

“There is a fundamental unity
among biological, chemical, and
physical systems in the sea.”

—Henry Bryant Bigelow

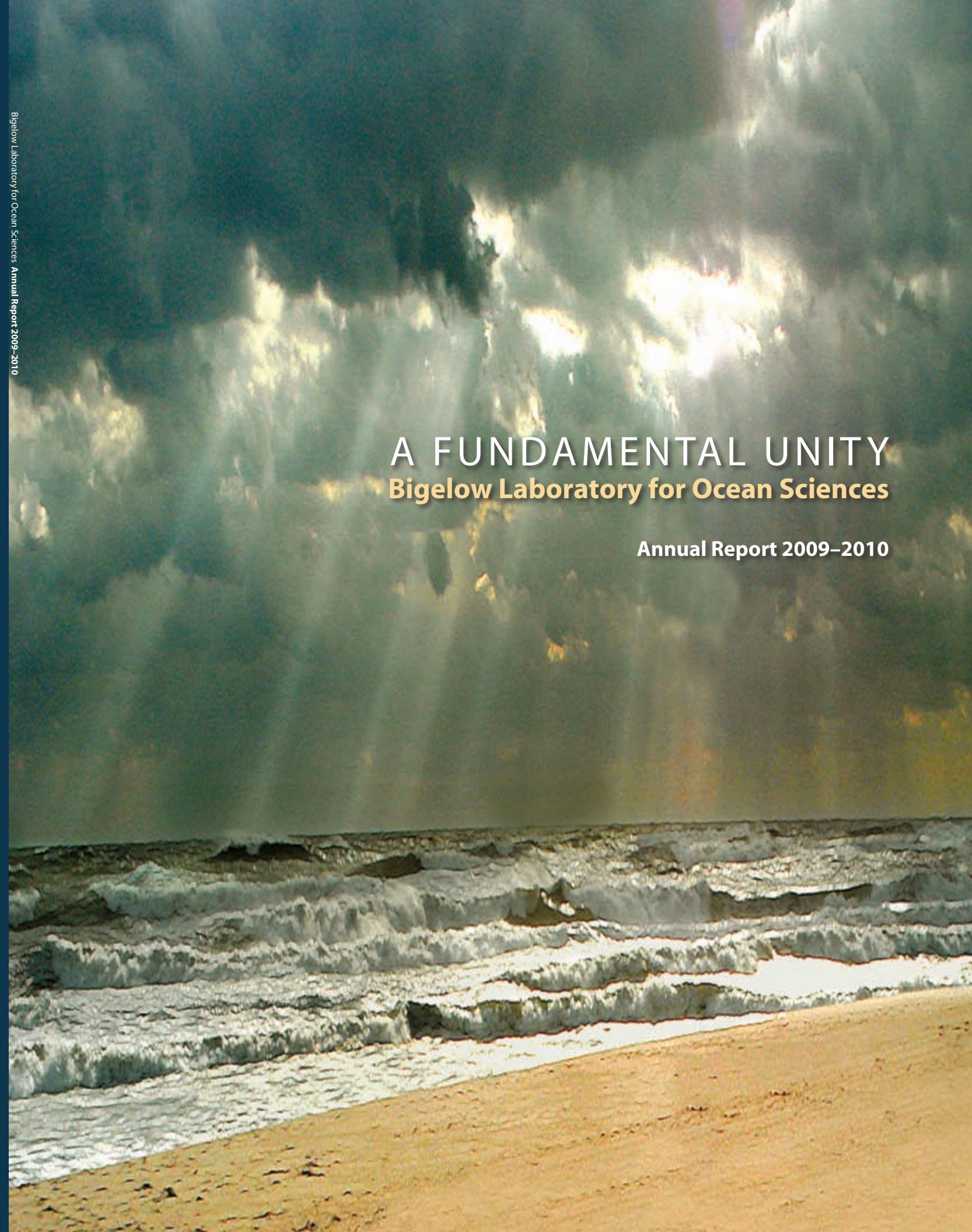
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A FUNDAMENTAL UNITY

Bigelow Laboratory for Ocean Sciences

Annual Report 2009–2010





“Science matters because it is the preeminent story of our age, an epic saga about who we are, where we came from, and where we are going.”

—Michael Shermer

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Strategy in Action

It has been a source of tremendous satisfaction for me to participate in the life of Bigelow Laboratory over the past eighteen months. The Laboratory's groundswell of accomplishments during this time have been extraordinary in their own right, but especially so in the context of a very tough economic climate. The Bigelow Strategic Plan is rapidly coming to fruition, focusing and spurring the organization's continued evolution within the three interrelated areas of basic research, education, and technology transfer. This strategy has been incorporated into a five-year Business Plan, which sets out objectives, timeframes, and resource allocations for implementing our ambitious new operating model.

The foundation for all that Bigelow Laboratory does is its commitment to delivering world-class research in fundamental ocean science. During the past eighteen months, this primary mission has been advanced by hiring several new senior scientists and by assembling over \$30 million to build a new Ocean Science and Education Campus in East Boothbay, Maine.

The groundbreaking ceremony for the new campus in early September was a transformational moment for Bigelow Laboratory and for the many, many dedicated researchers, staff, trustees, friends, and supporters who have shared in its 36-year history. U.S. Senator Susan Collins was the guest of honor at this ceremony, in recognition of all her support over the years and her help in securing federal funding for a major portion of the new campus facilities.

Over the summer, the Laboratory's ongoing commitment to education was greatly strengthened by two new academic relationships. Bigelow Laboratory and Colby College formed a strategic partnership, engaging the resources of both institutions and working together to create new programs to help train the next generation of ocean scientists.

During this same period, the Laboratory entered into a formal relationship with the Yale University School of Medicine. This relationship is designed to



Photo by Dennis Griggs

identify opportunities for Bigelow scientists to collaborate with researchers at Yale on projects that combine the results of the Laboratory's discoveries with potential applications in medical science.

Bigelow Laboratory's third strategic objective, commercialization of its intellectual property assets, was also advanced this year with the establishment of an Office of Technology Transfer. Private funding for this critical initiative has been committed and a Director of Technology Transfer hired, opening

new opportunities to generate revenue and channel the Laboratory's intellectual property into commercial markets for societal benefit.

Of course, it must be said that none of the objectives of the Strategic Plan and the Five-Year Business Plan could be achieved without strong leadership and unflagging commitment at all levels of the organization. In Dr. Graham Shimmield, Bigelow Laboratory is blessed to have an exceptional chief executive with internationally recognized credentials and experience. Working closely with Graham, the members of the Laboratory's Board of Trustees have been extremely active and generous with their financial support.

Finally, I'd like to recognize and thank Bigelow Laboratory's scientists. None of our ambitious plans would have any chance of success without these highly dedicated and talented individuals. Their commitment to advancing knowledge about the world's oceans and their search for discoveries that can improve our lives in the future are truly inspirational.

Thank you for your interest in Bigelow Laboratory. On behalf of the scientists, staff, and Board of Trustees, I welcome your further engagement in the activities of Bigelow Laboratory as we embark on a new era in our history.

David M. Coit
Chair of the Board of Trustees

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A New Day for Ocean Sciences at Bigelow Laboratory

The past year and a half has brought both a sea change in the public's appreciation of the oceans, and in the decisions the Laboratory has made about its own future. This juxtaposition is not altogether coincidental. We have witnessed the establishment of this country's first National Ocean Policy and National Ocean Council, mandating that "science-based information be at the heart of ocean policy decision-making." This was also the period that brought us the sobering images of the *Deepwater Horizon* spill, along with the unfolding wonders that marked the decadal culmination of the international Census of Marine Life. There is no doubt in my mind that this is the time in which ocean science has become part of the public vocabulary.

Bigelow Laboratory's current growth is occurring in the context of this new recognition, and the accompanying awareness that human impact on the ocean is increasing "at a rate that challenges our ability to manage significant and often competing demands" (Nancy Sutley, Chair of the White House Council on Environmental Quality). The Laboratory's strategy is anchored in the conviction that our science is of the highest quality, is independent, and is relevant to society as a whole. Rapid progress is taking place because of a convergence of planning, energy, and commitment on the part of everyone involved in our future. Specifically, we are investing in:

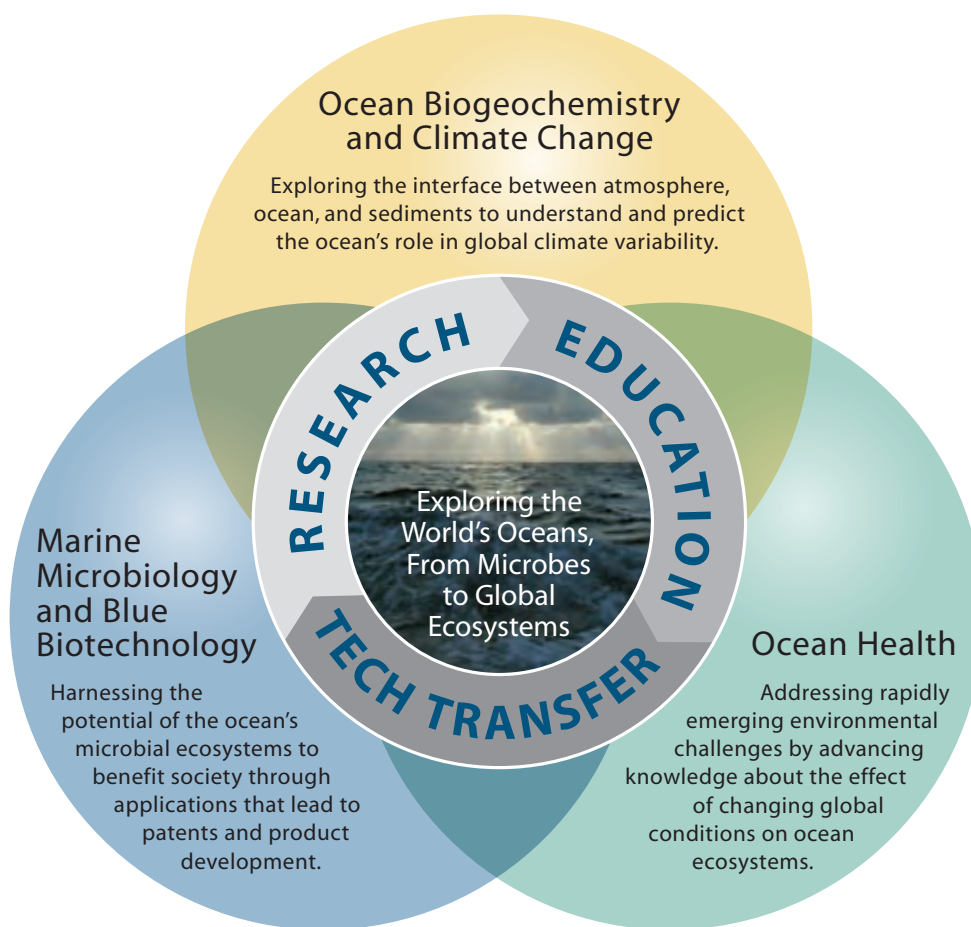
- a broadened identity and strategic scope, with core science centers that encompass an expanded operational focus for research, education, and technology transfer;
- new senior research scientists and institutional staff; and
- building our new Ocean Science and Education Campus facilities in East Boothbay, Maine, with the associated economic benefit this generates for the region.



Photo by Terry DeWan.

The ocean's microbial ecosystems drive the biogeochemical cycles that influence global climate and are vital to the planet's health. Our new campus facilities will allow our scientists to integrate bench-to-mesocosm-to-expedition scale discoveries, working at the critical interface between the ocean's smallest living particles and the global ecosystem processes that support life on Earth.

The new national mandate for conservation and sustainable use of the ocean's resources puts a priority on marine spatial planning, a comprehensive approach to ocean management policy that requires scientific understanding of ocean processes, their resilience, and their impact upon the global environment. Our core science centers in marine microbiology, and the associated applications that we call blue biotechnology; ocean health; and ocean biogeochemistry and climate change directly contribute to this understanding.



Bigelow Laboratory's Core Science Centers.

The National Ocean Policy also emphasizes the importance of training and recruiting future ocean scientists. The Laboratory has successfully launched new initiatives in mentoring and education programs. Specifically, we have created an academic partnership with Colby College, established a training program for our postdoctoral researchers, continued to develop our National Science Foundation-sponsored Research Experience for Undergraduates Program, and formalized a research agreement with the Yale University School of Medicine. Our long-standing BLOOM program annually introduces Maine high school students to the breadth of ocean science through an intensive, formative, week-long residency and research experience.

Over the past year, the Board of Trustees and Senior Research Scientists have reaffirmed the collective values of this unique institution. The spirit of independent investigation and the quality of our science are our touchstone for managing a period of

significant change. I commend this report to you, as a record of our collective endeavor. The following pages highlight the research our scientists have undertaken during the last eighteen months, and discuss “why it matters”—how our discoveries help to address the challenges society faces today, and in the years ahead.

This is the moment in history when, for the first time, the nation established a policy “to help the United States think comprehensively” about the fundamental unity that exists within the world’s ocean resources and ecosystems. Bigelow Laboratory has set a course to provide the integrated, interdisciplinary scientific foundation needed to discover the life-sustaining processes in the ocean and understand their essential relationship to the future of the planet.

Graham Shimmield, Ph.D., FRSE
Executive Director and President

Marine Microbiology and Blue Biotechnology



Scientists in this core group use molecular biology and microbial ecology methods to explore the vast reservoir of microbial organisms living in the world's oceans. Marine Microbiology and Blue Biotechnology programs investigate the evolution, ecology, and breadth of the ocean's microbial biodiversity and explore the potential of harnessing this diversity for new products and technologies to benefit society. Resources in this area include the world's first microbial single cell genomics facility; the Provasoli-Guillard National Center for the Culture of Marine Phytoplankton, including the world's first collections of marine bacteria and viruses; a bioreactor facility; and a state-of-the-art flow cytometry laboratory.

Single Cell Genomics

The Power of Sequencing Single Cells

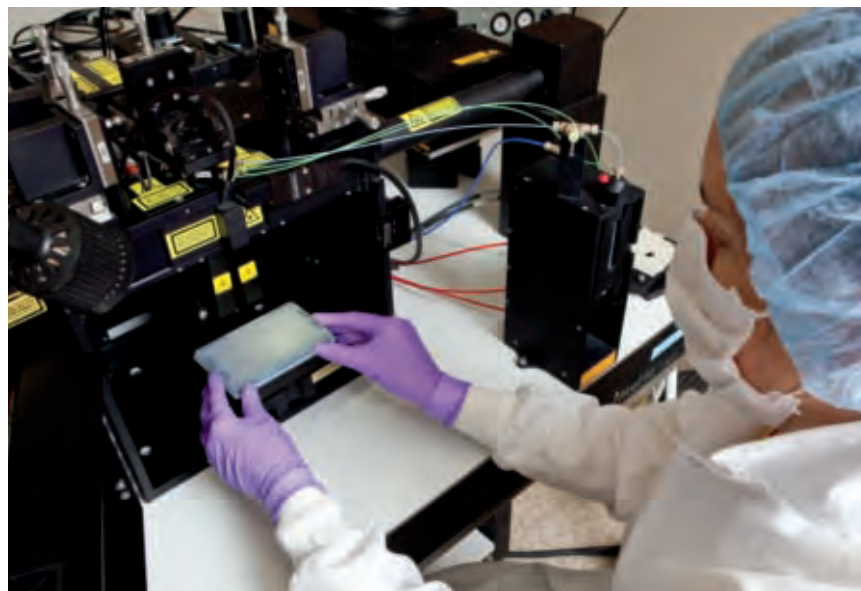
Single-celled microbes, invisible to us without magnification, are the oldest, most abundant, and most diverse forms of life on our planet. These elemental particles of life dominate many functions of the biosphere, including the productivity of the oceans; the health of larger organisms, such as humans; and the global cycles of carbon, nitrogen, and other essential elements.

The ocean's microbial genetic diversity offers significant potential for discovering new medicines and products, and developing clean energy sources.

Traditional microbiology has depended on access to microbes in pure cultures grown in the laboratory. Over 99% of the ocean's microbial species currently cannot be grown in laboratory cultures, however, making these species inaccessible to standard research techniques. Culture-independent, metagenomic studies, such as the Venter Institute's recent Global Ocean Sampling (GOS) expedition, demonstrated that the collective genetic material found in the ocean's microbial community—the ocean's "metagenome"—is fantastically immense—far greater than scientists' earlier estimates of microbial diversity in what used to be considered barren seas.

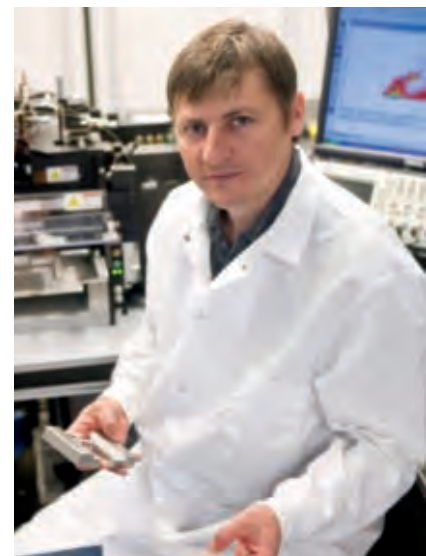
Most of the newly discovered bounty of marine microbial genes does not match those of the few hundred marine microbes that have been successfully "domesticated" in cultures, so the wealth of species within this "uncultured majority" remains unidentified.

