflagellate, a local isolate from Blaine, Washington was grown at three ecologically relevant pH values: 8.0 (control), 7.8, and 7.6. In addition to the pH stressor, these cultures were grown under macronutrient-replete and -deficient conditions, making this multi-stressor experiment multifactorial to replicate current and projected ocean conditions. We will present the toxin production rates, including relative proportion of dissolved versus particulate toxin fractions which may alter the risk to shellfish under future, more acidified conditions. These experiments will improve our understanding of how toxin-producing species react to anticipated climate stressors and the potential impacts of climate change on shellfish survival and harvest potential.

Liposomal Curcumin, a Novel Approach to HAB Mitigation

***William Scott*[1]**, *Cynthia Heil*[1], *Emily R. Hall*[1], *Al Place*[2], *Devin Burris*[1], *Jessica Frankle*[1], *Susan Launay*[1], *Sanjana Varanasi*[1]

[1]1Mote Marine Laboratory, Sarasota, Florida USA
[2]Institute of Marine and Environmental Technology, University of Maryland Center for Environmental Sciences, Baltimore, MD

Curcumin (*Curcuma longa*), a phytochemical derived from turmeric, has been shown to be efficient in reducing both cells and brevetoxins of the Florida Red Tide dinoflagellate *Karenia brevis*. However, curcumin's low solubility in deionized water (1.34 ± 0.02 mg L^{-1}) is the primary factor limiting its use for HAB mitigation. We have examined the efficacy of curcumin encapsulated into lecithin-based liposomes as a delivery system for HAB mitigation, which allows the curcumin to be taken up by mixotrophic dinoflagellates directly. Liposomes are vesicles consisting of a phospholipid bilayer and are used extensively in targeted medical delivery systems. In prior laboratory studies utilizing *K. brevis*, the minimum effective curcumin dose was reduced from 5 mg L^{-1} (solubilized in ethanol) to 1 mg L^{-1} with liposome encapsulation. Liposomal curcumin was effective in mitigating other HAB species such as *Alexandrium monilatum* and *A. tamarense*, however, these armored dinoflagellates require a higher minimum effective dose (5 mg L^{-1}) compared to *K. brevis* and additional exposure time in benchtop experiments, likely due to differences in cellular structure and permeability. The efficacy of this liposomal curcumin dose was confirmed in a replicated 18-liter aquaria experiment which examined the influence of liposomal curcumin on both *A. monilatum* and *A. tamarense* cells and toxins, water quality, nutrient and saxitoxin concentrations (via ELISA), and photosynthetic efficiency (PAM). The minimum effective dose for cell removal was tenfold lower than the 50 mg L^{-1} required for curcumin solubilized in ethanol. The results showed that a minimum effective dose of 5 mg L^{-1} reduced both toxin levels and cell density of both species by up to 82.07% by 48 hours after treatment addition. Liposomal delivery of mitigation compounds thus represents a promising targeted delivery system that is broadly applicable to multiple HAB species and potentially multiple HAB mitigation compounds.

Combating HABs Using Equilibrium Modulation

Nicholas Shannon[1]*, Vince Lovko*[1]*, George Philippidis*[2]*, Kruti Shukla*[3]*, David Fung*[3]

[1]Mote Marine Laboratory, Sarasota, Florida, United States
[2]USF, Tampa, Florida, United States
[4]EMF, Ottawa, Canada

HAB mitigation is a necessity in protecting marine life and human health. The three main types of mitigation (chemical, physical, and biological) all directly impact the water column by changing the water itself through adding chemicals or particulates to the system. These mitigation tactics can also cause negative effects on other marine life and long-term impacts are generally unknown. Equilibrium Modulation (EM) is a novel technology that uses weak (<1W) electromagnetic pulses to alter the quantum state of water, reducing viscosity and increasing the amount of oxygen that passes into the water across the air-water interface. The devices are small (~2' dia.), solar powered, low maintenance, and efficient, with one unit able to affect ≥50 acres. The increased oxygenation and peak pH moderation reduce the impact of hypoxic water on grazers, which can help mediate blooms and aid in the conversion of organic forms of nitrogen (that *K. brevis* can utilize) to simpler forms (NO_x) more readily used by non-harmful phytoplankton such as diatoms. EM devices deployed in freshwater systems showed significant changes to water quality by promoting nitrification. Previous studies show EM devices function in saltwater mesocosm systems to shift the ammonia-nitrate equilibrium in favor of nitrate and improve recovery time for non-HAB algae. These higher nitrate levels can promote the growth of diatoms to outcompete red tide blooms for nutrients in the water. In this study, EM devices are being deployed at multiple sites in canals along Longboat Key, Florida. Each site is sampled biweekly for water quality, phytoplankton community composition, and pulse amplitude modulated fluorometry. We expect to see shifts towards higher nitrate levels, an increase in the biodiversity of phytoplankton, and an improved recovery time after a red tide bloom. We are currently collecting data in this ongoing experiment; and available data will be presented.

Advances in Classification of Harmful Algae in Inland Waters Using Hyperspectral Remote Sensing Data

Samantha Sharp[1], *Alicia Cortés*[2], *Alexander L. Forrest*[3], *Liane S. Guild*[4], *Yufang Jin*[5], *Jeremy Kravitz*[6], *Lisl Lain*[7], *Carl Legleiter*[8], *Sifiso Mpapane*[7,9], *Rabelani Mudzielwana*[10], *Ryan E. O'Shea*[11,12], *Humeshni Pillay*[7,9], *Glynn Pindihama*[13], *S. Geoffrey Schladow*[3], *Marié Smith*[7,9] *and Juan Torres-Pérez*[4]

[1]NASA Postdoctoral Program Fellow, NASA Ames Research Center, Moffett Field, CA, USA
[2]University of Granada, Granada, Spain
[3]Tahoe Environmental Research Center, University of California, Davis, Davis, CA, USA
[4]Biosperic Science Branch, NASA Ames Research Center, Moffett Field, CA, USA
[5]Department of Land, Air and Water Resources, University of California, Davis, CA, USA
[6]Pixxel Space Technologies, El Segundo, CA, USA
[7]Council for Scientific and Industrial Research, Cape Town, South Africa
[8]Observing Systems Division, U.S. Geological Survey, Denver, CO, USA
[9]Department of Oceanography, University of Cape Town, Cape Town, South Africa
[10]Department of Geography and Environmental Sciences, University of Venda, Thohoyandou, South Africa
[11]Science Systems and Applications Inc., Lanham, MD, USA
[12]NASA Goddard Space Flight Center, Greenbelt, MD, USA
[13]Environment & Health Research Unit, South African Medical Research Council (SAMRC), Cape Town, South Africa

Phytoplankton community composition is an important measure of inland water body aquatic health. Shifts in phytoplankton populations towards cyanobacteria dominance are a concern due to the potential for toxin production. Therefore, tools for monitoring phytoplankton and cyanobacteria communities are important for management of these water resources. Increasingly available hyperspectral data from recent and upcoming satellite missions will allow for the development and testing of phytoplankton and cyanobacteria identification algorithms. This study evaluates the performance of the phytoplankton classification algorithm Phytoplankton Detection with Optics (PHYDOTax) and the cyanobacteria classification algorithm Spectral Mixture Analysis for Surveillance of Harmful Algal Blooms (SMASH). We apply these tools to inland waters in California, United States, and the Greater Cape Floristic Region, South Africa. PHYDOTax classifications are compared to in situ phytoplankton community composition determined from phytoplankton pigment measurements. SMASH cyanobacteria classifications are compared to cyanobacteria community measurements from microscopy data. We found promising performance of PHYDOTax applied to our in situ spectroradiometer measurements but less encouraging results of PHYDOTax applied to satellite- and airborne-based hyperspectral imagery despite attempts to improve atmospheric correction. We found limited success of SMASH using the original spectral library and improved classification when using a site-specific spectral library we developed from in situ spectroradiometer measurements. These initial studies illustrate the potential of hyperspectral data for classifying phytoplankton and cyanobacteria populations in inland waters and also identify areas where further research is needed.

Revisiting Aphanizomenon Flos-aquae, What Do We Actually Know About Its Physiology?

Cody Sheik,[1,2]*, Kaela Natwora*[1]*, Abby Smason*[1]*, Maya Casey* [1]

[1]Large Lakes Observatory, Duluth, MN, USA
[2]Biology Department, University of Minnesota Duluth, Duluth, MN, USA

Aphanizomenon flos-aquae blooms have become a common occurrence in Lake of the Woods and in the harbors of Duluth, MN, and Superior, WI that empty into Lake Superior. *Aphanizomenon flos-aquae* is visually identifiable by its characteristic trichome shape and is often seen with differentiated heterocyst cells. In Lake of the Woods, nitrogen depletion was thought to be a driver of *Aphanizomenon flos-aquae*'s success as a blooming species, as it was assumed it could fix nitrogen. However, metatranscriptomic studies during a bloom season found no *Aphanizomenon flos-aquae* nitrogenase genes expressed, despite nitrogen fixation rates correlating with the bloom. Subsequent metagenomic analysis confirms that *Aphanizomenon flos-aquae* genomes lack the full suite of nitrogenase genes (*nifHDK*) required for a functional nitrogenase. This begs the question of what's going on with this globally distributed organism. Here, we'll dive into the genomes of our and publicly available *Aphanizomenon flos-aquae* to describe the functional traits of these organisms, the potential reasons for the lack of nitrogenase genes in our Lake of the Woods strains, and the implications for bloom dynamics.

TAML/Sodium Percarbonate Synergism for Degradation of *Microcystis* and Microcystin

Vic Simons[1]*, Nicholas Onikian*[1]*, Catherina Fagan*[1]*, Christopher Sibley*[1]*, Terrence J. Collins*[2]*, Jennifer Toyoda*[1]

[1]Mote Marine Laboratory, Sarasota, Florida, USA
[2]Carnegie Mellon University, Pittsburg, PA, USA

The toxic cyanobacteria *Microcystis* aeruginosa is well-known for both the visible slicks it forms on ponds and the toxins it produces which lead to fish kills and poisoned water supplies. Many treatment strategies target this growing problem by either killing cells or destroying toxins, however an ideal method would tackle both issues. Hydrogen peroxide – which can be dosed in the form of sodium percarbonate (SPC) – has a long history of success at killing harmful algae like *Microcystis*, however research has shown it has little effect on toxins by itself. NewTAML catalysts (NTs) activate hydrogen peroxide and improve its oxidative activity on targets, including toxins like Microcystin-LR; we hypothesized that by combining these two compounds, both cells and toxins could be removed from freshwater effectively. We performed a flask test to compare the performance of 59.3 mg/L sodium percarbonate with NewTAML (NT 3) at three concentrations (250 nM, 500 nM, and 1 µM). In the first set of experiments, flasks were dosed with TAML and SPC simultaneously; in the second set of experiments, flasks were first dosed with SPC, then TAML was added 48-hours later. After simultaneous application, cell health decreased in all SPC treatments but rebounded in the presence of TAML; additionally, toxins were reduced only in TAML-treated conditions, however they rebounded over the course of the experiment alongside cell health. After serial application, cell health decreased immediately in all SPC-treated flasks (YII values below ~0.03), then toxins decreased to below 0.06 mg/L within 4-h of TAML addition and never rose above 0.1 mg/L for the rest of the experiment. These data show NT 3 enhances toxin removal compared to SPC alone, and serial application leads to greater decreases in both toxins and cell health, enabling less chemical use with greater HAB control response. Future work will test HAB control in natural blooms and toxicity testing on non-target native species. We gratefully acknowledge financial support from the U.S. Harmful Algal Bloom Control Technologies Incubator.

Management Decision Triggers in Drinking Water Reservoirs: Phosphorus Sequestration To Prevent HABs

Andrew Z Skibo

Amarûq Environmental Services & ClearChannelVM, Missoula, Montana, USA

[The successful mitigation of harmful blue-green (Cyanophyta) algae blooms (HABs) presents a significant challenge to the management of our nation's water open water storage resources, requiring timely monitoring of basic water quality parameters and biological indicators of HAB activity. An effective monitoring program allows for the coordination of proactive mitigation activities to occur duringearly-stage blooms prior to the potential formation of HAB-produced water pollutants such as cyanotoxins, taste, and odor compounds. Traditional monitoring techniques such as spot or grab sampling or term deployment of data loggers are frequently hindered in efficacy by factors such as collection frequency, sample count (n) relative to water body size and/or volume, and the timely return of laboratory-quantified data. The human detection threshold of many common taste and odor compounds is very low, thus the proactive mitigation of dormant benthic and early active, or incipient phase, HAB colonies is a benefit in reducing overall potential concentrations of their pollutant byproducts. Utilizing near-real time (nRT) water quality monitoring through the deployment of multiparameter sonde arrays equipped with remote telemetry collecting base water quality parameters and phycocyanin quantitation, in conjunction with quarterly spot sampling, allowed for the effective implementation of Management Decision Trigger-based nutrient mitigation through timely application of a lanthanum-modified bentonite (LMB) and dormant algal colony mitigation through the application of granular Sodium Carbonate peroxyhydrate. Treatment results and post-mitigation effort water quality monitoring data from the 2026 water season will be discussed.]

Eliminating Decades of Copper Sulfate Use Through Ultrasonic Mitigation at Syracuse Water Authority

Rob Slingerland

SonicPure LLC, Torrance, CA, Untied States

For over forty-four consecutive years, the Syracuse Water Department managed cyanobacteria blooms in the one-hundred-twenty-one-million-gallon Woodland Reservoir using significant annual applications of copper sulfate. These chemical treatments, often exceeding fifteen thousand pounds per year, were labor-intensive and provided only temporary suppression followed by rapid algal rebounds. Seeking a sustainable and cost-effective alternative for this unfiltered drinking water source, the department transitioned to a combined strategy of high-precision ultrasonic technology and diffused aeration. This presentation evaluates the operational performance and financial impact of ultrasonic units in successfully eliminating the need for chemical algaecides from two thousand nineteen through two thousand twenty-five. By targeting blue-green algae with specific resonant frequencies, the system disrupts cellular buoyancy and prevents the formation of surface blooms without releasing harmful toxins. Longitudinal data show that cell counts of dominant cyanobacteria, including *Chroococcus* and *Cyanobium*, decreased by over ninety percent compared to historical averages. Furthermore, the initial capital investment of twenty-six thousand dollars achieved a full return on investment in less than two years by eliminating the sixteen-thousand-dollar annual chemical budget. The success of this implementation demonstrates that ultrasonic intervention provides a reliable, chemical-free defense for municipal water authorities while improving water clarity, dissolved oxygen levels, and regulatory compliance. This case study offers a scalable model for other open-water reservoirs facing similar environmental and public health challenges.

Phenology of cHAB Species and Toxin Production in a Northern Freshwater Estuary

Abigail Smason[1,2]*, Christopher Filstrup*[2]*, and Cody Sheik*[1]

[1]Large Lakes Observatory, University of Minnesota Duluth, MN, USA
[2]Natural Resources Research Institute, University of Minnesota, MN, USA

The occurrence of cyanobacterial blooms in Lake Superior and the Duluth-Superior harbor has increased over the last 15 years. Putative toxin-producing genera, such as *Microcystis* and *Dolichospermum*, have been visually observed in isolated harbor blooms, raising concerns about their potential to bloom extensively under the right conditions and to move into Lake Superior. These blooms are also difficult to predict because of their ephemeral nature. To better understand the phenology of cyanobacteria in this system, we sampled 15 stations routinely from May to October of 2025 for water chemistry and microbial community composition as well as six bloom-prone sites to characterize cyanobacterial taxa blooming in this heterogeneous environment. During our study, one visible bloom occurred on October 3rd and was localized to a small inlet in the harbor. Interestingly, water quality parameters measured at the bloom-prone sites across the estuary the day before showed increased concentrations of the bloom indicators chlorophyll and phycocyanin, as well as a large spike in the cyanotoxin microcystin. The bloom had a mixed community structure comprising *Aphanizomenon*, *Microcystis*, and *Dolichospermum*, along with other less commonly observed bloomers in this region. Individual cyanobacterial taxa cliques show patterns of changing dominance across regions in the estuary throughout the summer, suggesting shifting microhabitats for cyanobacteria like the *Aphanizomenon* genus. Additionally, the abundance of bloomers across the estuary indicates hotspots that harbor these genera throughout the season until conditions allow for a bloom. Our monitoring data are providing new insights into the distribution and abundance of important cyanobacterial genera in the largest tributary to Lake Superior and suggest that molecular-based monitoring efforts may provide key information to understand how cyanobacteria in the tributary may move and proliferate into Lake Superior in the future.

Predicting Microcystin Concentrations During a Winter *Microcystis* Bloom in Agricultural Water Using Imaging Flow Cytometry

Jaclyn E. Smith[1,2,3]*, Jennifer L. Wolny*[2]*, James A. Widmer*[4]*, Yakov Pachepsky*[1]

[1]Environmental Microbial Food Safety Laboratory, United States Department of Agriculture – Agricultural Research Service, Beltsville, MD, USA

[2]Office of Applied Microbiology and Technology, Human Foods Program, US Food and Drug Administration, College Park, MD, USA

[3]Environmental Science and Technology Department, University of Maryland, College Park, MD, USA

[4]Department of Food Science and Technology, University of Georgia, Athens, GA, USA

Harmful cyanobacterial blooms (CyanoHABs) are an increasing threat to freshwater systems used in agriculture, such as those used for livestock watering and irrigation, especially during the summer. However, winter bloom events in agricultural waters remain poorly understood. This study investigated whether a high-throughput imaging flow cytometer (FlowCam), combined with machine learning–assisted taxonomic classification (EcoTaxa), could reliably predict microcystin concentrations during a winter bloom in an agricultural pond in Georgia, USA. Between December 2022 and March 2023, 72 samples were collected and analyzed, producing 166,783 particle images. Of these, 78,982 phytoplankton images were validated and grouped into 33 taxonomic categories utilizing EcoTaxa. Over the sampling period, microcystin concentrations ranged from 1.97 to 744 µg/L, with a February peak coinciding with elevated levels of *Microcystis aeruginosa*. Principal component analysis showed that PC1 and PC2 accounted for 98% of the variability in phytoplankton communities. Multiple linear regression models accurately predicted microcystin concentrations using cyanobacteria taxa as predictors for both particle-based (R^2 = 0.977) and area-based biomass (R^2 = 0.986) metrics. Sensitivity analysis identified *M. aeruginosa* as the most influential variable in predicting microcystin levels. The minimal differences observed between particle-based and area-based models suggest that simple particle counts, FlowCam's primary output, may serve as an effective indicator for CyanoHAB monitoring. Following validation, EcoTaxa achieved an average annotation accuracy of 76%, highlighting its capacity as a semi-automated monitoring tool. Overall, these results demonstrate that imaging flow cytometry, paired with machine learning-based classification, can rapidly assess cyanobacteria communities and associated toxin risks in agricultural water systems.

