16S tag data, metagenomic data, and a draft assembled genome of Altermonas macleodii derived from laboratory-maintained Trichodesmium erythraeum cultures

Website: https://www.bco-dmo.org/dataset/709113
Data Type: experimental
Version: 09 March 2018
Version Date: 2018-03-09

Project
» Adaptation of key N2-fixing cyanobacteria to changing CO2 (HiCO2_AdaptCyano)

Contributors	Affiliation	Role
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Dataset Description

These data are all derived from laboratory-maintained Trichodesmium erythraeum cultures and contain 16S tag data, metagenomic data, and a draft assembled genome of Altermonas macleodii.

3 DNA sequence datasets have been uploaded to NCBI in their appropriate locations. The accession information is presented here:

FastQ files of 16S rRNA amplicon data have been uploaded to NCBI's Sequence Read Archive (SRA) under accession number SRP078329.

FastQ files of 5 metagenomic sequence datasets have been deposited in NCBI's SRA under SRP078343.

A FastA file of a draft genome has been uploaded to NCBI's Whole Genome Shotgun (WGS) database under the accession MBSN00000000.

These datasets were released upon publication of the paper: *The Trichodesmium consortium: conserved heterotrophic co-occurrence and genomic signatures of potential interactions*, by Lee et al. (doi:10.1038/ismej.2017.49), published in April 2017. Detailed sample information is included in the supplemental spreadsheets to that publication, specifically tables S1 and S2.

These data were also utilized in the paper:
Walworth, N. G., Lee, M. D., Suffridge, C., Qu, P., Fu, F., Saito, M. A., ... & Hutchins, D. A. (2018). Functional genomics and phylogenetic evidence suggest genus-wide cobalamin production by the globally distributed marine nitrogen fixer Trichodesmium. *Frontiers in Microbiology*, *9*, 189. doi: 10.3389/fmicb.2018.00189

Methods & Sampling

For sampling and analytical methodology, refer to the paper:
Lee, at al. (2017) The Trichodesmium consortium: conserved heterotrophic co-occurrence and genomic signatures of potential interactions. The ISME Journal,11, 1813–1824; doi:10.1038/ismej.2017.49

Data Processing Description

BCO-DMO Processing:
-09 March 2018: added links to NCBI accession numbers.

Data Files

File
tricho_metagenomics.csv (Comma Separated Values (.csv), 938 bytes)   MD5:57adfc9d06c235908e83be8effb5f342   Primary data file for dataset ID 709113

Parameters

Parameter	Description	Units
accession_number	NCBI accession number	unitless
accession_link	Hyperlink to NCBI for the accession number	unitless
description	Description of the accession	unitless
BioProject_id	NCBI BioProject ID number for the accession	untiless
BioProject_link	Hyperlink to NCBI for the BioProject ID number	unitless

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 CO_2 levels (~750ppm) or current 380ppm levels (labeled 380) for four years.

Project Information

Adaptation of key N2-fixing cyanobacteria to changing CO2 (HiCO2_AdaptCyano)

Coverage: Culture study at the University of Southern California, Los Angeles

Description from NSF award abstract:
This study will employ a novel combination of experimental evolution techniques and state-of-the-art molecular methods to yield unique insights into adaptive changes in the keystone marine cyanobacteria *Trichodesmium* and *Crocosphaera* in response to selection by high CO2. Several studies have suggested that N2-fixation rates of the biogeochemically-critical cyanobacteria *Trichodesmium* and *Crocosphaera* may increase dramatically in the future high CO2 ocean, but these have all used the same limited set of cultured isolates and considered cells only briefly acclimated to elevated CO2. The investigator's new results, however, demonstrate that a broad diversity of high- and low-CO2 adapted ecotypes exists within each diazotroph genus. Furthermore, in a preliminary four year experimental evolution study with *Trichodesmium*, the PIs observed large adaptive responses following 500-700 generations of selection by high CO2- but in a completely unexpected way. All of the six replicate high CO2-adapted cell lines exhibited strong constitutive up-regulation of N2 fixation rates. These very elevated N2 fixation rates continued, even though the cultures have were switched back to low-CO2 conditions for many months. Expression of the nif operon and N assimilatory genes was also up-regulated in these cell lines, as is expression of many intergenic regions of the genome.

The investigators hypothesize that constitutive up-regulation of cellular N2 fixation systems may be a common adaptive response of both *Trichodesmium* and *Crocosphaera* under extended selection by elevated CO2. This project will test this hypothesis in a four-year experimental evolution study to determine the adaptive responses of both high- and low-CO2 specialized ecotypes of these two diazotrophs to increased CO2.

The investigators will grow representative high- and low-CO2 adapted ecotypes from each genus in well-replicated cell lines at 380 ppm and 750 ppm CO2 for up to 1000 generations. Periodically, they will perform "switch" experiments to measure N2 and CO2 fixation rates and growth rates of high CO2-selected cell lines grown briefly (one week) at low CO2, and vice versa. These switch experiments will allow screening for cell lines which exhibit adaptive changes in phenotypically-expressed rate parameters, such as those observed in the preliminary *Trichodesmium* study. Evolutionary mechanisms in the CO2-selected cell lines will be examined by comparison of changes in their genomes, transcriptomes, and proteomes over time relative to reference genomes, using frozen samples archived monthly during the preceding selection period. Examination of these molecular and biochemical changes will be coordinated with an in-depth array of physiological and biogeochemical analyses. This combined approach will allow an evaluation of potential adaptive mechanisms in diazotrophic cyanobacteria ranging from indel, duplication, single nucleotide polymorphism, and transposition mutations to altered putative non-coding RNA expression, protein expression, and post-translational protein modifications, and then allow the investigators to link these mechanisms directly with their potential impacts on ecosystem-level biogeochemical processes like N2 and CO2 fixation. Finally, the research team will determine how long term selection by high CO2 affects the iron and phosphorus requirements of *Trichodesmium* and *Crocosphaera*, since constitutive up-regulation of N2 fixation would also have major implications for limitation of diazotrophs by these two critical nutrients in the future high CO2 ocean.

Funding