The challenge of assembling billions of short DNA fragments from the GOS and other metagenomic studies was unresolved



—a task that has been described as putting thousands of separate jigsaw puzzles together out of billions of pieces without even knowing which pieces came from which boxes.

With funding from the National Science Foundation, Dr. Ramunas Stepanauskas, Dr. Michael Sieracki, and the research team at the Laboratory's Single Cell Genomics Center (SCGC) have developed the research tools needed to study such uncultured marine microbial species at the individual, single cell level. The researchers collaborated with an international group of scientists to test their pioneer-



Dr. Ramunas Stepanauskas.

Photo by Dennis Griggs (2).



Photo by Greg Bernard.

In September 2010, the SCGC held a week-long international workshop called “Redefining Microbial Genomics: The Power of Sequencing Individual Cells.” Its primary goal was to gather scientists from a variety of institutions who are using or planning to further develop microbial single cell genomics technology, exchange information, and make faster progress in this emerging field. More than seventy people, including scientists from the United States, France, Denmark, Spain, Sweden, the United Kingdom, Finland,

India, Saudi Arabia, The People’s Republic of China, Australia, and New Zealand attended. Sessions focused on the latest advances in gene sequencing technologies and the application of single cell genomics to wide range of research questions encompassing ecosystems, evolution, and microbial diversity. The workshop was sponsored in part by the National Science Foundation, the Gordon and Betty Moore Foundation, the U.S. Department of Energy, and the National Aeronautics and Space Administration.

ing approach—using fluorescence-activated cell sorting technology combined with multiple displacement amplification to isolate genetic material from individual microbial cells without the need for cultivation.

The international team of SCGC researchers led by Stepanauskas has successfully assembled the first high-quality, contamination-free genomes of uncultured microbes, working with only minute quantities of DNA within individual cells. This has made it possible to begin analyzing multiple genes, and even entire genomes, of the uncultured microbial species that dominate the ocean and most other environments.

Launched in 2009 with financial support from the National Science Foundation and the Maine Technology Institute, the Single Cell Genomics Center (SCGC) makes this technology available to the broad scientific community by implementing high-throughput robotics and information manage-

ment systems. During its first year in operation, SCGC contributed its unique services to research projects in over twenty organizations on three continents, analyzing over 100,000 individual microbial cells. This activity resulted in scientists’ access to genetic material from over 60 microbial phyla, about half of which do not have a single species in culture.

The kinds of samples processed by the SCGC range from marine to terrestrial to animal gut content, and the type of research questions

addressed encompass ecology, evolution, and human health. This major achievement is revolutionizing the study of microbial genetic information.

Ramunas Stepanauskas
Senior Research Scientist

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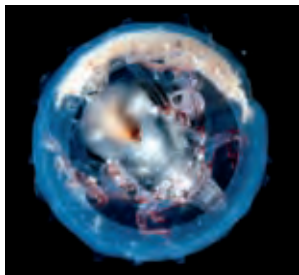
why it matters

By reading genetic information encoded within individual cells, scientists are able, for the first time, to investigate the unique metabolic capabilities, adaptations, and distribution of uncultured marine microbes. The new technology has allowed the SCGC to study the molecular ecology and evolutionary history of these microbes, including the bacterioplankton that harbor potential for bioenergy production. Single cell sequencing capability, together with mathematical modeling of population structure, are significantly advancing our understanding of the building blocks and basic principles that govern diversity in the world’s ocean.

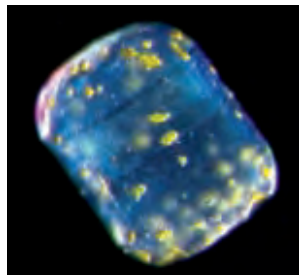
Aquatic Cytometry

Discovering an Ocean of Diversity

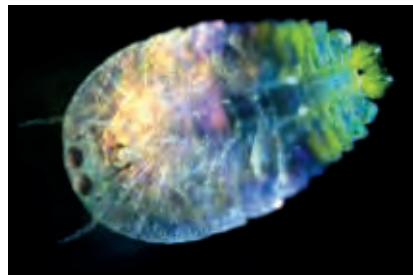
Major advances in cell measurement technology (cytometry) have expanded our ability to detect, count, isolate, measure, and analyze individual living cells. The Laboratory's aquatic cytometry researchers are refining and adapting basic cytometry techniques to investigate the ecology and biology of marine microbial ecosystems and populations, including methods of analyzing the biomass of some of the smallest organisms in the ocean.



Courtesy Mattias Ormestad/KahiKai.



Courtesy of Fonds Tara.



Courtesy of Fonds Tara.



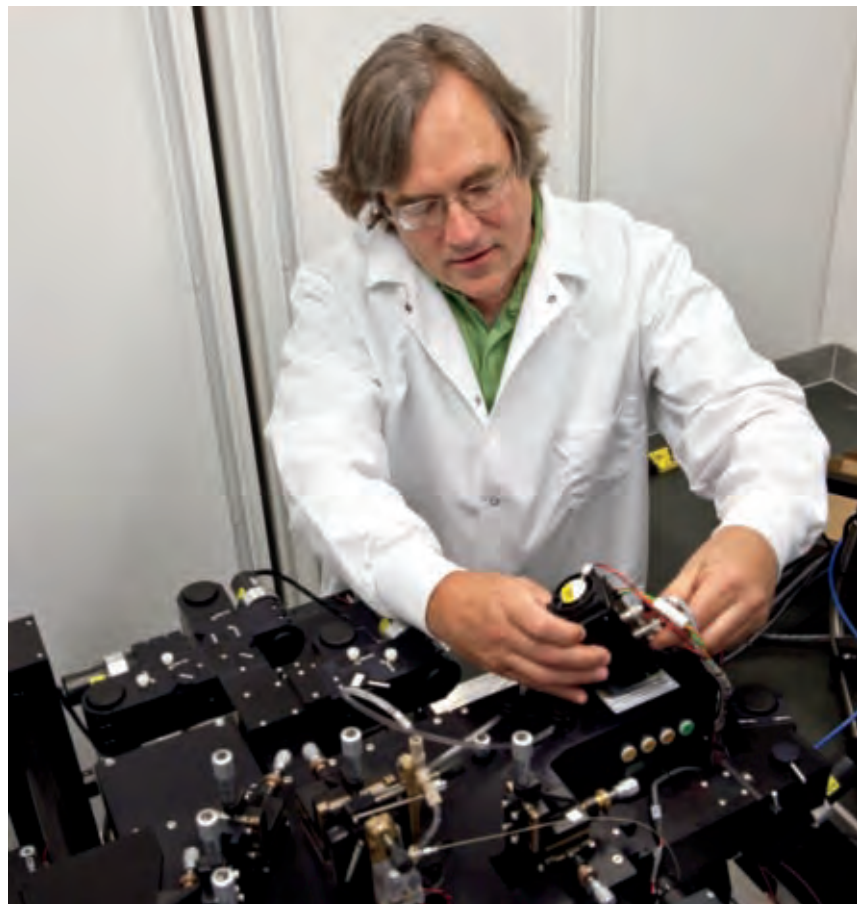
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New fluorescence techniques for flow and imaging cytometry developed at Bigelow Laboratory, along with the creation of a portable, at-sea cell-sorting laboratory, has made it possible to sort cells from fresh samples during research expeditions, and examine the dynamics at work among individual microscopic cells within the ocean's massive seasonal phytoplankton blooms.

Recent funding from the National Science Foundation and the Maine Technology Institute has provided support for Dr. Michael Sieracki and his research team to use single-cell sequencing techniques in combination with flow cytometry to examine the diversity of a specific size class (<10 μ m) of protists, a key part of the microbial food web both in the Gulf of Maine ecosystem and throughout the world's oceans.

Michael Sieracki
Senior Research Scientist

Nicole Poulton, *Research Scientist*
Brian Thompson, *Research Associate*
Ben Tupper, *Research Associate*

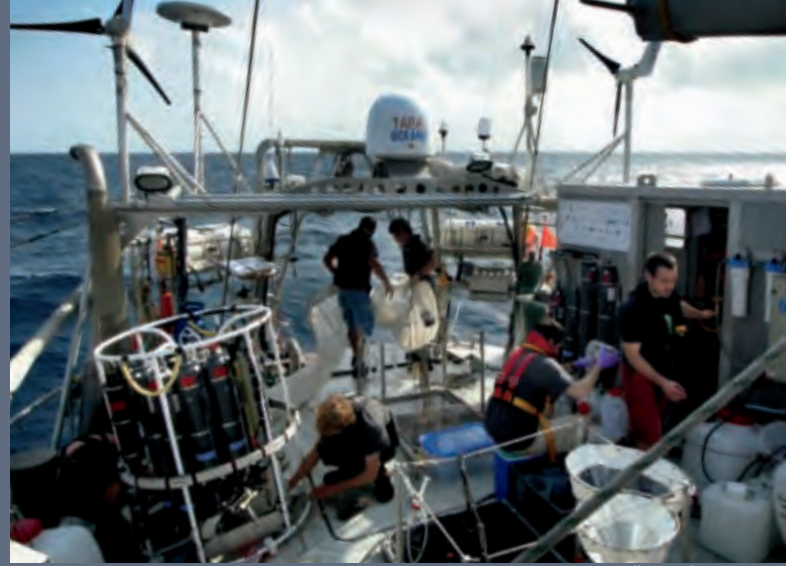


Dr. Michael Sieracki.

Photo by Dennis Griggs.



Photo © J.Girardot/Fonds Tara.



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Over the past year, Sieracki and his research group have worked with the international *Tara Oceans* Expedition to establish a cytometry, imaging, and single cell genomics capability aboard the three-year oceanographic expedition circumnavigating the planet. The expedition is studying the diversity of marine microorganisms and the effects that changing environmental conditions are having on this vital component of life in the oceans.

Sieracki led the *Tara* science team in the Mediterranean Sea for several weeks, sailing from Malta to Dubrovnik to train researchers aboard the vessel in the use of at-sea flow cytometry and imaging technology. *Tara's* cell imaging activity is dedicated to the observation of plankton from a few micrometers to a centimeter in size. Flow analyses continuously measure the variations of the surface water and its plankton community. The expedition's goal is to discover how the ocean's diverse microorganisms will react to the effects of climate change and ocean acidification, and how ocean ecosystems are responding to environmental change.

why it matters

Advanced technology for automated measurement and elemental analysis of single cells is allowing the Aquatic Cytometry research team to use the power of single cell genomics to increase our understanding of the magnitude and function of marine microbial diversity. By sorting and isolating cells from seawater samples, and then amplifying an individual cell's DNA and sequencing its genes, the team discovered a substantially greater level of diversity of protists than previously shown by sequencing DNA from whole seawater samples. These results provide the basis for a new and significantly more precise perspective about microbial community structure and function, as well as the resilience of marine ecosystems.

Geomicrobiology

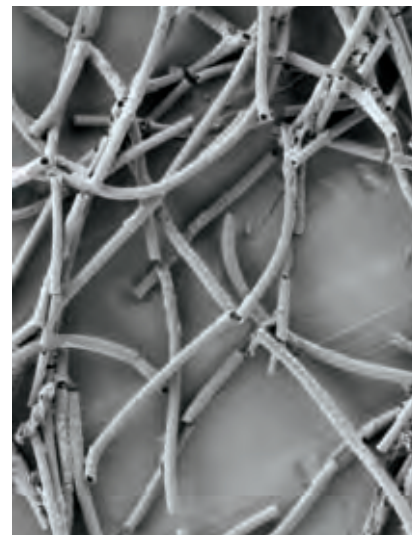
Unraveling the Ocean's Oldest Microbial Secrets

Growing on an enormous diversity of substrates, marine bacteria have been found at both the coldest and hottest temperatures at which life is known to survive. They are essential in maintaining ocean health, are of major commercial importance in biotechnology, and their ecology and evolutionary history are fundamental to understanding marine ecosystem processes.

The dynamic interface between ocean sediments and seawater is an important source of trace nutrients essential for the massive seasonal blooms of phytoplankton that occur throughout the global ocean. Climate change models predict that increased water temperature, increased nutrient loading, and increasing acidity of the water will have significant impact on coastal ocean areas, with profound effects on the bacterial processes associated with recycling these trace nutrients.

Dr. David Emerson and the Geomicrobiology research group at Bigelow Laboratory address the evolutionary history and ecological function of microbes in geochemical processes, particularly the role that bacteria play in marine and freshwater iron cycles.

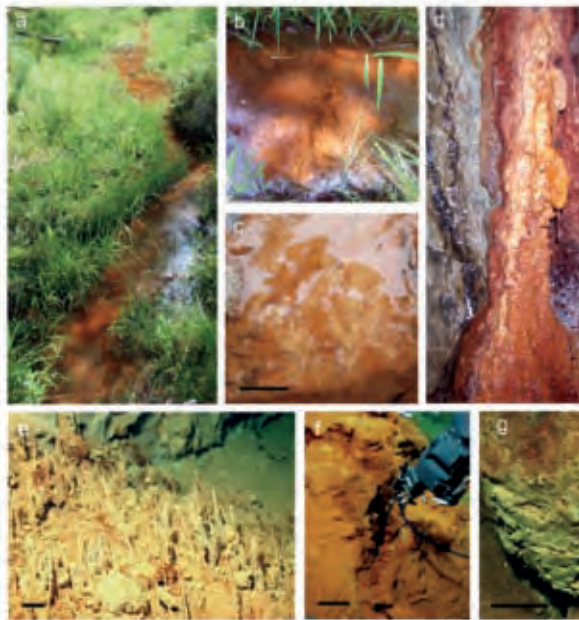
Iron-oxidizing bacteria (FeOB) are microbes that live by consuming iron in environments as varied as the deep-sea hydrothermal vents of undersea volcanoes, shipwrecks, and the root systems of wetland plants. FeOB can function both as a nuisance and a benefit—they are major agents of biofouling and biocorrosion in water distribution systems, but can aid in removal of harmful metals and organic pollutants in water treatment systems. The Office of Naval Research is funding Emerson's team to investigate the role of FeOB in corrosion of steel in the marine environment.



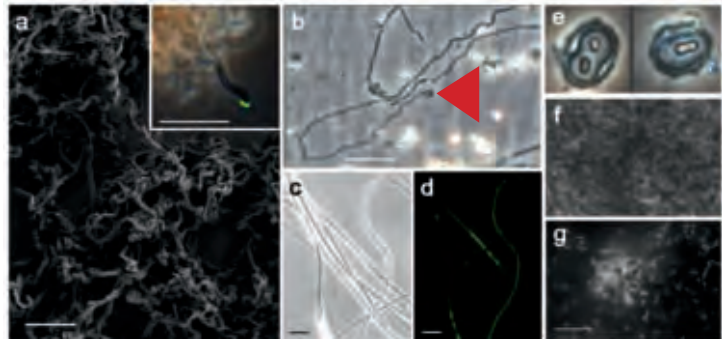
Left: Dr. David Emerson. Right: Scanning electron microscope image of the sheaths formed by the FeOB *Leptothrix ochracea*. Photos by Joyce McBeth.

Many FeOB have evolved to produce unique microstructures, commonly in the form of sheaths or stalks that create thick mats, consisting of a matrix of organic and mineral material. These structures influence the way the microbes interact with the environments in which they are found. Understanding the metabolism of these specialized microbes may provide clues about the potential for similar life forms to exist in habitats on other planets. The National Aeronautics and Space Administration (NASA) is funding research on the use of FeOB as biomarkers for life in ancient Earth habitats and in other potentially habitable zones in our solar system.

Among the extreme habitats on our own planet, seamount hydrothermal vents are a particularly rich source of information about the microbial lives of FeOB. The National Science Foundation has provided support for Emerson and his team to investigate the microbial ecosystem associated with seamount volcanism at Hawaii's underwater Loihi Volcano and to develop new microbial sampling technology for use with deep-sea submergence vehicles. This research has led to the discovery of a new, iron-based microbial ecosystem over three miles below the surface, the deepest level at which such ecosystems have been found.



A photomontage of sites occupied by FeOB: a) a typical fresh-water Fe-seep associated with a wetland in Maine; b) a close-up of the flocculant microbial iron mat from a; c) a condensed iron mat composed of FeOB in a faster flowing, Fe-rich stream; d) a deposit of iron oxyhydroxides on the wall of a mine that is fed with circumneutral groundwater rich in Fe(II); e) an iron mat associated with diffuse hydrothermal venting at Loihi Seamount (1300 mbsl), note the chimney like structures of oxides; f) a focused flow vent at Loihi (T = 50°C) surrounded by flocculant iron mat; g) close-up image of another iron mat at Loihi associated with focused venting, note the texture of the oxides.