Regional Multi-Toxin Bioaccumulation in Coastal Bivalves Across the Southern California Bight

***Jayme Smith*[1]**, *Alle A.Y. Lie*[1], *Samuel Lillywhite*[1], *Raphael M. Kudela*[2], *Kendra Negrey*[2], *Melissa Peacock*[3], *Martha Sutula*[1], *Alvine C. Mehinto*[1]

[1]Southern California Coastal Water Research Project, Costa Mesa, CA
[2]University of California, Santa Cruz, Santa Cruz, CA, USA
[3]Northwest Indian College, Bellingham, WA, USA

The land–sea interface is increasingly recognized as a region where freshwater- and marine-derived harmful algal bloom (HAB) toxins can co-occur within coastal food webs. However, the prevalence and magnitude of multi-toxin exposure across regional scales remain poorly resolved. This study evaluated the occurrence, concentrations, and co-occurrence of HAB toxins in bivalve tissues across the Southern California Bight, a large, urbanized coastal region spanning over 400 km of coastline from Point Conception to the U.S.–Mexico border. Mussels and oysters were collected from multiple sites during winter, spring, and summer 2024 and analyzed for domoic acid (DA), total microcystins (MCYs), and yessotoxin (YTX). DA was consistently detected at low concentrations across seasons and sites but remained well below the U.S. Food and Drug Administration regulatory threshold. In contrast, MCYs were frequently detected in both bivalve types, with exceedances of the California health-based guidance threshold observed in 12.5% of mussel samples and 40.6% of oyster samples, particularly during summer. YTX was also commonly detected, especially in mussels, though always at low concentrations. Co-occurrence of multiple toxins within individual samples was widespread, with two or more toxins detected at most sites and up to three toxins observed in a single sample. These findings indicate that bivalves may act as vectors of concurrent exposure to multiple HAB toxins with distinct biological effects. The results suggest that multi-toxin exposure is a persistent feature of coastal systems at the land–sea interface, even outside of major bloom events. Expanding monitoring and assessment frameworks to better account for co-occurring toxins may improve evaluation of risks to ecosystem and human health.

Multidisciplinary Approach to a Cross-regional Problem: *Dinophysis* and DSP Toxicity

Juliette L. Smith[1]*, Lisa Campbell*[2]*, Christopher Gobler*[3]*, Jonathan R. Deeds*[4]*, Stephanie Moore*[5]*, Michael Brosnahan*[6]*, Pearse McCarron*[7]*, Neil Harrington*[8]*, Vera Trainer*[9]

[1]Virginia Institute of Marine Science, Gloucester Point, VA, USA
[2]Texas A&M University, College Station, TX, USA
[3]Stony Brook University, Stony Brook, NY, USA
[4]US Food and Drug Administration Human Foods Program, College Park, MD, USA
[5]NOAA Fisheries, Northwest Fisheries Science Center, Seattle, WA, USA
[6]Woods Hole Oceanographic Institution, Woods Hole, MA, USA
[7]National Research Council Canada, Halifax, Nova Scotia, Canada
[8]Jamestown S'Klallam Tribe, Sequim, WA, USA
[9]Olympic Natural Resources Center, University of Washington, Forks, WA, USA

Species of *Dinophysis*, known to produce toxins that cause diarrhetic shellfish poisoning (DSP), have threatened the safety of shellfish consumers in Asia and Europe for decades. In 2008, DSP was first recognized as a human health threat in the USA. The presence of toxin-contaminated shellfish, from *D. ovum,* led to a harvesting closure along the coast of Texas, a product recall, and introduced the need to monitor and manage *Dinophysis* spp. and DSP. Shellfish with toxin loads that exceeded the US FDA regulatory limits, from *D. acuminata* and *D. fortii*, have since been found in Washington, New York, and Massachusetts. Precautionary closures have occurred in Maine due to a novel toxin, dihydro-dinophysistoxin-1 (dihydro-DTX1) with unknown toxicity, produced by *D. norvegica*. Chesapeake Bay and the larger DELMARVA region (Delaware, Maryland, and Virginia) also harbor toxin-producing species of *Dinophysis*; however, the region provides contrast as a relatively new area of concern, with evidence of an approaching tipping point. Research funded by the National Competitive ECOHAB program advanced the science and management related to *Dinophysis* HABs and DSP by 1) developing a network of IFCBs that were optimized for monitoring *Dinophysis* spp. blooms; 2) investigating environmental and biological drivers of *Dinophysis* spp. blooms and toxicity; 3) developing informative markers for species identification and investigation of physiological responses among *Dinophysis* spp.; 4) investigating relative toxicity for the new dihydro-DTX1 congener and developing methods for management; and 5) partnering with State, Tribal, and industry groups to address management needs, disseminate results, and aid regional management programs. Advancements and outcomes will be discussed as a means to identify future research and technology needs in the management of DSP in the USA.

An Innovative HPLC methodology for the Detection of a Suite of Chlorophylls and Carotenoids by Mass Spectrometry and/or Photodiode Array Detection

Zacharias J. Smith[1], *David E. Berthold*[2], *H. Dail Laughinghouse*[2], *Cathleen Hapeman*[1]

[1] USDA Agricultural Research Service, Hydrology and Remote Sensing Laboratory, 10300 Baltimore Ave, Beltsville, MD, USA
[2] Agronomy Department, Fort Lauderdale Research and Education Center, Institute of Food and Agricultural Sciences, University of Florida, 3205 College Avenue, Davie, FL, USA

Chlorophylls and carotenoid analyses are important in freshwater and marine systems as they are used to quantify algal biomass and to determine ecological composition. The methods used for these analyses have often been limited to spectrophotometric detection, with some methods incorporating chromatographic separation. Mass spectrometric detection offers improved sensitivity, selectivity, and structural information compared to spectroscopy, but requires a full redesign of the separation system as previous chromatographic separations used solvent systems that are incompatible with mass spectrometry. The separation developed here used a YMC C30 “Carotenoid Column” with a novel mobile phase and elution scheme to separate a suite of algal pigments. Detection can be performed using a photodiode array (PDA) alone, or in conjunction with mass spectrometry (MS). The system was able to separate dozens of pigments from complex mixtures, provide structural information for analytes without standards as the MS detector method was developed to be capable of ‘non-target’ analysis, allowing for the identification of isomers of known compounds and the assignment of putative molecular weights for unknown analytes. Method detection limits using only the PDA were below 1 ppb for all analytes, while the MS could detect many analytes in the parts-per-trillion range. We report for the first time that echinenone (CAS 432-68-8) is actually a pair of isomers, which may have significant implications for photosynthesis due to this carotenoid’s importance in the orange carotenoid protein. We also report the detection of new chlorophyll b analogs that we putatively believe may be hydroxylated or dehydroxy derivatives.

A State-of-the-Science Discussion of Freshwater PSP Toxins: Do They Pose a Significant Risk to Human Health?

Zacharias J. Smith[1]*, Kandis M. Arlinghaus*[2]*, Cathleen Hapeman*[1]

[1] USDA Agricultural Research Service, Hydrology and Remote Sensing Laboratory, 10300 Baltimore Ave, Beltsville, MD, 20705
[2].Oak Ridge Institute for Science and Education (ORISE), National Ocean Service, National Oceanic and Atmospheric Administration, 331 Fort Johnson Road, Charleston, SC, USA

Freshwater PSP toxins (PSPTs) have been studied since the 1960's. However, they have received relatively little attention outside of marine environments, with other cyanotoxins (such as the microcystins) receiving significantly more research focus. We have assembled the entire historical record of environmental freshwater PSPT research and will present a summary of our findings. We report on the suite of known PSPTs (84 congeners) and the likelihood of others, including the likely presence of novel PSPTs in the environment. Additionally, we there gaps in the existing toxicological assessment of PSPTs (including those related to acute exposure) and how application of the marine safety framework may put freshwater consumers at risk. In addition to problems with the existing toxicological profile, we discuss multiple toxicity endpoints that have generally not been considered in marine risk assessment, but are hugely important to a freshwater risk assessment, such as oxidative stress in the brain and liver. All of this data is only available from animal models, necessitating the incorporation of additional safety factors to consumption thresholds. We will discuss the broad incorporation of STX ELISA in PSPT analysis in the U.S., and how it is likely that its ubiquitous use has underestimated toxin prevalence in freshwater environments. We will present evidence that even when toxins are detected, the concentrations reported do not provide any meaningful value towards assessing risk, and that in many of its current use cases the assay is not fit for purpose. In isolation, these issues are concerning but do not constitute an emergency, but when the uncertainties are assessed in combination we believe that there may be considerable risks to human health that must be assessed in more detail.

Then & Now: Transforming HAB Science and Management Through NOAA Competitive Research

Bruna Fernanda Sobrinho*, Maggie Broadwater, Quay Dortch, Brittany King, Felix Martinez, Sarah Pease, and Marc Suddleson*

NOAA, NOS, NCCOS, CRP, Silver Spring, MD, USA

NOAA's HAB Competitive Research was first authorized in 1998 with the passage of the Harmful Algal Bloom and Hypoxia Research and Control Act (HABHRCA 1998), which has since been re-authorized in 2004, 2014 and 2019. Programs addressing HAB research to management, based on multiple community reports, include Ecology and Oceanography of HABS (ECOHAB), Monitoring and Event Response for HABs (MERHAB), Prevention Control, and Mitigation of HABs (PCMHAB), Social, Cultural, and Economic Assessment of HABs (SEAHAB), and HAB Event Response (HABER). Projects have varied in size and scale from regional-scale or cross-regional studies involving large teams of investigators conducting coordinated, multi-disciplinary field programs to targeted laboratory or field studies that address fundamental questions related to the occurrence of HAB events and their management. Until 2010, the ECOHAB program was funded by multiple federal agencies and all NOAA HAB competitive research has advanced the missions of agencies at all levels. Special oral sessions at this meeting, entitled "Then & Now: Transforming HAB Science and Management through NOAA Competitive Research" will summarize the research by region or species, focusing on the management benefits and future research needs. This is the first step in developing a special issue of a journal summarizing NOAA-funded HAB research. In this poster the funding will be analyzed according to region, subject, HAB species, and regional vs. targeted projects. An initial outline of the special issue will be presented.

NoHABs®: Carbon-Based Multi-Stage Process for Rapid Remediation of Cyanobacterial Harmful Algal Blooms

Leonard Sonnenschein

Sonnenschein Institute, Boca Raton , Florida, United States

Harmful algal blooms driven by cyanobacteria threaten freshwater ecosystems, water quality, and public health worldwide through nutrient enrichment, especially bioavailable phosphorus from agricultural runoff and wastewater. The Sonnenschein Institute developed NoHABs, a proprietary, environmentally safe, carbon-based treatment that rapidly neutralizes existing algae and toxins, cuts off phosphorus and nitrogen supplies, prevents regrowth, and provides sustained protection without introducing secondary pollutants. The process employs a clear three-stage protocol. Stage one applies a carbon-based activator that doubles dissolved oxygen levels, enhances microscopic carbon capture by beneficial diatoms, and initiates natural nutrient cycling to starve cyanobacteria. Stage two blocks additional phosphorus inflows from tributaries and runoff, neutralizes and removes active blooming algae, and suppresses germination of resting akinetes. Stage three consists of periodic monitoring and targeted re-application for long-term maintenance. Efficacy was validated in controlled jar tests using water from Port Myaca Lock. Within 96 hours, treated samples versus untreated controls demonstrated phosphate undetectable within 24 hours, nitrate reduced by 90 percent, nitrite reduced by 50 percent and stable, alkalinity stabilized in the optimal 100 to 200 parts per million range, and pH increased modestly from 6.0 to 7.0. Dissolved oxygen and ammonia levels also improved significantly. Tests confirmed that dying cyanobacteria release toxins, evidenced by a temporary rise in cyanuric acid, which fully disappears within three to four days under NoHABs treatment. Compared with conventional alternatives, NoHABs offers distinct advantages. It delivers rapid visible results within days, comprehensively addresses nutrients and both active and dormant algae, safely manages toxin release, doubles oxygen to support beneficial organisms, prevents recurrence, and leaves no harmful residues, making it faster, safer, and more sustainable for lakes, rivers, and coastal waters.

From Satellite to State Management: Responding to the Gulf of Maine *Karenia mikimotoi B*loom

***Tyler Spillane**, Bryant Lewis*

Maine Department of Marine Resources, West Boothbay Harbor, ME, USA

Remote sensing technology has become more readily available for end-users to access allowing state shellfish sanitation regulators such as the Maine Department of Marine Resources (ME DMR) to incorporate it into harmful algal bloom (HAB) event response. Access to high-resolution processed chlorophyll-α satellite imagery allows strategic planning and coordination of labor-intensive field-based sampling and monitoring efforts to most effectively target areas of greatest concern or impact during a large-scale bloom. This presentation will examine the key factors necessary for satellite-based tools to be actionable from the perspective of a state agency managing and coordinating HAB response.

We will use the recent example of the 2026 *Karenia mikimotoi* bloom in the Gulf of Maine to show how ME DMR uses these tools in a bloom event. We will discuss how we paired these tools with traditional on the ground field sampling to respond to the bloom. Through discussion of this event, we aim to highlight the strengths and limitations of the current tools available and generate discussion on how they can better serve state regulators in harmful algal bloom management.

A Survey and Algaecide Assessment of Overwintering Cyanobacteria Populations in a Large Source Water Reservoir

Margaret K. Spoo-Chupka

The Metropolitan Water District of Southern California, La Verne, CA, USA

Diamond Valley Lake (DVL) is the largest drinking water supply reservoir in Southern California with a capacity of 800,000 acre-feet and a maximum depth of 80 meters. Non-body contact recreational activities are allowed at DVL. Cyanotoxin-producing blooms are becoming more common at the reservoir. While drinking water supply has not been impacted, voluntary recreational advisories and closures have occurred. Surface algaecide application is a standard practice for management of cyanobacterial blooms but has not been performed at DVL due to practical and logistical constraints of treating a reservoir of this size. Many cyanobacteria that produce cyanotoxins survive through the winter months by going quiescent and forming deposits of overwintering cells on sediments. Surveys of DVL sediments identified locations, water column depths, sediment depths, and sediment types within the lake that had overwintering populations. Overwintering cells detected in the surveys were typically *Microcystis* spp. and *Gloeotrichia echinulata*, the same species that develop summertime cyanotoxin-producing blooms. Microcystins were detected in nearly all biomass recovered from sediments surveyed with a median value of 0.26 µg/L (IQR 0.2-0.8), demonstrating the presence of toxin producers in overwintering populations. Laboratory growth experiments on overwintering cell material suggest the populations at DVL are viable and can contribute to planktonic blooms when environmental conditions become favorable. Algaecide laboratory experiments using copper sulfate on collected overwintering cell material indicate these populations are sensitive to doses that would typically be used in traditional surface lake treatments. The results of this survey demonstrate that viable overwintering cyanobacteria occupy less area in the lake than a surface water bloom. A preventative targeted treatment of overwintering cyanobacteria populations at DVL and other bloom-susceptible lakes has the potential to mitigate cyanobacteria blooms during warm months and be more practical and cost-effective than surface treatments.

Anywhere, Anytime – A National Vision for Operational HAB Forecasting

Kari St.Laurent[1], *Alexandria Hounshell*[2], *Michelle Tomlinson*[1], *Richard Stumpf*[1]

[1]NOAA National Centers for Coastal Ocean Science, Silver Spring, MD, USA
[2]NOAA National Centers for Coastal Ocean Science, Seattle, WA, USA

NOAA NCCOS produces operational harmful algal bloom (HAB) forecasts in key U.S. coastal and Great Lake systems around the United States. Our vision of a national HAB Forecasting Network aims to produce HAB forecasts anywhere at any time intrinsically guided by user needs. This presentation will highlight the current status of operational HAB forecasts produced and disseminated by the NCCOS HAB Forecasting Branch (HAB-F), demonstrate ongoing enhancements and new capabilities, and discuss current research towards adaptive event response forecasting capabilities using innovative technologies and modeling approaches. HAB-F currently produces operational HAB forecasts for Lake Erie, the Gulf of Maine, and the US Gulf and eastern Florida Coast. The modeling approach and dissemination style for each forecast is customized to the region and particular HAB impact (e.g. drinking water contamination, fisheries, human health) demonstrating that there is no 'one size fits all' approach. HAB-F is working with partners to expand and enhance HAB forecasting services, including the development of Chesapeake Bay and Lake Okeechobee HAB forecast systems, the expansion of satellite monitoring and event response capabilities to all U.S. coastal and Great Lakes regions, and the transition of new forecast products such as the probability of toxin exceedance for Lake Erie. In addition, HAB-F has begun critical research to expand our forecasting toolkit to be more adaptive to HAB event response and emerging information needs. For example, HAB-F has begun exploring high resolution satellite imagery (e.g. smallsats), applying AI/MLI techniques to better characterize satellite-derived algal blooms, using existing hydrodynamic models to forecast bloom movement 'on demand', and developing novel tools (e.g. BloomSCOPE) to track satellite imagery as HAB features. This presentation will give a broad overview of the current and future HAB-F vision for a national HAB forecasting capability.

Breathtaking Science: Red Tide Respiratory Irritation Forecast Improvements

Kari St.Laurent[1], *Alexandria Hounshell*[2], *Emily Brown*[3], *Kathrine Collins*[4], *Chris Holland*[5], *Richard Stumpf*[1]

[1]NOAA National Centers for Coastal Ocean Science, Silver Spring, MD, USA
[2]NOAA National Centers for Coastal Ocean Science, Seattle, WA, USA
[3]RPI, Inc, Charleston, SC, USA
[4]CSS, Inc, Silver Spring, MD, USA
[5]NOAA National Centers for Coastal Ocean Science, Beaufort, NC, USA

The NOAA National Centers for Coastal Ocean Science (NCCOS) produces an operational respiratory irritation risk forecast for individual beaches along the Gulf Coast every 3 hours up to 30 hours into the future using cell counts of *Karenia brevis* combined with the beach shoreline orientation and NWS wind direction and speed forecasts. NCCOS has begun to advance this forecast, with an ambitious goal to transition from a respiratory irritation *symptom* risk to a *toxin* risk forecast. To achieve this, we are working with partners to establish the optimal, fit-for-purpose, method to capture, extract, and quantify aerosolized brevetoxins in a controlled laboratory environment. This derived laboratory method will be applied in the field during the next *K. brevis* bloom in southwest Florida to assess its performance alongside a high-volume air sampling as well as cell count and surface water toxin measurements. This initial field study will inform whether a relationship between *K. brevis* cell concentrations and aerosolized brevetoxins can be appropriately modelled. Additionally, NCCOS seeks to improve the spatiotemporal coverage of the respiratory irritation forecast by: a) exploring a blanket very low respiratory irritation risk designation at sites with strong offshore winds, b) adding an 'insufficient data' designation if not enough information is available to issue a forecast, and c) determining whether satellite-derived ocean color products could be used as an accurate proxy for *K. brevis* cell counts when an *in-situ* counts are unavailable. Finally, NCCOS plans to improve forecast visualizations by exploring approaches to convey forecast confidence and to better visualize temporal forecasts. Overall, this presentation will highlight the ways NCCOS is enhancing Gulf Coast red tide forecast capabilities by increasing accuracy and providing a greater spatiotemporal coverage.

