Changes in seasonal phytoplankton community composition as a response to temperature at the San Pedro Ocean Time-series.

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Project
» How does intensity and frequency of environmental variability affect phytoplankton growth? (Enviro variability and phytoplankton growth)
» Dimensions: Collaborative Research: Genetic, functional and phylogenetic diversity determines marine phytoplankton community responses to changing temperature and nutrients (Phytoplankton Community Responses)

Program
» Dimensions of Biodiversity (Dimensions of Biodiversity)

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Abstract
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Dataset Description

All scripts used to process elemental and sequencing data can be found on figshare at: *https://doi.org/10.6084/m9.figshare.7603790.v2*

Raw sequence data is available from NCBI under Bioproject PRJNA512541

Methods & Sampling

Sample Collection: Surface water for the experiment was collected from the Southern California Bight at the San Pedro Ocean Timeseries (SPOT) station (33˚33′ N, 118˚24′ W). Seasonal sampling in September 2016 (summer), November 2016 (fall), and May 2017 (spring) examined microbial communities collected at ambient surface water temperatures of 20.6°, 16.5° and 16.1°, respectively. Seawater was collected in carboys from 3 m depth, with 100 micron mesh prefiltration to remove zooplankton, and was then taken back to the University of Southern California, where it was stored overnight at collection temperature. Initial samples and the incubation-experiment setup used water combined from all the collection carboys. The remaining surface water was filtered through a 0.2 micron gravity filter and used for subsequent culture dilutions.

DNA collection and sequencing: Microbial diversity was sampled before nutrients were added, and at the end of the final temperature fluctuation cycle. Cells were filtered (1.2 micron polycarbonate) and stored in liquid nitrogen. Extractions used the DNeasy Power Soil kit (Qiagen, Hilden, Germany) modified to include a 10-min 65 degree celsius incubation before vortexing. Amplification and sequencing of the V4-V5 hypervariable region of the 16S rRNA gene was done using the primers 515F-Y (5′-GTGYCAGCMGCCGCGGTAA-3′) and 926R (5′-CCGYCAATTYMTTTRAGTTT-3′). These primers successfully amplify large proportions of known prokaryotes, and chloroplasts (via the 16S rRNA gene), as well as eukaryotes (via the 18S rRNA). Library prep and sequencing was done at Molecular Research DNA labs (MRDNA; Shallowater, TX, USA) on the Illumina Miseq plat-form producing 2 × 300 bp paired-end reads. DNA samples from the spring experiment were treated the same way as summer and fall DNA samples, but were sequenced on a different date. To avoid potential sequencing run-specific batch effects, each season was analyzed individually. The quality of DNA from one replicate in the spring future-constant treatment was low and consequently contained few reads. This replicate was excluded from sequence analysis.

Data Processing Description

Experimental setup: Because of the oligotrophic conditions and low biomass at SPOT, nutrients were added to stimulate photoautotrophic growth and so enable measurements of the effects of temperature on microbial communities. Each incubation experiment used triplicate one-liter flasks enriched with nitrate, silicate and phosphate added to final concentrations of 30, 30 and 2 micro molar, respectively. Iron, other trace metals, and vitamins were added at replete concentrations equivalent to Aquil medium to avoid micronutrient limitation. Enriched SPOT water was split into temperature treatments intended to simulate present and predicted-future surface-water temperatures at both constant and fluctuating temperatures. Present temperatures were set to match the temperature at SPOT at the time of collection. The present-constant treatments acted as our experimental control. Future temperatures were increased 4 °C (spring and fall) or 5 °C (summer) from the present temperature. The two fluctuating temperature treatments had the same means as the constant treatments, but they alternated between a warm phase above (+4 °C) and a cold phase below (−4 °C) the mean value sequentially every 24 h, yielding a 48 h complete thermal cycle.