A photomontage of FeOB: a) an SEM image of *Mariprofundus ferrooxydans* Fe oxyhydroxide stalks, the inset is a light microscope image of a live culture with a cell (stained green with a fluorescent DNA dye) growing at the end of a stalk (bar = 5 μm); b) *Gallionella ferruginea* growing in an Fe-seep, the arrow denotes a cell at the end of the stalk; c & d) *L. ochracea* enriched from an Fe-seep; c) is a phase contrast image; d) is the same epifluorescence image showing the filaments of cells inside the sheaths, note many of the sheaths are empty; e) *Siderocapsa* from an Fe-seep, note the cells inside a 'nest' of Fe-oxides; f & g) a pure culture *Sideroxydans lithotrophicus*; f) shows the amorphous oxides produced by these cells during growth; g) shows the cells on the oxides. All scale bars are 10 μm unless otherwise noted. Courtesy of Joyce McBeth.

Using genetic sequencing technology, Emerson and his research team are tracing the evolution of FeOB and have discovered an entirely new FeOB class, the Zetaproteobacteria, which are spread throughout the world's oceans. Zetaproteobacteria were first found at deep-sea hydrothermal vents in the Pacific Ocean, where they flourish and form large microbial mat ecosystems that can be over a meter thick and cover thousands of square meters of ocean floor. Based on these results, other researchers have confirmed the presence and dominance of Zetaproteobacteria at other hydrothermal vent systems that have abundant iron in the Pacific Ocean and Mediterranean Sea.

David Emerson
Senior Research Scientist

Emily Fleming, Postdoctoral Researcher
Joyce McBeth, Postdoctoral Researcher

why it matters

It is likely that FeOB influenced the biogeochemistry of our planet's early history by precipitating iron oxides and creating the banded iron formations that are the world's primary source of iron ore. Recently, Dr. Joyce McBeth, a postdoctoral researcher in Emerson's laboratory, discovered Zetaproteobacteria growing in estuarine sediments and near shore water far away from any hydrothermal inputs, and demonstrated that they play a role in colonization and corrosion of steel. These findings indicate that Zetaproteobacteria are far more widespread and may be playing a significantly more important role in the iron cycle than had previously been understood.

Algal Molecular Evolution

Climbing through the Tree of Life

More than a billion years ago, genetic changes occurred inside a few protist cells that allowed these ancient marine microbes to assimilate bacteria without digesting them. Instead, the protist “hosts” used their ingested bacteria to form internal structures called plastids that could make carbohydrates from sunlight, carbon dioxide, and water. This sequence of events created the world’s first plants.

By tracing the molecular steps that led to this pivotal development in the planet’s history, Dr. Hwan Su Yoon and the researchers in the Algal Molecular Evolution Laboratory are deciphering the genetic changes that have taken place during other major transitions in evolutionary history. Their research is uncovering pathways by which life evolved through time and providing a means to connect the branches in the Tree of Life.

Using genetic sequencing technology, the Algal Molecular Evolution group compared the genomes of two related species of *Paulinella* amoebas. The researchers identified the mechanism by which one of the *Paulinella* species recently made the same evolutionary jump as the ancient protist, evolving the ability to use an ingested cyanobacterium to generate food energy through photosynthesis. The other *Paulinella* species they studied remained a predatory amoeba, dependent on eating other microorganisms to survive.



Photo courtesy of NOAA.

Collage of red algae collected at the West Flower Garden Bank, including two undescribed species.



Photo by Greg Bernard.

Dr. Hwan Su Yoon, with visiting student researcher Kyeongmi Kim in the Algal Molecular Evolution Laboratory.

Yoon's current research also includes a collaborative phylogenetic and genomic analysis of Rhodophyta (red algae). The red algae comprise 6,000 species, making them one of the most important algal groups and a significant contributor to eukaryotic evolution. (Eukaryotes are all the multitude of life forms, including humans, whose cells have a distinct nucleus containing genetic material.) The red algae were the direct evolutionary source of plastids for a major category of protists called chromalveolates. Chromalveolates include the diatoms and dinoflagellates responsible for the ocean's massive seasonal phytoplankton blooms.

Hwan Su Yoon
Senior Research Scientist

Kim Hee Jeong, Research Technician
Kyeongmi Kim, Visiting Student Researcher
Su Yeon Kim, Visiting Student Researcher
Huan Qiu, Postdoctoral Researcher
Eun Chan Yang, Postdoctoral Researcher



Photo by Peter Siver.

Synura petersenii scales.

Venturing Further into Freshwater

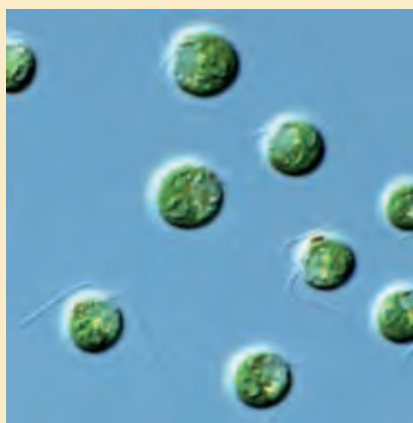
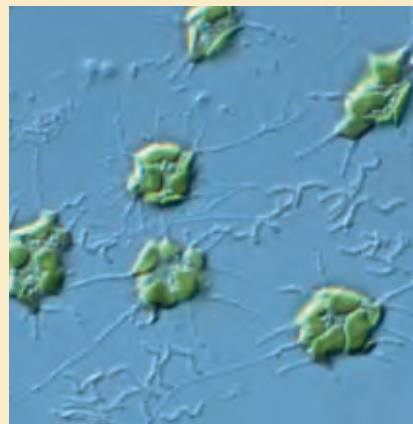
The global distribution, abundance, and diversity of freshwater phytoplankton exhibit a range of evolutionary adaptations that have enabled these species to overcome significant geographic barriers (e.g., dry land and seawater). The Yoon laboratory has conducted DNA and protein analysis of a freshwater alga called *Synura*, which demonstrates that this globally distributed algal group is significantly older and more diverse than previously thought. *Synura* have developed a complex geographic distribution pattern. Some *Synura* have retained their "cosmopolitan" distribution, while at the same time co-existing with other *Synura* species that have evolved adaptations to specific regional conditions. The story of *Synura* may contain important clues about the way populations of microorganisms are distributed and about the ongoing dynamics of genetic adaptation in a changing environment.

why it matters

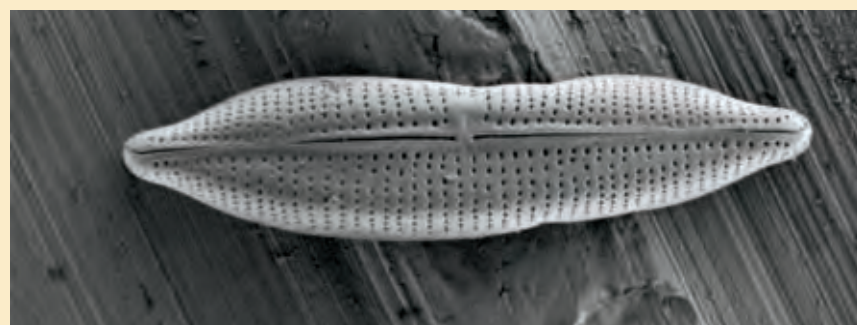
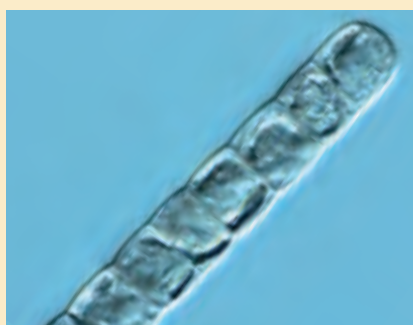
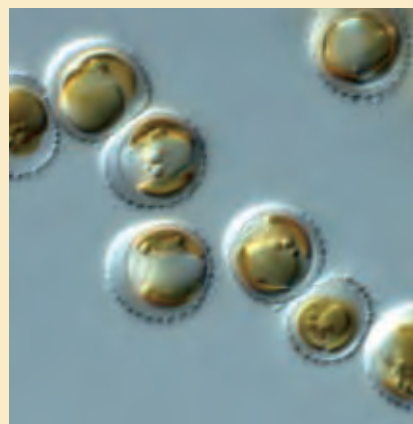
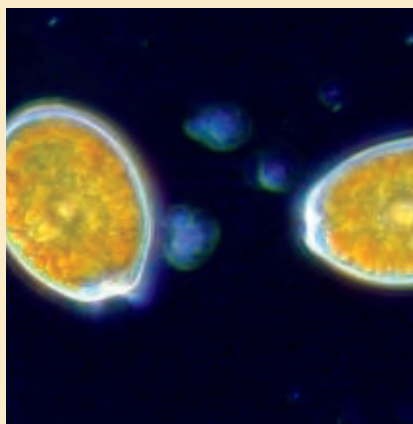
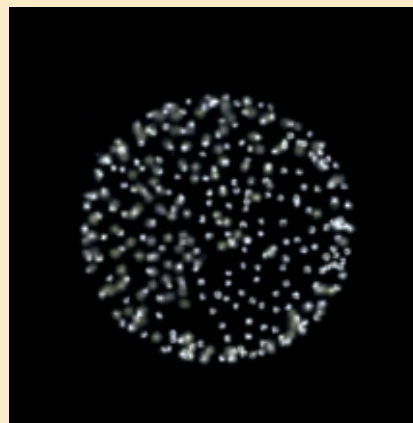
Rhodophyta and its plastid descendants are the dominant algal group in the ocean today. They are a key source of nutrition for people, and have a multitude of food, pharmaceutical, and industrial applications, such as production of agar and carrageenan. The goals of Yoon's National Science Foundation-sponsored project are to sample broadly across the major groups of red algae, reconstruct their phylogenetic history, determine genome sequences from 16 species to understand the evolutionary road that led to their diversification, and establish their fundamental place in the Tree of Life.

The Provasoli-Guillard National Center

A Growing Collection, A New Direction



At the end of June 2010, the National Science Foundation awarded a five-year, \$1,807,672 grant to support development of a self-sustaining operation at the Provasoli-Guillard National Center for Culture of Marine Phytoplankton. The Center is the largest repository of living marine phytoplankton in the United States, and the nation's official such collection. Annually providing thousands of cultures and DNA to scientists worldwide, the collection houses more than 2,700 strains of algae grown at temperatures ranging from tropical to polar ocean environments. Under the leadership of its new Director Dr. Willie Wilson, the Center is currently expanding to include the world's first living collections of marine viruses and bacteria.



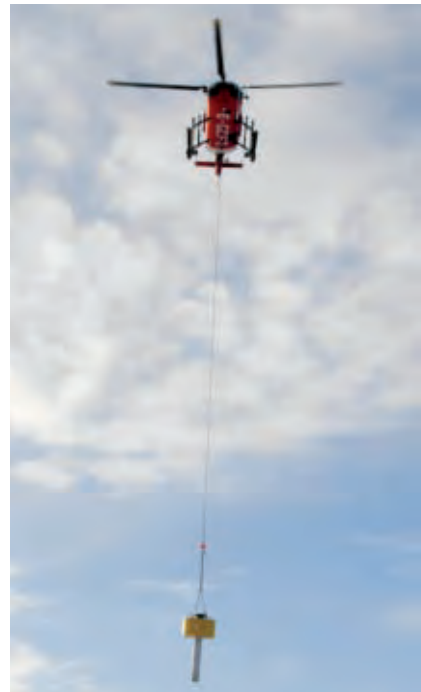
OCEAN BIOGEOCHEMISTRY AND CLIMATE CHANGE

The Laboratory's Ocean Biogeochemistry and Climate Change researchers explore the connection between atmosphere, ocean, and sediments to understand and predict the ocean's role in global climate variability. Questions of ocean biogeochemistry and climate change must be addressed at many scales, from local to global, and from individual cells to entire ocean basins. By bringing research programs in ocean observing, air-sea interactions, ocean biogeochemistry, cellular biogeochemistry, and land-sea interactions together, scientists are able to undertake the collaborative investigations necessary to discover the role of microscopic marine communities in global ocean processes and climate change.

Ocean and Atmospheric Chemistry: the O-Buoy Network

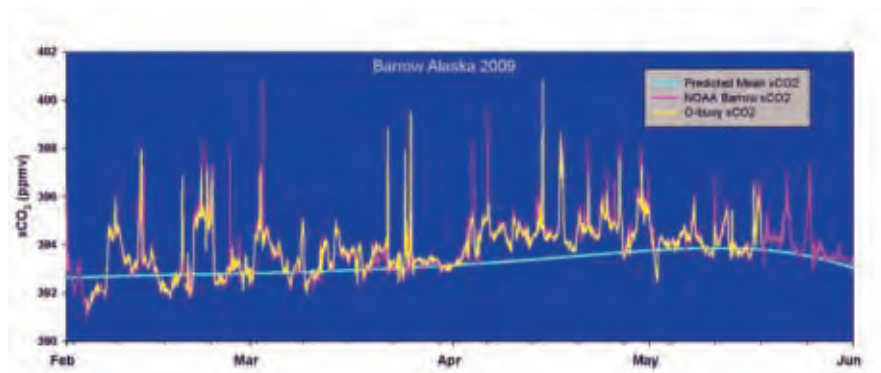
Streaming Real-Time, Ocean-Based, Atmospheric Data, for the First Time

Frequent and sustained observations of ocean conditions are essential to understand the interaction between ocean processes and changing climate patterns. The climate in the Arctic is changing more abruptly than anywhere else on the planet, and seasonal changes occurring in the atmosphere above the Arctic Ocean have direct impact on marine ecosystem productivity, ocean surface chemistry, and cloud formation.



A range of biogeochemical processes, particularly in Arctic regions, produce gases—including carbon dioxide (CO_2), ozone (O_3) and bromine monoxide (BrO)—that affect our climate.

Scientists believe that more open water from melting ice may make the Arctic Ocean into a larger carbon dioxide (CO_2) sink, but there are no long-term CO_2 measurements from and over the Arctic Ocean because of the



Atmospheric concentrations of CO_2 off Barrow, Alaska during a four month period in early 2009, as measured by O-Buoy. Significant short-term departures from the predicted mean are evident in this high-resolution record.



Photo by Dennis Griggs.

Dr. Patricia Matrai.

extreme logistical challenges involved in monitoring this remote ocean. Except for information collected from land, a few research vessels, aircraft, and satellites, there have been very few measurements of CO_2 , ozone, or other chemicals in the atmosphere above the surface of the Arctic Ocean. Measuring environmental variability in the fast-changing ice fields of different regions in the Arctic Ocean requires the ability to gather long-term, ocean-based, atmospheric data.

Dr. Patricia Matrai's Ocean and Atmospheric Chemistry Laboratory is leading a collaborative project funded by the National Science Foundation that has designed and deployed a network of robust, unattended, and self-contained monitoring buoys in the Arctic Ocean. Known as the O-Buoy Project, this suite of instruments lodged in the shifting sea ice of the Arctic Ocean is sending continuous measurements of atmospheric conditions back to the Laboratory's data servers.



O-Buoy 2 deployment in the Beaufort Sea. The buoy was delivered to the ice by the research ship's helicopter. Photos courtesy of Carlton Rauschenberg.



The current O-Buoy network, showing the positions of O-Buoys 1 through 4, and drift tracks for O-Buoys 1 and 2. Image by Google Earth and Ben Tupper.

The O-Buoy network is the first autonomous, ice-supported, atmospheric chemistry measurement system in the Arctic Ocean. Working with colleagues from the University of Alaska, Purdue University, Monterey Bay Aquarium Research Institute, the Stanford Research Institute, and the United States Army's Cold Regions Research and Engineering Laboratory, the Matrai team has developed the power management and instrumentation control necessary for the network to operate with minimal direct human interaction, while surviving harsh conditions during seasonal shifting and melting of Arctic sea ice.

The first O-Buoy was field tested in Elson Lagoon, in Barrow, Alaska, and later deployed in the

Beaufort Sea; a second O-Buoy is now sampling there. Additional O-Buoys have been stationed during 2010 in Hudson Bay in the Canadian Arctic, and the northern Beaufort Sea. Eleven more O-Buoys will be assembled and located throughout the Arctic Ocean over the next five years.

Patricia Matrai

Senior Research Scientist

Andrew Hind, *Postdoctoral Researcher*

Carlton Rauschenberg, *Research Associate*



why it matters

O-Buoy data are significantly increasing knowledge about changing environmental conditions in the Arctic Ocean and its effect on the planet's atmosphere. Part of the multi-institutional, multi-agency Arctic Observing Network, information from the O-Buoy system is freely available for use by the broader scientific community and will aid in developing future models of atmospheric chemistry and global climate change.

Ocean Observing and Optics

Sea Truth in a Changing Ocean

Burning of fossil fuels is predicted to increase the concentration of atmospheric carbon dioxide (CO₂) to levels that will cause a number of significant changes in the global environment, including increased temperatures, more rainfall, and lowering of the ocean's pH, a process called "ocean acidification."