Quantifying the Effect of Particle Sinking in Imaging FlowCytobot Concentration Estimates

***Michael Staiger**, Mrun Pathare, and Michael Brosnahan*

Woods Hole Oceanographic Institution, Woods Hole, MA, USA

This study explores the potential for undercounting large microplankton in standard analysis pipelines for Imaging FlowCytobot (IFCB) data. The IFCB phytoplankton sensor has emerged as a workhorse for several regional-scale HAB monitoring networks across the U.S. This device generates rich digital image records of individual particles in water samples, describing both the diversity and abundance of planktonic communities. The sensor's ability to characterize larger members of the community is impacted by size exclusion at the sample intake stage and particle settling during sample analysis. IFCB samples are stored in a syringe barrel as the sample is processed. Over this storage time, cells can settle out of suspension, affecting the resulting image record. This bias may be amplified when analyzing preserved samples, as fixed cells can't counteract settling through buoyancy regulation or swimming. To assess this effect, settling behavior and resulting concentration estimates were compared between live and fixed samples recorded using an IFCB and conventional light microscopy. Our results show size-dependent discrepancies in IFCB-derived concentration estimates, consistent with differential settling by larger phytoplankton and microzooplankton. Methods to lessen this effect during sample analysis and to correct counting bias are also explored in the context of 2023 IFCB recordings of a Tripos muelleri bloom in the Gulf of Maine and a mass bivalve spawning event in the Chukchi Sea. This work identifies a previously unrecognized source of bias in IFCB data records that should be considered, particularly when analyzing the occurrence of large plankton species or working with preserved samples.

Spatial and Temporal Variation of Riverine Algal Communities in the Illinois River, Illinois

Brianna C. Stanley

U.S. Geological Survey, Central Midwest Water Science Center, Urbana, Illinois, U.S.A.

Cyanobacterial harmful algal blooms (HABs) have contributed to degraded water quality in the upper Illinois River, Illinois (IL) posing health and financial risks on nearby communities that depend on this waterway for industry, drinking water, and recreation. In 2020, the Illinois River Basin was selected as the third basin in the U.S. Geological Survey's (USGS) Next Generation Water Observing System initiative to enhance water monitoring and improve understandings of HABs. The Illinois River was sampled for algal community composition from 2021 to 2025 to advance the understanding of timing, drivers, and spatial extent of HABs in this region. During this effort, samples were collected bimonthly from May to September at multiple USGS locations with well-established historical water quality data and on-going sensor monitoring, including the Illinois River at Starved Rock, IL (USGS-05553700) and Seneca, IL (USGS-05543010) monitoring locations. Algal community composition was enumerated and taxa identified by light microscopy. Concurrent discrete data collected included nutrients, cyanotoxins, and taste and odor compounds, which were used to help evaluate nutrient availability and harmful secondary metabolite production by cyanobacteria in the waterway. The taste and odor compounds geosmin and/or 2-methylisoborneol were detectable in every discrete sample collected during the sampling period. This presentation will summarize the changes observed in the Illinois River's algal community, providing the basis for evaluating both the contribution of potential HAB-forming cyanobacteria and the dynamics of the riverine phytoplankton community.

Diverse Harmful Algae in Louisiana Estuaries: Potential for Toxin Exposure and Animal Effects

Beth A. Stauffer[1]*, Jennifer Raabe*[1]*, Ann Fairly Pandelides*[1]*, Tessa Rock*[1,2]*, Raphael Kudela*[3]*, Kendra Negrey*[3]

[1]School of Biological Sciences, University of Louisiana at Lafayette, Lafayette, LA, USA
[2]Current affiliation: Florida Fish and Wildlife Conservation Commission, St. Petersburg, FL, USA
[3]Department of Ocean Sciences, University of California Santa Cruz, Santa Cruz, CA, USA

Harmful algae and their blooms (HABs) have historically been considered of little concern in Louisiana waters due to the influence of the Mississippi-Atchafalaya River System and consistently lower coastal salinities. However, many marine HAB species have been detected at least once in estuarine or continental shelf waters and routine monitoring is lacking. Over the course of 1.5 years, we quantified "marine" HABs in 5 Louisiana oyster growing estuarine regions and detected potentially toxic species in the genera *Pseudo-nitzschia*, *Alexandrium*, *Prorocentrum* and *Protoceratium*, as well as a species of *Chattonella* that is still being identified. We also focused on enumerating cyanobacteria at two estuarine locations representing higher and lower salinity conditions, tracking microcystins through multiple matrices (particulate, dissolved, SPATT), and into oyster tissues. Even with low concentrations of microcystins in the water column (pMC mean = 0.004 μg L^{-1}; dMC mean = 0.275 μg L^{-1}), accumulation in oyster tissues was detected using the Microcystin-DM ELISA in 50% of samples when paired with an extraction/cleanup method which improved relationship with LC-MS analyses. Lab-based work investigating the effects of microcystin exposure on oyster valve behavior and physiology indicate that oysters close more when exposed to toxic *Microcystis aeruginosa* cultures, with implications for their energy budgets. More recently, we've tracked toxins into specific tissues within the oyster following different feeding and depuration periods. Preliminary results show maximum concentrations in gut/hepatopancreas tissues and increased toxin concentrations with longer periods of feeding (48 and 72h, v. 24) and shorter depuration times (6h, v. 12 or 24h). Together, these results provide a broad view of HABs in the heavily river-influenced estuaries of Louisiana while tying water column toxins to effects on shellfish, both as consumers, themselves, and as possible vectors to humans.

Quantifying Cyanotoxins Across Matrices Using Diverse Tools: Challenges, Opportunities, and Insights

Beth A. Stauffer*, Panchali Hazarika, Maya Lombardi, Jennifer Raabe, Julia A. Sweet*

School of Biological Sciences, University of Louisiana at Lafayette, Lafayette, LA, USA

Quantifying cyanobacteria presence, taxonomic identity, and toxin production remains a core challenge to researching and monitoring for cyanobacterial harmful algal blooms (CyanoHABs) and managing or mitigating their effects. Through multiple projects in oligo- and mesohaline estuaries in Louisiana, we've utilized a variety of tools to quantify biomass, ranging from continuous measures to extracted estimates of pigment fluorescence and molecular enumeration of 16S phycocyanin gene copies. We've also employed multiple methods for measuring cyanotoxins, including immunoassays, single-toxin qPCR (for microcystins via *mcyD*), and multi-toxin qPCR (via Phytoxigene assay). Each method provides a slightly different picture of the presence of cyanobacteria and cyanoHABs in our estuaries. For example, ratios of phycocyanin to chlorophyll-*a* from the CyanoFluor instrument showed generally less variability (CV = 27%) than extracted phycocyanin concentrations (CV = 142%) throughout an 8-month project in Barataria Bay; however, the lab-based phycocyanin methods require multiple rounds of freeze/thaw along with sonication and are laborious. Toxin quantifications using the Microcystin/Nodularin-ADDA ELISA yielded a number of detections above the minimum detection level (0.15 µg L^{-1}) for both particulate and dissolved microcystins, and with varying distributions from up- to down-estuary. In contrast, the Phytoxigene assay showed no detections of microcystin (based on the *mcyE* gene) in the Barataria Bay dataset. Saxitoxin (based on *sxtA* gene) was detected at low copy number in 3 samples collected from up-estuary locations that also showed high abundances of *Raphidiopsis* and *Dolichospermum*. We are currently working to compare microcystin detections based on *mcyE*, *mcyD*, and ELISA from two locations. Together, results from these studies are building our understanding of cyanoHABs in Louisiana estuaries while also informing on best approaches for effectively monitoring these organisms.

Bridging the Gap Between Needs and Impacts: Guiding Questions for Co-Producing Actionable Satellite HAB Tools

Elizabeth A. Staugler[1], *Alexandria Hounshell*[2], *Kari St. Laurent*[3], *Richard Stumpf*[3], *Michelle Tomlinson*[3]

[1]Florida Sea Grant, University of Florida, Gainesville, FL, USA
[2]National Centers for Coastal Ocean Science, NOAA, Seattle, WA, USA
[3]National Centers for Coastal Ocean Science, NOAA, Silver Spring, MD, USA

Satellite-based tools are increasingly used to monitor and forecast harmful algal blooms (HABs) across diverse aquatic systems, yet challenges persist in translating satellite data into products that are trusted, actionable, and sustained in operational settings. Drawing on perspectives shared across this session, this presentation frames guiding questions that connect the individual talks and support discussion across the co-production continuum, from identifying user needs to long-term operational use.

The discussion will examine how data producers decide when a satellite HAB product is likely to be useful and how potential stakeholders and end-users are identified early in development. This includes consideration of new product development versus refinement of existing tools, as well as identifying stakeholder needs that tend to be prioritized or overlooked during initial design stages. We will also explore what "actionable" means in practice, recognizing that definitions vary across users, regions, and decision timelines. These differences influence product design choices, acceptable uncertainty, resolution, delivery formats, and the consequences of false positives versus false negatives or misaligned timelines.

Attention will be given to where co-production efforts most commonly encounter challenges during the product development lifecycle, and to practical mechanisms that have supported sustained user engagement, feedback, and trust over time. This includes discussion of whether early engagement is sufficient or whether ongoing feedback structures are needed, and how co-production can be supported within realistic timelines and funding constraints. Finally, we will explore what signals indicate readiness for transition from research to operations, how those determinations are made, and how usability and relevance are reassessed as tools mature and user needs evolve.

Together with the other talks in this session, these questions are intended to stimulate dialogue and inform a synthesis to guide future collaboration between satellite data producers and HAB tool users.

When Science Meets the Shoreline: How Intermediaries Shape HAB Risk Communication

Elizabeth A. Staugler[1]*, Chris Simoniello*[2]*, Paul Monaghan*[3] *and Lisa S. Krimsky*[4]

[1]Florida Sea Grant, University of Florida, Gainesville, FL , USA
[2]Gulf of America Coastal Ocean Observing System, Texas Agricultural and Mechanical University, College Station, TX
[3]Agricultural Education and Communication, University of Florida, Gainesville, FL , USA
[4]Florida Sea Grant, Indian River Research and Education Center, Institute of Food and Agricultural Sciences, University of Florida, Ft. Pierce, FL , USA

Harmful algal blooms (HABs) present profound implications for public health, coastal economies, and community well-being. In Florida, blooms of *Karenia brevis* ("red tide") pose recurring challenges not only for environmental management but also for effectively communicating risk to diverse audiences. This study examines red tide communication through the perspectives of professional intermediaries—tourism officials, hospitality and small business representatives, media professionals, and public information officers—who translate scientific information into actionable guidance for residents and visitors.

Using four focus groups (n = 36), we explored how these communicators interpret available red tide data, respond to public concerns, and navigate tensions between accurately conveying health risks and avoiding unnecessary economic harm. Participants emphasized that audiences prioritize timely, hyper-local, and health-relevant information, particularly guidance related to respiratory effects, beach conditions, and seafood safety, rather than delayed or highly technical metrics such as cell counts. Challenges included fragmented information platforms, delays in data reporting, and the rapid spread of misinformation and outdated imagery on social media, which can amplify perceived risk and prolong economic impacts even after conditions improve.

Despite these barriers, participants identified successful communication practices, including sustained interagency coordination, consistent messaging across jurisdictions, real-time visual tools (e.g., beach cameras), and direct engagement with community members. Opportunities for improvement centered on integrating disparate data streams into user-friendly, location-based tools; developing shared communication toolkits with adaptable visuals and plain-language messaging; and adopting preparedness-oriented approaches similar to hurricane communication models.

By centering intermediary communicators as everyday "risk amplification stations," this study illustrates how the social construction of HAB risk shapes public understanding, behavior, and trust. Findings offer transferable lessons for improving HAB communication globally, highlighting best practices and practical tools that support rapid response, empower communities, and balance public health protection with economic resilience.

Dynamics of Bacterial Human Pathogens in the *Microcystis* Microbiome

Morgan M. Steffen

James Madison University, Harrisonburg, VA, USA

Cyanobacterial harmful algal blooms (cHABs) are made up of diverse networks of interacting microbes from all domains of life. Bacterial constituents of these bloom communities in freshwater systems can include human pathogens belonging to the genera *Klebsiella, Pseudomonas, Aeromonas,* and *Escherichia*, among others. Individual isolates belonging to these taxa have the capability to confer a growth benefit to *Microcystis*, in particular some isolates of *K. pneumoniae* isolated from Lake Erie and Taihu. As global temperatures continue to rise, these human pathogens with higher optimum growth temperatures may outcompete other native bacteria in the freshwater cHAB microbiome, which often have a lower optimum growth temperature. We have isolated ~100 potential opportunistic human bacterial pathogens from *Microcystis* blooms and culture isolates and tested their impact on the growth and physiology of *Microcystis*, both in co-culture and in a larger consortium. We have identified their antibiotic resistance profiles and potential antagonistic interactions with bacteria not known to be human pathogens from the *Microcystis* microbiome. Moving forward, it is critical to understand the dynamics of these bacterial populations as global temperatures rise and disturbances related to environmental change continue to shape cHAB populations in critical freshwater environments like the Great Lakes.

Novel Controlled Release Microencapsulation Technique Induces Phosphorus and Cyanobacteria Bloom Mitigation

Sophia Steffensmeier[1], *Benjamin Marics*[2], *Matthew Kirby*[1], *Barry H. Rosen*[1]

[1]Florida Gulf Coast University, Fort Myers, FL, USA
[2]Conservancy of Southwest Florida, Naples, FL, USA

Cyanobacteria possess ecological strategies that enable them to multiply and dominate a waterbody. When ample nutrients and warm temperatures are present, rapid growth occurs, often resulting in a harmful algal bloom (cyanoHAB). These blooms disrupt ecosystems by depleting dissolved oxygen levels and potentially releasing cyanotoxins, which threaten fish and wildlife populations. Due to increased industrial development and urbanization in Florida's natural waterbodies, cyanoHABs have become a growing concern. Traditional methods for mitigation are often short-term and can lyse cells, releasing cyanotoxins into the water column. Accordingly, the objective of this project was to develop a novel approach for cyanoHAB mitigation, utilizing the encapsulation of iron. Floating microcapsules were designed to release an iron core that causes cyanobacterial flocculation, agglomeration, and subsequent settling to the bottom of the water column. Capsules were developed using a microencapsulator and evaluated in controlled laboratory cyanobacterial blooms. Flocculation and sinking were assessed by quantifying cyanobacterial natural unit counts and area using an Imaging FlowCytobot (IFCB) and MATLAB. These findings indicate that the capsules successfully triggered flocculation and sinking, demonstrating a highly promising approach for cyanoHAB mitigation. This method may offer a critical advantage over traditional mitigation approaches by enabling localized treatment, preventing immediate toxin release, and reducing the risks of chemical overuse.

Co-creating a HABs Impact Assessment Framework with Coastal Alaskan Communities to Support Food Secure Futures

Margaret Rudolf[1], ***Taylor R. Stinchcomb***[2], *Lauren M. Divine*[3], *Rachel Lekanoff*[4], *CLAMS for HEALING Workshop Participants*[5]

[1]International Arctic Research Center, Fairbanks, Alaska, USA
[2] Wildlife Conservation Society, Arctic Beringia Program, Fairbanks, Alaska, USA
[3]Anchorage, Alaska, USA
[4]Alaska Conservation Foundation, Anchorage, Alaska, USA
[5]Various Tribal and Community Organizations, Alaska, USA

Rapidly changing ocean conditions have increased the frequency and severity of harmful algal blooms (HABs) across Alaska. HABs can affect marine food webs, from shellfish to Pacific walrus and other marine mammals, and thus may have critical impacts on the food security of Indigenous communities who rely on these foods for all aspects of wellbeing. Assessing these impacts requires first understanding what Indigenous food security means and what a food secure future looks like across different regions and cultures. The CLAMs for HEALING project brought together 14 staff from Alaska Native organizations, members of coastal Alaskan communities, and HABs researchers to participate in a two-day workshop to (1) develop frameworks that center Indigenous communities' visions of food secure futures; (2) identify the risks and impacts to food security driven by HABs in a changing climate; and (3) identify leverage points to support the resilience of food security. Using a modified Theory of Change process, participants co-produced an Indigenous Food Security Framework with four overarching dimensions: Culture, Health, Accessibility, and Relationships. We conducted thematic analysis to translate these into a preliminary Impact Assessment Framework that incorporates cultural, ecological, and governance indicators into HABs impact monitoring. The preliminary Impact Assessment Framework will be workshopped with additional coastal Alaska Native communities for refinement and relevance to their specific contexts. Following refinement and feedback, we will collaborate with communities to test and evaluate the Impact Assessment Framework in 2027. Our work supports community-led monitoring of HAB impacts and informs more holistic, relational decision-making around HAB mitigation and coastal community resilience.

Socio-economic Impact of Sargassum on Coastal Communities and Fisheries in the Southeast Region

Brent Stoffle

NOAA, SEFSC/SSRG, Miami, FL, USA

Sargassum inundations across the tropical and subtropical Atlantic emerged as a persistent and intensifying phenomenon with significant impacts on coastal communities and fisheries. In the diverse U.S. Southeast region, including Florida, Puerto Rico, and the U.S. Virgin Islands, recurrent landings of pelagic Sargassum have disrupted coastal economies, degraded critical habitats, and strained local infrastructure. This presentation synthesizes recent NOAA-led and partner-supported assessments of the socio-economic impacts of Sargassum on coastal communities and fisheries, with an emphasis on the intersection of ecological change and socio-economic impacts.

The findings highlight direct and indirect impacts across fishing sectors, tourism, public health, and management. Accumulations of Sargassum in nearshore and estuarine environments can reduce water quality, contribute to hypoxic conditions, and alter fish behavior and distribution, thereby affecting catch rates, gear efficiency, and fisher safety. Concurrently, coastal tourism—an economic cornerstone of the Southeast and US Caribbean—experiences declines associated with beach fouling, odor from decomposition, and reduced aesthetic value. Public expenditures for removal and disposal have increased substantially, placing disproportionate burdens on small and resource-limited communities.

Case studies highlight adaptive responses, including early warning systems, coordinated cleanup strategies, and emerging valorization pathways for Sargassum biomass. However, gaps remain in forecasting precision, cross-jurisdictional coordination, and long-term mitigation planning.

The findings underscore the need for integrated, multidisciplinary approaches that couple monitoring with socio-economic resilience planning. Strengthening partnerships among federal, territorial, and local entities will be critical to developing scalable, equitable responses to this evolving and complex coastal issue.