Elemental analysis: To measure particulate organic carbon (POC) and nitrogen (PON),samples were filtered onto precombusted GF/F filters (2h at 450 °C) and analyzed using a Costech Elemental Combustion system (Valencia, CA, USA). POC was used to estimate bulk assemblage growth rates by recording the change in particulate organic carbon over 2 days, capturing growth during both cool and warm periods. To measure biogenic silica (BSi), samples were filtered onto 3 micron polycarbonate filters and measured to estimate diatom biomass. Similar to POC-derived growth rates, changes in BSi over two days were used to derive diatom-specific growth rates in our treatments. Cells were filtered onto precombusted GF/F filters for particulate organic phosphorus (POP) measurements. In addition to indirectly measuring Chlorophyll using in vivo fluorescence, we measured total chlorophyll by filtering onto GF/F filters and extracting in 90% acetone for 24h. Extracted Chlorophylla and in vivo fluorescence were measured on a Turner AU-10 (Turner Designs Inc., Sunnyvale, CA). During spring and fall experiments, carbon fixation rates were measured by spiking 30 ml of each enrichment with 50 microliter of 14C labeled sodium bicarbonate, then incubated for 3h, filtered onto GF/F filters, and placed in 4.5 ml of scintillation solution.Total radioactivity (TA) was measured using triplicate solutions of combined isotope and scintillation solution spiked with 100 µl of phenyethlamine. We accounted for filter absorption using 10ml from each replicate-enrichment spiked with identical amounts of isotopes and filtered immediately. Samples were incubated in the dark overnight and radioactivity was measured with a Tri-Carb 2500TR liquid scintillation counter after 24h (Beckman Coulter Inc., Brea, CA).

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Related Publications

Kling, J. (2019). *Processed_16s_output* [Data set]. figshare. https://doi.org/10.6084/M9.FIGSHARE.7603790.V2
https://doi.org/10.6084/m9.figshare.7603790.v2
Results

Kling, J. D., Lee, M. D., Fu, F., Phan, M. D., Wang, X., Qu, P., & Hutchins, D. A. (2019). Transient exposure to novel high temperatures reshapes coastal phytoplankton communities. The ISME Journal, 14(2), 413–424. doi:10.1038/s41396-019-0525-6
Results

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Parameters

Parameters for this dataset have not yet been identified

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Project Information

How does intensity and frequency of environmental variability affect phytoplankton growth? (Enviro variability and phytoplankton growth)

Coverage: laboratory experiment

NSF Award Abstract:
Microscopic plants called phytoplankton are key members of global oceanic ecosystems, since their photosynthesis supports the majority of the marine food chain and produces about as much oxygen as land plants. Because of this, oceanographers have often carried out experiments examining how factors such as temperature and carbon dioxide levels may affect phytoplankton growth. Most previous experiments have used constant levels of temperature and carbon dioxide, but it is clear from looking at measurements from real ocean ecosystems that these two factors often vary greatly over timescales of days to weeks. Using field and laboratory experiments along with computer modeling, this project will test how the growth of several major groups of phytoplankton differs under constant conditions of temperature and carbon dioxide, compared to conditions in which these factors fluctuate in intensity and frequency. This research will give marine scientists a better picture of how phytoplankton may respond to a varying natural environment today and in the future, and therefore help us to understand how ocean food webs function to support critical living resources such as fisheries. The project will train graduate and undergraduate students and a postdoctoral researcher, and the lead scientists will be involved in an ocean science education program for largely minority high school students from a downtown Los Angeles school district.

The goal of this project is to use laboratory culture and natural community experiments to understand how realistically fluctuating temperature and pCO2 conditions may affect globally important phytoplankton groups in ways that differ from the artificial constant exposures used in previous work. Culture experiments will test how the intensity and frequency of short-term thermal and carbonate fluctuations affects the growth responses of diazotrophic and picoplanktonic cyanobacteria, coccolithophores, and diatoms under both current and projected future environmental conditions. These lab results will be supported and extended by parallel experiments using mixed natural assemblages from the California upwelling regime, allowing us to test these same questions using phytoplankton communities that experience large seasonal shifts between highly dynamic thermal and carbonate system conditions during the spring upwelling season, and relatively much more static conditions during fall stratification events. These results will be synthesized using a new generation of numerical models that employ novel approaches to incorporating realistic environmental variations to allow more accurate predictions of phytoplankton responses to a dynamic environment in today's marine ecosystems, and in the future changing ocean.