The impact of these changes on phytoplankton populations affects both the ocean's biological productivity and the biogeochemical processes that help reduce CO₂ in the atmosphere through export of organic carbon to the deep ocean.

Ocean observation by direct sampling and satellite remote sensing are critical tools for understanding the distribution and abundance of single-celled phytoplankton called coccolithophores, which precipitate calcium carbonate shells and contribute significantly to carbon export from the surface ocean. Coccolithophores are expected to respond dramatically to increased atmospheric carbon dioxide levels and ocean acidification. Changes in the abundance of coccolithophores and other calcifying phytoplankton within the marine phytoplankton



The microscopic single-celled coccolithophore *Emiliana huxleyi*, covered in protective calcium carbonate plates. Courtesy of the Provasoli-Guillard National Center.

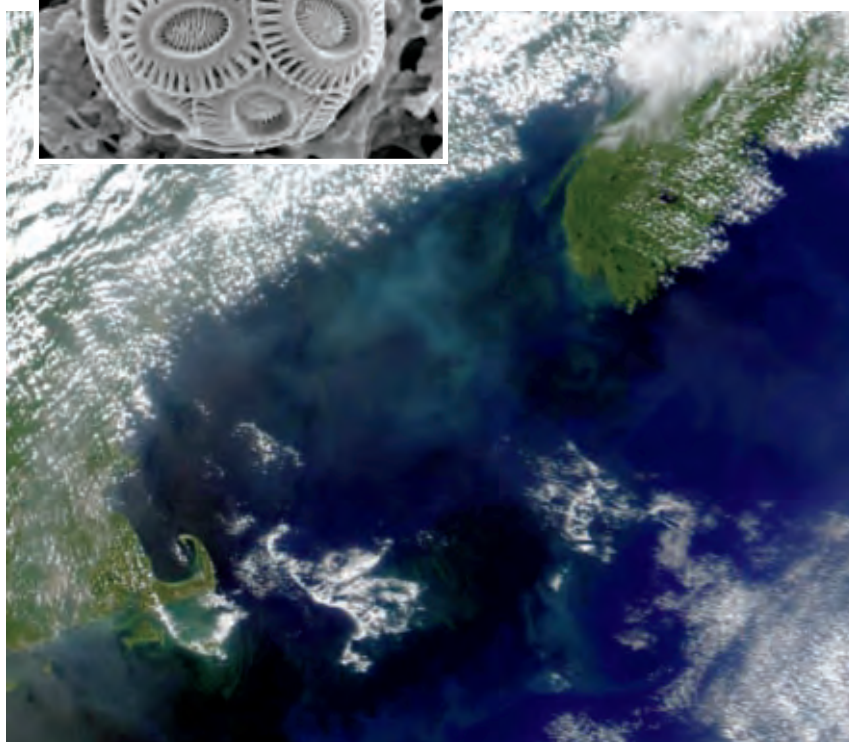


Image courtesy of NASA.

The Gulf of Maine.



Photo by Rebecca Fowler.

Dr. Barney Balch.

community could alter the ocean's ability to reflect, absorb, or scatter light, potentially triggering significant feedbacks for climate change.

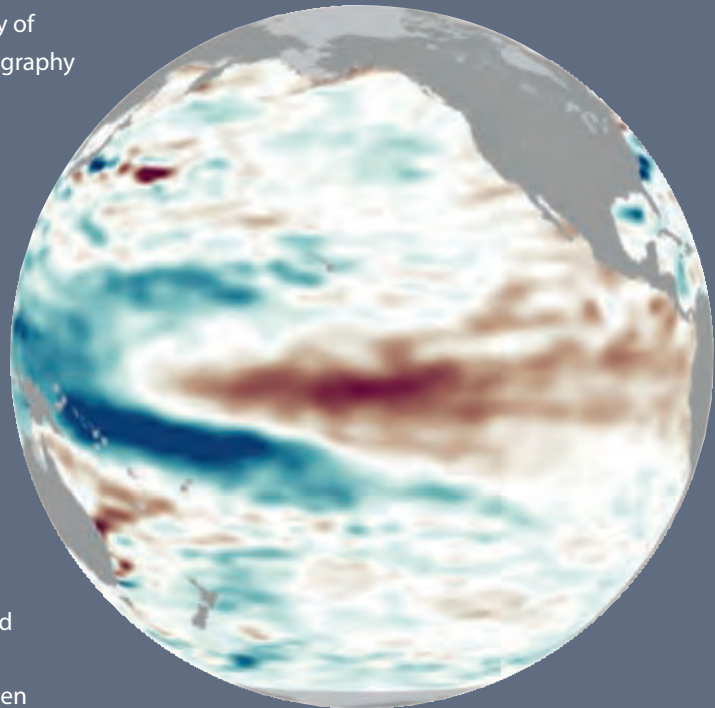
Dr. Barney Balch and the Laboratory's Ocean Observing research group uses advanced technology in ocean optics to study the composition of phytoplankton communities by measuring their biomass and light absorption properties.

Over the past 12 years, the researchers have created and operated a platform for a long-term time series, known as the Gulf of Maine North Atlantic Time Series (GNATS).

GNATS measures physical, chemical, and biological conditions in the Gulf of Maine and monitors temperature, biomass, and primary productivity in this

Collaborating with researchers from the University of California-Santa Barbara and the National Oceanography Centre in the United Kingdom, Balch and his team have recently published findings from a National Science Foundation-funded study of the relationship between nutrients, phytoplankton biomass, and carbon fixation in the eastern and central Equatorial Pacific. This region of the ocean is generally considered to be significantly less biologically productive than expected (given the high concentrations of nutrients) and their research is focused on unraveling the reasons for this.

Measurements of phytoplankton biomass and primary productivity were taken from research ships in the Pacific during both warm and neutral El Niño periods. The data showed that biomass and primary production were highest both along the equator itself and at the convergence zone between the North Equatorial Counter Current and the South Equatorial Current, a region known to accumulate enhanced phytoplankton biomass. They postulate that the factors controlling primary productivity and phytoplankton community structure involve more than simply nutrient availability, and that production (and carbon export) in this vast region of the Pacific Ocean results from a complicated and delicate balance among different classes of phytoplankton and other characteristics, such as the abundance and diversity of grazing populations of zooplankton.



Above-normal sea surface temperatures during the El Niño-Southern Oscillation are maintained by waves of warm water that travel across the Pacific from Indonesia toward South America. Higher-than-average sea surface height (shown above in brown) on February 15, 2010, indicates a deeper-than-normal layer of warm water. Image courtesy of NASA.

regionally significant ecosystem. The program utilizes commercial ferries, small research vessels, and an autonomous glider to collect data on the biogeochemistry of the Gulf of Maine between Portland, Maine and Yarmouth, Nova Scotia. Such data are critical for understanding physical and chemical controls on biological productivity in the Gulf.

Barney Balch
Senior Research Scientist

Danielle Alley, *Research Technician*
Bruce Bowler, *Research Associate*
Dave Drapeau, *Research Associate*
Emily Lyczkowski, *Research Technician*
Laura Lubelczyk, *Research Technician*



why it matters

Balch uses GNATS data to “sea-truth” satellite data by calibrating information from satellites with real-time observations at sea. Using ocean color and temperature data from satellite images, scientists are able to calculate rates of photosynthesis, and estimate the amount of chlorophyll, phytoplankton particulate organic carbon, and particulate inorganic carbon in ocean ecosystems throughout the world. Observations of regional and global patterns of sea surface temperature, sea level height, phytoplankton biomass, productivity, rainfall, and river discharge are making it possible to assess the large-scale impact of climate change on ocean biogeochemistry.

Trace Metal Biogeochemistry

Picturing the Role of Metals in Diatom Biology and Global Biogeochemical Cycles

The ocean's phytoplankton communities form the foundation of the planet's marine food web and have a key role in the global carbon cycle. Global climate change is altering the availability and distribution of essential nutrients that these communities need for growth.

As carbon dioxide levels increase and the ocean becomes more acidic, changes in the cycling of trace metals can have significant impact on phytoplankton physiology and community structure, with consequences that reverberate throughout the world's ocean ecosystems.

The Bigelow Trace Metal Biogeochemistry Laboratory delves into the interactions between microorganisms and trace metals in the ocean and investigates how varying levels of metals in the surrounding seawater affect phytoplankton growth. This research directly addresses the interconnected processes by which essential elements are cycled through the oceans by living organisms and the key interactions that determine basin-wide plankton ecology and biogeochemistry.



Photo by Dennis Griggs.

Dr. Ben Twining.

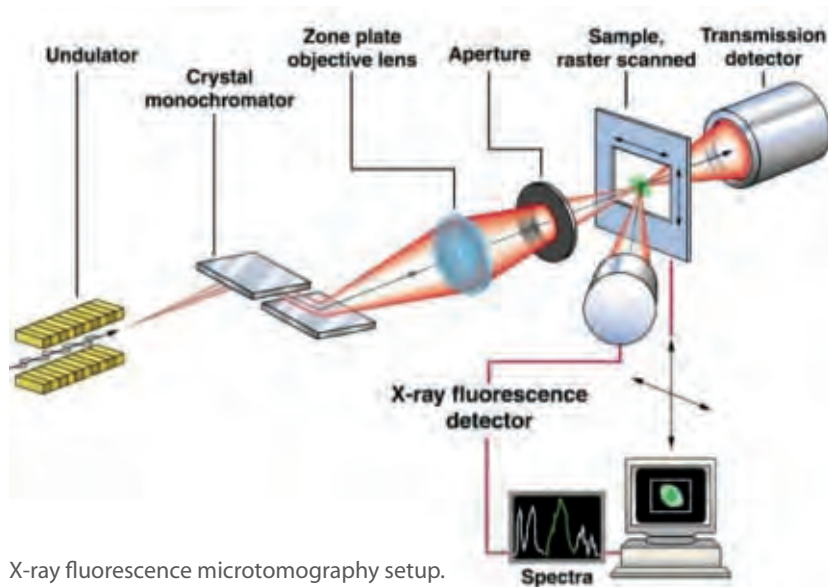


Scanning electron microscope image of *Cyclotella meneghiniana*. Courtesy of the Provasoli-Guillard National Center.

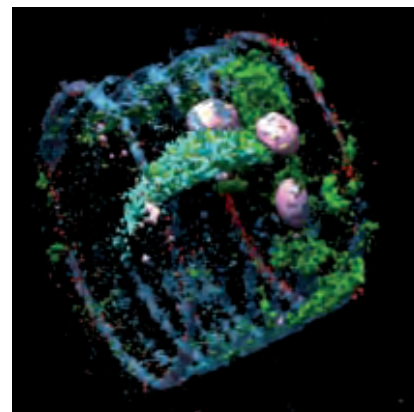
Dr. Ben Twining and his research team are examining the distribution of specific elements within individual cells to discover how marine microorganisms use and accumulate very low concentrations of essential metals in seawater, how they modify the bioavailability of these "micro-nutrients," and their impact on global biogeochemical cycling. By combining field studies with advanced analytical tools, Twining has made the first direct measurements of trace metal nutrients

in natural phytoplankton groups from major oceanic regions, including the equatorial Pacific Ocean, the sub-tropical Pacific near New Zealand, and the Sargasso Sea.

Twining is a member of a multi-institutional research group using a powerful new microscopy technique called X-ray fluorescence microtomography to create three-dimensional maps of the structural distribution of elements within cells. This technology allows scientists to study the



X-ray fluorescence microtomography setup.



Internal organization of *Cyclotella meneghiniana*.

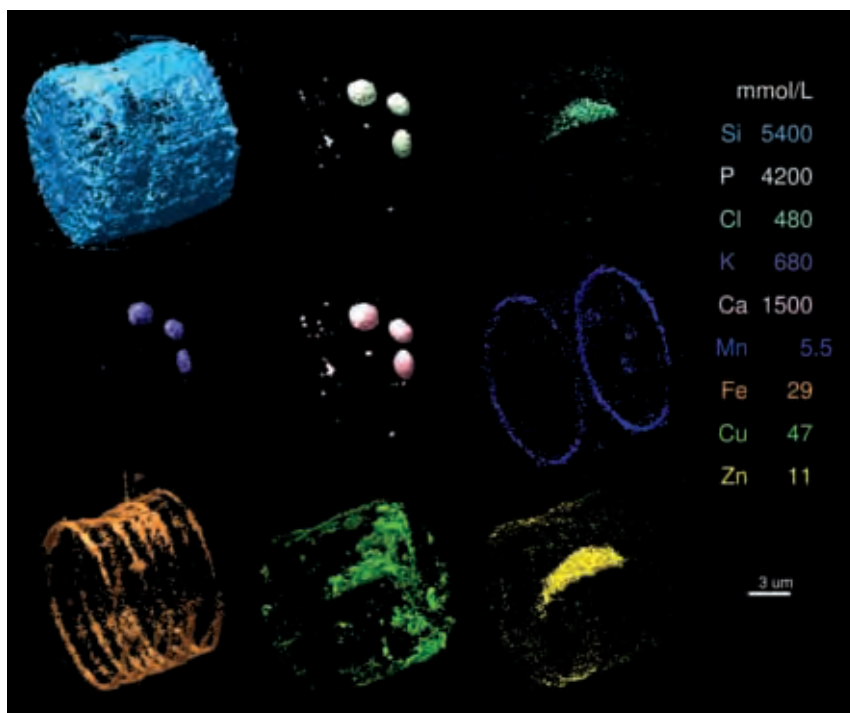
internal structure of whole cells by combining a series of two-dimensional views at various angles to construct a three-dimensional image.

The researchers have used a freshwater diatom, *Cyclotella meneghiniana*, to test the effectiveness of X-ray fluorescence microtomography in quantifying the three-dimensional distribution of trace amounts of silicon, phosphorus, sulfur, chlorine, potassium, calcium, manganese, iron, copper, and zinc at previously unavailable, submicron-levels of spatial resolution.

These results demonstrate that the same technique can be used to study marine phytoplankton, making it possible to learn about environmental factors affecting trace element content of diatoms, improve the ability to reconstruct past climate and ocean conditions, and predict future environmental changes.

Ben Twining
Senior Research Scientist

Jochen Nuester, Postdoctoral Researcher
Sara Rauschenberg, Research Associate



3D renderings of elemental distributions in *Cyclotella meneghiniana*.

Image courtesy of Ben Twining (3).

why it matters

Creating an accurate picture of the quantity and distribution of elements within a cell provides new data about cellular processes, and can show how trace elements are accumulated through the food chain. Understanding the elemental composition of individual phytoplankton cells at the ocean's surface provides important insights about ocean biochemistry, and can significantly improve estimates about how much carbon dioxide phytoplankton cells remove from the ocean and sequester in the deep sea.

Biogeochemistry at Sea

Carbon Cycling in the Amazon Plume

The flow of freshwater from the Amazon River is the largest of any river in the world. Because the Amazon River flows through the planet's most densely populated forest basins, it carries massive amounts of sediments and organic material into the western Atlantic Ocean, visible from space as a greenish brown plume stretching thousands of miles out to sea.

The Amazon Plume is unique in its remarkably efficient, phytoplankton-driven biological "pump," which draws carbon dioxide from surface waters and exports it to the deeper ocean. The plume can pump up to four times as much carbon to the ocean floor than surrounding waters, making information about the dynamic processes at work within the plume ecosystem vital for understanding regional and global human impacts on the tropical ocean and their potential feedbacks to climate change.



Photo by Dennis Griggs.

Dr. Joaquim Goés.