The Effects of Environmentally Relevant Nitrogen Concentrations on Growth and Physiologyof Toxic and Non-Toxic Microcoleus strains

Sydney Stubler[1], *Jacob Mormando*[1], *Abeer Sohrab*[2], *Fiza Mansoor*[2], *Ramesh Goel*[2], *Joanna Blaszczak*[3], *Robert Shriver*[3], *Sophia Galova*[4], *Kalina Manoylov*[5], *Emily Garlock*[6], *Zac Triumph*[6], *Gregory L. Boyer*[6] *and Rosalina Stancheva*[1]

[1]Department of Environmental Science & Policy, Potomac Environmental Research and Education Center, George Mason University, Fairfax, VA, USA
[2]Department of Civil and Environmental Engineering, University of Utah, Salt Lake City, UT, USA
[3]Department of Natural Resources & Environmental Science, University of Nevada, Reno, NV, USA
[4]Department of Chemistry and Biochemistry, University of California San Diego, La Jolla, CA, USA
[5]Department of Biological and Environmental Sciences, Georgia College & State University, Milledgeville, GA, USA
[6]Department of Chemistry, State University of New York College of Environmental Science and Forestry, Syracuse, NY, USA

Microcoleus is a common benthic cyanobacterium proliferating in low-nutrient rivers globally. It is of growing concern due to the ability of some species to produce the potent neurotoxin, anatoxin-a (ATX). In this study, we cultured three non-axenic unialgal *Microcoleus* strains, isolated from the Eel River and Scott River in California, under four total dissolved inorganic nitrogen (DIN) concentrations. Treatment DIN concentrations were 0.62 ± 0.09 mg/L for the ultra-low nitrogen (ULN) treatment, 1.98 ± 0.16 for the low nitrogen (LN) treatment, 4.85 ± 0.27 for the medium nitrogen (MN) treatment, and 23.77 ± 1.25 mg/L for the high nitrogen treatment (HN). Samples were harvested in a time-series on days 3, 7, 10, 14, 17, 21, 28, and 31. *Microcoleus anatoxicus* strain ER4 produces mainly ATX with lower quotas of dihydroanatoxin-a (dhATX), *M. anatoxicus* strain SR17 produces both congeners, and *Microcoleus* sp. 1 strain ER12 is non-toxic. At each harvest, cell density, chlorophyll *a*, and anatoxin concentrations were measured. Additionally, DIN concentrations were measured at every other harvest to estimate DIN consumption by the *Microcoleus* consortia (including heterotrophic microbiome). Under the lowest DIN concentrations, the morphology of *Microcoleus* sp. 1 strain ER12 was indicative of lower physiological stress compared to the toxic strains. The highest growth of *Microcoleus* strains occurred under the higher nitrogen treatments, with *Microcoleus* sp. 1 strain ER12 achieving significantly higher cell densities than the toxic strains. There were no significant differences in total ATX production between treatments across both toxic strains. However, different DIN concentrations affected the timing of peak toxin quotas and fractions of anatoxins produced (ATX versus dhATX, intracellular versus extracellular toxins). Toxic strains consumed significantly higher concentrations of DIN compared to the non-toxic strain, likely due to the nitrogen need for ATX production.

A Perspective on Monitoring Blooms with Different Satellite-based Sensors

Richard P. Stumpf[1], *Michelle C. Tomlinson*[1], *Sachidananda Mishra*[2], *Timothy T. Wynne*[1], *Andrew Meredith*[2]

[1]NOAA, National Centers for Coastal Ocean Science, Silver Spring, MD, USA
[2]CSS, Fairfax, VA, USA

Freshwater cyanobacterial blooms frequently have high biomass, which makes them amenable to detection with satellites. For many years, operational satellite missions were designed for land or the open ocean. In the last decade, satellite missions have had sensors that are more suitable for detecting blooms in lakes and estuaries, particularly because of the addition of one or more bands in the spectral region between red and near-infrared light. The key challenges in using these sensors for bloom detection are the trade-offs between spatial and temporal discrimination, and between spectral and sensitivity discrimination. The sensor mission of greatest interest is the OLCI on Sentinel-3, which is the reference for satellite-based water color observations (300 m pixel, daily coverage, good spectral resolution), and is well established for monitoring freshwater blooms, provided the water body is wider than about 1 km. Higher spatial resolution missions that may supplement OLCI include the Sentinel-2 MSI (20 m, 5-day repeat), and commercial sensors such as the Planet SuperDove (up to 3 m, and potentially daily coverage); however, they are more limited in discrimination and sensitivity. There are multiple ways to evaluate the products from these sensors. Ultimately, the goal is to determine whether they can accurately provide us with important and timely information about cyanobacteria bloom presence, extent, and intensity with sufficient confidence to support management needs.

Contrasting Bulk and Single-cell Bacterial Communities of Marine Dinoflagellates Across Coastal Regions

***Jiyeon Sung**, Christopher J. Gobler*
Stony Brook University, Stony Brook, NY, USA

Marine phytoplankton blooms are not simply the result of the proliferation of a single organism, but rather complex ecological processes shaped by interactions with diverse microbial communities. In particular, dinoflagellates coexist with heterotrophic bacteria in marine environments, where such interactions can influence host physiology, survival, and ecosystem functioning. Recent studies suggest that phytoplankton may harbor recurring core microbial assemblages, and that host species identity or genetic characteristics may contribute to shaping these associated microbiomes. However, most of these findings are derived from culture-based or controlled systems, and it remains insufficiently understood how host-associated and environmental factors jointly structure microbial communities in natural marine settings. To address this gap, we analyzed seawater and phytoplankton samples collected across five coastal regions on Long Island, New York, USA. We employed a dual approach combining bulk microbial community profiling and single-cell–associated microbiome analysis. Bulk samples were fractionated (0.2–20 μm and >20 μm) to distinguish free-living and dinoflagellate-associated microbial communities, while single-cell isolation enabled direct assessment of bacteria associated with individual dinoflagellate cells, allowing a more host-associated perspective on microbial composition. The observed phytoplankton included *Alexandrium catenella, Dinophysis acuminata, Margalefidinium polykrikoides,* and *Prorocentrum cordatum*. Among these, *Dinophysis* and *Margalefidinium* were repeatedly detected across multiple regions, providing a consistent framework for comparison. We examined how bacterial assemblages associated with the same host varied across geographic locations and whether such variation reflects environmental recruitment or host-driven selection. The objectives of this study were to (1) compare microbial community structures between bulk and single-cell fractions, (2) assess geographic variation in host-associated microbiomes, and (3) evaluate the relative contributions of host selection and environmental processes in shaping these interactions. This work aims to advance our understanding of the diversity and ecological significance of dinoflagellate–bacteria associations in marine ecosystems.

Population Connectivity of Coastal *Dinophysis* Blooms Resolved Using Transcriptome-Derived SNPs

Serena Sung-Clarke[1,2]*, Harriet Alexander*[1]*, Carolyn Tepolt*[1]*, Arianna Krinos*[3]*, Sara Shapiro*[1]*, David Beaudoin*[1]*, Savannah Davis*[3]*, Michael Staiger*[1,2]*, Nour Ayache*[5]*, Rayna Hamilton*[1]*, Juliette Smith*[6]*, Michael Brosnahan*[1]

[1]Woods Hole Oceanographic Institution, Woods Hole, MA, USA
[2]MIT-WHOI Joint Program in Applied Ocean Sciences and Engineering, Cambridge, MA, USA
[3]Brown University, Providence, RI, USA
[4]North Carolina Agricultural and Technical State University, Greensboro, NC, USA
[5]French Research Institute for Exploitation of the Sea (IFREMER), Nouméa, New Caledonia, France
[6] Virginia Institute of Marine Science, Gloucester Point, VA, USA

Dinophysis are kleptoplastidic dinoflagellates, and many species in this genus cause diarrhetic shellfish poisoning (DSP). Some of the densest Dinophysis blooms observed historically occurred in temperate coastal embayments, and often in the absence of Mesodinium, its obligate prey. Despite their regular occurrence, it is not understood how these prey-free Dinophysis blooms initiate. Here, we investigated blooms at two nearby, but distinct, tidal embayments on the Cape Cod National Seashore from January 2024 – July 2025 to assess population connectivity between these sites and across years. In Salt Pond, the northern of the two sites, blooms were exceptionally dense in June and July in both 2024 and 2025 (>1M cells/L); in Meetinghouse Pond, a large bloom persisted from January – June, 2024 (>100K cells/L). To understand the genetic relationship between these bloom populations, a novel bioinformatic approach was taken to identify neutral SNP markers in single-copy genes from both meta- and single-cell-transcriptomes. These markers were used to compare the genetic distance between and within these Cape Cod National Seashore blooms, as well as between various Dinophysis culture isolates and bloom metatranscriptomes in the Eastern Atlantic Ocean. This work highlights some novel approaches for using transcriptomic data for dinoflagellate population genetics and can help elucidate the roles of local vs transported populations in seeding blooms.

Effects of Organic Carbon on Nutrient Concentrations, Carbonate Chemistry, and Metals Following Modified Clay Flocculation in Seawater – Understanding Chemical Impacts of Red Tide Mitigation Techniques

Kathleen Sway[1]*, Emily R. Hall*[1]*, Jessica Frankle*[1]*, Salvatore Caprara*[2]*, Kristen N. Buck*[2]*, Donald M. Anderson*[3]

[1] Mote Marine Laboratory
[2] Oregon State University
[3]Woods Hole Oceanographic Institute

Modified Clay II (MCII), a formulation of kaolinite clay combined with poly-aluminum chloride (PAC), is currently being evaluated as a mitigation strategy for reduction of blooms of *Karenia brevis*. Several laboratory studies have been performed in filtered or treated seawater with cultured *K. brevis*, yet there is evidence that elevated concentrations of dissolved organic matter (DOM) and other natural particles may influence flocculation, metal concentrations, and nutrient binding capabilities of MCII. To test this, MCII was applied to seawater from New Pass (low DOM) and from Placida Harbor (high DOM) without the addition of *K. brevis*. For this study, we examined changes in nutrient concentrations, carbonate chemistry, metals, and MCII settling rates in natural seawater with differing DOM profiles. There were significant differences in seawater carbonate chemistry parameters and flocculated clay nutrient concentrations. Settling rates were also compared between the two water sources and though not significantly different, high DOM seawater showed greater variability. This study provides insights into seawater chemical characteristics with the addition of MCII.

The Mitigation of Marine HABs (*Alexandrium catenella, Pseudo-nitzschia multiseries*) by Cultivable Seaweeds

Laine H. Sylvers[1]*, Christopher J. Gobler*[1]

School of Marine and Atmospheric Sciences, Stony Brook University, Southampton, NY

Although many macroalgae have been shown to inhibit and lyse HAB phytoplankton and have even been shown to decrease toxin buildup in co-cultivated shellfish, much of this research has been performed in small-volume experiments with results that may not be applicable to aquaculture systems. Here, we present results from experiments investigating the effects of *Ulva lacinulata* and sugar kelp (*Saccharina latissima*) on blooms of both *Alexandrium catenella* and *Pseudo-nitzschia multiseries* in mesocosm and raceway experiments of moderate volume (75-300L) with daily water exchange to simulate tidal exchange. Algicidal activity was present for all seaweed/HAB pairs. *P. multiseries* was strongly inhibited by *U. lacinulata* in all experiments in a dose-dependent manner, with 49%+ reduction in cell density from 1 g L^{-1} *U. lacinulata*, and 78%+ reduction from 2 g L^{-1}. *S. latissima* (1 g L^{-1}) also displayed significant algicidal activity (41-71% reduction in *P. multiseries* cell density). In experiments with variable water exchange, *U. lacinulata* and *S. latissima* still significantly reduced *P. multiseries* cell density at water exchange rates of exceeding 30% of volume per day. In 300L mesocosm experiments, *S. latissima* significantly reduced the densities of *A. catenella* by 46-60% within 48h. In the mesocosm experiment using a low-moderate density bloom of *A. catenella* (1.4×10^3 cells L^{-1}), there was a 27% reduction in total mussel toxicity in the kelp treatment ($p = 0.057$), while in the experiment with a high-density bloom (4.7×10^5 cells L^{-1}), there was no difference in toxin accumulation between treatments. Data will also be presented from raceway and mesocosm experiments investigating the effects of variable water exchange rate on the algicidal activity of *S. latissima* on *A. catenella* from April-May 2026.

Emerging Technologies for HAB Monitoring: Uncrewed Aircraft Sampling of Water and Aerosols in Lake Okeechobee

*Kevin A. Adkins [1], Justin Fratto[2], Marc Compere[2], Avinash Muthu Krishnan[3], **Kayla D. Taylor[4]**, Emel Sen Kilic[5], Mauricio Arias[6], Eric Milbrandt[7], Cassondra Armstrong[8], Jason Evans[9], David Zink[10], Nickolas D. Macchiarella[3]*

[1]College of Aviation, Embry-Riddle Aeronautical University, Daytona Beach, FL, USA
[2]Department of Mechanical Engineering, Embry-Riddle Aeronautical University, Daytona Beach, FL, USA
[3]Aeronautical Science Department, Embry-Riddle Aeronautical University, Daytona Beach, FL, USA
[4]Department of Electrical Engineering and Computer Science, Embry-Riddle Aeronautical University, Daytona Beach, FL, USA
[5]Department of Human Factors and Behavioral Neurobiology, Embry-Riddle Aeronautical University, Daytona Beach, FL, USA
[6]Department of Civil & Environmental Engineering, University of South Florida, Tampa, FL, USA
[7]Sanibel-Captiva Conservation Foundation, Sanibel, FL, USA
[8]South Florida Water Management District, West Palm Beach, FL, USA
[9]Institute for Water and Environmental Resilience, Stetson University, DeLand, FL, USA
[10]School of Graduate Studies, Embry-Riddle Aeronautical University, Daytona Beach, FL, USA

Harmful algal blooms pose significant environmental and socioeconomic threats to many areas in South Florida, including Lake Okeechobee and its distribution canals. These blooms can simultaneously lead to the widespread mortality of aquatic life and to the emergence of public health hazards, which are especially detrimental to the localized economies around Lake Okeechobee that depend highly on fishing and water-related tourism. Lake Okeechobee has been monitored for water quantity and quality for several decades, providing an excellent context and opportunity to test and implement a new generation of bloom sampling techniques. One challenge that has stymied the progress of understanding bloom dynamics is the event-driven nature of data collection, given that blooms often appear and mobilize within days, so collection techniques often miss the initiation of the bloom and cannot sufficiently track a bloom's movement and growth along a body of water. Compared to traditional hand collection techniques from crewed boats, uncrewed aircraft borne systems can enhance bloom sampling with automation, precision flight, and machine-level consistency in sampling. This work describes the first-year progress of an interdisciplinary, multi-year project to develop an uncrewed-aircraft-hosted water and aerosol sampling technique for blooms on Lake Okeechobee. The project plans to test the sampling techniques and collect samples across two summer and two fall field campaigns. The engineering design process of the techniques is presented, including initial testing and validation results of the techniques on an experimental body of water in Volusia County, FL. Finally, results from the first of three planned summer field campaigns are presented.

Cyanobacterial Bloom Exposure Amplifies COVID-19 Risk in Colorado Patients

***Anne E Thessen**, Shawn T O'Neil, Melissa A Haendel*

Department of Genetics, Genetic Medicine Research Building, 120 Mason Farm Rd, Chapel Hill, NC, USA

Environmental exposures shape human disease in profound ways, yet they remain dramatically understudied compared to genomic and molecular drivers of illness. Among the most underappreciated threats are chronic, low-level exposures to cyanobacterial toxins. Using a novel, multi-source data integration approach, we conducted a retrospective analysis of real-world electronic health records to investigate whether proximity to cyanobacterial blooms worsens COVID-19 outcomes in Colorado patients. By linking a large real-world data source with satellite imagery from the USEPA CyAN project and field observations from the Colorado Department of Public Health & Environment (CDPHE), we constructed a uniquely rich dataset capturing both environmental exposures and clinical outcomes. A propensity-score matched logistic regression revealed that COVID-19 patients living near recurring cyanobacteria blooms faced 2.75 times higher odds of severe outcomes (hospitalization or death) compared to unexposed individuals. Notably, COVID-19 vaccination reduced the odds of severe outcomes by more than half. While the precise mechanism linking cyanobacterial toxin exposure to COVID-19 severity remains to be elucidated, this study provides compelling evidence that environmental exposures can meaningfully amplify the risk of severe infectious disease outcomes. We call for accelerated investment in in situ monitoring programs, biomarker discovery, and longitudinal studies to quantify the true burden of chronic cyanobacterial toxin exposure on human health.

The Role of nitrogen and Phosphorus Limitation in Controlling Saxitoxin-Production in Harmful Cyanobacteria, *Dolichospermum* and *Aphanizomenon*

John Thraen, *Christopher Gobler*

School of Marine and Atmospheric Sciences, Stony Brook University, Southampton, NY, USA

Toxin production by cyanobacterial harmful algal blooms (CHABs) can be influenced by nitrogen (N) or phosphorus (P), yet little is known regarding how nutrient balance may alter cyanobacterial saxitoxin (STX) production. Here, we investigated the influence of N and P limitation on the production of STX in multiple strains of the freshwater cyanobacteria, *Dolichospermum circinale* and *Aphanizomenon gracile*. Strains were grown semi-continuously and exposed to differing concentrations of N and P, and growth rates, photosynthetic efficiency, N2 fixation rates, alkaline phosphatase activity (APA), and STX cell quotas were quantified. Despite diazotrophic capabilities, growth rates of the cyanobacteria could be limited by low levels of N or P. For all strains, low P conditions (0-1 µM orthophosphate; 0 - 31µg L-1) led to significant increases in STX quotas and APA, indicating P limitation at this range of P concentration was accompanied by higher STX per cell. N2 fixation rates were significantly lowered by P limitation. P limitation responses differed across strains, with *D. circinale* strain ACMB05 exhibiting larger reductions growth rate and photosynthetic efficiency at low P, while *D. circinale* strain ACBU02 and the *A. gracile* were less sensitive, but *A. gracile* also showed the greatest difference in STX quota between P-limited and P-replete conditions. Low P conditions tended to increase the abundance of the congeners GTX2, STX, and dcGTX, further enhancing total toxicity of cells in low P conditions. This study demonstrates that while N and P availability can constrain diazotrophic cyanobacterial cell growth, P limitation also serves as a physiological trigger for increasing cellular STX quotas. Differences in sensitivity to P coupled with the consistent upregulation of STX and APA under low P conditions suggest that while sensitivity to P-limitation can vary by strain, P-deficiency is universal stressor that may exacerbate the public health risks associated with STX-producing CHABs.

Canyons to Confluences: Characterizing Benthic Cyanobacteria in the U.S. EPA's Region 8 Utah Pilot Sites

Marcie L. Tidd

U.S. EPA Region 8 Laboratory Services and Applied Science Division, Lakewood, Colorado, USA

Growing recognition of potentially toxigenic benthic cyanobacteria in U.S. rivers and streams has heightened the need for coordinated monitoring and management. The U.S. EPA Region 8 participated in nationwide studies (2023–2025) lead by EPA scientists to evaluate field and laboratory approaches for characterizing the occurrence and toxin production of benthic cyanobacteria in river systems. Study locations spanned multiple regions, with Region 8 focal sites in Grand Staircase–Escalante National Monument and the Virgin River watershed of Utah, including Zion National Park. These efforts were enabled by close collaboration with State and Federal partners that supported planning, access, logistics, and analytical expertise. This poster summarizes the field sampling framework used to estimate the distribution and spatial extent of benthic mats (e.g., reach-scale transects, percent-cover assessments, transect sampling-point-intercept methodology, and georeferenced photo documentation); to collect representative mat, substrate, and co-located water samples; and to characterize environmental covariates relevant to benthic cyanobacteria proliferation. Laboratory analyses included those for nutrients, chlorophyll, cyanotoxins via Enzyme-linked Immunosorbent Assay and Liquid Chromatography / Mass Spectrometry, qPCR for toxin-linked genes, eDNA, and microscopy. Preliminary findings include estimates of benthic mat coverage and cyanotoxin occurrence from the Utah focal systems, contextualized by hydrologic setting and riverbed characteristics. Lessons learned inform risk screening, monitoring design, and targeted follow-up investigations. The work underscores how regional coordination and sustained partnerships with State and Federal agencies accelerate method advancement and translate emerging science into actionable management for benthic cyanobacteria in flowing waters.

