

Accessions for clones of heterotrophic "helper" bacterium *Alteromonas* EZ55 grown at elevated and ambient CO₂.

Website: <https://www.bco-dmo.org/dataset/735669>

Data Type: Other Field Results

Version: 1.1

Version Date: 2025-02-25

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
Dyhrman, Sonya T.	Lamont-Doherty Earth Observatory (LDEO)	Principal Investigator
Morris, James Jeffrey	University of Alabama at Birmingham (UA/Birmingham)	Co-Principal Investigator
Hennon, Gwenn	Lamont-Doherty Earth Observatory (LDEO)	Scientist
Copley, Nancy	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract

This dataset includes a link to *Alteromonas/Prochlorococcus* clone NCBI BioProject "Impacts of Evolution on the Response of Phytoplankton Populations to Rising CO₂", and a listing of the associated FASTQ files.

PRJNA377729: <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA377729>

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Dataset Description

This dataset includes a link to *Alteromonas/Prochlorococcus* clone NCBI BioProject "Impacts of Evolution on the Response of Phytoplankton Populations to Rising CO₂", and a listing of the associated FASTQ files.

PRJNA377729: <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA377729>

These data were published in:

Hennon et al. "The impact of elevated CO₂ on *Prochlorococcus* and microbial interactions with 'helper' bacterium *Alteromonas*" (2018) ISME. Supplemental Table 4

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 Alteromonas clones from co-culture experiments was grown axenically in ambient or elevated CO₂ in co-culture with Alteromonas, in PEv media.

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 the draft EZ55 genome (Genbank accession SRX022631) using bowtie2 with sensitive end-to-end mode. 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

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Data Files

File
Alteromonas_accessions.csv (Comma Separated Values (.csv), 4.83 KB) MD5:632455c9e97e50cbfa7b0024605d5320

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Related Publications

Hennon, G. M., Morris, J. J., Haley, S. T., Zinser, E. R., Durrant, A. R., Entwistle, E., ... Dyhrman, S. T. (2017). The impact of elevated CO₂ on Prochlorococcus and microbial interactions with “helper” bacterium Alteromonas. The ISME Journal, 12(2), 520–531. doi:[10.1038/ismej.2017.189](https://doi.org/10.1038/ismej.2017.189).
Results

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Parameters

Parameter	Description	Units
bioproject_accession	NCBI BioProject accession number; a collection of biological data related to a single initiative	unitless
bioproject_link_url	Link to NCBI	unitless
bioproject_link_text	NCBI Accession ID	unitless
bioproject_link	url for collection of biological data related to a single initiative	unitless
biosample_accession	NCBI BioSample accession number	unitless
library_ID	short unique identifier for the sequencing library	unitless
title	BioSample title	unitless
library_strategy	type of sequencer used	unitless
library_source	sequencing location	unitless
library_selection	library preparation kit used	unitless
library_layout	Paired-end or Single	unitless
platform	type of DNA sequencing instrument	unitless
instrument_model	model of DNA sequencer	unitless
design_description	description of the methods used to create the sequencing library	unitless
filetype	type of file: FASTQ	unitless
filename	FASTQ file name	unitless
filename2	additional FASTQ filename	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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