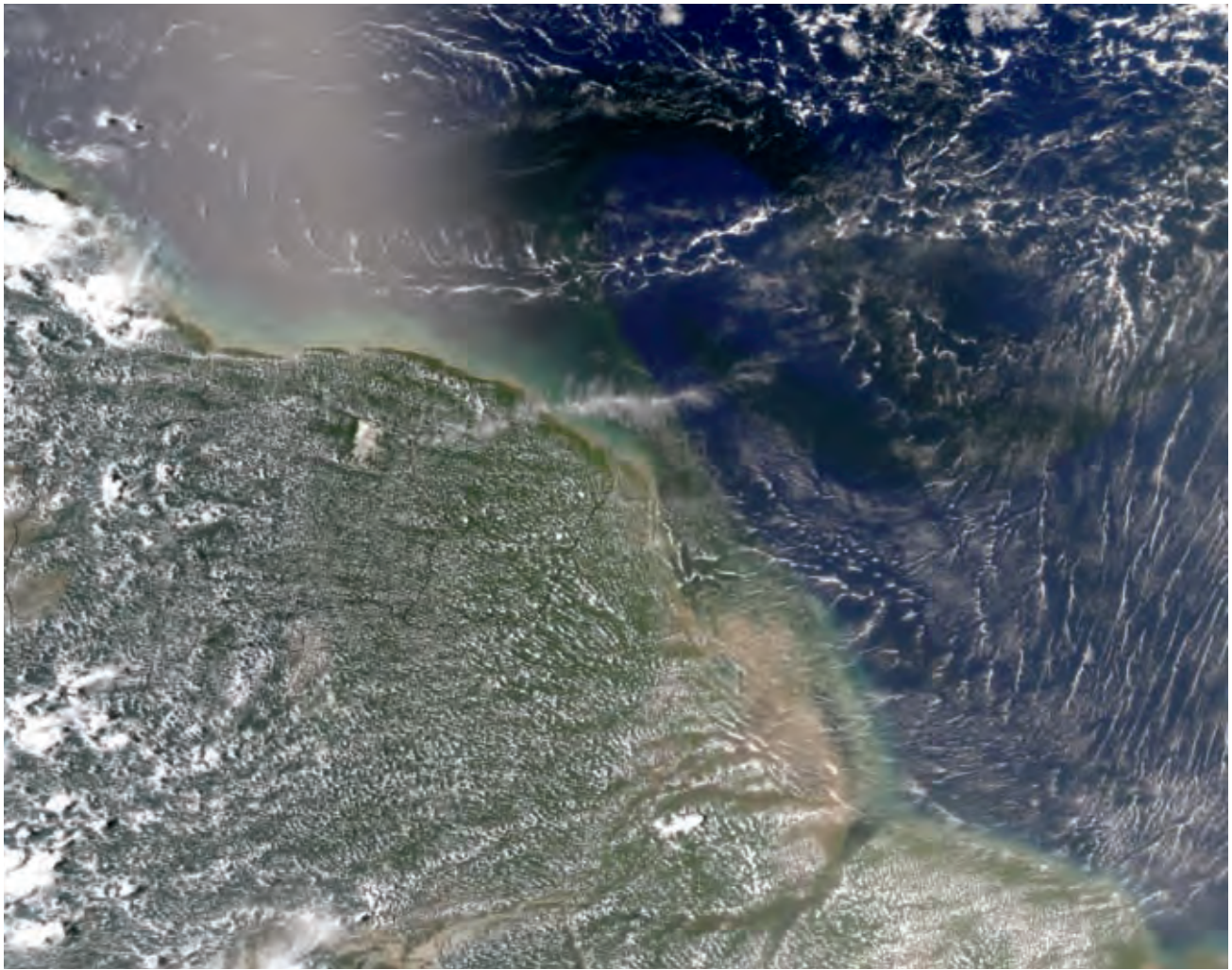


Photo by Joaquim Goés.

Colby College student and Amazon Plume expedition intern Courtney Beaulieu (left) with Dr. Helga do Rosario Gomes. The *R/V Knorr* is in the background.

In the spring of 2010, Dr. Joaquim Goés and his staff in the Ocean Biogeochemistry and Climate research group joined an international team of 47 multi-disciplinary researchers on the *R/V Knorr* off the coast of South America to study carbon and nitrogen cycling in the Amazon Plume. Bigelow expedition intern Courtney Beaulieu from Colby College in Maine was also on board as one of fourteen student researchers in the project.

During the expedition, the Goés team investigated the ecological relationships of the plume's phytoplankton community and how they may contribute to this increased carbon export. The scientists' primary focus was on the plume's unusual symbiotic assemblages of diatoms and nitrogen-fixing bacteria (known as diazotrophs) capable of fixing large amounts of carbon dioxide in the plume ecosystem.



Water within the Amazon Plume has such a high volume and is moving so fast that it remains concentrated enough to be seen meandering many kilometers across the Atlantic. The plume is a band of dark water that first sweeps, then loops, east on the North Equatorial Counter Current. Image courtesy of NASA.

Nutrient and other environmental conditions within the Amazon Plume provide an ideal niche for diatom-diazotroph assemblages (DDAs) to flourish. Previous research addressed the behavior of DDAs in response to external forcing from dust and runoff, but until now, the ecology of these organisms, and their impact on biological productivity and carbon export, remained largely unstudied.

Joaquim I. Goés,
Senior Research Scientist

Maria Fatima Helga do Rosario Gomes,
Research Scientist

Elin Haugen, *Research Technician*



why it matters

The Goés research team conducted a suite of laboratory, field, satellite, and modeling studies of Amazon Plume ecology, phytoplankton community structure, and nutrient cycling by DDAs. Data from the expedition are being analyzed to determine the distribution, nutrient demands, and activity of DDAs in the context of phytoplankton species succession. Measuring the proportion of sinking organic matter that reaches the seafloor provides a way to calculate the efficiency of the biological pump. These findings will help establish a much-needed ecological model with which to evaluate observations from satellites and future field studies in the context of tropical climate change in the Atlantic basin. Because DDAs have been found in other large tropical river systems, it is possible that they are a globally significant, yet previously unexamined, biological component of the global carbon cycle.

Ocean Health

Ocean Health programs address rapidly emerging environmental challenges by investigating the effect of changing global conditions on the ocean. The impact of microbial communities on ocean health and productivity is a critical component of ocean ecosystems. Advances in genomic research, microbiology, and bioinformatics are allowing scientists at the Laboratory to develop a fundamental new paradigm for ocean systems biology that represents a significant step beyond the traditional approach of field-to-laboratory study. The Ocean Health group is accelerating our knowledge of the ocean's microbial systems to enable sustainable management and stewardship of the world's marine ecosystems.



Sensory Ecology and Zooplankton Physiology

Environmental Signals in a Microscopic World

Aquatic microorganisms live in a vast, three-dimensional world with few geographical barriers. Despite their extraordinary numbers, their small size means that these organisms are often separated by hundreds or thousands of body lengths (roughly equivalent to having our nearest neighbor half a mile away), resulting in a relatively dilute, watery world.

For many of these organisms, searching out potential food items or finding each other in order to mate would be a nearly impossible task without the ability to detect sensory cues. Understanding which sensory signals these organisms use is fundamental to interpreting the distribution patterns of species throughout the ocean, and ultimately to understanding the biological-ecological links between species and communities.

Led by Dr. David Fields, the Sensory Ecology and Zooplankton Physiology Laboratory investigates the sensory mechanisms that drive behavioral responses in ecologically and commercially important zooplankton species. The sensory systems of small, neurologically



Above: A scanning electron micrograph (SEM) of 3 segments from the antennule of a marine copepod. The long hair detects mechanical signals, while the shorter hairs detect both mechanical and chemical signals.



Photo by Dennis Griggs.

Dr. David Fields.

Right: The fluid disturbance created by a 2 mm-long copepod swimming through the water. The white line is the body of the animal; colored lines indicate water speed. Other organisms, including fish, detect the copepod based on the size and strength of the disturbance.

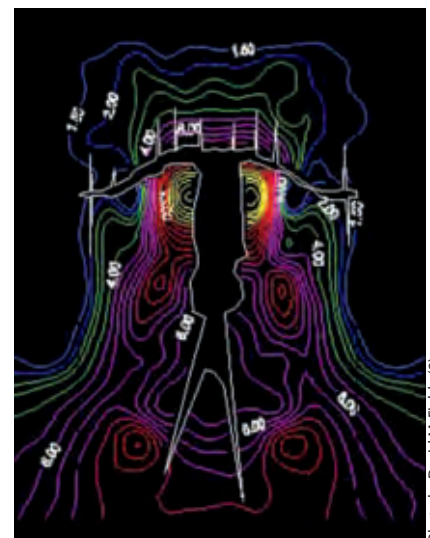


Photo by David M. Fields. (2)



Endangered North Atlantic Right Whale with calf.

Photo courtesy of NOAA.

The Laboratory's Sensory Ecology projects are currently funded by the National Science Foundation (NSF) and the Office of Naval Research (ONR). NSF is supporting the investigation of fluid signal patterns created by moving organisms and how these signals are detected and interpreted at the level of an individual sensory hair. This research can provide an innovative approach to managing aquaculture pests, such as commercially damaging salmon lice, and help explain how a range of animals—from copepods, to fish, to seals and manatees—find their mates and their food, and avoid predators in a complex, fluid environment.

ONR is funding research focused on predicting a larger scale phenomenon—where patches of krill, a tiny crustacean that is one of the major food sources for the threatened North Atlantic Right Whale, are likely to form. In the Gulf of Maine, right whales often aggregate in regions where there are abundant food resources. Unfortunately, these rich feeding grounds sometimes coincide with shipping lanes or areas under intense fishing pressure. Fields is investigating the environmental conditions that cause krill to form large swarms in order to predict where and when this will happen.

simple organisms are often exquisitely tuned for particular signals that are directly relevant to their survival. Discovering the means by which these organisms detect signals in their environment and ascertaining their sensitivity has helped scientists predict where they live; determine how they find their food; and understand the ecological relevance of their behavior, smell, and color.

Ultimately, all sensory information (light, sound, smell) must pass through the water to be perceived by marine organisms. Subtle changes in the properties of the water, such as temperature or penetration of light, can have complicated and profound effects on the ability of these organisms to function. For example, the Arctic Ocean is predicted to increase in temperature by 5° to

10°C over the next 50 to 100 years. This change in temperature will alter the water's viscosity, changing the patterns of fluid disturbances.

Although shifting temperatures may not be large enough to kill animals directly, damage to their ability to find a mate will undoubtedly cause broad scale disruptions in the marine food web. A copepod that is trying to detect a mate based on these

changed fluid signals will face a challenge analogous to a human being trying to identify another person's high-pitched voice after inhaling helium gas. The shift in tone and pitch alters the ability to discriminate among different sounds.

David M. Fields
Senior Research Scientist

Steve Shema, *Research Technician*



why it matters

Discovering how small, but ecologically indispensable organisms are able to distinguish among the myriad physical messages in their fluid environment is essential to understanding basic zooplankton processes. This knowledge will help predict predator-prey population fluctuations and how global changes in zooplankton distribution affect the health of ocean ecosystems.

Evolutionary Bioinformatics and Molecular Phylogenetics

Tracking Adaptation on a Molecular Scale

Bioinformatics combines molecular biology and mathematical modeling of biological data with computational methodology, allowing scientists to quickly process and analyze vast amounts of information.

Rapid advances in gene sequencing technologies allow scientists to study how life evolves in extraordinary detail, discovering direct genetic connections among organisms, populations, and species, and strong correlations between environmental change and molecular adaptations. The Evolutionary Bioinformatics and Molecular Phylogenetics group at Bigelow Laboratory is using bioinformatics to study evolution and adaptation at the level of molecules and proteins.

Together with recent statistical innovations, it has become possible to estimate the rate of genetic change, describe demographic histories of species, and identify phylogenetic relationships in populations over space and time. This research is providing a new perspective about the effects of natural selection on the biodiversity of our planet.



Photo by Greg Bernard.

Dr. David McClellan.



Photo courtesy of NOAA.

Dolphins are marine mammals that have evolved the ability to remain underwater significantly longer than land mammals.

Dr. David McClellan is working in collaboration with empirical researchers from around the world to develop analytical methodology and computer software to study evolutionary adaptation in a variety of organisms. These research methods can be applied to a wide range of species, including large plants and animals, but by far the richest source of these data are bacteria and viruses, whose fast rate of mutation makes it easy to see evolution happening in relatively short periods of time.

The mechanism and extent to which specific genes spread throughout different evolutionary

lineages in marine communities depends on environmental conditions such as temperature, light intensity, density, and dissolved CO₂ concentrations, among many other factors. By combining computer modeling, genomics, and bioinformatics, McClellan and his colleagues are developing methods to sample and compare marine genomes and metagenomes across space and time, providing a way to track specific evolutionary adaptations in response to environmental changes in the ocean.

This approach is being used as part of a current National Aeronautics and Space Admin-

TreeSAAP: Looking Deep Inside

Working with a colleague from the Department of Biomedical Engineering at Johns Hopkins University, McClellan has refined a powerful software program that can detect and characterize the effects of natural selection on amino acids that form proteins. Known as TreeSAAP (Selection on Amino Acid Properties using phylogenetic trees), the program was originally developed by McClellan, colleagues, and students. It measures selective influences on structural and biochemical amino acid properties and performs statistical tests on these data. TreeSAAP's recent improvements have achieved a nearly 90% level of accuracy, making it possible to conduct detailed studies of individual changes in amino acids and their role in protein function. This approach allows specific adaptive changes to be mapped onto three-dimensional structures to assess the positive benefits of adaptation on cellular function, offering significant promise for its use as a biomedical research tool.

Cytochrome bc1 Complex

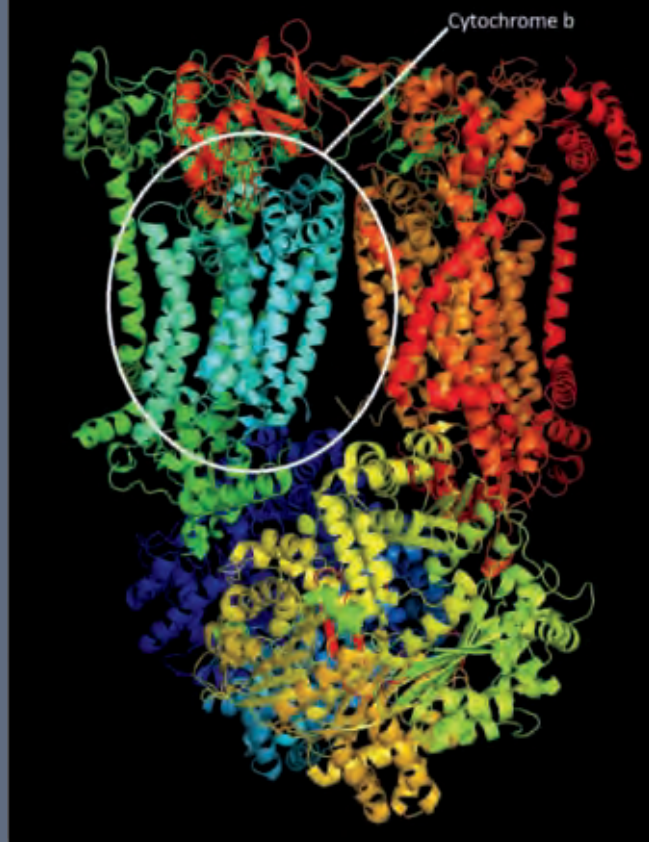


Illustration by Rachelle Campbell.

A three-dimensional protein structure of the cytochrome bc1 complex, which includes the central catalytic protein cytochrome b. This complex of proteins is responsible for pumping hydrogen ions (protons) across the inner mitochondrial membrane to create the proton gradient necessary for oxidative phosphorylation of ATP (adenosine triphosphate) molecules, the fuel of all cells. This structure was used to identify those amino acid residues responsible for the adaptation that allows whales and porpoises to stay submerged underwater several times longer than humans.

illustration /EPSCoR (Experimental Program to Stimulate Competitive Research) grant from the Maine Space Grant Consortium investigating the evolution of biological iron-oxidation and oxygen respiration in marine bacteria.

David McClellan
Senior Research Scientist

why it matters

Theoretical, computational, and empirical bioinformatics research is making significant contributions to the efficiency and accuracy of DNA and protein sequence analysis, and is supporting the investigation of molecular mechanisms involved with the development of drug and vaccine resistance in viruses and bacteria. Besides its contribution to biomedical advances, evolutionary bioinformatics is supplying the analytical tools needed to link protein evolution with habitat and climate change, and understand the effects of global and local environmental pressures on humans and other life forms at the most basic, molecular level.

Marine Virology

Discoveries on the Boundary of Life

A single teaspoon of seawater is likely to contain up to a hundred million viruses. Marine viruses catalyze global biogeochemical cycles by breaking down phytoplankton cells and releasing their contents, accelerating the recycling of organic compounds.

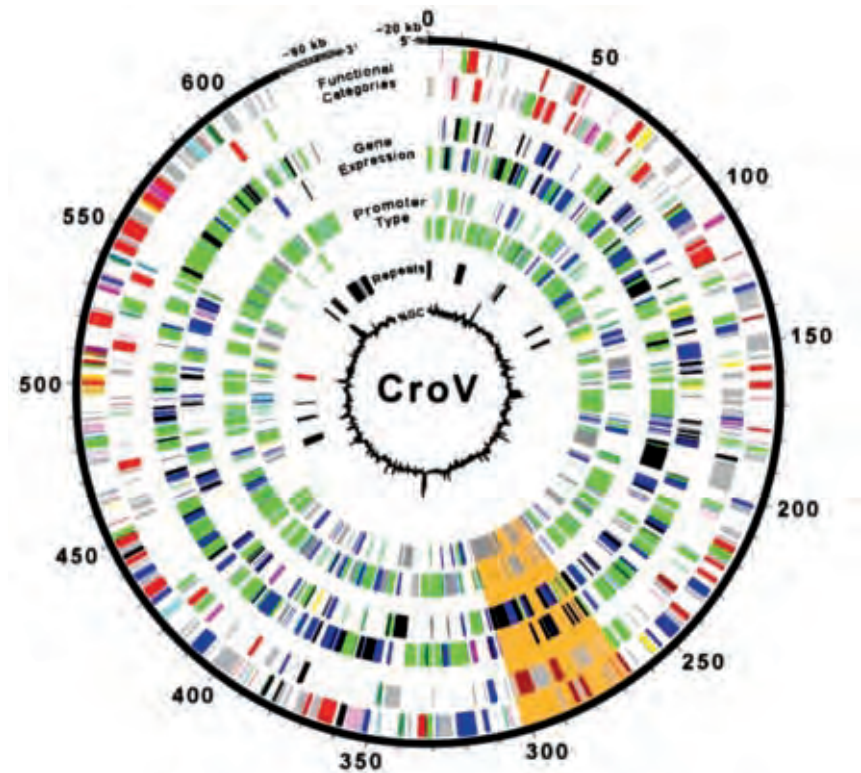
By regulating seasonal phytoplankton blooms and influencing nutrient flow in the ocean, viruses recycle approximately 25% of the carbon captured by photosynthesis, making them an essential part of the global carbon cycle.