Incorporating the SuperDove Constellation into a Harmful Algal Bloom Monitoring and Forecasting System

Michelle C. Tomlinson[1]*, Cynthia Arguijo*[2]*, Xin Yu*[3]*, Sachidananda Mishra*[3]*, Kari St.Laurent*[1]*, Richard P. Stumpf*[1]

[1]NOAA, National Centers for Coastal Ocean Science, Silver Spring, MD, USA
[2]Smith College, Northampton, MA, USA
[3]RPI, Tallahassee, FL, USA

Harmful algal blooms (HABs) pose a risk to human and ecological health in waterbodies around the US. In coastal and estuarine waters, these blooms are patchy, and change their extent hourly to daily, often occurring in small tributaries and near shorelines. To monitor and forecast HABs, NOAA's National Centers for Coastal Ocean Science (NCCOS) has incorporated satellite ocean color imagery from the 300 m spatial resolution Ocean Land Colour Instrument (OLCI). While these daily images have been useful for monitoring for blooms and initiating HAB forecast models, they often cannot delineate the patchiness of algal blooms or resolve and detect blooms in narrow estuaries or along the shore where recreational beaches, drinking water intakes, and aquaculture farms may reside. SuperDove data provide 3 m spatial resolution imagery at an almost daily frequency in most locations. This commercial data source, which has been made available for government use, could improve the initiation of HAB forecasting models and expand the model domain to make bloom transport and extent forecasts more accurate. A short-term forecast model has been developed for Margelefidinium polykrikoides, a dinoflagellate which impacts fisheries in the lower Chesapeake Bay tributaries, using OLCI imagery as input. We will present an evaluation of the accuracy of Planet imagery compared to OLCI and an assessment of how it could improve short-term forecasts in this region. The exploration of this higher spatial resolution satellite data could make forecasts more applicable to fisheries and aquaculture HAB concerns in the Chesapeake Bay and other highly complex estuaries.

Impact of *Mulinia lateralis* on Phytoplankton Biomass and Community Composition in Baffin Bay, Texas

***Kalie Tovar**, Laura Beecraft, Michael Wetz*

Harte Research Institute at Texas A&M University-Corpus Christi, Corpus Christi, Texas, United States of America

Baffin Bay, a lagoonal estuary located in South Texas, has been experiencing symptoms of eutrophication over the past 3-4 decades, including a doubling of chlorophyll a concentrations, episodic hypoxia, fish kills and recurring Aureoumbra lagunensis ("brown tide") blooms. Brown tide blooms are known to decrease benthic diversity and threaten the bay's popular recreational and commercial fisheries, generating stakeholder interest in exploring potential mitigation methods. One proposed method, requiring further study, is utilizing the dominant bivalve filter feeder, the Dwarf Surf Clam (*Mulinia lateralis*). Previous laboratory studies demonstrated *M. lateralis*' ability to filter *A. lagunensis* at bloom concentrations, making it an important consideration as a possible top-down biological control of *A. lagunensis*. This study quantified the impact of M. lateralis filtration on phytoplankton biomass and community composition by conducting in-situ seasonal mesocosm experiments in Baffin Bay. Two treatments were employed, including: 1) addition of M. lateralis at naturally occurring abundances, and 2) a control without *M. lateralis*. Results from fall and winter experiments showed no consistent effect of *M. lateralis* on total chlorophyll a or size fractionated chlorophyll a. Reductions in the <2 µm and 2-20 µm size fraction occurred in the *M. lateralis* treatment in winter, but not in the fall. The fall experiment showed a community shift from diatoms to dinoflagellates and ciliates in the *M. lateralis* treatment, but in winter experiments, dominant taxa remained unchanged. Additional experiments will be conducted in spring and summer, 2026, when *A. lagunensis* blooms are more pronounced and *M. lateralis* is expected to be more active. Results from this research will be useful for determining if *M. lateralis* can be utilized as a biological control to mitigate the proliferation of *A. lagunensis*.

TAML/Oxidant Provides a Safe and Sustainable by Design Approach for Controlling Marine and Freshwater HABs

Jennifer H. Toyoda[1]*, Nicholas R. Ohnikian*[1]*, Vic E. Simons*[1]*, Christopher D. Sibley*[1]*, Xiaowei Ma*[2]*, Terrence J. Collins*[2]

[1]Mote Marine Laboratory, Sarasota, FL, USA
[2]Carnegie Mellon University, Pittsburg, PA, USA

There is an urgent need to control active HABs with technologies that are effective in removing cells and toxins, environmentally sustainable, fair, and economically viable. NewTAML catalysts (NTs) are bioinspired, small-molecule replicas of peroxidase enzymes which activate commodity oxidants to degrade toxins and disrupt HAB cells; NT and oxidant concentrations are low. NTs are non-toxic, non-bioaccumulative, and non-endocrine disrupting. Paired with widely used oxidants such as hydrogen peroxide or sodium percarbonate, NT/oxidant provides an innovative, environmentally responsible, and fast-acting control technology. This project investigated NT/oxidant for control of the marine dinoflagellate, *Karenia brevis*, and the freshwater cyanobacteria, *Microcystis aeruginosa*. We performed flask and mesocosm mitigation experiments to evaluate effects on cells, toxins, and water parameters. In marine HAB experiments, NT/hydrogen peroxide rapidly and effectively reduced *K. brevis* cell concentrations, though brevetoxin removal lagged. Acute toxicity tests were performed on two estuarine species, *Menidia beryllina* and *Americamysis bahia*. No mortalities were observed after 96 h exposure of NT or NT/hydrogen peroxide in doses far exceeding intended environmental use. Freshwater HAB experiments showed simultaneous application of NT/sodium percarbonate rapidly eliminated microcystins, but inefficient cell removal led to toxin rebound within 72 h. However, when applying sodium percarbonate first followed by NT, cells and toxins were eliminated with no rebound by 168 h. Together these data show NTs at very low concentrations can supercharge low-concentration oxidants for HAB control in both marine and freshwater settings while achieving excellent safety profiles. Future work will focus on generating data for Experimental Use Permit applications, investigating ecosystem impacts such as non-target organism and nutrient effects, continuing NT product innovations to advance scalability and make NT/Oxidant a highly adaptable HAB solution. We gratefully acknowledge financial support from the U.S. Harmful Algal Bloom Control Technologies Incubator.

Grazer-Induced Toxin Production: Applications for toxin monitoring on the Pacific Coast

***Aubrey Trapp*[1]*, Raphael M. Kudela*[2]*, Melissa B. Peacock*[3]

[1]Salish Sea Research Center at Northwest Indian College, Bellingham, WA, USA
[2]University of California Santa Cruz, Santa Cruz, CA, USA
[3]Salish Sea Research Center at Northwest Indian College, Bellingham, WA, USA

Grazers exert top-down pressures on the phytoplankton community, yet the mechanisms and impacts of these interactions, such as induction of chemical defenses in phytoplankton, remain poorly understood. Copepodamides, a group of polar lipids exuded by copepods, are known to induce toxin production across multiple genera of harmful algae, including *Pseudo-nitzschia* spp. diatoms and *Alexandrium* spp. dinoflagellates. Toxins from harmful algal blooms (HABs) bioaccumulate through marine food webs posing challenges and health risks to coastal communities. HAB monitoring systems seek to mitigate the negative effects of HABs by tracking seasonal trends and providing early warning of toxin events. Here we investigate toxin induction by copepods and copepodamides in harmful algal bloom (HAB) species from the United States pacific coast using both observational and experimental approaches. Two years of weekly copepodamide monitoring via solid phase adsorption toxin tracking (SPATT) passive samplers showed potential for improving predictions of *Pseudo-nitzschia* abundance and domoic acid concentration in Monterey Bay, CA. The method was also adapted for the Salish Sea, WA where paralytic shellfish toxins are more prevalent. Complementary experiments with grazers and grazer cues explored toxin induction of local HAB species from both locations. Together, these results encourage development of novel approaches to include top-down information in HAB monitoring and early warning systems.

Paralytic Shellfish Toxin Accumulation and Depuration in North Atlantic Bivalves Fed Saxitoxin-Producing *Dolichospermum circinale*

Blythe Triplett*, Marcella Kretz Wallace, Jiyeon Sung, John Thraen, Ronojoy Hem, Christopher J. Gobler*
School of Marine and Atmospheric Sciences, Stony Brook University, Southampton, NY, USA

Paralytic shellfish toxins (PSTs) are a group of neurotoxins that include saxitoxin and are produced by marine dinoflagellates and some genera of freshwater cyanobacteria, including *Dolichospermum* species pluralis. While PST accumulation in bivalves feeding on dinoflagellates is well understood, little is known regarding how exposure to PST-synthesizing cyanobacteria influences saxitoxin accumulation, despite the growing recognition that freshwater cyanobacteria are transported to, and persist in, estuarine environments. This study assessed the clearance rates and saxitoxin accumulation and depuration of two marine bivalves (the Eastern oyster, *Crassostrea virginica*, and the blue mussel, *Mytilus edulis*) adapted to 15 PSU and fed a saxitoxin-synthesizing strain of *Dolichospermum circinale* in the presence of a nontoxic alga, *Diacronema lutheri*. During experiments, oysters were observed to preferentially consume *Dolichospermum* over *Diacronema* during short-term exposure (1-hour), but significantly decreased clearance of the cyanobacteria over longer exposures (12-hour). In contrast, mussels displayed equal clearance of the two algae over both time horizons. When fed *Dolichospermum* for 96 hours, oysters accumulated high levels of PSTs (120 micrograms of saxitoxin per 100 grams of tissue) in 24 hours but began depurating the toxin after 72 hours, despite continued exposure. In contrast, mussels progressively accumulated ~90 micrograms of saxitoxin per 100 grams of tissue after 96 hours of exposure. While depuration rates were similar between species, mussels depurated all toxin congeners equally, while oysters preferentially depurated carbamate congeners. Both bivalves retained over 20 micrograms of saxitoxin per 100 grams of tissue after 96 hours of depuration, evidencing the persistence of PSTs. Given these findings and the increasingly recognized discharge and persistence of freshwater cyanobacteria and their toxins in estuaries, monitoring PSTs downstream of saxitoxin-producing cyanobacterial blooms seems warranted.

Direct Photolysis of Anatoxin-a in Sunlight: Comprehensive Characterization of Rates, Photoproducts, Mechanism, and UV-Vis Spectrum

***Zac Triumph**, Xingye Yang, David Kieber, David Kiemle, Nicholas C. Pflug, Gregory L. Boyer*
SUNY ESF, Syracuse, NY, United States

Harmful algal blooms are a growing problem in freshwater systems. Toxin type and level are highly variable based on algal species and site conditions, but persistence of toxins after blooms is poorly understood. Anatoxin-a (ATX) is an acute neurotoxin responsible for canine fatalities in the last century. It is photolabile in sunlight, especially under basic conditions, but the degradation rates have previously been quantified in hours of exposure rather than quanta of sunlight. Here, we measured the apparent first-order degradation rates of ATX in lake water where natural sunlight showed a half-life ($t_{1/2}$) of 162 µEinstein cm^{-2} (7.8 hr) and artificial sunlight showed a $t_{1/2}$ of 108 µEinstein cm^{-2} (5.2 hr). We identified the novel structure of the major photodegradation product using mass spectrometry (MS) and nuclear magnetic resonance (NMR) spectroscopy. Based on this structure, we propose a photoisomerization mechanism that justifies the reported trends of low pH inhibiting degradation of ATX. We measured the first high-definition UV-Vis absorption spectrum showing an absorption band from 300–310 nm, which explains ATX's relatively modest degradation rates observed under natural sunlight. We also report the molar absorptivity constant of 13650±140 cm^{-1} mol^{-1} at 229.0 nm (λ_{max} for ATX), which is useful for accurate quantification of ATX in lieu of advanced techniques such as LC-MS/MS. Overall, this work provides a comprehensive overview of the direct photolysis of ATX and highlights the need for further investigation of photolability in anatoxins as a whole.

Water Quality Drivers of Harmful Algal Blooms in Cedar Lake and Lake Nokomis

Rachael Crabb[1], ***Katie Turpin-Nagel***[2], *Joe Bischoff*[2]

[1]Minneapolis Park and Recreation Board, Minneapolis, MN, USA
[2]Barr Engineering Co., Minneapolis, MN, USA

Cedar Lake and Lake Nokomis are regionally significant lakes that are heavily used for swimming and recreational boating during open water season as well as ice skating and skiing in the winter. While both lakes are meeting state phosphorus standards, the increasing frequency of toxic harmful algal blooms (HABs) represents a serious and growing concern. The Minneapolis Park and Recreation Board (MPRB) has observed microcystin, cylindrospermopsin, and anatoxin-a above detection limits on numerous occasions with levels exceeding recreational thresholds and causing beach closures in 2021. Given these concerns, the MPRB completed a stressor analysis to identify the primary drivers of HABs in these lakes and identify management strategies. Seven potential drivers were evaluated—phosphorus (P) enrichment, nitrogen dynamics, temperature, light, micronutrients, zooplankton predation, and detention time. Study results indicate that internal P loading is the primary driver of HABs in both lakes. Strong stratification in Cedar Lake promotes persistent hypolimnetic (often > 500 µg/L) and metalimnetic (often > 300 µg/L) P concentrations and steep vertical nutrient gradients favoring buoyancy-regulating taxa. These conditions are likely exacerbated by climate change where the extent and duration of stratification are increased as temperatures warm. In contrast, Lake Nokomis exhibits weak stratification but extensive anoxia, facilitating sediment P release and episodic mixing into the photic zone. Furthermore, cyanobacteria dominance and high toxin production has persisted into the winter months, driven by sufficient under-ice P and increased light availability from snow removal activities for recreational skating highlighting that HAB drivers may extend beyond the growing season. Since internal P loading from sediments was identified as the primary driver of cyanobacteria blooms, controlling sediment release is expected to reduce cyanobacteria bloom frequency and intensity.

Standard Method 10120; QPCR detection for Cyanobacteria and Cyanotoxin Producing Genes

Mark Van Asten[1,2] *Leonardo B. Pinheiro*[3]

[1]Phytoxigene, Inc. Akron, OH USA
[2]University of NSW, Sydney, NSW.
[3] National Measurement Institute, Chemical & Biological Metrology, Sydney, New South Wales, Australia

Accurate identification and reporting of Harmful Algal Blooms is critical for managing their threats. The current CyanoDTec Quantitative PCR (qPCR) assay has been in use to screen for potential risk of Microcystin/Nodularin, Cylindrospermopsin and Saxitoxin, plus measuring total cyanobacteria since 2016. However, even though data has consistently shown that there is a very high correlation between the presence of toxin genes and toxins and in some jurisdictions a rapid uptake in their use for ongoing monitoring, uptake more broadly has been limited. One of the hesitations for the use of qPCR is the lack of consensus, standardization of methods and the interpretation of results. Guidelines remain ambiguous and reliance on visualization and enumeration still remain the main tool for monitoring HABs. Standard Methods is a consensus organization supported by the American Water Works Association and American Public Health. The Organization's function is to review and revise existing methods and the development of new methods. Within the framework for any method consideration, it's critical that it's shown to perform reliably across multiple laboratories. In a 2025 study it was demonstrated that with the use of standardized reagents combined with highly characterized nucleic acid Reference Materials, qPCR quantification technology is able to reach levels of accuracy and reproducibility comparable to those achieved with digital PCR. The results from this study facilitated the consideration of a qPCR method for approval and publication by the Board of Standard Methods. The presentation will outline the results of the 2025 Interlaboratory study along with the approval process of the qPCR Standard Method. There is clearly a need for more reliable and reproducible methods to facilitate better monitoring and prediction of HABs, establishing a Standard Method should be a key milestone in gaining acceptance for the utilization of qPCR as a monitoring tool.

Assessing the Epifaunal Community of Pelagic Sargassum in Nearshore Coastal Habitat in St. Thomas

Helen Van Houten[1]*, Jessica Michael*[1]*, Avery Coble*[2]

[1]Coral World Ocean and Reef Initiative, St. Thomas, Virgin Islands, US
[2]University of the Virgin Islands, St. Thomas, Virgin Islands, US

Pelagic Sargassum serves as essential habitat for diverse marine species, yet massive inundations pose significant ecological and economic threats to Caribbean coastlines. This study aimed to determine what epifauna is associated with Sargassum rafts within the USVI and if their community composition changes as it gets closer to shore. Our research focused on sampling rafts on the east end of St. Thomas, given this is the area Sargassum enters the region, and utilized dip net sampling and raft volume estimates to enumerate clinging fauna. We visualized the community composition of clinging fauna using Non-Metric Multidimensional Scaling with Bray-Curtis metrics. Environmental gradients, including depth, distance from shore, and a calculated isolation index, were analyzed via Permutational Multivariate Analysis of Variance (PERMANOVA). Additionally, the fauna fitness was assessed by determining individuals with eggs or parasites attached as unfit. Difference in fauna fitness based on depth was analyzed using a Students T-test. No significant differences in composition were found regarding depth, distance from shore, or isolation index. Furthermore, depth did not significantly impact faunal fitness status. While the first season did not reveal a definitive transitional point, these data provide a baseline for identifying what epifauna species are associated with Sargassum within this region and a potential transition point when the Sargassum rafts stop being ideal habitats. Continued research is essential to improve management practices for Sargassum inundation events in the territory.

Florida Gulf Coast Spatio-Temporal Assessment of Acidification Associated with *Karenia brevis* Blooms and Storm Events

Emily R. Hall[1], ***Sanjana Varanasi***[1], *Janet J. Reimer*[2], *Kimberly K. Yates*[3], *Mitch Lemon*[4], *Matthew Garrett*[5], *Katherine A. Hubbard*[5]

[1]Mote Marine Laboratory, Sarasota, FL
[2]Mid-Atlantic Regional Council on the Ocean, Washington, D.C.
[3]Gulf of America Coastal Ocean Observing System, College Station, TX
[4]University of South Florida, St. Petersburg, FL
[5]Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, St. Petersburg, FL

Coastal and ocean acidification along the Florida Gulf coast is driven by multiple stressors, including rising atmospheric CO_2, eutrophication, riverine discharge, and episodic disturbance events such as storms and harmful algal blooms (HABs). Coastal waters of southwest Florida experience high biomass HABs of the dinoflagellate *Karenia brevis* near annually, while storm events deliver pulses of freshwater, nutrients, and organic matter that can rapidly alter carbonate chemistry. Monthly sampling was conducted along two coastal transects, from Tampa Bay to Charlotte Harbor, between July 2020 and May 2025, capturing carbonate chemistry dynamics before, during, and following both *K. brevis* blooms and storm events. Conductivity, temperature, and depth profiles as well as discrete water samples for *K. brevis* cell abundance, nutrients, and carbonate chemistry were evaluated to characterize how these episodic events drive shifts in carbonate system parameters. This study aims to link observed changes in carbonate chemistry to high biomass blooms of *K. brevis* and storm-driven disturbances in Southwest Florida. Elevated pCO_2 and reduced pH_T were associated with bloom and post-bloom periods, while storm events introduced additional variability through freshwater inputs and nutrient loading. Our findings highlight the need for integrated monitoring to resolve how storms and HAB events contribute to acidification trends across local to regional spatial scales and event to decadal timescales.

