Clones of Prochlorococcus MIT9312 mixed with clonal isolates of the heterotrophic "helper" bacterium Alteromonas EZ55 (P-ExpEv project)

Website: https://www.bco-dmo.org/dataset/688162
Data Type: Cruise Results
Version: 1
Version Date: 2017-04-24

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
Clones of Prochlorococcus MIT9312 mixed with clonal isolates of the heterotrophic "helper" bacterium Alteromonas EZ55 (P-ExpEv project).

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Coverage

Temporal Extent: 2015-12 - 2015-12

Dataset Description

This dataset includes a link to Prochlorococcus clone NCBI BioProject and associated metadata.
PRJNA377729: https://www.ncbi.nlm.nih.gov/bioproject/PRJNA377729

Methods & Sampling

Six clones of high light II Prochlorococcus VOL4, a streptomycin-resistant derivative of strain MIT9312 were isolated by dilution to extinction in Pro99 media pretreated with the helper bacterium Alteromonas sp. strain EZ55. Prochlorococcus clones were made axenic by addition of streptomycin. For co-culture experiments, Alteromonas bacteria were introduced to Prochlorococcus cultures prior to growth experiments. Alteromonas

was diluted onto YTSS agar plates and each Prochlorococcus culture was inoculated with a single separate colony. Alteromonas stock cultures were grown in YTSS liquid medium and cryopreserved in 20% glycerol at -80 C.

Each of the six Prochlorococcus clones was grown in ambient or elevated CO2 in co-culture with Alteromonas, in PEv media.

The mRNA libraries were prepared for Illumina Hi-seq 2500 paired-end sequencing (PE100) with TruSeq RNA sample Prep Kit v2 (Illumina, San Diego, CA. Samples were barcoded for multiplex sequencing and run on in a single lane by the Columbia University Genome Center (CUGC) (New York, NY).

RNA extractions were performed with the RNeasy Mini Kit.

Data Processing Description

Sequence reads were de-multiplexed and trimmed to remove sequencing barcodes. Trimmed reads were aligned to both the MIT9312 gene models (accession: NC_007577.1) and the draft EZ55 genome (Genbank accession TBD) using bowtie2 with sensitive end-to-end mode. Reads aligning to coding sequences in the MIT9312 gene models were counted with samtools idxstats. Reads aligning to the EZ55 draft genome were counted with HT-seq count.

BCO-DMO Processing Notes:
- added conventional header with dataset name, PI name, version date
- modified parameter names to conform with BCO-DMO naming conventions
- added links to NCBI BioProject page
- replaced blanks with nd (no data)

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Data Files

File
Pro_ancestor.csv (Comma Separated Values (.csv), 8.38 KB) MD5:dbc2079cbd98a30a17ad4b2ef5721685 Primary data file for dataset ID 688162

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Parameters

Parameter	Description	Units
sample	sequencing facility sample identifier	unitless
sample_title	laboratory sample identifier	unitless
NCBI_BioProject	collection of biological data related to a single initiative	unitless
BioProject_link	url for collection of biological data related to a single initiative	unitless
organism	bacterium used in this study	unitless

strain	population of organism that descends from a single organism or pure culture isolate	unitless
isolate	specific individual from which this sample was obtained	unitless
isolation_source	physical/ environmental/ geographic source of the sample	unitless
collection_date	date sample was obtained	date
geo_loc_name	geographical origin of the sample	unitless
sample_type	sample type such as whole organism, mixed culture, cell culture, metagenomic assembly	unitless
biomaterial_provider	laboratory and principal investigator where sample came from	unitless
collected_by	laboratory and principal investigator where organism was isolated	unitless
lat_lon	geographical coordinates of the location where the sample was collected; north and east are positive	decimal degrees
depth	vertical distance below the surface where sample was collected	meters
env_biome	descriptor of the broad ecological context of sample	unitless
genotype	observed genotype	unitless
passage_history	number of sample generations	generations
samp_size	amount of sample collected	number of cells
temp_C	temperature at which sample was collected	degrees Celsius
light_level	light level at which sample was collected	micromol photons m-2 s-1
light_dark_hr	number of hours of light:dark for a 24 hour period	hours:hours
CO2	carbon dioxide concentration	ppm

Alkalinity	buffering capacity of water	umoles/kg
pH	scale of acidity	unitless
DIC	dissolved inorganic carbon concentration	umoles/kg
co_cultured_with	additional organisms grown with the primary organism	unitless
Media	type of water or broth organism was grown in	unitless

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Instruments

Dataset-specific Instrument Name	Illumina Hi-seq 2500 paired-end sequencing (PE100) with TruSeq RNA sample Prep Kit v2 (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	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

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Deployments

Dyhrman_2013

Website	https://www.bco-dmo.org/deployment/692263
Platform	LDEO
Start Date	2013-01-01
End Date	2017-03-31
Description	Phytoplankton studies

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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.

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Program Information

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

Website: https://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 (https://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-FY2011
NSF 12-500, FY 2012
NSF 12-600, FY 2013
NSF 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)

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Funding

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

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