Dimensions: Collaborative Research: Genetic, functional and phylogenetic diversity determines marine phytoplankton community responses to changing temperature and nutrients (Phytoplankton Community Responses)

Coverage: Narragansett Bay, RI and Bermuda, Bermuda Atlantic Time-series Study (BATS)

NSF Award Abstract:
Photosynthetic marine microbes, phytoplankton, contribute half of global primary production, form the base of most aquatic food webs and are major players in global biogeochemical cycles. Understanding their community composition is important because it affects higher trophic levels, the cycling of energy and elements and is

sensitive to global environmental change. This project will investigate how phytoplankton communities respond to two major global change stressors in aquatic systems: warming and changes in nutrient availability. The researchers will work in two marine systems with a long history of environmental monitoring, the temperate Narragansett Bay estuary in Rhode Island and a subtropical North Atlantic site near Bermuda. They will use field sampling and laboratory experiments with multiple species and varieties of phytoplankton to assess the diversity in their responses to different temperatures under high and low nutrient concentrations. If the diversity of responses is high within species, then that species may have a better chance to adapt to rising temperatures and persist in the future. Some species may already be able to grow at high temperatures; consequently, they may become more abundant as the ocean warms. The researchers will incorporate this response information in mathematical models to predict how phytoplankton assemblages would reorganize under future climate scenarios. Graduate students and postdoctoral associates will be trained in diverse scientific approaches and techniques such as shipboard sampling, laboratory experiments, genomic analyses and mathematical modeling. The results of the project will be incorporated into K-12 teaching, including an advanced placement environmental science class for underrepresented minorities in Los Angeles, data exercises for rural schools in Michigan and disseminated to the public through an environmental journalism institute based in Rhode Island.

Predicting how ecological communities will respond to a changing environment requires knowledge of genetic, phylogenetic and functional diversity within and across species. This project will investigate how the interaction of phylogenetic, genetic and functional diversity in thermal traits within and across a broad range of species determines the responses of marine phytoplankton communities to rising temperature and changing nutrient regimes. High genetic and functional diversity within a species may allow evolutionary adaptation of that species to warming. If the phylogenetic and functional diversity is higher across species, species sorting and ecological community reorganization is likely. Different marine sites may have a different balance of genetic and functional diversity within and across species and, thus, different contribution of evolutionary and ecological responses to changing climate. The research will be conducted at two long-term time series sites in the Atlantic Ocean, the Narragansett Bay Long-Term Plankton Time Series and the Bermuda Atlantic Time Series (BATS) station. The goal is to assess intra- and inter-specific genetic and functional diversity in thermal responses at contrasting nutrient concentrations for a representative range of species in communities at the two sites in different seasons, and use this information to parameterize eco-evolutionary models embedded into biogeochemical ocean models to predict responses of phytoplankton communities to projected rising temperatures under realistic nutrient conditions. Model predictions will be informed by and tested with field data, including the long-term data series available for both sites and in community temperature manipulation experiments. This project will provide novel information on existing intraspecific genetic and functional thermal diversity for many ecologically and biogeochemically important phytoplankton species, estimate generation of new genetic and functional diversity in evolution experiments, and develop and parameterize novel eco-evolutionary models interfaced with ocean biogeochemical models to predict future phytoplankton community structure. The project will also characterize the interaction of two major global change stressors, warming and changing nutrient concentrations, as they affect phytoplankton diversity at functional, genetic, and phylogenetic levels. In addition, the project will develop novel modeling methodology that will be broadly applicable to understanding how other types of complex ecological communities may adapt to a rapidly warming world.

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Program Information

Dimensions of Biodiversity (Dimensions of Biodiversity)

Website: http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503446

Coverage: global

(adapted from the NSF Synopsis of Program)
Dimensions of Biodiversity is a program solicitation from the NSF Directorate for Biological Sciences. FY 2010 was year one of the program. [MORE from NSF]

The NSF Dimensions of Biodiversity program seeks to characterize biodiversity on Earth by using integrative,

innovative approaches to fill rapidly the most substantial gaps in our understanding. The program will take a broad view of biodiversity, and in its initial phase will focus on the integration of genetic, taxonomic, and functional dimensions of biodiversity. Project investigators are encouraged to integrate these three dimensions to understand the interactions and feedbacks among them. While this focus complements several core NSF programs, it differs by requiring that multiple dimensions of biodiversity be addressed simultaneously, to understand the roles of biodiversity in critical ecological and evolutionary processes.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1538525
NSF Division of Ocean Sciences (NSF OCE)	OCE-1638804

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