Estimated thermal traits for phytoplankton

Website: https://www.bco-dmo.org/dataset/839689
Data Type: Other Field Results
Version: 1
Version Date: 2021-02-04

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
Rynearson, Tatiana A.	University of Rhode Island (URI-GSO)	Principal Investigator
Anderson, Stephanie I.	University of Rhode Island (URI-GSO)	Contact
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Estimated thermal traits for phytoplankton assessed in Anderson et al., Marine Phytoplankton Functional Types Exhibit Diverse Responses to Thermal Change (in review).

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Coverage

Spatial Extent: **N**:74.65 **E**:174.81 **S**:-65 **W**:-155

Dataset Description

Phytoplankton thermal traits were estimated for diatoms (n=135), dinoflagellates (n=46), coccolithophores (n=30), and cyanobacteria (n=32). This dataset contains estimated traits and parameters presented in Thomas et al (2012) as well as those for 59 additional strains (Anderson et al, in review). Study selection followed the criteria outlined in Thomas et al (2012) and Anderson et al (in review).

Methods & Sampling

Thermal reaction norms were used to describe phytoplankton thermal responses following the equation presented in Thomas et al. (2012). For strains compiled previously, parameters for thermal reaction norms were provided (Thomas et al 2012 & 2016). For added strains, parameters were estimated using the thermal

growth rates found in the related dataset, https://www.bco-dmo.org/dataset/839696, and the maximum likelihood approach described in Thomas et al. (2012) and the bbmle package in R 3.6.1 (2019).

Traits were then estimated for each strain using their respective thermal reaction norms, as outlined previously (Thomas et al. 2012 & 2016; Anderson and Rynearson, 2020). This included the thermal optima (Topt), thermal maxima (Tmax) and thermal niche width. The thermal maxima were quality controlled according to Thomas et al. (2016) to ensure validity.

Data Processing Description

BCO-DMO Processing:
- replaced "NA" with "nd" as missing data value;
- renamed fields (replaced periods with underscores);
- removed commas from "study" and "source" columns;
- replaced commas with semi-colons in the "name", "strain", and "clone" columns;
- replaced comments with codes due to length and generated file "derived_traits_comment_codes.csv";
- replaced/removed un-renderable characters from the "source" column.

Definitions/descriptions for "comment_code" columns:
Note 1 = Latitude approximate. Based on information from Jacques (1983), Fiala & Oriol (1984), & Fiala & Oriol (1990), there are 5 possible isolation locations, all along the same longitude: 48S, 54S, 58S, 60S, and 65S. In the absence of further information from the authors, I have used the median location.

Note 2= Growth rates estimated from nonlinear fitting. One value presented was measured in previous study.

Note 3 = location approximate

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Data Files

File	
derived_traits.csv	(Comma Separated Values (.csv), 82.02 KB) MD5:b3cb1b99d5ccdfd25422e1f64d1cada8
Primary data file for dataset ID 839689	

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Supplemental Files

File	
data_sources.pdf	(Portable Document Format (.pdf), 144.02 KB) MD5:c6fb59a3eca1a2654a9e1a49c12b8ecf
Complete citations for the papers referenced in the "study" column of dataset 839689.	
derived_traits_comment_codes.csv	(Comma Separated Values (.csv), 467 bytes) MD5:4bfd2ca2b91639cbf70effcf56d49ff1
Complete comments/notes for the codes in the "comment_code" column of dataset 839689.	

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Related Publications

R Core Team (2019). R: A language and environment for statistical computing. R v3.5.1. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/

Software

Thomas, M. K., Kremer, C. T., & Litchman, E. (2015). Environment and evolutionary history determine the global biogeography of phytoplankton temperature traits. Global Ecology and Biogeography, 25(1), 75–86. doi:10.1111/geb.12387
Methods

Thomas, M. K., Kremer, C. T., Klausmeier, C. A., & Litchman, E. (2012). A Global Pattern of Thermal Adaptation in Marine Phytoplankton. Science, 338(6110), 1085–1088. doi:10.1126/science.1224836
Methods

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Related Datasets

IsRelatedTo

Rynearson, T. A. (2021) **Estimated thermal capacities for phytoplankton strains.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-02-04 doi:10.26008/1912/bco-dmo.839713.1 [view at BCO-DMO]

Rynearson, T. A. (2021) **Literature compilation of thermal growth rates from four phytoplankton functional types.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2021-02-04 doi:10.26008/1912/bco-dmo.839696.1 [view at BCO-DMO]
Relationship Description: Contains the thermal growth rates used to fit thermal reaction norms.

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Parameters

Parameter	Description	Units
isolate_code	Unique isolate ID adpated from Thomas et al. (2012).	unitless
study	source publication; refer to supplemental file "data_sources.pdf" for complete citations	unitless
source	geographical location of isolation	unitless
isolation_latitude	latitude of isolation location	degrees North
isolation_longitude	longitude of isolation location	degrees East (-180 to 180)
habitat	isolation location habitat type: marine or estuarine	unitless
name	Full current name of species with strain or clone name if available	unitless
speciesname	Full current name of species, omitting strain and clone names	unitless

strain	strain name, if given	unitless
clone	clone name, if given	unitless
species	taxonomic classification, species name	unitless
genus	taxonomic classification, genus name	unitless
family	taxonomic classification, family name	unitless
order	taxonomic classification, order name	unitless
class	taxonomic classification, class name	unitless
phylum	taxonomic classification, phylum name	unitless
kingdom	taxonomic classification, kingdom name	unitless
domain	taxonomic classification, domain name	unitless
group	phytoplankton functional type that the species belongs to	unitless
mu_wlist	estimated thermal niche width (parameter 'omega' in the thermal reaction norm model)	unitless
mu_alist	estimate of parameter ‘a’ in the thermal reaction norm model	unitless
mu_blist	estimate of parameter ‘b’ in the thermal reaction norm model	unitless
mu_c_opt_list	estimate of parameter ‘z’ in the thermal reaction norm model	unitless
mu_c_opt_val_list	estimated specific growth rate (per day) when temperature is at ‘z’ (i.e. mu.c.opt.list)	per day
mu_g_opt_list	estimated optimum temperature for growth	degrees Celsius
mu_g_opt_val_list	estimated maximum specific growth rate (per day) based on the thermal reaction norm model fit	per day

mu_n	number of points (i.e. number of growth rate measurements) in the curve	unitless
tmin	Tmin, or minimum persistence temperature, estimated from the thermal reaction norm model fit	degrees Celsius
tmax	Tmax, or maximum persistence temperature, estimated from the thermal reaction norm model fit	degrees Celsius
minqual	quality of Tmin estimate (quality control criteria found in supplementary info)	unitless
maxqual	quality of Tmax estimate (quality control criteria found in supplementary info)	unitless
comment_code	notes about isolation location, taxonomy, and other sources of uncertainty; refer to metadata 'Processing Description' for definitions or to the supplemental file "derived_traits_comment_codes.csv"	unitless

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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-1638834

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