Effects of Temperature and N:P Stoichiometry on the Elemental Composition and Eco-physiology of *Microcystis*

Nicole D. Wagner[1], *Tessa V. Wallace*[1], *Olivia H. Sowa*[1], *Ryan J. Andrews*[1], *Clay Prater*[2]

[1]Department of Biological Sciences, Oakland University, Rochester, Michigan, USA
[2]Department of Biological Sciences, University of Arkansas, Fayetteville, Arkansas, USA

Cyanobacteria blooms are increasing in frequency, intensity, and duration globally. Major drivers of cyanobacterial bloom formation include the concentration of nitrogen (N) and phosphorus (P), the N:P stoichiometry, temperature, water column stability, and light. Although the drivers of bloom formation are known, predicting bloom formation, size, and cyanotoxin potential remains elusive. One potential research area that has received little attention is how the elemental composition changes beyond carbon, N, and P, particularly with different N forms and across temperature gradients that may provide insights into bloom formation and expansion. Here, we examined how temperature, nitrogen form, and supply N:P affect the ionome (i.e., elemental composition beyond carbon, N, and P) and eco-physiological traits of *Microcystis aeruginosa* (LE 3). We grew quadruplicates consisting of nitrate or urea as the N-form, at a N:P of 2, 16, 30, and 50, and across a four-temperature gradient ranging from 20 to 32 degrees Celsius and measured the volume corrected, cell quotas, and biovolume of the ionome, and chlorophyll a. We found numerous two-way and three-way interactions among the N:P supply, N-form, and temperature. The ionomic composition was affected by N:P supply, N-form, and temperature. Overall, our results highlight the interconnectedness of the ionomic composition within and among N:P supply and N-form and, when incorporated into a predictive framework, may be better at predicting bloom size and toxin potential.

Economic Benefits of CyanoHAB Mitigation in US Freshwater Systems

Lisa A. Wainger[1]*, Matt A. Weber*[2]*, Eva M. Bailey*[1]*, Kehinde Ojo*[3]*, Emily Hoyt*[3]*, Anjali Gulati*[3]*, Elizabeth W. Price*[1]*, Scott Knoche*[3]

[1]University of Maryland Center for Environmental Science, Solomons, MD, USA
[2]Independent Consultant, Corvallis, OR, USA
[3]Morgan State University, PEARL, St. Leonard, MD, USA

Although the ecological and social harms of CyanoHABs are increasingly recognized, the economic benefits of their mitigation remain poorly quantified. We are developing a national-scale assessment of the expected benefits of mitigating CyanoHABs (reducing frequency, extent and/or duration) using emerging technologies in freshwaters. Two complementary economic approaches are being developed. A return-on-investment (ROI) analysis will explore how implementing new control technologies could reduce future management expenditures. Second, a cost-benefit analysis (CBA) will quantify the public value of enhancing ecosystem service benefits.

For the ROI analysis, we are fitting a regression model to estimate future CyanoHAB management costs. The data are being collected through interviews and web/literature sources. In the 29 states where we conducted interviews, agency managers said monitoring and public warnings were their main activities. A web search revealed that 20 state governments conduct some level of control. Important context for these results is that freshwater resource managers consistently report that funding is insufficient to meet the current management challenge.

For the CBA analysis, we are conducting a stated preference economic valuation survey to assess willingness to pay for reductions in HAB intensity. Benefit categories are recreation safety, ecosystem condition, and access to real-time lake status data. Focus groups used to refine the survey indicated that even people unfamiliar with harmful algae and who do not use lakes, were willing to pay substantial amounts for improvements. Control scenarios are being developed to estimate the net benefits of projected changes in cyanoHAB intensity and associated ecological outcomes.

The research products will provide an integrated economic framework for evaluating CyanoHAB mitigation technologies across US freshwater systems. Funding is from the USACE ERDC.

Moving towards a Regional HABs Observing Network – Co-production of Data Tools

Kirstin Wakefield[1]*, Sheri Schwartz*[2]*, Michelle C. Tomlinson* [3]*, Jen Maucher Fuquay* [4]*, Caroline Owens*[5]*, Margaret Mulholland*[6]*, Greg Silsbe*[7]*, Emily Brownlee*[8]*, Cathy Wazniak*[9]*, Mary Ford*[1]

[1]MARACOOS, Washington DC, USA
[2]Tetratech, South Kingstown, Rhode Island, USA
[3]National Centers for Coastal Ocean Science, NOAA, Silver Spring, Maryland, USA
[4]National Centers for Coastal Ocean Science, NOAA, Charleston, South Carolina, USA
[5]RPI, under contract to NOAA, Tallahassee, Florida, USA
[6]Old Dominion University, Norfolk, VA, USA
[7]University of Maryland Center for Environmental Science, Cambridge, Maryland, USA
[8]St Mary's College of Maryland, St Mary's City, MD, USA
[9]Maryland Department of Natural Resources, Annapolis, Maryland, USA

The Mid-Atlantic is a complex region for harmful algal bloom (HAB) monitoring and management. Major currents influence phytoplankton transport along the coastal shelf. Phytoplankton monitoring is implemented with multiple technologies, at various scales, across numerous agencies and organizations. HAB detections are reported on multiple disparate platforms collected at varying timescales, even within the same body of water. Building a regional HAB observing network to provide early detection and rapid response requires timely access to monitoring data and phytoplankton imaging classifiers from a centralized location. To address these challenges, support real-time decision-making, and enable future predictive capabilities, the Mid-Atlantic Regional Association Coastal Ocean Observing System (MARACOOS), is developing a prototype Chesapeake Bay HABs data portal to support a regional HABs observing network in partnership with researchers, state agencies, and NOAA. Integration of phytoplankton data from state monitoring programs, NOAA's community science based Phytoplankton Monitoring Network, the MERHAB Planktoscope network, and NOAA's satellite remote sensing products will be discussed. The curation of Mid-Atlantic Phytoplankton Imaging Libraries for Imaging Flow CytoBots (IFCB), FlowCam, and Planktoscopes to provide regionally-specific classifiers, standardized metadata, and SOPs and the process to build a community framework for contributions will also be described. Improved IFCB classifiers are also underway for the Mid-Atlantic through interrogations of the New England LTER database and ECOMON cruises. This multi-pronged approach to creating a regional prototype for the National HABs Observing Network (NHABON) will increase the Mid-Atlantic's capacity for early detection and provide more timely bloom species information to coincide with satellite remote sensing that drives forecast products. With fisheries valued at over eight billion dollars and a rapidly expanding aquaculture sector that together support over 60,000 jobs, a HABs observing network can furnish managers and shellfish growers with the data necessary for rapid response to existing and emerging HABs.

Improved Extraction of DSP Toxins from Mussels Reveals Risks of Underreporting in Monitoring Programs

***Zhihong Wang**, Claire Sears, Tod Leighfield, John S. Ramsdell*

NOAA/National Ocean Service, National Centers for Coastal Ocean Science, Charleston, SC, USA

Methanolic extraction of diarrhetic shellfish poisoning (DSP) toxins is critical for public health monitoring, yet inconsistent recoveries remain a significant challenge. We investigated the causes of variable extraction efficiency for okadaic acid (OA) and dinophysistoxin-1 (DTX1) using mussel homogenates freshly prepared or frozen for durations ranging from days to years. Recoveries were notably low (41–62%) in fresh or recently frozen samples but reached ~100% in samples frozen for eight years or heated (76°C, 20 min) prior to extraction. Re-extraction of samples frozen for 1.5–2 years also yielded higher toxin levels. These results suggest that under-recovery is likely due to toxin sequestration by active protein-enzyme complexes—specifically protein phosphatases—or entrapment within intracellular vacuoles. The restoration of recovery via heat or long-term storage points toward a mechanism involving enzymatic inactivation and the structural breakdown of cellular sequestration sites, highlighting a critical gap in standard protocols for fresh samples. To address this, we developed an optimized method that disrupts toxin-matrix interactions, eliminates cleanup beyond filtration, and simplifies liquid chromatography conditions to enhance mass spectrometry (MS) sensitivity while reducing MS contamination. Accuracy ranged from 80–120% across spike levels using solvent and matrix-matched standards for calibrations. These findings demonstrate that conventional protocols can underestimate DSP concentrations in fresh shellfish, with direct implications for regulatory monitoring. Incorporating enzyme-inactivation or enhanced extraction is recommended to ensure accurate quantification, prevent underestimation of risk, and avoid erroneous management decisions. These improved methods strengthen public health protection and regulatory confidence.

Addressing HABs at the Sediment-Water Interface

Justin L Wank, *John A Collins*

AquaBlok Ltd., Swanton, Ohio, United States of America

Harmful algal blooms (HABs) are driven largely by excess phosphorus inputs, including both external loading and internal recycling from sediments. The presentation focuses on internal recycling from sediments and presents a nutrient management approach designed to target bioavailable phosphorus at the sediment-water interface. The system utilizes an engineered particle for controlled delivery of buffered aluminum sulfate. It utilizes a coated limestone core to provide both rapid settling and placement of the active material at the sediment surface and additional buffering capacity. The material, which is called AquaGate+Alum, is a combination of powdered aluminum sulfate, bentonite and limestone, which efficiently descends through the water column and forms a reactive layer at the sediment surface. The released alum binds dissolved reactive phosphorus (DRP), also referred to as Free Reactive Phosphorus (FRP) converting it into stable, insoluble forms, thereby reducing phosphorus bioavailability. Simultaneously, the bentonite and limestone core provides localized buffering capacity, supporting favorable pH conditions during treatment. The dual-function design enables effective interception of phosphorus flux from sediments while also reducing concentration in overlying water column. Bench-scale and field-informed evaluations demonstrate that the material performs across a range of freshwater environments, including lakes, ponds, reservoirs, stormwater systems, and engineered water bodies. The technology can also be adapted to flow-through applications such as stormwater conveyance channels, where it has the potential to capture soluble phosphorus prior to downstream transport. Optimal performance is observed under moderate pH (6.5-8.0) and alkalinity (50-200mg/L as $CaCO_3$), with flexibility for site-specific adjustment based on water chemistry. By addressing both internal and external phosphorus sources, AquaGate+Alum provides a proactive and scalable approach to nutrient management. This technology offers water resource managers a proactive tool to reduce HAB risk, improve water quality, and support long-term ecosystem stability.

Community Reorganization Following *Planktothrix* Bloom Collapse: Differential Responses Across the Microbial Plankton

Christopher S. Ward[1,2]*, Margaret E. Rettig*[2]*, Alexis E. Heath*[2]*, George S. Bullerjahn*[2]

[1]School for Marine Science and Technology, University of Massachusetts Dartmouth, New Bedford, MA, USA
[2]Center of Great Lakes and Watershed Studies, Bowling Green State University, Bowling Green, OH, USA

Hydrological alteration can act as a major ecosystem disturbance, reshaping nutrient delivery, residence time, and biological interactions in downstream aquatic systems. Sandusky Bay, a shallow embayment of western Lake Erie, provides a rare opportunity to evaluate microbial plankton responses following the 2018-2019 removal of a defunct hydroelectric dam on the Sandusky River. Prior to dam removal, Sandusky Bay experienced persistent summer-long blooms of microcystin-producing *Planktothrix agardhii* for more than a decade. In the years following dam removal, spring TN:TP ratios increased and *Planktothrix* largely disappeared, marking a pronounced cyanobacterial bloom regime shift. Here, we examine how this bloom collapse affected the broader microbial plankton community, with particular attention to whether different groups responded uniformly or exhibited contrasting levels of resistance and reorganization. Following the decline of *Planktothrix*, *Cyanobium* emerged as the dominant cyanobacterial group, while other potentially toxigenic cyanobacteria, including *Aphanizomenon*, *Dolichospermum*, and *Cylindrospermopsis/ Raphidiopsis*, appeared as transient summer peaks rather than persistent bloom-formers. Concurrent shifts among heterotrophic bacteria and microeukaryotes suggest that the collapse of the longstanding *Planktothrix* bloom reorganized multiple components of the microbial food web. However, the disturbance response was not uniform across the microbial plankton. Some groups exhibited sensitivity to the altered environmental and phytoplankton regime, while others were comparatively resistant, maintaining similar structure despite major changes in cyanobacterial dominance. These differential responses suggest that microbial plankton communities contain both disturbance-responsive and disturbance-resistant components, with implications for microbial diversity, biogeochemical processing, and ecosystem function following HAB regime shifts.

The Science Behind and Field Use of PAA (Peracetic Acid) and Peroxide in the Control of Cyano/Bacteria

Tom Warmuth

BioSafe Systems, LLC, East Hartford, CT, United States

Peracetic Acid (PAA) / Peroxide based algaecides have been shown to be effective in mitigation and control of cyanobacteria in various methods of application. Lab scale trails of liquid Peroxyacetic acid (PAA)/hydrogen peroxide and solid SCP (sodium carbonate peroxyhydrate) on cyanobacteria give direction on developing effective dosing in field applications for cyanobacterial harmful algal blooms (cHAB) in-season as well as early season/overwintering benthic populations from which planktonic blooms develop later in the spring and summer. More recently, extensive research through private and federal (ACOE) researchers have shown that stand alone use and use alongside phosphorus binding technologies, these overwintering treatments appear to be potentially effective options to minimize the impacts, severity, or frequency of cyanobacterial blooms.

Nanobubble Ozone Technology for Cyanobacterial Harmful Algal Bloom Control: Mechanisms and Design Considerations

*Haley E. Syed[1], **Linda Weavers**[1], Heather Raymond[2], Justin Chaffin[3], Rachel Gabor[4], David Berthold[5], Eugene Braig IV[4], Katherine Gaffney[4], Michael Herman[6], Dail Laughinghouse IV[5], Forrest Lefler[5], Keara Stanislawczyk[4]*

[1]Civil, Environmental and Geodetic Engineering, Ohio State University, Columbus, OH, USA
[2]College of Food, Agricultural and Environmental Sciences, Ohio State University, Columbus, OH, USA
[3]F.T. Stone Laboratory and Ohio Sea Grant, Ohio State University, Put-In-Bay, OH, USA
[4]School of Environment and Natural Resources, Ohio State University, Columbus, OH, USA
[5]Fort Lauderdale Research and Education Center, University of Florida, Davie, FL, USA
[6]Environmental Science Graduate Program, Ohio State University, Columbus, OH, USA

In this study we evaluated the effectiveness of ozone nanobubbles for controlling cyanobacterial harmful algal blooms (CHABs). Mesocosm nanobubble ozone treatment (NBOT) experiments were conducted in 2022, 2023, and 2025. We evaluated the efficacy of NBOT across various water quality conditions, focusing on ozone to dissolved organic carbon (DOC) ratio and high and low bloom densities. Measurements of total and extracellular toxins, nutrients, chlorophyll-a, organic matter and algal class abundances were used to evaluate effectiveness of NBOT on CHABs. Following treatment, rapid cell lysis, increase in aqueous cyanotoxins, and increase in DOC is observed. Greater than 90% reduction in cyanobacteria is observed. 96 hour after treatment, green algae, diatoms and cryptophytes make up approximately 50% of the phytoplankton abundance. We observed that a O_3: DOC dose of at least one yielded best results. With higher O_3:DOC doses population rebounds after 96 hours were not observed while lower doses resulted in less change to the biomass. A second application of ozone 1 hour after treatment resulted in treatment of the aqueous cyanotoxins released due to cell lysis.

Measuring the Socioeconomic Value of the SoundToxins Partnership to the Commercial Shellfish Industry

Michael J. Weir[1]*, Leif Anderson*[2]*, Teri King*[3]*, Jerry Borchert*[4]*, Tracie Barry*[4]*, Michelle Lepori-Bui*[5]*, Melissa Petrich*[5]*, Vera L. Trainer*[6]

[1]Woods Hole Oceanographic Institution, Woods Hole, MA, USA
[2] [2]Northwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Seattle, WA, USA
[3]West Coast Regional Office, National Oceanic and Atmospheric Administration, Lacey, WA, USA
[4]Office of Shellfish and Water Protection, Washington State Department of Health, Tumwater, WA, USA
[5]Washington Sea Grant, Seattle, WA, USA
[6]Olympic Natural Resources Center, University of Washington, Forks, WA , USA

The SoundToxins phytoplankton monitoring and research partnership supports the Washington State Department of Health (WDOH) biotoxin monitoring program by providing an early warning system of harmful algae bloom species, and monitoring phytoplankton at strategic locations near shellfish harvesting sites throughout Puget Sound. SoundToxins partners are Tribal biologists, Federal, State and County researchers, University staff and students, environmental educators, shellfish and finfish producers and community members. When harmful algae are detected by SoundToxins, an alert notifies WDOH managers who can take action including prioritizing shellfish sample analysis at the Public Health Laboratory and request shellfish samples. This study is the first to estimate company-level valuation of the benefits provided by SoundToxins program to the shellfish industry using an economic survey distributed using both in-person and online convenience sampling approaches. This study demonstrated that the average shellfish grower is willing to pay $533.31 per year to support SoundToxins. These findings are consistent with other studies which concluded that protecting public health and resilient coastal industries via continuous environmental monitoring and management of early warning systems is worthwhile.

Development of a Coastal Harmful Algal Bloom Monitoring Plan for Texas

Michael Wetz[1]*, Laura Beecraft*[1]*, Susana Gonzalez*[1]*, Liana Garcia*[2]*, Alex Nuñez*[2]

[1]Harte Research Institute, Texas A&M University-Corpus Christi, Corpus Christi, Texas, USA
[2]Texas Parks & Wildlife Department, Corpus Christi, TX, USA

In Texas, harmful algal bloom (HAB) monitoring by state agencies centers on event response to blooms. Sustained monitoring for early warning purposes is accomplished by Imaging FlowCytobots (IFCB) that until recently were limited to two locations along the 367 miles of coastline, emphasizing the likelihood that HABs not in their immediate vicinity would be missed. Estuaries, where most recent blooms of novel HAB taxa have been documented, are particularly under sampled. This presentation describes the data-driven framework for development of a coastal HAB monitoring plan for Texas. The plan was built upon knowledge of historical coastal HAB events and existing monitoring efforts, stakeholder input, locations of oyster farms and fish/shellfish hatcheries, and an analysis of water quality "hot spots" to identify high priority locations for improving HAB monitoring. Key recommendations of the plan include: 1) close IFCB-based monitoring gaps at ocean inlets where early warning of *Karenia brevis* and *Dinophysis* blooms is possible, and augment IFCB-based monitoring with measurements of environmental data (e.g., salinity, temperature, nutrients) to better understand drivers of blooms, 2) implement new HAB monitoring or support existing HAB monitoring within high priority estuaries, and 3) remove logistical barriers to routine HAB monitoring in Texas' coastal waters by identifying dedicated funding sources, supporting skills-based training to ensure reliability and comparability of data, and increasing coordination and communication to maximize collaboration potential and monitoring effectiveness. Progress towards implementation of plan recommendations will be discussed in more detail in the presentation.

