Daily growth rates for Thermal Performance Curve (TPC) of Chaetoceros simplex in nitrogen-replete evolved populations after about 200 generations of evolution at eight temperatures, 10-35 degrees C.

Website: https://www.bco-dmo.org/dataset/778779
Data Type: experimental
Version: 1
Version Date: 2019-10-07

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
Litchman, Elena	Michigan State University (MSU)	Principal Investigator
Klausmeier, Christopher	Michigan State University (MSU)	Co-Principal Investigator
Kremer, Colin T.	Michigan State University (MSU)	Scientist
Aranguren-Gassis, Maria	Universidad de Vigo	Contact
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Daily growth rates for Thermal Performance Curve (TPC) of Chaetoceros simplex in nitrogen-replete evolved populations after about 200 generations of evolution at eight temperatures, 10-35 degrees C.

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Coverage

Spatial Extent: **Lat**:42.4061 **Lon**:-85.4007
Temporal Extent: 2016-06 - 2016-10

Dataset Description

Daily growth rates for Thermal Performance Curve (TPC) of *Chaetoceros simplex* in nitrogen-replete evolved populations after about 200 generations of evolution at eight temperatures, 10-35 degrees C.

After ~ 200 generations of evolution (165–186 days: 194–232 generations), we characterised the TPCs of two randomly selected N-replete evolved populations that were 34 °C-tolerant (see the 34 °C challenge section below) and the control and an ancestral population. Assay temperatures were 10, 20, 25, 29, 31, 32, 34 and 35 °C, and three replicate populations were grown in 50-mL culture flasks (instead of well plates) (96 growth rate estimates).

Methods & Sampling

Chaetoceros simplex cultures, were obtained from population strain CCMP 200 (National Center for Marine Algae and Microbiota, NCMA).

Thermal performance curve (TPC) assays:
We assayed the TPCs of our populations twice during the evolution experiment. This involved pre-acclimating sub-cultures from each population to 28 °C (in-between the 25 °C control and 31 °C experimental treatment) in N-replete medium for 20 days (20–25 generations) to remove any effects of acclimation to previous temperatures (31 or 25 °C) and N levels. Subsequently, separate flasks containing N-replete medium were placed at each assay temperature, inoculated with pre-acclimated populations, and allowed to acclimate for six more days.

After ~ 200 generations of evolution (165–186 days: 194–232 generations), we characterised the TPCs of two randomly selected N-replete evolved populations that were 34 °C-tolerant (see the 34 °C challenge section below) and the control and an ancestral population. Assay temperatures were 10, 20, 25, 29, 31, 32, 34 and 35 °C, and three replicate populations were grown in 50-mL culture flasks (instead of well plates) (96 growth rate estimates). We measured in vivo chlorophyll-a fluorescence (excitation wavelength: 436 nm, emission wavelength: 680 nm) daily using a SpectraMax M5 microplate reader (Molecular Devices, Sunnyvale, CA, USA) to estimate the growth rate.

Growth rate calculations:
From the daily biomass estimations (in vivo chlorophyll-a fluorescence), we calculated population growth rates (day−1), as the slope of the linear regression of ln(biomass) vs. time (days).

Also see data for 100 generations: https://www.bco-dmo.org/dataset/778749
More details in Aranguren-Gassis et al. 2019, Ecology Letters.

Data Processing Description

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- reduced precision of Growth_rates from 9 to 1 decimal places.

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Data Files

File
200gen.csv (Comma Separated Values (.csv), 1.57 KB) MD5:553541790d8d1d88be3b6d60d57666f4 Primary data file for dataset ID 778779

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Related Publications

Aranguren-Gassis, M., Kremer, C. T., Klausmeier, C. A., & Litchman, E. (2019). Nitrogen limitation inhibits

marine diatom adaptation to high temperatures. Ecology Letters. doi:10.1111/ele.13378
Results

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Parameters

Parameter	Description	Units
Evol_strain	evolved population identifier; L1 signifies strains raised in 'regular' medium at 884 micromoles nitrate; 5 signifies medium with reduced nitrate at 5 micromoles. Control refers to the population maintained at 25ºC during the evolution experiment as a temperature control population. 'Ancestral' refers to the initial population cryopreserved at the beginning of the experiment.	unitless
Temperature	Culture maintenance temperature	Celsius degrees
Flask_replicate	Replicate number	unitless
Growth_rate	Growth rate calculated from biomass	day-1

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Instruments

Dataset-specific Instrument Name	SpectraMax M5 microplate reader (Molecular Devices, Sunnyvale, CA, USA)
Generic Instrument Name	plate reader
Generic Instrument Description	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: http://en.wikipedia.org/wiki/Plate_reader, 2014-09-0-23.

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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

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-1638958
NSF Division of Ocean Sciences (NSF OCE)	OCE-1638804
NSF Division of Ocean Sciences (NSF OCE)	OCE-1638834

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