Maximum growth rates for G. huxleyi RCC874 and RCC914 N amendment laboratory-based culture experiment

Website: https://www.bco-dmo.org/dataset/999165
Data Type: experimental
Version: 1
Version Date: 2026-05-21

Project
» Collaborative Research: Defining the role of the pan genome in Emiliania huxleyi ecology and biogeography (ECO-PAN-EHUX)

Contributors	Affiliation	Role
Alexander, Harriet	Woods Hole Oceanographic Institution (WHOI)	Co-Principal Investigator
Dyhrman, Sonya T.	Lamont-Doherty Earth Observatory (LDEO)	Co-Principal Investigator
Haley, Sheean	Lamont-Doherty Earth Observatory (LDEO)	Scientist

Abstract
Environmental factors associated with climate change alter the interactions between bacteria and their algal hosts, known as the phycosphere, with broader implications for marine microbial community ecology. We examined the interactive effects of warming and nitrogen limitation on two strains of Gephyrocapsa huxleyi (RCC874 and RCC914), a widely abundant and physiologically flexible coccolithophore, and their phycospheres in response to N-replete and low N conditions. From daily cell counts derived from flow cytometry, we calculated the maximum exponential growth rate of the two strains in culture to assess whether co-stress had a significant impact on growth rate.

Table of Contents

Coverage

Location: Laboratory-based experiment

Methods & Sampling

G. huxleyi strains RCC874 and RCC914 were obtained from the Roscoff Culture Collection (RCC). The cultures were transferred from the maintenance stock into artificial seawater (40 g Instant Ocean® Sea Salt per L Milli-Q® water) amended with nutrients, trace metals, and vitamins according to the L1 recipe (https://ncma.bigelow.org/algae-media-recipes) without silica (herein reported as L1-Si). The temperatures were selected to simulate no heat stress (18°C), moderate heat stress (22°C), and high heat stress conditions (25°C and 28°C for RCC874 and RCC914, respectively). The cultures were acclimated to the temperature conditions under a 14:10 light/dark cycle for approximately 10 days prior to the start of the experiment.

Following acclimation, cultures were transferred in triplicate into 2.8 L Fernbach flasks at an initial concentration of 1.0×10^5 cells mL^{-1}. The cultures were divided into two conditions: nitrogen-replete (N replete; L1-Si with standard 8.82×10^{-4} M $NaNO_3$) and nitrogen-limited (N limited; L1-Si with 8.82×10^{-5} M $NaNO_3$). Cell

abundances and optical properties were measured daily using flow cytometry with a BD Accuri C6 Plus equipped with a C-Sampler (BD, USA).

Data Processing Description

FCS data were processed using flowCore version 2.18 in R version 4.4.0. Maximum exponential phase-specific growth rate in cells per day was calculated in R version 4.4.0 using the growthrates package version 0.8.4, using the function all_splines() (spar = 0.5) (Petzoldt, 2022).

BCO-DMO Processing Description

- Loaded data from "MaxGrowthRate_GhuxleyiCultures_WHOI_Oct2023-Jan2024.xlsx" (sheet 1) with header row 1, treating empty strings and "nd" as missing values
- Set column types: Strain and n_conc as integer, temp_c as integer, rep as string, mumax and y0 as number
- Output written to 999165_v1_G_huxleyi_maximum_growth_rates.csv

Problem Description

No problems or issues have been reported by the dataset authors.

[table of contents | back to top]

Parameters

Parameters for this dataset have not yet been identified

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	BD Accuri C6 Plus equipped with a C-Sampler (BD, USA)
Generic Instrument Name	BD Biosciences Accuri C6 Plus flow cytometer
Dataset-specific Description	Cell abundances and optical properties were measured daily using flow cytometry with a BD Accuri C6 Plus equipped with a C-Sampler (BD, USA).
Generic Instrument Description	A flow cytometer designed to detect fluorochromes (including FITC, PE, APC), polymer dyes, and fluorescent proteins (including GFP, YFP, mCherry). The instrument is equipped with a blue and red laser, two light scatter detectors, and four fluorescence detectors with user-interchangeable filters. A non-pressurised peristaltic pump system drives the fluidics. The system monitors the sample volume pulled per run and can calculate absolute counts or sample concentration per microliter (uL). In the standard configuration (3-blue/1-red), three detectors read fluorescence emissions from fluorochromes excited by the blue laser, while a fourth detector reads emissions from fluorochromes excited by the red laser. The optional Selectable Laser Module allows the system to operate in 2-blue/2-red and 4-blue configurations. The minimum detectable particle size and sample volume are 0.5 micrometers (um) and 0.5 uL respectively. The maximum number of events is 1 million with an acquisition rate of up to 10,000 events/second.

[table of contents | back to top]

Project Information

Collaborative Research: Defining the role of the pan genome in Emiliania huxleyi ecology and biogeography (ECO-PAN-EHUX)

NSF Award Abstract:
Emiliania huxleyi is a numerically and ecologically important phytoplankton species in the ocean known for its cosmopolitan distribution and ability to form large blooms in coastal and open ocean regions. Studies of E. huxleyi variants in culture have found differences in growth, function and activity potential among them. The E. huxleyi variants also differ in some of the genes they carry. It has been hypothesized that this genomic variability may underlie the global success of this phytoplankton species by allowing adaptation of variants to diverse environments. Yet, the direct connection between genomic content and ecological success remains unclear. This project investigates how the conserved and variable portions of E. huxleyi genome may be connected to its success and its dynamics under varied environmental conditions. This work is critical to our understanding of how this important phytoplankton species may shift and respond to future changes. This project also supports the development of a series of hands-on activities designed to teach middle school students advance computational data analysis in ocean science. These activities are in collaboration with the Girls Who Code Club at the Our Sisters School, a tuition-free, non-sectarian, independent school for girls from low-income families, located in New Bedford, MA.

Understanding how phytoplankton diversity and phenotype are driven by changes in the environment is crucial for better predicting carbon cycle dynamics in the future ocean. While much work has investigated competition among phytoplankton species, intraspecific diversity and dynamics remain largely unknown for many eukaryotic phytoplankton. The overarching goal of this project is to define the role of the pan genome (set of variable genes) in E. huxleyi ecology and biogeography through a series of genomic analyses, computational field surveys, and laboratory-based experiments. This project is sequencing the genomes of several E. huxleyi isolates from across the global ocean and combining them with existing genome sequences to constrain the core and variable portions of the pan genome. Using this new pan genome reference database and leveraging global scale metagenomics and metatranscriptomic surveys, this project is estimating ecotype diversity of E. huxleyi across ocean regions to identify patterns of environmental selection. This project additionally focuses on identifying the physiological and transcriptional responses of a selection of sequenced strains and their responses to shifts in their nutrient environments in controlled laboratory studies. As E. huxleyi plays such a significant role in marine ecosystems and the global carbon cycle it is important that its pan genome and its impact on the biogeography and ecology of E. huxleyi is taken into consideration. It is likely that these dynamics are acutely important to predicting how this genus, and perhaps others, respond to changing environmental conditions in the future ocean.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1948025
NSF Division of Ocean Sciences (NSF OCE)	OCE-1948409

[table of contents | back to top]