Long-term Water Quality Changes in Baffin Bay (Texas, USA) with Relevance to *Aureoumbra lagunensis* Blooms

***Michael Wetz**, Laura Beecraft*

Harte Research Institute, Texas A&M University-Corpus Christi, Corpus Christi, Texas, USA

Baffin Bay, Texas (USA), is a eutrophying lagoonal estuary that is prone to *Aureoumbra lagunensis* ("brown tide") blooms. Using data from a 13-year citizen science water quality monitoring program, here we quantify variability and long-term changes in phytoplankton biomass and community composition in Baffin Bay. High chlorophyll *a* concentrations (>20 µg/l) that were reflective of dense, spatially extensive *A. lagunensis* blooms, occurred during low rainfall, long residence time and hypersaline conditions in 2013-2015 and in early-mid 2018, whereas diatom blooms were observed following episodic floods in late 2018 to mid-2019 and mid-2021 to mid-2022. Since 2022, there has been a noticeable decrease in chlorophyll *a* in the system, and high biomass of *A. lagunensis* has been limited to one tributary of Baffin Bay despite widespread hypersaline conditions. The reason(s) for the decreasing chlorophyll *a* and prevalence of *A. lagunensis* blooms is unclear but possibilities include: 1) recent watershed nutrient reduction efforts that began in earnest in 2022, 2) sea level rise (~6 mm/year increase over the study period), which brings an influx of lower chlorophyll *a* water into Baffin Bay and decreases the influence of sediment-derived nutrients on the water column via an increase in water depth, and/or 3) a 2-fold increase in silicate concentrations over the study period, possibly due to increasing water temperatures and silicate remineralization, that may favor diatoms over *A. lagunensis*. These findings highlight the complex dynamics that shape water quality, phytoplankton dynamics and *A. lagunensis* bloom prevalence in Baffin Bay, with clear expression of eutrophication symptoms for most of the study period that are hypothesized to be increasingly modulated by large-scale climate drivers and watershed nutrient reduction efforts that will be expanding in scale/coverage.

Why *Microcystis*?

Steven W Wilhelm

Department of Microbiology, The University of Tennessee, Knoxville, TN, USA

Algal blooms degrade aquatic ecosystems worldwide and disrupt essential ecosystem services. In freshwater systems, blooms dominated by cyanobacteria are especially concerning because they produce secondary metabolites, including taste- and odor-causing compounds as well as potent hepatotoxins and neurotoxins. These blooms can have major environmental and socioeconomic impacts.

Although cyanobacterial blooms have long been linked to nutrient enrichment, nutrient loading alone does not fully explain why certain species dominate. To address this gap, we are investigating the traits that give Microcystis a competitive advantage in large, temperate lakes. These traits include the ability to respond to shifts in nutrient chemistry, alter local pH, react strongly to short-term temperature changes, and withstand viral predation—factors that help Microcystis persist at high biomass.
We will present these findings in the broader context of why Microcystis blooms occur in large lakes such as Lake Erie and Lake Taihu.

Ammonium as a Metabolite Proxy for DinoSHIELD: Enabling Regulatory Quantification of a Naturally-Derived Algicide

***Lynn Wilking*[1], *William C. Holland*[2], *D. Ransom Hardison*[2], *Kathryn Coyne*[3], *Kaytee Pokrzywinski*[2]**

[1]CSS Inc. under contract to NOAA-NCCOS, Beaufort, NC, USA
[2]NOAA-NCCOS, Beaufort, NC, USA
[3]University of Delaware, Lewes, DE, USA

DinoSHIELD is an algicide produced by the marine bacterium *Shewanella* sp. IRI-160 that selectively targets harmful dinoflagellates like *Karenia brevis*, the species responsible for red tide in Florida. While highly effective against *K. brevis* (87-97% activity), the identity of the bioactive compound(s) remains unknown, creating regulatory challenges for environmental tracking and permitting. *Shewanella* sp. IRI-160 produces both algicidal metabolites and ammonium (NH_4^+). Studies have shown that the algicidal components in DinoSHIELD and NH_4^+ toxicity function through independent pathways, indicating NH_4^+ is not the driver of algicidal activity. Direct comparisons show that at equivalent concentrations (60µM NH_4^+), DinoSHIELD produces 45-50% algicidal activity while NH_4^+ alone causes only 8-15% growth inhibition on *K. brevis*. Transcriptomic analysis confirms 83% of biological processes are uniquely regulated by DinoSHIELD rather than NH_4^+, further demonstrating independence. However, NH_4 concentrations are strongly correlated with algicide potency across three formulations: natural seawater, seawater + casamino acids, and pure water. This covariation enables NH_4^+ to serve as a quantifiable proxy for the algicidal compounds. The relationship follows a saturation curve: activity increases rapidly at lower NH_4^+ concentrations and plateaus at ~90-100% once a threshold is exceeded. The pure water formulation EC_{50} (27µM NH_4^+) and EC_{95} (99µM NH_4^+) provide regulatory reference points. Safety margins remain substantial: the most sensitive non-target organism (copepod nauplii) show LC_{50} is 10X the effective dose at 272µM NH_4^+. Using NH_4^+ as a proxy validates data across laboratory monocultures, natural bloom microcosms, repeated-dosing community experiments, and non-target studies. This proxy addresses key regulatory requirements while maintaining biological relevance that is especially valuable for securing EPA experimental use permits for this promising HAB control technology.

Distribution of PSP-causing *Alexandrium catenella* blooms in Chiniak Bay, Kodiak Island, Alaska

*Steven R. Kibler[1], Julie A. Matweyou[2], Mark W. Vandersea[1], Leanne M. Poussard[1], **Lynn E. Wiking**[3], Connor P. Cleary[4], Jennifer R. McCall[5], Andie A. Wall[6], Isaiah Dela Cruz[6]*

[1]NOAA National Centers for Coastal Ocean Science, Beaufort Lab, Beaufort, NC, USA
[2]University of Alaska Fairbanks, Kodiak Seafood and Marine Science Center, Kodiak, AK, USA
[3]Consolidated Safety Services, Inc., under contract to NOAA NCCOS, Beaufort Laboratory, Beaufort, NC, USA
[4]NOAA Alaska Fisheries Science Center, Kodiak Lab, Kodiak, AK, USA
[5]Center for Marine Science, University of North Carolina Wilmington, Wilmington, NC, USA
[6]Kodiak Area Native Association, Kodiak, AK, USA

Communities in the Kodiak Archipelago of Alaska contend with serious risks from paralytic shellfish poisoning (PSP), a potentially fatal illness caused by ingestion of shellfish containing neurotoxins from the toxic dinoflagellate *Alexandrium catenella*. Blooms of this species occur each spring and summer (May-Aug), where they reduce food security for Kodiak subsistence harvesters and impose economic risks to local shellfish growers. The limited toxicity monitoring that occurs in the archipelago is restricted largely to the ~40-mile road system encompassing the city of Kodiak and the shoreline of the surrounding Chiniak Bay. Local testing data demonstrate a complex pattern of shellfish toxicity, where some locations in the bay exhibit high PSP toxin levels, while other sites are relatively toxin-free. In such a spatially complex environment, the factors governing *Alexandrium* bloom intensity and distribution must be identified to build a more effective monitoring strategy and reduce toxicity risks. As part of a 2023–2028 MERHAB project characterizing HAB occurrence in the eastern Kodiak Archipelago, bloom mapping surveys in Chiniak Bay were completed in May, June, and August of 2024 and 2025. Additionally, a 2024 sediment survey confirmed that these blooms are supported by local beds of benthic resting cysts. The cysts overwinter and germinate in the early spring to seed *Alexandrium* blooms in the water column. Here we present data on *Alexandrium* bloom and resting cyst distribution in the Chiniak Bay area in relation to hydrographic drivers. Patterns of cell and cyst abundance are discussed in comparison with shore-based shellfish monitoring data, locations where subsistence harvesting occurs, and sites of shellfish mariculture. These preliminary findings account for recurrence of Kodiak *A. catenella* blooms and have implications for PSP risks to subsistence harvesters and new mariculture operations in the area.

Identifying Mid-Atlantic *Karenia*: Novel Use of the Covaris ML230 Focused-Ultrasonicator to Recover DNA from Single-Cells

***Jennifer L. Wolny*[1], *Elizabeth S. Hunter*[1], *Sameer Vasantgadkar*[2], *William Heddendorf*[3] & *Sara M. Handy*[1]**

[1]US Food and Drug Administration - Human Foods Program, College Park, MD, USA
[2]Covaris LLC, Woburn, MA, USA
[3]New Jersey Department of Environmental Protection - Bureau of Marine Water Monitoring, Leeds Point, NJ, USA

During the past decade, *Karenia* species have been detected more frequently in mid-Atlantic coastal waters than previous decades, with blooms occurring in mid-summer and autumn. These blooms are often dominated by *Karenia papilionacea* (10^5 cells L^{-1}) recognized via its unique butterfly-shape morphology. However, cells that resemble the highly toxigenic sister-taxon, *Karenia brevis*, are also found within the blooms at concentrations that trigger resource management actions to ensure shellfish in impacted areas are safe for human consumption (10^3 cells L^{-1}). Routine monitoring of coastal waters by state government and academic partners, using traditional light microscopy and Imaging Flow Cytobot (IFCB) methods, has allowed for the morphological examination of these populations, but obtaining genetic confirmation has been elusive since cultures of *Karenia* species are difficult to establish. The Covaris ML230 Focused-Ultrasonicator was evaluated for DNA recovery from single *Karenia* cells of varying morphologies in Lugol's preserved field samples. This study applied Covaris' Adaptive Focused Acoustics (AFA) technology to these specific protistan samples, extending the system's routine application for nucleic acid and protein extraction from mammalian, fungal, and bacterial matrices. The successful recovery of high-quality DNA from preserved *Karenia* cells allowed us to establish the genetic identity of taxa from a September 2025 *Karenia* bloom that occurred along the New Jersey coast. Analysis of the LSU D1-D2 gene coding region indicated that cells with the butterfly-shape and the *K. brevis*-like cells were both *K. papilionacea*. Additionally, the New Jersey *K. papilionacea* cells were a 99.3% match to *K. papilionacea* populations reported from Newfoundland, Canada and were genetically distinct from *K. papilionacea* populations from Asia and Australia.

Modeling Ciguatera Risk: A Benthic-Pelagic Framework for *Gambierdiscus* Transport and Trophic Transfer in Hawai‘i

Jennifer A.T.K. Wong-Ala, Eileen Nalley

University of Hawaii Sea Grant College Program, Honolulu, HI, U.S.A.

Gambierdiscus spp. are epiphytic dinoflagellates that are widespread across the Pacific Ocean, the Gulf of Mexico, and the Caribbean Sea, where they can produce potent ciguatoxins that cause ciguatera poisoning. Forecasting where these dinoflagellates thrive and how they accumulate in reef fish is a complex problem that requires targeted modeling to protect fishers' health. In the Hawaiian archipelago, fishers are affected by ciguatera poisoning, a public health issue that remains highly underreported. To address this threat, our research outlines a plan to develop a biophysical ecosystem model to explore high-risk areas and time periods for ciguatera poisoning. This poster introduces our proposed conceptual framework and initial implementation strategy. Given the significant environmental unknowns and cryptic diversity of *Gambierdiscus* in Hawai‘i, our initial framework uses a simplified approach centered on the prevalent species *Gambierdiscus australes*. We plan to pair this biological target with a heat map of macroalgae around the island of O‘ahu. Using a coupled benthic-pelagic simulation framework, we intend to model the physical detachment, pelagic transport, and reattachment of cells driven by wave-induced bottom shear stress. The subsequent phase will couple another model to simulate ciguatoxin bioaccumulation in target reef fish species heavily implicated in local poisoning events, such as kole (*Ctenochaetus strigosus*). By presenting this foundational roadmap that links macroalgal habitat mapping, individual-based hydrodynamic tracking, and localized trophic transfer, we aim to discuss our scalable tool for regional risk assessment and coastal management.

Genomic Detection of Domoic Acid Biosynthesis Uncovers Expanded Toxigenic Diversity Across *Pseudo-nitzschia* Diatoms

Steffaney M. Wood-Rocca [1, 2] †, *Zoltán Füssy* [2, 3] †, *Monica Thukral* [2, 3], *Andres Mauricio Caraballo-Rodriguez, Hong Zheng* [2, 3], *Shelly A. Wanamaker* [4, 5], *Jennifer M. Polinski* [5], *Alexandra DeSmidt* [6], *Freya Hammar* [2, 3], *Brian D. Bill* [7], *Hannah McGrath* [8], *Nathalie Choisne* [10], *Florian Maumus* [10], *Tom. O. Delmont* [11], *Katherine A. Hubbard* [6], *Pieter C. Dorrestein, Matthew J. Harke* [5]*, *Bradley S. Moore* [1, 9]*, *Andrew E. Allen* [2, 3]*

[1] Center for Marine Biotechnology and Biomedicine, Scripps Institution of Oceanography, University of California San Diego, La Jolla, CA, USA
[2] Microbial and Environmental Genomics Group, J. Craig Venter Institute, La Jolla, CA, USA
[3] Integrative Oceanography Division, Scripps Institution of Oceanography, University of California San Diego, La Jolla, CA, USA
[4] School of Aquatic and Fishery Sciences, University of Washington, Seattle, WA, USA
[5] Gloucester Marine Genomics Institute, Gloucester, MA, USA
[6] Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, St. Petersburg, FL, USA
[7] Environmental and Fisheries Science Division, Northwest Fisheries Science Center, National Marine Fisheries Service, National Oceanic and Atmospheric Administration, Seattle, WA, USA
[8] Moss Landing Marine Labs, 8272 Moss Landing Road, Moss Landing, CA, USA
[9] Skaggs School of Pharmacy and Pharmaceutical Sciences, University of California San Diego, La Jolla, CA, USA
[10] Université Paris-Saclay, INRAE, AgroParisTech, Institute Jean-Pierre Bourgin for Plant Sciences, 78000, Versailles, France
† Contributed equally to this work.

Domoic acid production by the diatom genus *Pseudo-nitzschia* drives recurrent harmful algal blooms with major consequences for marine ecosystems, fisheries, and human health. Predicting domoic acid risk remains challenging because toxin production is unevenly distributed across morphologically similar and cryptic lineages, and species-level assignments based on morphology or single marker genes often fail to resolve toxigenic potential. Here, we expand genomic resources for *Pseudo-nitzschia* by generating and compiling high-quality genomes spanning diverse species and biogeographic origins, enabling a genus-wide phylogenomic framework to investigate the distribution and evolution of the domoic acid biosynthesis gene cluster. Comparative analyses show that domoic acid biosynthetic capacity is consistently associated with the presence of the domoic acid biosynthesis pathway, which we detect only in species with confirmed domoic acid production. While the cluster exhibits a conserved core structure, several lineages display signatures of ongoing evolution, including intronization, locus rearrangement, pseudogenization, as well as the emergence of a biochemically functional kainoid synthase relocated to a distinct genomic locus in *P. australis*. Metatranscriptomic surveys reveal widespread environmental domoic acid biosynthesis expression, across size classes and species, implicating taxa not typically associated with environmental domoic acid events such as *P. obtusa* and *P. plurisecta*. Finally, nutrient limitation experiments in the inconsistent domoic acid producer *P. pseudodelicatissima* uncovered coordinated domoic acid biosynthesis expression in response to silicon limitation across distinct co-expression modules. Together, these results refine the phylogenetic scope of domoic acid production and provide a genome-resolved basis for improved molecular monitoring of toxigenic diversity.

Decoding the Hidden Chemistry of Harmful Algal Blooms: MS^2 as a Window into Cyanobacterial Metabolites

Runjie Xia [1],*Lindsey Ahn*[1],*Michaela Burkhauser*[1], *Ross Youngs*[2] *and Matthew J. Bertin*[1]

[1]Department of Chemistry, Case Western Reserve University, Cleveland, OH , USA
[2]Biosortia, Inc., Columbus, OH, USA

Cyanobacterial harmful algal blooms produce complex mixtures of cyanopeptides, including microcystins and micropeptins, which vary in structure, toxicity, and abundance. Traditional isolation followed by NMR-based structure elucidation provides definitive structural confirmation but limits our understanding of the full chemical landscape. In this talk, I will show how tandem mass spectrometry, combined with molecular networking and product ion searches, allows us to rapidly decode the structures of cyanopeptides, especially micropeptins, in environmental samples. By leveraging diagnostic fragments, we can identify core scaffold types, side-chain modifications, and even residue-specific modifications, building a "chemical atlas" of bloom metabolites. This approach not only highlights structural diversity and biosynthetic flexibility but also can be used as a valuable tool for compound dereplication, structural prediction, and environmental monitoring.

The Detection of Total Microcystins and Nodularins in Water Samples with an ADDA-Targeted ELISA

***Jingping Xie**, Peter Robinson, Titan Fan*

Beacon Analytical Systems, Inc., Saco, ME, USA

Microcystins (MC) and Nodularins (NOD) are prominent hepatotoxins produced by cyanobacteria during harmful algal blooms (HAB). Monitoring of these environmental toxins is necessary to the management of inland fisheries and aquafers. Total MC and NOD were determined by developing a competitive enzyme-linked immunosorbent assay (ELISA) targeting their characteristic ADDA (3-amino-9-methoxy-2,6,8-trimethyl-10-phenyldeca-4,6-dienoic acid) amino acid side chain. For the detection of this shared side chain, rabbit anti-ADDA polyclonal antibodies were produced. Relative to MC-LR (100%), cross-reactivity was observed as follows: NOD (132%), MC-*dm*LR (110%), MC-LA (90%), MC-RR (81%), MC-LW (78%), MC-LF (65%), and MC-YR (58%). This broad congener cross-reactivity, assay sensitivity of 0.1 ppb (calibrator range 0.1 to 6 ppb MC-LR), and 60 minute microtiter plate format allows for a uniquely rapid, robust, and cost effective solution for total MC and NOD detection. Method performance was evaluated using negative pond water samples collected locally in Saco, Maine. Samples were spiked with MC-LR at levels of 1, 3, and 3.5 ppb, yielding recoveries of 102%, 110%, and 125% respectively. Proficiency testing samples comprised of raw source or recreational fresh water and recovered 67% to 120% of the target. No matrix effects were observed with sodium thiosulfate (<10 mg/mL), seawater (salinity <3.8%), and ascorbic acid (<1 mg/mL).

