Gene expression profiles from high through put Illumina sequencing of multiple long-term evolved lines of Trichodesmium, 2011-2013 (Trichodesmium in High CO2 project)

Website: https://www.bco-dmo.org/dataset/4007
Version:
Version Date: 2013-07-30

Project
» Gene Expression Patterns in High CO2-Adapted Trichodesmium (Trichodesmium in High CO2)

Contributors	Affiliation	Role
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Dataset Description

NOTE: This dataset were released at NCBI on 2014-07-11. For questions, please contact Eric Webb, eawebb@usc.edu.

This EAGER funded dataset contains GenBank accession numbers for the gene expression profiles obtained from high through put illumina sequencing of multiple long-term evolved lines of Trichodesmium. In these experiments transcriptome samples (labeled 750) were obtained from cultures grown in either projected year 2100 CO2 levels (~750ppm) or current 380ppm levels (labeled 380) for four years. Additional files include the transcriptomic profiles from cells lines that were switched form their longterm conditions to either lower or higher CO2 conditions. These samples are labeled 750-380 for the switch from high CO2 to low and 380-750 for the switch from low to high.

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Data Files

File
trich_accession.csv(Comma Separated Values (.csv), 1.81 KB) MD5:55f4366bf0b56b78cef251de54a4e6a3 Primary data file for dataset ID 4007

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Parameters

Parameter	Description	Units
accession_number	database identifier assigned by repository and linked to GenBank	unitless
taxon_code	identification number of experimental organism	unitless
organism	taxonomic name of experimental organism	unitless
isolate	isolate number of experimental organism	unitless
BioProject_id	identification code of BioProject experiment	unitless

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Deployments

lab_Webb_Hutchins_Fu

Website	https://www.bco-dmo.org/deployment/59058
Platform	Webb-Hutchins-Fu USC
Start Date	2011-08-15
End Date	2013-03-31
Description	Lab experiments of transcriptome samples (labeled 750) obtained from cultures grown in either projected year 2100 CO2 levels (~750ppm) or current 380ppm levels (labeled 380) for four years.

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Project Information

Gene Expression Patterns in High CO2-Adapted Trichodesmium (Trichodesmium in High CO2)

Project Description from NSF Abstract:

The potential for biogeochemically-critical marine organisms, such as the N2-fixing cyanobacterium Trichodesmium, to adapt to a rapidly changing environment is a poorly understood but key determinant of future ocean food webs and elemental cycles. Despite an exponential increase in the sophistication of molecular tools available to the ocean science community, no study has yet applied these methods to relevant marine organisms in conjunction with microbial evolution experiments such as those pioneered by R.E. Lenski and colleagues for the model enteric bacterium Escherichia coli.

Intellectual Merit:
In this EAGER project, the PIs will conduct an exploratory approach that uses tiled microarray methods to evaluate changes in the expression of both coding and non-coding regions of the genome in Trichodesmium cultures that have been maintained in long-term (>3 years) high CO2 adaptation experiments. The objective of this work is to demonstrate that a novel combination of evolutionary experimental techniques and state-of-the-art gene expression methods can be used to yield unique insights into adaptive changes in keystone marine micro-organisms such as Trichodesmium in response to selection by environmental change variables. The over-arching goal is to increase our mechanistic understanding of the ways that evolution could shape the responses of marine biota to future changes in ocean chemistry and climate.

Broader Impacts:
This project will help support and train a new USC Ph.D. student, and research activities will include USC undergraduate biology majors. Public education and communication efforts for this project will be greatly enhanced by an annual series of public outreach and professional colloquia sponsored by a USC-funded "2020" initiative to integrate scientific and societal responses to climate change in the Southern California region. Any evolution-driven shifts in the growth and N2 fixation patterns of Trichodesmium, a keystone oceanic functional group, have large consequences for marine ecology, carbon cycling, and the food chains that support important living resources. The biggest scientific impact of this EAGER project could be to offer verification of a pioneering new approach to help determine how the microbes that are fundamental to today's ocean biogeochemical cycles will adapt to anticipated and unprecedented rates of change in marine ecosystems.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1143760

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