NCBI accessions of the harmful alga Heterosigma akashiwo (CCMP2393) grown under a range of CO2 concentrations from 200-1000 ppm

Website: https://www.bco-dmo.org/dataset/747872

Data Type: experimental

Version: 1

Version Date: 2018-10-11

Project

» Impacts of Evolution on the Response of Phytoplankton Populations to Rising CO2 (P-ExpEv)

Program

» Science, Engineering and Education for Sustainability NSF-Wide Investment (SEES): Ocean Acidification (formerly CRI-OA) (SEES-OA)

Contributors	Affiliation	Role
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Abstract

This dataset includes metadata associated with NCBI BioProject PRJNA377729 "Impacts of Evolution on the Response of Phytoplankton Populations to Rising CO2" PRJNA377729: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA377729. The alga Heterosigma akashiwo was grown at CO2 levels from about 200 to 1000 ppm and then the DNA and RNA were sequenced.

Table of Contents

Coverage

Temporal Extent: 2017-06-21 - 2017-07-13

Dataset Description

This dataset includes metadata associated with NCBI BioProject PRJNA377729 "Impacts of Evolution on the Response of Phytoplankton Populations to Rising CO2" PRJNA377729: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA377729. The alga Heterosigma akashiwo was grown at CO2 levels from about 200 to 1000 ppm and then the DNA and RNA were sequenced.

Acquisition Description

Uni-algal, non-axenic cultures of Heterosigma akashiwo (CCMP2393) were grown in L1 medium (without silicate) made with a Long Island Sound seawater base collected from Avery Point, CT, USA (salinity 32) at 18°C with a 14:10 (light:dark) cycle with an irradiance of approximately 100 µmol m-2 s-1 . Cells were acclimated in exponential growth phase to different carbonate chemistries in 1.2 L of L1 media in 2.5-L polycarbonate bottles. To control the carbonate chemistry of the water, the headspace of each bottle was purged continuously with a custom gas mixture of ~21% oxygen, ~79% nitrogen and either 200, 400, 600, 800 or 1000 ppmv CO2 (TechAir, NY).

At the point of harvest, 150 mL (~6 x 106 cells) were filtered on to 5 µm pore size, 25 mm polycarbonate filter and flash frozen in liquid nitrogen. Genetic material from samples was extracted with the RNeasy Mini kit (Qiagen, Valencia, CA) and DNA was removed on-column using the RNase-free DNase Set (Qiagen), yielding total RNA. Total RNA extracts of the triplicate cultures were quantified on a 2100 Bioanalyzer (Agilent, Santa Clara, CA). Libraries were prepared using poly-A pull down with the TruSeq Stranded mRNA Library Prep kit (Illumina, San Diego, CA). Library preparation, barcoding, and sequencing from each library was performed by the JP Sulzberger Columbia University Genome Center (New York, NY).

Sequence reads were de-multiplexed and trimmed to remove sequencing barcodes. Reads were aligned using Bowtie2 (Langmead and Salzberg 2012) to the MMETSP consensus contigs for Heterosigma akashiwo CCMP2393 (https://omictools.com/marine-microbial-eukaryotic-transcriptome-sequenci...).

Significant differences between physiological parameters by CO2 treatment were assessed with analysis of variance (ANOVA) and Tukey's honestly significant differences test (aov and TukeyHSD, stats, R). Differential expression of genes in any CO2 treatment compared to modern was determined using the general linear model (GLM) exact test (edgeR, R). Briefly, the read counts were normalized by trimmed mean of M-values (TMM) using the function calcNormFactors, tagwise dispersions were calculated with the function estimateGLMTagwiseDisp, a GLM was fit using glmFit, and log2 fold change (logFC) for each treatment was calculated relative to average expression at modern CO2. P-values from likelihood ratio tests were corrected for multiple testing using the false discovery method (fdr).