Short-term *Sargassum* Trajectory Forecast for the Gulf of America and East Coast of Florida

Haibo Xu*, Yonggang Liu, Yuyuan Xie, Brian Barnes, Chuanmin Hu, Junnan Jiao*

University of South Florida, St. Petersburg, College of Marine Science, St. Petersburg, FL, USA

A short-term Sargassum trajectory forecast product is developed by integrating satellite imagery with numerical ocean circulation models. Satellite images are available at two resolutions: basin-scale coverage at 1 km resolution, and higher-resolution (60 m) coverage of coastal sea adjacent to land, where moderate-resolution imagery has no data. The circulation models include the West Florida Coastal Ocean Model (WFCOM), the East Florida Coastal Ocean Model (EFCOM), and the Global Hybrid Coordinate Ocean Model (HYCOM). Once detected by satellite, Sargassum patches are tracked by a Lagrangian particle-tracking model, using WFCOM or EFCOM for high-resolution coastal inundation forecast and HYCOM for more offshore regions. The daily automated system produces 1-day hindcast and 3.5-day forecast of Sargassum trajectories, along with the percentage of coverage within each satellite pixel representing the local Sargassum density. A sensitivity study is also conducted to evaluate the impact of different windage coefficients (0.5% - 3% of the surface wind velocity) on trajectory predictions.

Have Florida's Red Tides Increased over the Past 40 years? In situ and Satellite Observations

Yao Yao[1]*, Chuanmin Hu*[1]*, Brian B. Barnes*[1]*, Katherine A. Hubbard*[2]*, Cheng Xue*[1]*, Jennifer P. Cannizzaro*[1]

[1]College of Marine Science, University of South Florida, St. Petersburg, Florida, USA
[2]Fish and Wildlife Research Institute, Florida Fish and Wildlife Conservation Commission, St. Petersburg, Florida, USA

Harmful algal blooms (HABs) caused by Karenia brevis (commonly known as 'red tides') have a long occurrence history on the West Florida Shelf (WFS). While recent history shows roughly annual frequency, it is unclear if these red tides have changed over the past decades. Elucidating any such trend appears simple but is notoriously difficult due to the "observer effect" in field measurements, lack of reliable remote sensing algorithms, and inconsistencies between satellites. This study integrates in situ K. brevis cell abundance records with historical (1978–1986) and modern (2003–2019) satellite observations to reconstruct red tide patterns across the WFS, filling a long-standing gap in the late-1970s to mid-1980s record. Our analysis reveals that while the seasonality of red tides has remained largely consistent over the past several decades, indicators of bloom spatial extent and persistence suggest notable increases in recent years. The annual probability of fall bloom occurrence rose from 75% to more than 90%, and the mean duration of red tide events extended from 3.0 to 6.1 months. For the HABs "epicenter" region from Tampa Bay to Charlotte Harbor, annual occurrence frequency also increased from historical era to modern era, but the spatial extent remained stable, suggesting that most of the observed changes are due to HABs expansion in other regions of the WFS.

Perspectives on Detecting, Predicting and Managing Harmful Algal Blooms in Rivers from an Interdisciplinary Collaboration

Mindy Yeager-Armstead[1], *Anna Linhoss*[2], *Justin Murdock*[3], *Prem Parajuli*[4], *Jimmy Fox*[5] *and Bill Ford*[6]

[1]Department of Natural Resources and Earth Sciences, Marshall University, Huntington, West Virginia, USA
[2]Department of Biosystems Engineering, Auburn University, Auburn, Alabama, USA
[3]Department of Biology, Tennessee Tech University, Cookeville, Tennessee, USA
[4]Department of Agricultural and Biological Engineering, Mississippi State University, Mississippi State, Mississippi, USA
[5]Department of Civil Engineering, University of Kentucky, Lexington, Kentucky, USA
[6]Biosystems and Agricultural Engineering, University of Kentucky, Lexington, Kentucky, USA

A collaborative project is underway to fill data gaps around algal dynamics in a managed river system incorporating diverse strategies including remote sensing, laboratory studies, hydrodynamic and hydrologic modeling, and machine learning. Focused on the Greenup Pool of the Ohio River, this work aims to understand the role of hydrology in structuring algal communities and bloom potential in lotic systems, identify the sources of plankters that contribute to riverine productivity, and identify HAB triggers including drivers of cell growth and toxin production. The knowledge gained is then used to inform detection and prediction of blooms in support of aquatic resource management through multiple tools having variable strengths and limitations. Specifically, strategies for HAB detection utilize remote sensing and in-situ monitoring with machine learning while HAB forecasting is maximized with neural networks. Testing of HAB management scenarios and predictions of HAB potential under future climate scenarios are accomplished by hydrodynamic and hydrologic modeling. Laboratory and field studies validate remote sensing and inform machine learning and model development. The suite of methodologies employed provides scalable and transferable workflows for HAB detection, prediction and management in riverine ecosystems and converges on the importance of tributary sources of algae, and drivers of algal growth in the mainstem of the Ohio River.

Cyanobacterial Bloom Dynamics and Microcystin Risk in Mississinewa Reservoir, Indiana: Spatial Gradients, Temporal Escalation, and Nitrogen-Dominated Toxin Production

Nileshwari R.Yewle*, Isaac Bradford, Keith Cherkauer*

Department of Agricultural and Biological Engineering, Purdue University, West Lafayette, Indiana, USA

Mississinewa Reservoir (Miami County, Indiana) is a 3,180-acre impoundment subject to recurring cyanobacterial harmful algal blooms driven by agricultural nutrient loading from the Mississinewa River watershed. We conducted an integrated water quality assessment across 17 fixed stations along a 13.9-km longitudinal transect from dam to open water, over 11 sampling campaigns from June 2024 to September 2025 (148 observations; 22 variables). Microcystin exceeded WHO drinking-water and recreational guidelines in 57% and 12% of samples, respectively, peaking at 23.61 micrograms per litre in August 2025 concurrent with an Indiana Department of Environmental Management Beach Advisory Alert, representing a 24-fold escalation from 2024 levels. Spearman rank correlations identified significant positive longitudinal gradients in chlorophyll-a, dissolved oxygen, turbidity, and pH with distance from dam, and a negative gradient in nitrate-nitrite, consistent with biological nitrogen assimilation in the lacustrine zone. The molar nitrogen-to-phosphorus ratio was the dominant predictor of Microcystin concentration, followed by total nitrogen and dissolved organic carbon; soluble reactive phosphorus was non-significant after detection limit correction, indicating nitrogen-limited toxin biosynthesis. Bloom conditions exceeded non-bloom Microcystin by 7.5-fold. Principal component analysis and Ward linkage hierarchical clustering resolved 84% of site variance and identified three ecologically distinct reservoir zones corresponding to dam-proximal, mid-reservoir, and upstream open-water areas with differential bloom risk. These findings implicate watershed nitrogen loading as the proximate driver of cyanotoxin production in Mississinewa Reservoir and support a dual-nutrient management framework, a chlorophyll-a early warning threshold, and risk-stratified monitoring at upstream sentinel sites.

Continuous In-Situ Estimation of Cyanobacterial Abundance Using a Multi-Probe Submersible Fluorescence Monitoring System

Lawrence Younan

Turner Designs, San Jose, CA, USA

Monitoring phycocyanin (PC) to chlorophyll (CHL) ratios in the field has proven to be a reliable way to estimate cyanobacterial abundance within a mixed phytoplankton population and predict the onset of harmful algal blooms (HABs). Until now, this approach has been limited to grab sample analysis using handheld instruments, which restricts the temporal resolution of monitoring efforts. To address this limitation, we present a continuous *in situ* monitoring system utilizing various fluorescence probes to estimate cyanobacterial abundance in real time. This system simultaneously measures a fluorescence matrix – including chlorophyll, CDOM, and turbidity – providing the optical information needed to accurately estimate cyanobacterial abundance in real-world water conditions. The system is designed for flexible deployment in lakes, reservoirs, and drinking water intake environments. Here we compare continuous *in situ* cyanobacterial abundance estimates against discrete sample measurements and discuss how this approach gives water managers a practical, high-frequency early warning tool without a proportional increase in monitoring effort.

A Risk Characterization Tool for HABs on the Ohio

Greg Youngstrom

ORSANCO, Cincinnati, Ohio, USA

Twenty-five years of Ohio River discharge data were used to develop Bayesian regression models that are currently applicable to 20 sites spread-out along the entire 1579 km of the river's length. Prediction probabilities are served in real time as a component of a risk characterization tool/web application. In addition to presenting the model's results, the tool was designed with visualization options for studying water quality trends among eight river sites currently collecting data that could be associated with or indicative of bloom conditions. Ongoing improvements to the tool include bringing in satellite imagery as well as real-time data from sondes. The tool is made accessible to river water quality professionals to support risk communication to stakeholders, as well as serving as a real-time water data monitoring utility.

Multiplex ddPCR Enables High-Throughput Microcystin Gene Quantification in Freshwater Systems

Wafa Youssf, *Wen Zhang*

Department of Civil Engineering, University of Arkansas, Fayetteville, AR 72701, USA

Harmful cyanobacterial blooms pose increasing ecological and public health risks due to production of microcystins, which are potent hepatotoxins in freshwater systems. Reliable assessment of bloom toxicity requires simultaneous quantification of cyanobacterial abundance and toxin biosynthesis potential, which remains a key limitation in current monitoring approaches. This study developed and validated a multiplex droplet digital polymerase chain reaction assay for concurrent quantification of four key microcystin biosynthesis genes, *mcyA*, *mcyB*, *mcyD* and *mcyE,* together with total cyanobacterial abundance. The assay demonstrated high analytical sensitivity with a limit of detection of 0.5 gene copies per microliter and a limit of quantification of 5 gene copies per microliter, strong linearity with $R^2 > 0.9998$, and consistent agreement between single target and multiplex formats with minimal interference. Method performance was validated using laboratory cultures and extended to a three-year freshwater monitoring dataset from Lake Fayetteville, enabling evaluation across controlled and natural variability. The assay reliably detected toxin producing populations over a wide range of gene copy numbers and captured temporal dynamics associated with environmental fluctuations. Agreement between formats remained high, with differences typically below 10% and minor deviations only at concentration extremes consistent with expected droplet partitioning behavior. This multiplex approach improves analytical efficiency by enabling simultaneous multi gene and abundance assessment within a single reaction, reducing workload and increasing throughput. By integrating long term field monitoring with laboratory validation, this work establishes a robust molecular framework for tracking toxin producing cyanobacteria and supports improved early warning and risk assessment for harmful algal blooms.

Harmful Algal Bloom (HAB) Forecast for the lower Chesapeake Bay

Xin Yu[1], *Michelle C. Tomlinson*[2], *Yizhen Li*[3], *Alexandria G. Hounshell*[2], *Kari St.Laurent*[2]

[1]RPI. Under Contract to NOAA
[2]National Centers for Coastal Ocean Science (NCCOS), NOAA
[3]CSS. Inc. Under Contract to NOAA

HABs are routinely identified in Chesapeake Bay (CB) in both the mainstem and tributaries. Understanding and predicting the timing and movement of these blooms is critically important to help enable better coastal resource and ecosystem management. To fill this gap, we are developing a 1-D time-dependent model to understand the biophysical drivers and initiation for HAB occurrence in the York River estuary combined with a 3-D coupled biophysical model for short-term HAB forecasts. The 1-D model simulates hourly changes of phytoplankton biomass based on hourly data of tide, river inflow, water temperature and salinity, as well as monthly nutrient data (linearly interpolated into hourly). By integrating the growth function of HAB species, the model successfully captures most of the bloom/non-bloom years of *Margalefidinium polykrikoides* (*M. polykrikoides*) over the past 15 years, but fails to capture non-bloom years such as 2019, when there was a major hurricane impacting the region. The 1-D model, however, does not take into account spatial variability of the bloom. For this end, we used the 3-D bio-physical model to simulate HAB mixotrophic growth, respiration, and vertical diurnal migration, and predict the spatial distribution and temporal evolution of *M. polykrikoides* blooms in the lower Chesapeake Bay. Particle release location was identified using a fluorescence based, red-edge (RE10) satellite algorithm while particle density was inferred from satellite-derived chlorophyll-a concentrations both obtained from Ocean Land Colour Imager (OLCI) satellite imagery on the Sentinel-3 Mission. This model framework has been tested and validated for *M. polykrikoides* blooms in the York River, James River, and lower main-stem of the Bay from 2018 to 2023. We will discuss the advantages, limitations, and future direction of both 1-D and 3-D models for successful bloom prediction and tracking.

Spatiotemporal Variation in Algal and Bacterial Assemblages Associated with Toxigenic Benthic Cyanobacteria *Microcoleus* and *Anabaena* in Northern Californian Rivers

Jordan Zabrecky[1]*, Taryn Elliott*[1]*, Meaghan Hickey*[1]*, Raina Fitzpatrick*[2]*, Rosalina Stancheva*[3]*, Keith Bouma-Gregson*[4]*, Laurel Genzoli*[1]*, Grant Johnson*[5]*, Shadman Kaiser*[6]*, Abeer Sohrab*[6]*, Ramesh Goel*[6]*, Joanna Blaszczak*[1]

[1]University of Nevada, Reno, NV, USA
[2]Northern Arizona University, Flagstaff, AZ, USA
[3]George Mason University, Fairfax, VA, USA
[4]U.S. Geological Survey California Water Science Center, Sacramento, CA, USA
[5]Karuk Tribe Department of Natural Resources, Happy Camp, CA, USA
[6]University of Utah, Salt Lake City, UT, USA

Proliferations of benthic cyanobacteria associated with the production of neurotoxic cyanotoxins known as anatoxins have been increasingly observed in rivers worldwide. However, controls on their anatoxin production are poorly understood, as previous studies have found weak relationships between anatoxins and environmental factors. This suggests that biotic factors, such as species interactions among co-occurring taxa, may influence anatoxin production. In this study, we investigated how microbial assemblages within cyanobacterial benthic mats varied among rivers, across time, and with varying anatoxin concentrations. From June to September in 2022, we collected separate *Microcoleus* and *Anabaena* composite mat samples biweekly from the South Fork Eel, Russian, and Salmon Rivers in northern California. We analyzed samples for anatoxins using liquid chromatography tandem mass spectrometry, quantified assemblage composition with both microscopy and amplicon metabarcoding of the 16S rRNA gene and used PICRUSt2 to predict the functional profile of assemblages. Preliminary results indicate that both microscopically- and molecularly-identified *Microcoleus* assemblages significantly differed among rivers while those of *Anabaena* were similar. *Microcoleus* assemblages from the South Fork Eel River contained nitrogen-fixing taxa such as *Nostoc*, *Anabaena*, and *Epithemia* and had higher bacterial diversity in contrast to those from the Salmon River (mean Shannon index 5.7 vs. 4.6). Among all three rivers, *Anabaena* assemblages always included other anatoxin-associated taxa including, *Leptolyngbya*, *Geitlerinema*, and *Microcoleus*, and shared a similar bacterial diversity (mean Shannon index ranging from 6.4 to 6.7). In the South Fork Eel River, where anatoxin concentrations ranged from non-detection to 120 µg anatoxins per gram organic matter, we found that while microscopically- and molecularly- identified assemblages significantly differed with varying anatoxin concentrations, phylogenetically inferred functional profiles did not. This suggests that biotic factors may still influence anatoxin production, but process-based approaches are needed to determine the underlying mechanisms.

Culture Conditions Impact Culturability of Bacteria from Freshwater Systems

***Alyssa Zeniak**, Jackson Corbeil, Marisol Ballout, Elise Geller, Morgan M. Steffen*

James Madison University, Harrisonburg, VA, USA

It is well-established that over 99% of all bacteria on the planet are not able to be cultured in laboratory settings. When we attempt to culture bacteria from environmental systems for experimentation, enrichment conditions are often set to mimic one set of environmental measurements that most closely represent natural conditions. This may skew our ability to capture the most diverse libraries of bacterial isolates and therefore limit our experimental capacity. Here we tested the impact of media type and temperature on our ability to culture bacteria from freshwater systems, specifically from xenic cultures of freshwater cyanobacteria and Lake Erie cyanobacterial harmful algal blooms (cHABs). Cultures were grown in three to four different media types (CTTY, L1TY, TSB, and R2A) and incubated at 26 °C and 37 °C for 72 hours, with time points collected every eight hours. Bacterial growth was monitored using optical density measurements. Results showed that growth patterns varied depending on incubation conditions. Freshwater bacteria reached exponential phase and peak population density more rapidly in CTTY and L1TY media at 37 °C, with peak optical density occurring between 32 and 64 hours. In contrast, TSB supported greater growth at 26 °C, with maximum optical density observed between 40 and 64 hours. findings demonstrate that both temperature and media composition significantly influence the growth and culturability of Lake Erie bacterial isolates, emphasizing the importance of multiple incubation conditions in environmental microbiology studies to target a more diverse representation of the freshwater bacteria microbiome in culture.

Diel Dynamics of *Microcystis* Ecophysiology in Lake Erie

Brittany N. Zepernick[1,2]*, Anna G. Boegehold*[3]*, E. Anders Kiledal*[4]*, Emily E. Chase*[1,5]*, Robbie M. Martin*[1]*, Casey M. Godwin*[3]*, Trisha L. Spanbauer*[6]*, Gregory L. Dick*[3,4]*, Reagan M. Errera*[7]*, Steven W. Wilhelm*[1]

[1]Department of Microbiology, University of Tennessee, Knoxville, TN, USA
[2]Department of Biology & Marine Biology, University of North Carolina Wilmington, Wilmington, NC, USA
[3]International Joint Commission, Windsor, ON, CA
[4]Department of Earth and Environmental Sciences, University of Michigan, Ann Arbor, MI, USA
[5]Department of Biology, University of Winnipeg, Winnipeg, MB, CA
[6]Department of Earth and Environmental Sciences, University of Kentucky, Lexington, KY, USA
[7]Great Lakes Environmental Research Laboratory, National Oceanic and Atmospheric Administration, Ann Arbor, MI, USA

Lake Erie, like many large, shallow lakes, experiences recurring cyanobacterial harmful algal blooms (cHABs). Monitoring at monthly, weekly, and daily scales has improved our ability to identify bloom drivers and predict bloom events. However, one important temporal dimension remains largely unexplored: Diel (day–night) variation. Although diel changes may seem subtle, marine studies have shown that the day–night partitioning of microbial physiology can substantially influence community-level dynamics. Previous work in Lake Erie detected diel shifts in cyanobacterial gene expression, but limited data and the absence of statistical tests for diel periodicity constrained the resolution and broader interpretation of those findings. To address this gap, we carried out the Diel Assessment of Life in Lake Erie (DALLE) cruise at a fixed station in the western basin. Over a two-day period in July 2023, we collected samples at five time points each day - 2:00, 8:00, 14:00, 17:00, and 21:00 hours - to capture key stages of the diel cycle. Metatranscriptomic analyses revealed *Microcystis* dominated the transcriptionally active community, accounting for up to 47% of total transcriptional activity. Using RAIN (Rhythmicity Analysis Incorporating Nonparametric) methods, we found that approximately 8% of cyanobacterial genes exhibited significant diel periodicity. Together with a broader analysis of the full microbial community, these results deepen our understanding of cHAB dynamics across within-day temporal gradients and strengthen our capacity to anticipate the ecological drivers of future blooms.