Using a range of molecular biology tools, Dr. Willie Wilson and his team in the Laboratory's Marine Virology research group are investigating the role of viruses in ocean ecosystem dynamics by studying the genetics involved in predator-prey interactions between viruses and their hosts. Their work, in collaboration with scientists from the University of British Columbia and the Plymouth Marine Laboratory, has led to the discovery of a giant virus called CroV, which contains the largest genome of any marine virus isolated to date.



Photo by Dennis Griggs.

Dr. Willie Wilson.



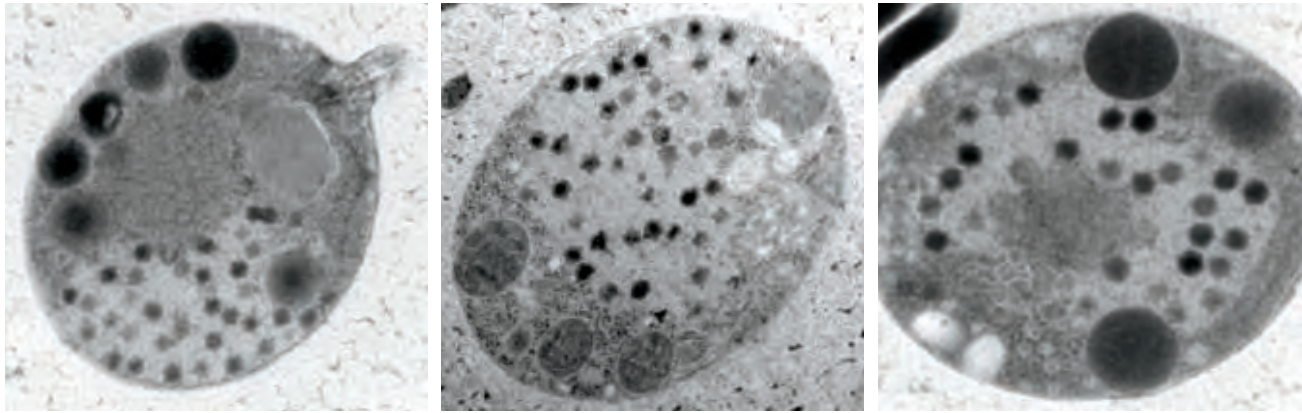
Genome diagram of CroV, a giant among viruses. Illustration by Matthais Fischer.

CroV infects the predatory single-celled microflagellate *Cafeteria roenbergensis*, which exists in large numbers throughout the world's oceans and provides a critical link in the marine food web by grazing on bacteria and other viruses. Thus far, only one other virus has been identified that is larger than CroV, the freshwater Mimivirus, which infects amoebas. Giant viruses are loosely defined as having a genome greater than 280,000 base pairs. There are currently less than 20 full virus genome sequences in this size range.

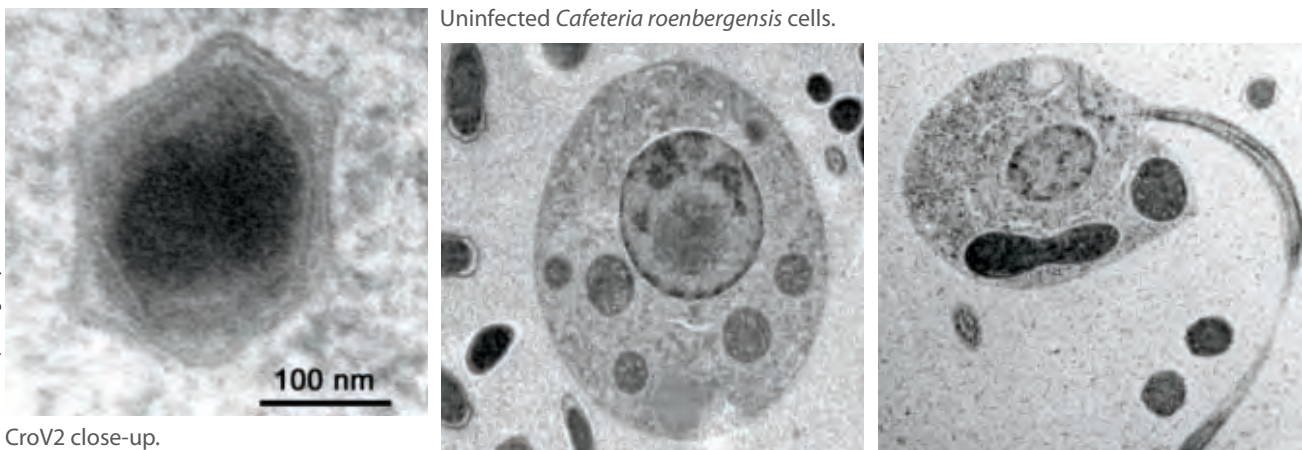
Unlike most of the known viruses, which have a relatively small number of genes, CroV has a 730,000 base pair DNA genome, comprising 544 genes and making it larger than some of the smallest bacteria. Its ability to synthesize proteins and sugars, and perform some of the same functions as living cells, has strengthened the case for considering at least some viruses to be genuine life forms.

An ecologically important marine virus, CroV is the first highly complex virus infecting a key microzooplankton predator to be studied in genetic detail.

Cafeteria roenbergensis cells infected with CroV.



Uninfected *Cafeteria roenbergensis* cells.



Microscope images by Matthais Fischer.

CroV2 close-up.

Analysis of its genetic structure is yielding new information about gene transfer, DNA replication, protein synthesis, and carbohydrate metabolism at the molecular level. The researchers in the Marine Virology group expect that CroV is the first of many giant marine viruses yet to be discovered.

Preliminary observations and analysis of the Global Ocean Sampling database suggest that giant viruses are extremely abundant, and those that have been isolated contain novel genes that encode important functions and metabolic pathways. Funding from the National Science Foundation is supporting single virus sorting and analysis of the genetic information found in a group of previously unstudied giant algal viruses.

Advances in flow cytometry sorting technology at Bigelow Laboratory and enhanced single virus genome sequencing at Oak Ridge National Laboratory (in collaboration with Dr. Steven Wilhelm at the University of Tennessee, Knoxville) are offering the researchers new perspective on the profusion and genetic potential of these infinitesimal oceanic “leviathans.”

Willie Wilson
Senior Research Scientist

Sheri Fløge, Research Assistant
Ilna Gilg, Research Assistant
Scott Lawrence, Visiting Student Researcher
Joaquín Martínez-Martínez,
Postdoctoral Researcher

why it matters

Marine viruses represent arguably the largest untapped biotechnological resource on the planet. They offer the potential for new products and medicines that are of direct benefit to humans, including their use in phage therapy to control harmful bacteria. New research is revealing the effect marine viruses have on ocean ecosystems at the genetic level, and uncovering the critical role they play in maintaining marine biodiversity and driving evolutionary processes in the sea.

Marine Microbial Ecology

Diving into Diversity

Microscopic single-celled organisms called protists are part of a major lineage of life—including complex multi-cellular plants and animals—known as eukaryotes. From an evolutionary perspective, protists are a step up on the Tree of Life compared to other microbes.

Unlike bacteria and archaea, protists (and their fellow eukaryotes) have evolved a distinct, membrane bound nucleus that contains each cell's genetic instructions.

Sequencing DNA in samples of seawater has shown that protists flourish in all marine ecosystems, with estimates of diversity comparable to the multitudes of different bacteria in the oceans. Hundreds of protist species can often be found in a single seawater sample. Large-scale DNA sequencing of samples from major oceanic regions is helping to determine the amount of protistan diversity in the oceans and the global distribution of diverse lineages. These data are providing clues about the function of protistan assemblages in the marine microbial food web and their role in maintaining ecosystem resilience and stability under changing environmental conditions.

Dr. Pete Countway has participated in manned submersible dives to survey protistan diversity in two physically distinct deep-sea hydrothermal vent ecosystems—

Samples for microbial eukaryote diversity at deep-sea hydrothermal vents were collected from protist traps placed at precise locations around vent ecosystems (yellow sponges in tubes), from cores of microbial mats and surrounding sediments, and by “vacuuming” samples off the seafloor at discrete sites.

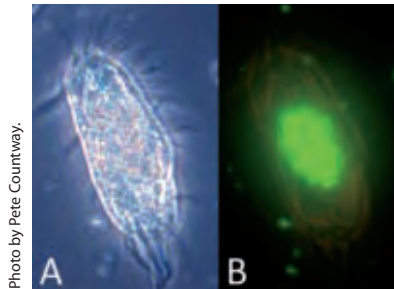


Photo by Pete Countway.

Deep-sea hydrothermal vent ciliate shown by (A) brightfield and (B) epifluorescence illumination. The bright green area in panel B is the result of grazing by the ciliate on Green Fluorescent Protein (GFP) expressing bacteria that were introduced to a natural sample.



Relative abundance of major microbial eukaryote lineages in a coastal seawater sample. Data from Caron, Countway, and Brown (2004). *J.Euk.Microbiol.*

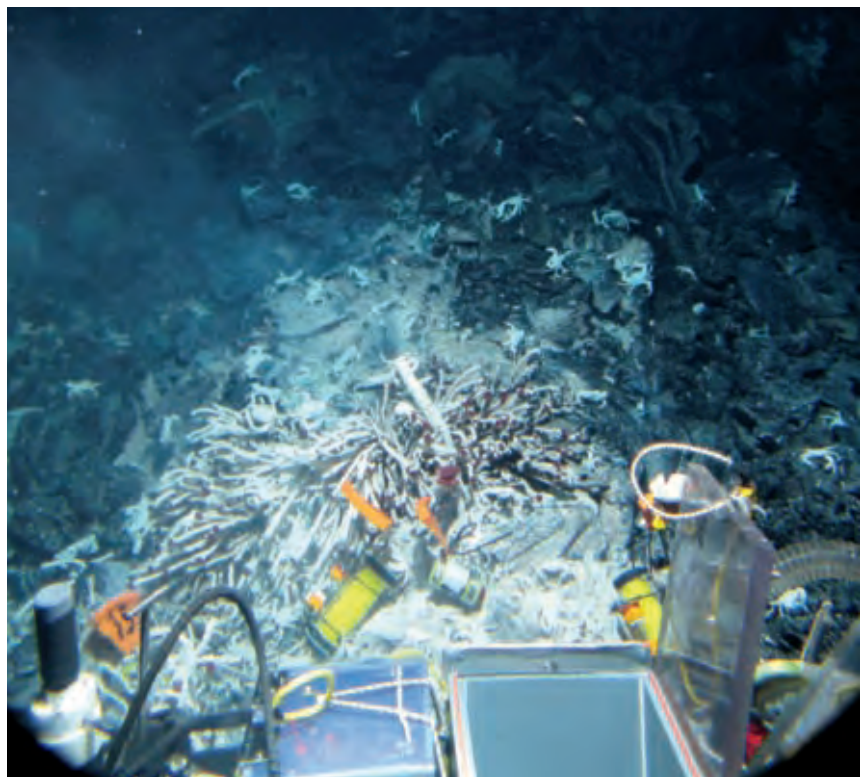
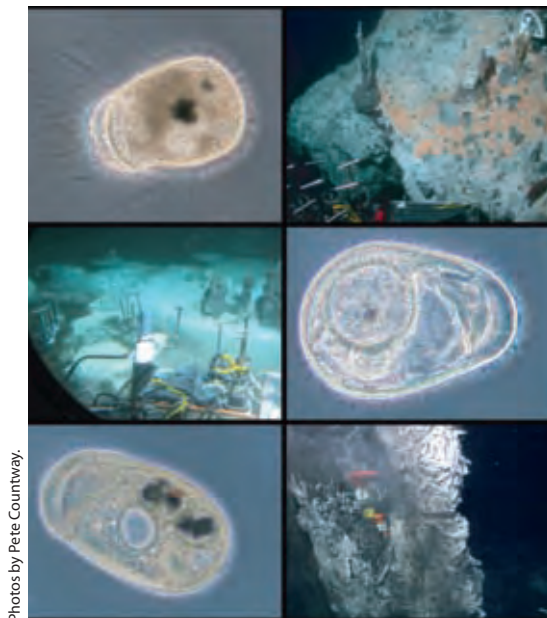


Photo by Pete Countway.



Photos by Pete Countway.



Courtesy of Google Earth.

Left: Deep-sea hydrothermal vent ciliates and the types of habitats that were sampled within the hydrothermal vent ecosystem, ranging from microbial mats growing atop hydrothermal features, sedimentary environments, and traps that were placed on hydrothermal chimneys. Right: Areas of study.

the sediment-dominated Guaymas Basin in the Gulf of California and the basalt-based vent system located at 9° N along the East Pacific Rise. Preliminary studies of protistan grazing on bacteria, “at sea” microscopy of live samples, and DNA sequencing reveal diverse and active protistan assemblages in and around deep-sea hydrothermal vents. Data from this research suggest that deep-sea hydrothermal vent protists are

largely unique and some resemble those in similar habitats with sharp chemical gradients and reduced oxygen levels at shallower depths.

Countway’s findings indicate that protistan assemblages can undergo rapid rearrangement of dominant types, while overall diversity is maintained by a background “rare” biosphere of less abundant protist species. Controlled experimental simula-

tion of environmental change in the laboratory offers the potential to investigate the role of protistan diversity in maintaining ecosystem function and to isolate, develop, and scale-up promising protist strains for biofuels and natural products.

Pete Countway
Senior Research Scientist



Photo by Greg Bernard.

Dr. Pete Countway.

why it matters

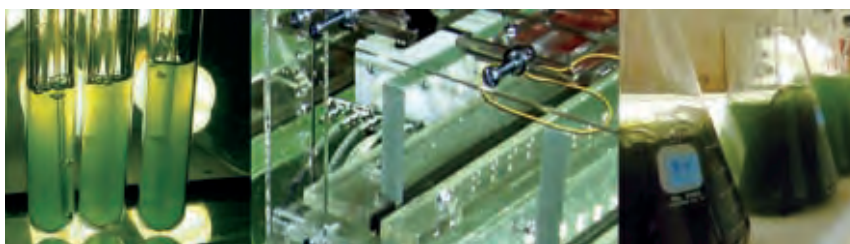
On a global scale, many of the most abundant protists are distributed throughout similar ecosystems in both the Atlantic and Pacific Oceans. The diversity of protistan assemblages in the upper water column is becoming increasingly well-characterized. Protistan diversity, abundance, and activity in the deep-sea, however, remains largely unexplored, even within the oases of life surrounding deep-sea hydrothermal vents. The ecological role of protists in these extreme habitats offers significant opportunities to discover how microbial life responds and adapts to abrupt physical and chemical changes in ocean ecosystems.

Corporate Alliances and Technology Transfer

Building an Entrepreneurial Ecosystem

Over the years, the Laboratory has developed substantial intellectual property, funded primarily by competitive grant awards from federal research agencies. In partnership with the private sector, this intellectual property has the potential to solve problems for industry and benefit society through a process known as innovation commercialization (also referred to as “technology transfer”)—the legal and economic process of converting scientific findings from research endeavors into useful products.

Because the oceans of the world represent such a vast frontier of undiscovered compounds and organisms, the prospect exists for Bigelow Laboratory to work with numerous private industries to explore commercial opportunities for new products and technologies in markets including biofuel, pharmaceuticals, cosmeceuticals and nutraceuticals, as well as single cell genome analysis, bioinformatics, and optical/chemical sensing. Private industry is increasingly seeking relationships with independent research laboratories to identify intellectual property that has commercial promise. The Laboratory has established the Department of Corporate Alliances and Technology Transfer to work with its Senior Research Scientists in managing the intellectual property and technology transfer aspects of their research, and to accelerate the migration of ideas from the lab bench to practical commercial application.



Over the past year and a half, the Laboratory began two collaborative initiatives with the private sector. Funding from the National Marine Fisheries Service’s Saltonstall-Kennedy Grant Program is supporting a project with Micro Technologies, a private animal health company in Richmond, Maine, to establish an experimental biologics production facility and develop new therapies for the aquaculture industry. During this same period, the National Science Foundation funded a Small Business Innovation Research project for the Laboratory to collaborate with Bodega Algae, LLC in Massachusetts, a renewable energy company that is developing photobioreactor technology needed to grow algae for use in production of biofuel.



