Gene expression data from nitrate-limited chemostat cultures of the diatom Thalaisiosira pseudonana subjected to varying CO2 concentrations

Website: https://www.bco-dmo.org/dataset/546449
Version: 30 Jan 2015
Version Date: 2015-01-30

Project
» A systems biology approach of diatom response to ocean acidification and climate change (diatom response to OA and CC)

Contributors	Affiliation	Role
Orellana, Monica V.	Institute for Systems Biology (ISB)	Principal Investigator
Armbrust, E. Virginia	University of Washington (UW)	Co-Principal Investigator
Hennon, Gwenn	University of Washington (UW)	Contact
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Table of Contents

Dataset Description

Gene expression data from nitrate-limited chemostat cultures of the diatom *Thalaisiosira pseudonana* subjected to CO2 concentrations ranging from 300-800 ppm.

Access to the dataset is restricted until the manuscript publication of our manuscript (currently under review for Nature Climate Change). Upon acceptance of the manuscript, data will be submitted to NCBI and the accession numbers will be provided here.

Methods & Sampling

For a full description of chemostat culturing methods see Hennon et al. (2014). Briefly, cells in chemostats were acclimated to 10 uM nitratelimitation at 70% of max growth rate for >10 days (equivalent to >15 generations) at 300, 475 or 800 uatm CO2, verified by pH and DIC measurements. After steady-state acclimation, ~1 x 10^8 cells were harvested on 0.2 micron polycarbonate filters by gentle vacuum filtration and flash frozen. Transition samples were collected daily as CO2 levels were increased from 300-800 ppm over four consecutive days (equivalent to 6 generations) after pre-acclimation to 300 ppm CO2 and nitrate limitation. ~1.5x10^7 cells were harvested from each day of the transition experiment on 0.2 micron polycarbonate filters by gentle vacuum filtration and flash frozen. Each sample condition was reproduced with four biological replicates. A total of 28 barcoded transcriptome libraries were prepared; 12 libraries (three treatments x four biological replicates) from steady-state culture experiments and 16 libraries (four days x four biological replicates) from transition experiments. RNA was extracted from filtered cells using the ToTALLY RNA kit. Messenger RNA was selectively amplified using MessageAmp II aRNA Amplification kit creating the antisense aRNA complement to mRNA from the sample. SOLiD barcoded libraries were prepared from aRNA as described in SOLiD Total RNA-seq kit and sequenced on a SOLiD 5500XL sequencer in two runs: one containing steady-state barcoded libraries and one containing transition barcoded libraries.

Reference:
Hennon, G. M. M., Quay, P., Morales, R. L., Swanson, L. M., & Armbrust, E. V. 2014. Acclimation conditions modify physiological response of the diatom *Thalassiosira pseudonana* to elevated CO2 concentrations in a nitrate-limited chemostat. Journal of Phycology, 253, 243–253. doi:10.1111/jpy.12156.

Data Processing Description

Reads were quality controlled (using a cut-off of p = 0.99 and minimum length = 30), trimmed, and aligned to *T. pseudonana* gene models using the Burrows-Wheeler Alignment tool and the SEAStAR tool (https://github.com/armbrustlab/SEAStAR). The aligned reads were counted for each gene model (Joint Genome Institute: thaps3 extended models) using the SEAStAR tool.

[table of contents | back to top]

Parameters

Parameters for this dataset have not yet been identified

[table of contents | back to top]

Project Information

A systems biology approach of diatom response to ocean acidification and climate change (diatom response to OA and CC)

Description from the NSF award abstract:
Advances in systems biology enable new approaches to understand the carbon cycle and carbon sequestration research across different scales of organization, linking single cells to ecosystems, with broad impacts. Systems biology is a robust, holistic, hypothesis-driven, quantitative, integrative and iterative discipline that enables comprehensive understanding of model organisms by utilizing genomic and computational tools that provide the power for linking gene expression, phenotype, and the environment. In a systems approach, cells are studied as an integrated whole to explain the overall response and dynamic change in the full spectrum of molecules (DNA, RNA proteins and metabolites), and their relationships (biological networks). The publication of the genome of T. pseudonana allows a universal analysis and understanding of the regulation of primary production of diatoms in response to ocean acidification and climate change. Global understanding of the mechanisms of regulation of carbon fixation by diatoms is now possible. This project will focus on characterizing - at molecular and cellular levels using a systems approach - the response of diatoms to ocean acidification and climate change, essential to understanding the future of the ocean's "biological pump". The broader goal of this project is to understand the contribution by diatoms to carbon cycling at a biogeochemical level. This project will generate a model of the global expression of all genes in the diatom T. pseudonana and will enable us to anticipate how higher CO2 and temperatures, lower pH will affect the ability of diatoms to sequester carbon in the oceans.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Emerging Frontiers Division (NSF EF)	EF-1316206
NSF Division of Ocean Sciences (NSF OCE)	OCE-0928561

[table of contents | back to top]