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
- reformatted date from DD-Mmm-YYYY to yyyy-mm-dd
- changed entries of 'not applicable' to 'nd'

[table of contents | back to top]

Related Publications

Hennon, G. M., Williamson, O. M., Limón, M. D. H., Haley, S. T., & Dyhrman, S. T. (2019). Non-linear Physiology and Gene Expression Responses of Harmful Alga Heterosigma akashiwo to Rising CO2. Protist, 170(1), 38-51. Protist Supplemental Table 2

[table of contents | back to top]

Parameters

Parameter	Description	Units
sample_name	A unique name for the sample	unitless
sample_title	Title of the sample	unitless
bioproject_accession	The accession number of the BioProject(s) to which the BioSample belongs.	unitless
organism	The most descriptive organism name for this sample	unitless
strain	The microbial or eukaryotic strain name	unitless
isolate	Identification or description of the specific individual from which this sample was obtained	unitless
host	The natural (as opposed to laboratory) host to the organism from which the sample was obtained.	unitless
isolation_source	Describes the physical - environmental and/or local geographical source of the biological sample from which the sample was derived.	unitless
collection_date	Date of sampling formatted as yyyy-mm-dd	unitless

geo_loc_name	Geographical origin of the sample	unitless
sample_type	Sample type	unitless
biomaterial_provider	Name and address of the lab or PI or a culture collection identifier	unitless
collected_by	Name of persons or institute who collected the sample	unitless
depth	Sample collection depth	meters
env_biome	Descriptor of the broad ecological context of a sample.	unitless
genotype	Observed genotype	unitless
lat_lon	latitude and longitude of sample colllection	decimal degrees
passage_history	Number of passages and passage method	unitless
samp_size	Amount or size of sample that was collected	unitless
temp_C	Temperature of the sample at time of sampling	degrees Celsius
light_level_umol_m2_s	Light level	micromol photons m-2 s-1
light_dark_hr	duration of light and dark cycles	hours
Media	Type of growth medium used	unitless
CO2_ppm	CO2 concentration	parts per million
Alkalinity	Alkalinity of sample	micromol per kilogram (umol/kg)
pH	The measure of the acidity or basicity of an aqueous solution	unitless; pH scale

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina Hi-seq 2500 paired-end sequencing (PE100) with TruSeq RNA sample Prep Kit (Illumina, San Diego, CA)
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Used to prepare the mRNA libraries. Samples were barcoded for multiplex sequencing and run on in a single lane by the Columbia University Genome Center (CUGC) (New York, NY).
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

[table of contents | back to top]

Project Information

Impacts of Evolution on the Response of Phytoplankton Populations to Rising CO2 (P-ExpEv)

Coverage: Experiment housed in laboratories at Michigan State University

Note: This project is also affiliated with the NSF BEACON Center for the Study of Evolution in Action. Project Description from NSF Award: Human activities are driving up atmospheric carbon dioxide concentrations at an unprecedented rate, perturbing the ocean's carbonate buffering system, lowering oceanic pH, and changing the concentration and composition of dissolved inorganic carbon. Recent studies have shown that this ocean acidification has many short-term effects on phytoplankton, including changes in carbon fixation among others. These physiological changes could have profound effects on phytoplankton metabolism and community structure, with concomitant effects on Earth's carbon cycle and, hence, global climate. However, extrapolation of present understanding to the field are complicated by the possibility that natural populations might evolve in response to their changing environments, leading to different outcomes than those predicted from short-term studies. Indeed, evolution experiments demonstrate that microbes are often able to rapidly adapt to changes in the environment, and that beneficial mutations are capable of sweeping large populations on time scales relevant to predictions of environmental dynamics in the coming decades. This project addresses two major areas of uncertainty for phytoplankton populations with the following questions: 1) What adaptive mutations to elevated CO2 are easily accessible to extant species, how often do they arise, and how large are their effects on fitness? 2) How will physical and ecological interactions affect the expansion of those mutations into standing populations? This study will address these questions by coupling experimental evolution with computational modeling of ocean biogeochemical cycles. First, cultured unicellular phytoplankton, representative of major functional groups (e.g. cyanobacteria, diatoms, coccolithophores), will be evolved under simulated year 2100 CO2 concentrations. From these experiments, estimates will be made of a) the rate of beneficial mutations, b) the magnitude of fitness gains conferred by these mutations, and c) secondary phenotypes (i.e., trade-offs) associated with these mutations, assayed using both physiological and genetic approaches. Second, an existing numerical model of the global ocean system will be modified to a) simulate the effects of changing atmospheric CO2 concentrations on ocean chemistry, and b) allow the introduction of CO2-specific adaptive mutants into the extant populations of virtual phytoplankton. The model will be used to explore the ecological and biogeochemical