As this report goes to press, Mark G. Bloom has begun his appointment as Director of the Laboratory’s new Department of Corporate Alliances and Technology Transfer (DCATT). Bloom is an internationally-recognized intellectual property attorney and technology transfer professional. He received a B.S. in Microbiology from Ohio State University and a J.D. from Franklin Pierce Law Center (Concord, NH). He is designated as a Certified Licensing Professional (CLP®) and is registered to practice before the U.S. Patent and Trademark Office.

OCEAN SCIENCE EDUCATION



A commitment to educating the next generation of ocean scientists and sharing our discoveries with students, educators, and the public are integral to the Laboratory's research programs and long-range objectives. Our education initiatives have expanded significantly in the past months to include partnerships with two academic institutions, a rigorous postdoctoral training initiative, and new opportunities for undergraduates, along with ongoing programs for high school science students and the public.

Postdoctoral Training

Becoming a Professional Scientist

Bigelow Laboratory is actively engaged in training postdoctoral researchers by encouraging development of the knowledge, skills, and professional ethics that are at the foundation of a high quality career in ocean science.



Photo by Greg Bernard.

By working with senior research scientists, assisting in submission of grant proposals, and participating in communication of research results, the Laboratory's postdoctoral researchers gain exposure to skills that will be crucial in their own future research programs.

Training in responsible research practices is an essential part of a scientist's professional education. Responsible conduct of research is critical for achieving scientific excellence and maintaining public trust in science. The Laboratory includes a strong focus on scientific ethics as part of a formal Postdoctoral Education and Training Program.

Under the leadership of Dr. David McClellan, the program has been designed to contribute to an individual's professional growth in areas including research ethics, grant proposal writing, peer-reviewed scientific publication, and application for academic faculty and senior research positions. The technical portion of the program provides direct experience that builds competence in bioinformatics, microscopy, and flow

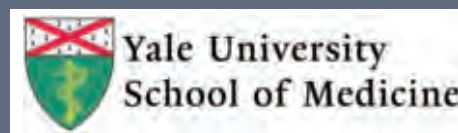
cytometry, along with skills in written communication and oral presentation. Additional topics will be considered as the program continues in future years.

Postdoctoral researchers attend seminars and committee meetings, present research, and invite and host speakers as part of the Laboratory's regular research seminar series. They are also an integral part of the Laboratory's education and public outreach programs, helping mentor and guide students in the Laboratory's high school and undergraduate programs.

The Laboratory's postdoctoral researchers: (from left to right): Emily Fleming, Geomicrobiology; Joyce McBeth, Geomicrobiology; Huan Qui, Algal Molecular Evolution; Jochen Nuester, Trace Metal Biogeochemistry; Joaquin Martínez Martínez, Marine Virology; Manuel García, Single Cell Genomics; Andy Hind, Ocean and Atmospheric Chemistry; and Brandon Swan, Single Cell Genomics. Not pictured: Eun Chan Yang, Algal Molecular Evolution.

Exploring Joint Initiatives with Yale University School of Medicine

In the summer of 2010, Yale University School of Medicine and Bigelow Laboratory signed a



Memorandum of Agreement for Academic Collaboration to further mutual research and collaboration goals. The agreement is intended "to strengthen mutual understanding, foster friendly communication, and promote academic collaboration and exchange." The agreement enables Bigelow scientists and Yale researchers to develop joint research projects, work with new funding agencies, and organize joint conferences.

Ten Weeks of Summer

Gulf of Maine and the World Ocean: Research Experience for Undergraduates

Now embarking on its third year, the Laboratory's National Science Foundation Research Experience for Undergraduates (REU) Program, known as *Gulf of Maine and the World Ocean*, recruits highly motivated undergraduates interested in conducting independent research projects with guidance from scientist mentors.

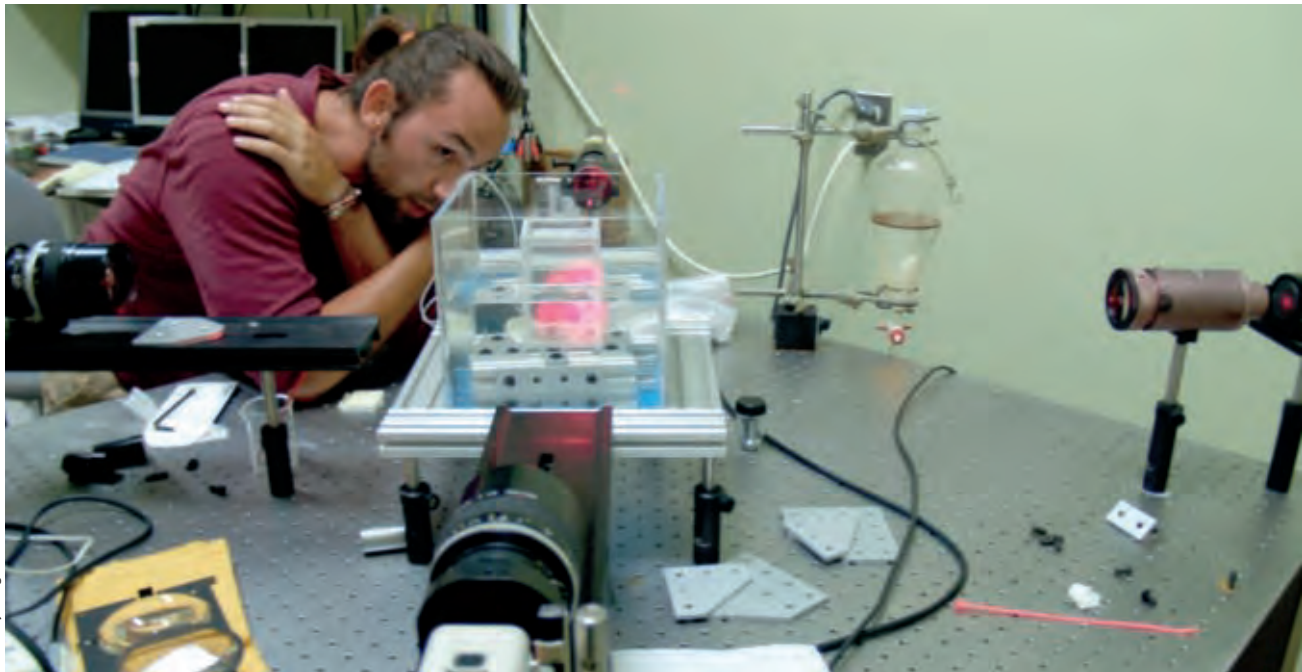


Photo by Greg Bernard.

2010 REU Student Brandon Walus in the Sensory Ecology Laboratory.

Undergraduates are selected from a nationwide pool of applicants to spend ten weeks investigating current areas of research within the Laboratory's core science centers.

Based on mutual research interests, each REU student is placed in a Senior Research Scientist's laboratory. Research areas include the marine microbial food web, fisheries oceanography, ocean biogeochemistry, optical oceanography, remote sensing, sensory biology, and climate change. Students identify a research question, develop a proposal, conduct their proposed work, prepare an abstract and

poster, and present their research at a formal student symposium at the close of the program.

REU participants are immersed in the Bigelow community and take part in seminars, field trips, and Laboratory social events.

Living as a community of young scientists is both an academic and personal growth experience for REU students, one that creates friendships and networks that form a lasting foundation for future careers in ocean research.

"I would like to thank Bigelow for one of the best summers I've ever had. I finally participated in a program in which I got to do work that I was passionate about and it helped me confirm my desire to enter the academic world of ocean sciences. I'll always be grateful for the experience and confidence that I gained from attending this program."

— 2010 REU Student



Photo by Dennis Griggs.

REU Program mentors Drs. David Emerson (left) and David Fields.

REU Class of 2009

David Brazel

Colby College, Maine

A time course study of bacterial community dynamics

Mentor: Dr. Ramunas Stepanauskas

Ashley Couture

University of Maine, Machias, Maine

Ciliate time series from a long-term dock study

Mentor: Dr. Michael Sieracki

Alexis Gillmore

Estrella Mountain Community College, Avondale, Arizona

Determining the interrelationship between growth rate and silica content of diatoms and the grazing rates of mesozooplankton

Mentor: Dr. David Fields and Mr. Steven Shema

Amanda Graumann

University of Wisconsin, Superior, Wisconsin

The relationship between biogenic silica (BSi), diatom concentration, and temperature in the Gulf of Maine

Mentor: Dr. William Balch

Andrew R. Gross

Pennsylvania State University, Pennsylvania

Iron enrichment: Natural causes and anthropogenic effects

Mentors: Dr. Joaquim Goés, Dr. Helga do Rosario Gomes, Ms. Stacey Keith

Amy Langdon

Swarthmore College, Pennsylvania

Leptothrix ochracea: An old and rusty phylogenetic mystery

Mentors: Dr. David Emerson and Dr. Emily Fleming

Hannah C. McDaniel

University of Maine, Orono, Maine

Potential regulation of Synechococcus growth and silica content by silicic acid concentrations in seawater

Mentors: Dr. Benjamin Twining, Dr. Jochen Nuester, Ms. Sara Rauschenberg

Noah Oppenheim

Reed College, Portland, Oregon

In situ monitoring of tethered lobsters reveals diel shifts in predation intensity and cannibalism

Mentor: Dr. Richard Wahle

Katherine M. Farrar

Bowdoin College, Maine

Addressing iron-oxidizing bacteria associated with steel corrosion in near shore marine environments.

Mentors: Dr. David Emerson and Dr. Joyce McBeth.



Photo by Greg Bernard.

2009 REU Student Amy Langdon in the Geomicrobiology Laboratory.



Katherine Farrar presenting her research at the 2009 REU Symposium.

REU Class of 2010

Macon "Joey" Brown

Indiana University-Purdue University, Indianapolis, Indiana

Defining the major lineages of red algae (Rhodophyta).

Mentors: Dr. Eun Chan Yang and Dr. Hwan Su Yoon

Rachelle R. Campbell

Southern Maine Community College, South Portland, Maine

What freed Willy: Ancient respiratory adaptations in whales.

Mentor: Dr. David McClellan

Meaghan Daley

University of Massachusetts, Boston, Massachusetts

Linking growth, Fe uptake, and Fe distribution in Trichodesmium to Fe availability.

Mentors: Dr. Jochen Nuester and Dr. Benjamin Twining

Jennifer R. Fownes

Dartmouth College, Hanover, New Hampshire

Novel methods for visualizing iron-oxidizing bacteria on mild steel.

Mentors: Dr. David Emerson and Dr. Joyce McBeth

Dr. Paty Matrai with 2010 REU student Angel Mojarro.

Ileana M. Freytes Ortiz

University of Puerto Rico, Rio Piedras, Puerto Rico

Cobble-dwelling fauna: Inter-oceanic differences in trophic structure.

Mentors: Ms. Charlene Bergeron and Dr. Richard Wahle

Brittney Honisch

Western Washington University, Washington

Iron requirements for growth in coastal and ocean strains of Emiliana huxleyi.

Mentors: Ms. Sara Rauschenberg and Dr. Benjamin Twining

April Klein

University of Texas, Arlington, Texas

Marine viruses: A study on host-virus response response to elevated levels of CO₂.



Photo by Greg Bernard.

Mentors: Ms. Ilana Gilg, Dr. Joaquin Martínez Martínez, and Dr. Willie Wilson

Angel Mojarro

Brown University, Providence, Rhode Island

Microgels and DMSP in marine phytoplankton.

Mentors: Mr. Andy Hind and Dr. Patricia Matrai

Jasper Nutt

University of Maine, Orono, Maine

Phage therapy as a vaccine for Aeromonas salmonicida.

Mentors: Ms. Ilana Gilg and Dr. Willie Wilson

Brandon Walus

University of Maine, Orono, Maine

Effects of sub-lethal concentrations of crude oil on copepod behavior: Acartia tonsa.

Mentors: Dr. David Fields and Mr. Steven Shema

Whitney M. Westman

Florida Institute of Technology, Melbourne, Florida

Barnacles: Fans of viscosity. The effects of kinematic viscosity on feeding behaviors in Balanus balanoides.

Mentors: Dr. David Fields and Mr. Steven Shema

Well Met

A Strategic Partnership with Colby College

In July 2010, the Laboratory entered into partnership with Colby College in Waterville, Maine, marking the beginning of a relationship that will increase educational and research opportunities for both institutions.

The new partnership formalizes connections between Bigelow scientists and Colby faculty and students that have been evolving steadily over the past several years. Colby undergraduates have participated in the Laboratory's NSF Research Experience for Undergraduates Program and served as expedition interns for Bigelow scientists aboard research ships.

In January 2010, Bigelow scientists taught courses in bioinformatics and in oceans and climate change as part of the College's January Program, an intensive four-week term during which students focus on a single course, internship, or research project. A key component of the partnership is a commitment to extend the January Program course offerings designed and taught by Bigelow scientists through 2013.

The partnership supports expansion of the marine sciences curriculum at Colby College and an increase in undergraduate student research, as well as increased research collaborations between the two institutions. The vision for the evolution of this partnership includes collaborative teaching opportunities that take advantage of the resources at both institutions, semester-long in-residence study by Colby students at Bigelow Laboratory, and curricular innovations that combine scientific research with economic and social policy analysis.

"We are very excited about the potential for this partnership. For our students and faculty, it will provide access to ocean research at a level simply not possible before, and it is hard to overstate the academic possibilities that will present themselves in the coming years."

— William "Bro" Adams, *President, Colby College*



Photo by Dennis Griggs (2).

In Full BLOOM

Hands-on Ocean Research for Maine High School Students

The annual Keller BLOOM (Bigelow Laboratory Orders of Magnitude) Program selects sixteen Maine high school juniors from across the state to spend four days with Bigelow scientists engaged in hands-on laboratory and field research.

The residential ocean science program consists of a full day aboard a research vessel collecting samples at a series of stations in the Sheepscot River estuary; data analysis using the Laboratory's state-of-the-art instrumentation; public presentation of research results; and time to discuss science and public policy, scientific ethics, and future career directions. Professional evaluation of the long-term impact of the program conducted in 2010 found that 100% of BLOOM students attend college; 62% major in STEM (Science, Technology, Engineering, and Mathematics) fields; 88% graduate from college; 57% pursue STEM careers; and 60% now live and work in Maine.



2010 BLOOM Students:

Samuel Albert
Fort Kent Community School

Kaitlyn Alley
Jonesport-Beals High School

Alyssa Beaupre
Lewiston High School

Maureen Blanchard
South Portland High School

Alison Clift
Bonny Eagle High School

Paul Elish
Presque Isle High School

Morgan Forni
Sumner Memorial High School

Hailey Gossard
Traip Academy

Marissa Heikkinen
Home Schooled

Blaise Jenner
Isleboro Central School

Kristina Kelley
Belfast Area High School

Mariam Khan
Waterville High School

Sophie Oullette
*Wisdom Middle/High School
(Frenchville)*

Zachery Shaw
Morse High School

Kristin Trenholm
Mt. Abram High School

Wade Valleau
Mount Desert Island High School

2009 BLOOM Students:

Douglas Blasius
Medomak Valley High School

Natasha Boada
Narraguagus High School

Amanda Bouchard
Monmouth Academy

Steven Chesley
Brunswick High School

Kayla Cobb
Scarborough High School

Dakota Cuninghame
Bucksport High School

Magnolia Dixon
Mt. Abram Regional High School

Arthur Govoni
Islesboro High School

Meghan Harbourne
and Emily Bell-Hoerth
Morse High School

Hayli Kinney
Rockland District High School

Jordan Leathers
*Upper Kennebec Valley Memorial
High School*

Justin Lewin
Presque Isle High School

Jenn Stauffer
Mount View High School

Katrina Ternus
Biddeford High School

Courtney Withee
Foxcroft Academy



Photo by Greg Bernard (3).

Talking Science

Free and Open to the Public

The Laboratory has expanded its annual Boothbay Harbor summer science conversations, part of the international Café Scientifique movement, to include special talks throughout the year in a variety of mid-coast Maine venues.

Our researchers and guest speakers are drawing record crowds at these events. The participants' interest in ocean science and global environmental issues is a welcome barometer of the public's commitment to talking about recent discoveries and the state of the world's oceans. The Laboratory also regularly participates in numerous community events and festivals, and continues to host an annual open house that brings local residents and visitors of all ages into our individual laboratories for tours and hands-on demonstrations of ocean science in its natural habitat.



Bigelow Laboratory
OPEN HOUSE
Ocean Science in Action

Join us for Laboratory tours and a personal view of a world-class research and education center.

August 3, 2009 • 1–3 p.m.
180 McKown Point Road • West Boothbay Harbor, Maine

- Meet Henry the Underwater Glider
- Watch real-time wave action on computers
- See amazing microscopic creatures
- Talk to scientists

All activities are free and open to the public, of all ages.

Bigelow Laboratory is committed to sharing information about current scientific issues, research, and education.

www.bigelow.org



BIGELOW LABORATORY FOR OCEAN SCIENCES PROUDLY PRESENTS

CAFÉ SCIENTIFIQUE 2010
Summer Science Conversations
on the Maine Coast

Bigelow Laboratory scientists and their guests invite you to be part of this summer's lively and informal discussions about ocean exploration and discovery.

