

# Fluorescence spectra for 3 strains of *Synechococcus* while increasing temperatures to detect the photosystem components disassociation temperature

**Website:** <https://www.bco-dmo.org/dataset/782322>

**Data Type:** experimental

**Version:** 1

**Version Date:** 2019-11-20

## Project

» [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)

Contributors	Affiliation	Role
<a href="#">Hutchins, David A.</a>	University of Southern California (USC)	Principal Investigator
<a href="#">Copley, Nancy</a>	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

## Abstract

Fluorescence spectra from 600-700nm at 530nm excitation for 3 strains of *Synechococcus* while increasing temperatures to detect the photosystem components disassociation temperature.

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## Coverage

**Spatial Extent:** N:41.7129 E:-71.2674 S:41.4471 W:-71.4007

**Temporal Extent:** 2017-01-01 - 2018-10-31

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## Dataset Description

Fluorescence spectra from 600-700nm at 530nm excitation for 3 strains of *Synechococcus* while increasing temperatures to detect the photosystem components disassociation temperature

## Methods & Sampling

Natural seawater was enriched for photoautotrophs and split into multiple temperatures for two weeks. After the enrichment period, *Synechococcus* was isolated from each temperature. Each isolate's thermal niche was measured through a series of lab experiments and sequenced.

200ml of dense culture was concentrated by centrifuging 25,000 x g for 15 minutes. The subsequent cell pellet was resuspended in 5ml of sterile growth media. Cell concentrate was dark acclimated for 10 minutes and 200ul was used to measure the fluorescence spectra. After each measurement, the temperature increased and cells were dark acclimated at that temperature for an additional 10 minutes. This continued until the fluorescence decreased to ~0 indicating the disassociation of the photosynthetic apparatus. This was done following the methods published in Pittera et al., 2017.

## Data Processing Description

### BCO-DMO Processing Notes:

- added conventional header with dataset name, PI name, version date

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## Data Files

File
<b>Syn_fluor_degen_temp.csv</b> (Comma Separated Values (.csv), 53.10 KB) MD5:88d4216a4d54a18e8ea4fb200df9e038 Primary data file for dataset ID 782322

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## Related Publications

Pittera, J., Partensky, F., & Six, C. (2016). Adaptive thermostability of light-harvesting complexes in marine picocyanobacteria. The ISME Journal, 11(1), 112–124. doi:[10.1038/ismej.2016.102](https://doi.org/10.1038/ismej.2016.102)  
*Methods*

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## Parameters

Parameter	Description	Units
Temperature	experimental temperature	degrees Celsius
Em_nm	Experimental wavelength	nanometers
LA31_A	Percentage change in fluorescence emission at 530nm excitation for strain LA31 subsample A	percent
LA31_B	Percentage change in fluorescence emission at 530nm excitation for strain LA31 subsample B	percent
LA31_C	Percentage change in fluorescence emission at 530nm excitation for strain LA31 subsample C	percent
LA126_A	Percentage change in fluorescence emission at 530nm excitation for strain LA126 subsample A	percent
LA126_B	Percentage change in fluorescence emission at 530nm excitation for strain LA126 subsample B	percent
LA126_C	Percentage change in fluorescence emission at 530nm excitation for strain LA126 subsample C	percent
LA127_A	Percentage change in fluorescence emission at 530nm excitation for strain LA127 subsample A	percent
LA127_B	Percentage change in fluorescence emission at 530nm excitation for strain LA127 subsample B	percent
LA127_C	Percentage change in fluorescence emission at 530nm excitation for strain LA127 subsample C	percent

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## Instruments

<b>Dataset-specific Instrument Name</b>	centrifuge
<b>Generic Instrument Name</b>	Centrifuge
<b>Dataset-specific Description</b>	Used to create a pellet of cells.
<b>Generic Instrument Description</b>	A machine with a rapidly rotating container that applies centrifugal force to its contents, typically to separate fluids of different densities (e.g., cream from milk) or liquids from solids.

<b>Dataset-specific Instrument Name</b>	SpectraMax m2 (Molecular Devices, CA)
<b>Generic Instrument Name</b>	plate reader
<b>Dataset-specific Description</b>	Used to measure the fluorescence spectra
<b>Generic Instrument Description</b>	<p>Plate readers (also known as microplate readers) are laboratory instruments designed to detect biological, chemical or physical events of samples in microtiter plates. They are widely used in research, drug discovery, bioassay validation, quality control and manufacturing processes in the pharmaceutical and biotechnological industry and academic organizations. Sample reactions can be assayed in 6-1536 well format microtiter plates. The most common microplate format used in academic research laboratories or clinical diagnostic laboratories is 96-well (8 by 12 matrix) with a typical reaction volume between 100 and 200 uL per well. Higher density microplates (384- or 1536-well microplates) are typically used for screening applications, when throughput (number of samples per day processed) and assay cost per sample become critical parameters, with a typical assay volume between 5 and 50 µL per well. Common detection modes for microplate assays are absorbance, fluorescence intensity, luminescence, time-resolved fluorescence, and fluorescence polarization. From: <a href="http://en.wikipedia.org/wiki/Plate_reader">http://en.wikipedia.org/wiki/Plate_reader</a>, 2014-09-0-23.</p>

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## Project Information

**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](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
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1638804</a>

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