impacts of beneficial mutations in realistic environmental situations (e.g. resource availability, predation, etc.). Initially, the model will be applied to idealized sensitivity studies; then, as experimental results become available, the implications of the specific beneficial mutations observed in our experiments will be explored. This interdisciplinary study will provide novel, transformative understanding of the extent to which evolutionary processes influence phytoplankton diversity, physiological ecology, and carbon cycling in the near-future ocean. One of many important outcomes will be the development and testing of nearly-neutral genetic markers useful for competition studies in major phytoplankton functional groups, which has applications well beyond the current proposal.

[table of contents | back to top]

Program Information

Science, Engineering and Education for Sustainability NSF-Wide Investment (SEES): Ocean Acidification (formerly CRI-OA) (SEES-OA)

Website: http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503477

Coverage: global

NSF Climate Research Investment (CRI) activities that were initiated in 2010 are now included under Science, Engineering and Education for Sustainability NSF-Wide Investment (SEES). SEES is a portfolio of activities that highlights NSF's unique role in helping society address the challenge(s) of achieving sustainability. Detailed information about the SEES program is available from NSF (http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=504707). In recognition of the need for basic research concerning the nature, extent and impact of ocean acidification on oceanic environments in the past, present and future, the goal of the SEES: OA program is to understand (a) the chemistry and physical chemistry of ocean acidification; (b) how ocean acidification interacts with processes at the organismal level; and (c) how the earth system history informs our understanding of the effects of ocean acidification on the present day and future ocean. Solicitations issued under this program:NSF 10-530, FY 2010-FY2011NSF 12-500, FY 2012NSF 12-600, FY 2013NSF 13-586, FY 2014 NSF 13-586 was the final solicitation that will be released for this program. PI Meetings:1st U.S. Ocean Acidification PI Meeting(March 22-24, 2011, Woods Hole, MA)2nd U.S. Ocean Acidification PI Meeting(Sept. 18-20, 2013, Washington, DC) 3rd U.S. Ocean Acidification PI Meeting (June 9-11, 2015, Woods Hole, MA – Tentative) NSF media releases for the Ocean Acidification

Program: Press Release 10-186 NSF Awards Grants to Study Effects of Ocean Acidification Discovery Blue Mussels "Hang On" Along Rocky Shores: For How Long? Discovery nsf.gov - National Science Foundation (NSF) Discoveries - Trouble in Paradise: Ocean Acidification This Way Comes - US National Science Foundation (NSF) Press Release 12-179 nsf.gov - National Science Foundation (NSF) News - Ocean Acidification: Finding New Answers Through National Science Foundation Research Grants - US National Science Foundation (NSF) Press Release 13-102 World Oceans Month Brings Mixed News for Oysters Press Release 13-108 nsf.gov - National Science Foundation (NSF) News - Natural Underwater Springs Show How Coral Reefs Respond to Ocean Acidification - US National Science Foundation (NSF) Press Release 13-148 Ocean acidification: Making new discoveries through National Science Foundation research grants Press Release 13-148 - Video nsf.gov - News - Video - NSF Ocean Sciences Division Director David Conover answers questions about ocean acidification. - US National Science Foundation (NSF) Press Release 14-010 nsf.gov - National Science Foundation (NSF) News - Palau's coral reefs surprisingly resistant to ocean acidification - US National Science Foundation (NSF) Press Release 14-116 nsf.gov - National Science Foundation (NSF) News - Ocean Acidification: NSF awards $11.4 million in new grants to study effects on marine ecosystems - US National Science Foundation (NSF)

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1314336

[table of contents | back to top]