Results from metal limitation experiments (Cu, Zn, Fe, Mn) conducted in the diatom T. pseudonana carried out in the Kustka and Allen labs at Rutgers in Newark, NJ from 2007-2011

Website: https://www.bco-dmo.org/dataset/3668
Data Type: experimental
Version: 1
Version Date: 2012-06-27

Project
» Expression profiling and functional genomics of a pennate diatom: Mechanisms of iron acquisition, stress acclimation, and recovery (Pennate Diatom Genomics)

Contributors	Affiliation	Role
Allen, Andrew E.	J. Craig Venter Institute (JCVI)	Principal Investigator
Kustka, Adam	Rutgers University	Contact
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
Results from metal limitation experiments (Cu, Zn, Fe, Mn) conducted in the diatom T. pseudonana carried out in the Kustka and Allen labs at Rutgers in Newark, NJ from 2007-2011

Table of Contents

- Dataset Description
    - Data Processing Description
- Data Files
- Parameters
- Deployments
- Project Information
- Funding

Dataset Description

Results of metal limitation experiments (Cu, Zn, Fe, Mn) conducted in the diatom *T. pseudonana*.

Data Processing Description

PI-provided parameter names were modified to conform with BCO-DMO conventions.

[table of contents | back to top]

Data Files

File
tpseudonana_growth.csv(Comma Separated Values (.csv), 570 bytes) MD5:52bf38a9be366b5d846f46a3e44a24d8 Primary data file for dataset ID 3668

[table of contents | back to top]

Parameters

Parameter	Description	Units
sample	Vial sample numbers (unique ID's).	dimensionless
metal	Metal of interest.	dimensionless
condition	Condition of the metal of interest under which the experiment was carried out.	dimensionless
growth_rate	Cell specific growth rate (per day), calculated as the slope of the linear regression between ln (cell density) versus time.	ln(cell density)/day
growth_rate_se	Standard error of growth_rate.	dimensionless
p_fe_prime	The negative log of fe_prime concentration (which is the summed concentration of all Fe species not complexed to EDTA). The additional effect of photochemistry of FeEDTA complexes on calculating fe_prime_log was considered. Originally notated as pFe'.	dimensionless
p_cu_prime	The negative log of Cu prime concentration (which is the summed concentration of all Cu species not complexed to either EDTA or TETA). Originally notated as pCu'.	dimensionless
p_mn_prime	The negative log of the Mn prime concentration (which is the summed concentration of all Mn species not complexed to EDTA). Originally notated as pMn'.	dimensionless
p_zn_prime	The negative log of the Zn prime concentration (which is the summed concentration of all Zn species not complexed to EDTA). Originally notated as pZn'.	dimensionless

[table of contents | back to top]

Deployments

lab_Kustka_Allen

Website	https://www.bco-dmo.org/deployment/58828
Platform	Rutgers_Newark
Start Date	2007-09-01
End Date	2011-08-01
Description	Research for the project 'Expression profiling and functional genomics of a pennate diatom: Mechanisms of iron acquisition, stress acclimation, and recovery' was conducted at Dr. Kustka's lab at the Rutgers-Newark campus: 101 Warren Street, Smith Hall Room 140 Newark, New Jersey, 07102

[table of contents | back to top]

Project Information

Expression profiling and functional genomics of a pennate diatom: Mechanisms of iron acquisition, stress acclimation, and recovery (Pennate Diatom Genomics)

Abstract:
Iron (Fe) availability plays an increasingly well known role regulating the fate of upwelled nitrate and determining the size structure and community composition of phytoplankton assemblages in the ocean. All Fe enrichment experiments conducted to date have reported increases in the biomass and photosynthetic capacity of

diatoms. Mounting evidence from field experiments, detailed physiological investigation, and genomic sequence data suggest fundamental differences in Fe bioavailability and uptake mechanisms, storage capacity, and stress recovery between pennate and centric diatoms. Pennate diatoms often dominate the phytoplankton assemblage after mesoscale Fe addition experiments because, in part, they are able to maintain cell viability during long periods of chronic Fe stress. The underlying molecular bases for these adaptations are virtually unknown. Preliminary primary metabolite data of Fe-limited *P. tricornutum* suggest that metabolic reconfigurations are necessary to meet increased demand for Fe-stress metabolites such as those involved in defense from reactive oxygen species (ROS) and intracellular metal chelation. Cellular nitrogen (N) status, and the accumulation of glutamate in particular, appears likely to play a primary role in recovery from Fe stress. This project capitalizes on the extremely well annotated *Phaeodactylum tricornutum* genome sequence to characterize global patterns of gene expression in response to shifts into and out of Fe and N stress and over the course of the diel cycle. The primary goal is to determine the molecular and physiological processes that constrain and define different phases and levels of Fe-stress acclimation. Oceanic physiological regimes have recently been defined according to different combinations of Fe and N availability and physiological indicators of the resident phytoplankton. This research will provide molecular-level insights into defense, acclimation, and regulatory mechanisms and pathways that govern survival strategies in situations of oceanographically-relevant stress and thus are of major ecological and biogeochemical consequence. Preliminary EST and partial genome microarray data, for example, indicate that chaperones and proteases play a significant role in monitoring cellular health and balancing the difference between investment in defense or activation of programmed cell death (PCD).

The proposed research will provide insights into the regulation of this fascinating and delicate balance. Such basic cellular processes play an important biogeochemical role in controlling bloom dynamics and regulating particle flux. Analysis of global gene expression will be compared with state of the art monitoring of intracellular metal levels and primary metabolite profiles using ICP-MS and gas chromatograph-mass spectroscopy (GC-MS) to determine the factors that determine cell survivability. The combination of global gene expression profiling and analysis of intracellular metal and metabolite pools will supply, for the first time, a holistic picture of the global cellular response of a marine pennate diatom to Fe-stress. *P. tricornutum* transcriptome profiles resulting from exposure to Fe - hydroxamate siderophores and heme-bound Fe (two classes of Fe binding ligands that are believed to comprise two major components of Fe in seawater) will be evaluated to understand the network of genes involved in recognizing and assimilating these compounds. An advanced reverse-genetics system for manipulating levels of gene expression in *P. tricornutum* will be used to evaluate the specific role of particular genes and pathways in facilitating Fe stress acclimation.

Broader Impacts: This research integrates important current themes in biogeochemistry, microbial ecology, marine sciences, and genome biology and will provide insight into factors that control the distribution and nutrient biogeochemistry of diatoms. By partnering with Affymetrix, through their Microbiology Program, a diatom microarray resource will be made available for the first time for open purchase and use. As part of the proposed research, a high school teacher from one of the local school systems with large underrepresented student populations will be recruited to work on a related topic. Upon completion of his/her paid internship, the teacher will design a classroom activity for use the following school year. As a further point of dissemination, the activity will be incorporated into a curriculum installment focused on marine and phytoplankton genomics for an existing mobile laboratory program called DISCOVER GENOMICS!, which interacts with middle school students in the Washington, D.C. Metropolitan area.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-0727997

[table of contents | back to top]