Every Tuesday,
beginning June 15, 2010,
from 6–7 p.m.
and then Tuesday evenings,
June 29–August 24, 2010

Opera House, Boothbay Harbor
86 Townsend Avenue • Free and Open to the Public

Come Join the Conversation!
A cash bar is available to help set the mood.

The Laboratory has been part of the international Café Scientifique movement since the 1980s. There are currently more than 150 active groups in 26 countries engaged in such activities.

For a complete program and more information, visit
www.bigelow.org

Making History

Groundbreaking for the Ocean Science and Education Campus

More than two hundred of the Laboratory's friends and neighbors gathered in a rough clearing of our 64-acre East Boothbay property on September 7, 2010 to witness the official groundbreaking for the Bigelow Center for Blue Biotechnology, the first facility being built on the Ocean Science and Education Campus.

Guest of honor U.S. Senator Susan Collins, whose help was instrumental in making the day a reality, was on hand to take part in the ceremony.

Funding from a diversity of sources made the historic day possible, including the National Oceanic and Atmospheric Administration, the National Institute of Standards and Technology, the National Science Foundation, the Maine Technology Asset Fund, the First National Bank of Damariscotta, the support of Maine's entire Congressional delegation, and the steadfast generosity of the Laboratory's private donors.

The years, months, weeks, and days leading up to this moment are a story of vision, determination, talent, and generosity on the part of a long list of people who believe that discoveries in ocean science

are important to everyone, and that world-class ocean science should have a permanent home on the coast of Maine. We thank them all.



U.S. Senator Susan Collins with State Office Representative William Card en route to the groundbreaking site.



Photo by Dennis Griggs

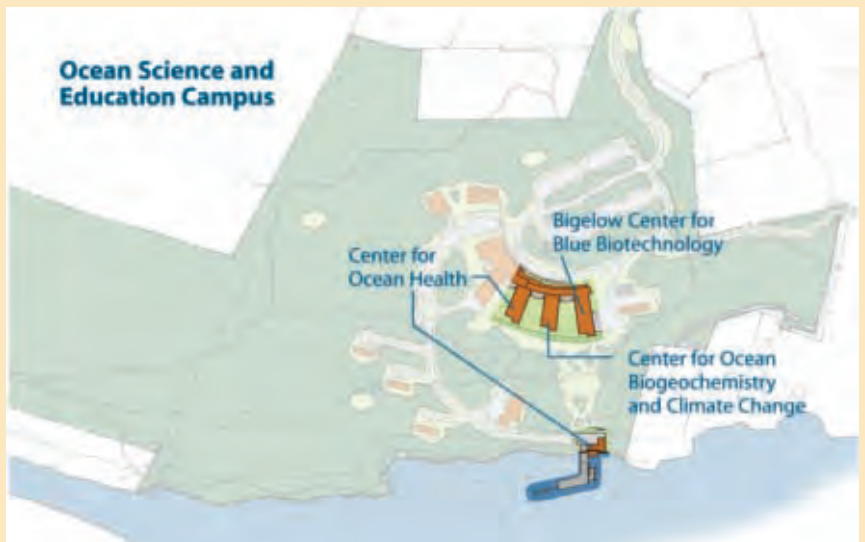
Photo by Terry DeWan (2)



Photo by Greg Bernard (3).

Campus Development Goals

The design of the Ocean Science and Education Campus is based on expression of world-class science, while at the same time ensuring optimal land use, stewardship, and sustainability. The campus is being built to integrate with the natural environment and the local community, and will include over a mile of public walking trails. The campus also represents the Laboratory's commitment to a future for global ocean research on the coast of Maine, creating new jobs in Maine's innovation economy, and pioneering ways to harness the ocean's enormous potential for the benefit of society through research, education, and technology transfer.



Active Grants and Contracts

January 1, 2009–June 30, 2010

Title	Funder	Principal Investigator(s)	Award Total
Bacterial dormancy, bacterivory, and bacterioplankton diversity in the ocean	NSF	Stepanuskas/Sieracki	659,836
Collaborative Research: Producing an Updated Synthesis of the Arctic's Marine Primary Production Regime and Its Controls	NSF	Matrai	306,793
ITR Collaborative Research: Interactive Software Systems for Expert-Assisted Analysis and Classification of Aquatic Particles	NSF	Sieracki/Balch	1,555,515
Analysis and Classification of Aquatic Particles COSEE	UME/NSF	Sieracki/Goés/Fields	622,108
The Collaborative O-Buoy Project: Development of a Network of Arctic Ocean Chemical Sensors for the IPY and beyond	NSF	Matrai	413,994
Collaborative Research: The role of phytoplankton ballast material in deterring copepod grazing	NSF	Fields/Sieracki	462,847
Provasoli-Guillard National Center for Culture of Marine Phytoplankton	NSF	Wilson	1,915,968
Development of "Eye-in-the-Sea" (EITS), an Unobtrusive Camera System using Far-Red Illumination for in-situ Observation	NSF	Widder	671,828
Collaborative Research: From structure to information in mechanosensory systems: The role of sensor morphology in detecting fluid signals	NSF	Fields	322,532
Collaborative Research: Phytoplankton Community Dynamics and Physiological Status in the South Atlantic Subtropical Gyre and Benguela Upwelling Systems	NSF	Sieracki	228,646
Collaborative Research: Marine Microgels: A microlayer source of summer CCN in high Arctic ocean leads	NSF	Matrai	498,722
Patagonian Shelf Coccolithophores: Ecological Factors Regulating the Southern Hemisphere's Largest Recurring Coccolithophore Bloom	NSF	Balch	495,729
Functional Genomics of phosphate acquisition during virus infection of <i>Emiliana huxleyi</i>	NSF	Wilson/Stepanuskas	808,750
Collaborative Research: Loihi Seamount as an Observatory for the Study of Neutrophilic Iron-Oxidizing Bacteria and the Microbial Iron Cycle	NSF	Emerson	114,695
Collaborative Research: Plant Regulation of Competition Between Methanogens and Iron-Reducing Bacteria in Freshwater Wetlands	NSF	Emerson	100,721
Collaborative Research: Autonomous Measurements of Carbon Fluxes in the North Atlantic Bloom	UME/NSF	Sieracki	40,000
Collaborative Research: Biological and physical controls on DMS production and emission during VOCALS	NSF	Matrai	320,000
Collaborative Research: FeCycle II—Natural Variability in Plankton Iron Quotas During an Unamended Lagrangian Experiment	NSF	Twining	181,090
Unlocking the Mysteries of Plastid Origin through Comparative Genomic Analysis of Two <i>Paulinella</i> Species	NSF	Yoon	993,911



Title	Funder	Principal Investigator(s)	Award Total
Single Cell Genome Sequencing of Uncultured Prokaryotes from the South Atlantic Mesopelagic	NSF	Stepanauskas/McClellan/Sieracki	976,747
Collaborative Research: Quantitative Importance and Trophic Role of <i>Noctricula</i> Blooms in the Arabian Sea	NSF	Goés	296,905
Collaborative Research: Grazing and Iron Controls of Diatom Blooms in the Arabian Sea	NSF	Goés	139,819
Establishing Marine Archaeal, Bacterial, and Viral Collections to Complement the CCMP at Bigelow Laboratory	NSF/FSML	Emerson/Wilson	335,341
REU Site: Bigelow Laboratory for Ocean Sciences—Undergraduate Research Experience in the Gulf of Maine and the World Ocean	NSF/REU	Wahle/Fields	258,685
MRI: Acquisition of equipment for microbial single cell genomics research	NSF/MRI	Stepanauskas/McClellan/Sieracki	574,045
SGER: Giant Virus Regulation of Cocclithophorid Dynamics	NSF	Wilson	69,523
Collaborative Research: Agent-based Modeling and Observation of Intra-Population Variability in Phytoplankton	NSF	Twining	137,756
Collaborative Research: Iron Storage in Diatoms and N ₂ Fixing Cyanobacteria: Mechanisms, Regulation, and Biogeochemical Significance	NSF	Twining	257,021
Identification of photoheterotrophic microorganisms in temperate freshwater lakes	NSF	Stepanauskas/Sieracki	650,000
Role of Latent Virus Infection in Marine Phytoplankton	NSF	Wilson	549,105
Collaborative Research: Decoding Virus Leviathans	NSF	Wilson/Stepanauskas	338,950
Collaborative Research: Impacts of Changing Seasonality of Wind-driven Mixing on the Arctic System	NSF-ARRA	Matrai	104,337
Collaborative Research: RedToL—Phylogenetic and Genomic Approaches to Reconstructing the Red Algal (Rhodophyta) Tree of Life	NSF	Yoon	1,353,152
Collaborative Research: ETBC: Amazon Influence on the Atlantic Carbon Export from Nitrogen Fixation by Diatom Symbioses (ANACONDAS)	NSF	Goés	333,261
Acquisition of a Confocal Laser Scanning Microscope at the Bigelow Laboratory for Ocean Sciences	NSF/FSML	Emerson/Twining/Fields/Yoon	341,265
Collaborative Research: High Resolution Bacterial Mat Sampler for Operation with Deep Submergence Vehicles	NSF	Emerson	115,372
LSCBR: The Provasoli-Guillard National Center for Culture of Marine Phytoplankton	NSF	Wilson	1,807,672
Light Delivery Enhancement of Photobioreactors	Bodega/NSF	Wilson	25,033
GEOTRACES: Atlantic Section: Characterization of phytoplankton trace metal quotas and their contribution to the particulate metal pool in the upper ocean	NSF	Twining	331,838

Active Grants and Contracts

Title	Funder	Principal Investigator(s)	Award Total
Collaborative Research: The Great Southern Coccolithophore Belt	NSF	Balch/Twining	1,065,191
Microbial Systems in the Biosphere: Unraveling the lifestyles of dominant freshwater Fe-oxidizing bacteria	NSF	Emerson	610,893
GNATS, The Gulf of Maine North Atlantic Time Series: Integrating terrestrial and ocean carbon cycles in a coastal shelf sea through coordinated ship and satellite observations	NASA	Balch	800,386
Climate change and its impact on the ecosystem of the Arabian Sea	NASA	Goés	966,277
Spatial and temporal variability in chlorophyll, primary production, and carbon export in the Bering Sea linked to climate change (NSPIRES)	NASA	Goés	745,316
Biosphere of Mars: Ancient and Recent Studies	UCB/NASA	Emerson	217,845
Astrological Pathways: From the Interstellar Medium, through Planetary Systems, to the Emergence and Detection of Life	CIW/NASA	Emerson	55,854
Differentiating Sources of Backscattering in the Southern Ocean: Calcite, Bubbles, and Other Optical Constituents	UCONN/NASA	Balch	437,025
Using Remote Sensing to Understand Carbon Flow and Its Transformations from Upland Ecosystems into the Coastal Ocean	NASA	Balch	524,795
Ecosystem Carbon Dynamics in High-latitude Seasonal Seas of the Subarctic North Pacific and North Atlantic	OSU/NASA	Sieracki	115,846
A Proposal for Refinement of the MODIS Calcite Algorithm and CAL/VAL Activities Towards Assembly of Earth System Data Records	NASA MODIS	Balch	676,980
Lobster Settlement Forecasting in the Gulf of Maine	UME/NASA	Wahle	66,535
Reducing Uncertainty in the Marine Carbon Cycle by Coupling Satellite and In-water Robotic Measurements	UME/NASA	Sieracki	86,455
Characterization of Large and Unusual <i>Nocticula</i> Blooms in the Northern Arabian Sea and Their Role in Carbon Cycling During the Winter Monsoon	NASA	Goés	830,056
The Autonomous Polar Productivity Sampling System (APPSS)	UWA/NASA	Matrai	445,171
DEPSCoR—Energy transfer to Upper Trophic Levels on a Small Offshore Bank	USM/ONR DEBSCoR	Fields	136,513
Role of Fe-oxidizing Bacteria in Metal Bio-corrosion in the Marine Environment	ONR	Emerson	418,877
Developing Genetic Fingerprinting Techniques in Lobster Seeding Trials	UMESeagrant/NOAA	Wahle	161,844
Development of a technology platform for the assessment and controlled delivery of therapeutic bacteriophage in aquaculture	MT/NOAA	Wilson	112,655



Title	Funder	Principal Investigator(s)	Award Total
Developing Tools to Evaluate Spawning and Fertilization Dynamics of the Giant Sea Scallop, <i>Placopecten magellanicus</i>	NOAA RSA	Wahle	183,270
Research on Lobster Age-Size Relationships: Developing Regionally Specific Growth Models from Meta-analysis of Existing Data	DMR	Wahle	70,000
A proposal to add two Slocum Gliders to the Gulf of Maine North Atlantic Time Series (GNATS)	MTI	Balch	141,200
Establishment of a LC-MS Facility for Research and Education in Marine Sciences	MTI	Goés	346,000
Investigate Effects of Commercial Rockweed Harvesting on the Associated Macroinvertebrate Community (Cobscook Bay)	DMR	Larsen	7,551
Lobster Settlement Update	DMR	Wahle	6,000
Bigelow Center for Blue Technology	MTAF	Shimmield/Wilson	4,453,971
Depth-related Settlement Patterns of the American Lobster in Southern New England and the Gulf of Maine	UNH/NEC/NOAA	Wahle	264,735
Using FlowCAM Technology to Measure High Frequency Spatial and Temporal Variations in Phytoplankton and Zooplankton Species Composition and Develop State of the Art Plankton Monitoring	CA DWR	Poulton	24,000
O-Buoy	CPW	Matrai	310,000
Examining settlement dynamics of postlarval American lobster, (<i>Homarus americanus</i>), in Lobster Management Area 2	SNECRI	Wahle	7,808
Automated O-Buoy	CPW	Matrai	19,000
MSGC Fellowships for Three Summer Interns (Goés)	MSGC	Goés	9,000
Collaborative Research: ATOL: Deep Brown—A phylogenic and genomic investigation of the Algal Heterokont Tree	NSF	Andersen	751,465
Mechanoreception in Marine Copepods: Detecting Complex Fluid Signals	NSF	Fields	201,148
Climate-Related Interannual Variability of Potential New Production Over the Western North Atlantic Ocean	NASA	Goés	180,095
Organic Matter Metabolism in a Coastal Ocean Ecosystem	NASA	Matrai/Sieracki	719,053
Facilities to Catalyze a Center for Ocean Microbial Systems Science	MTI	Sieracki	160,000
Historical Records of Fouling Organisms on the Coast of Maine	ME DEP	Larsen	2,500
Historical Records of Fouling Organisms on the Coast of Maine	CBEP/USM	Larsen	500

Summary Financial Statements

Statement of Activities and Changes in Net Assets

(For fiscal years ended June 30)

	2010	2009	2008
Operating Activities			
Operating Revenue and Support			
Grants and contracts for research and education	\$6,141,056	\$5,280,659	\$4,889,104
Contributions to growth fund	1,514,844	73,725	469,688
Other revenue, including course fees	662,180	577,186	324,064
Contributions to Annual Fund	338,326	304,509	268,641
Total Operating Revenue and Support	8,656,406	6,236,079	6,180,481
Operating Expenses			
Research and Education	7,084,982	6,630,744	5,733,334
Unallocated management and general	449,404	354,459	415,508
Development	368,396	377,245	248,629
Total Operating Expenses	7,902,782	7,362,447	6,397,471
Change in Net Assets from Operating Activities	753,624	-1,126,368	-216,990
Non-Operating Revenue and Support			
Grants for equipment and construction	788,806	362,730	273,521
Change in Net Assets from Non-Operating Activities	788,806	362,730	273,521
Total Change in Net Assets	1,542,430	-763,639	-172,453

Statement of Financial Position

(At June 30)

	2010	2009	2008
Assets			
Cash	\$350,481	\$270,617	\$108,052
Investments	1,614,537	1,688,474	2,533,757
Property and Equipment, Net	6,542,677	5,190,054	5,459,860
Other	2,267,809	1,836,593	1,348,424
Total Assets	10,775,504	8,985,738	9,450,093
Liabilities and Net Assets			
Liabilities	1,094,214	846,864	547,584
Net Assets			
Unrestricted	6,102,203	5,766,256	5,882,690
Temporarily Restricted	3,376,943	2,170,845	2,818,775
Permanently Restricted	202,144	201,769	201,044
Total Net Assets	9,681,290	8,138,870	8,902,509
Total Liabilities and Net Assets	10,775,504	8,985,734	9,450,093


Bigelow Laboratory for Ocean Sciences was formed in 1974. The Laboratory is a Maine nonprofit public benefit corporation and is qualified as a tax-exempt organization under Sec. 501(c)(3) of the Internal Revenue Code. The Laboratory's financial statements for fiscal years 2008, 2009, and 2010 were audited by Macdonald Page & Co. The summary financial statements shown here are derived from the audited financial statements. Copies of the audited financial statements are available on request from the Director of Finance, Bigelow Laboratory for Ocean Sciences, P.O. Box 475, West Boothbay Harbor, ME 04575; or by email to: finance@bigelow.org

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