Diel proteomes of cultured Trichodesmium erythraeum sp. IMS101 from laboratory experiments conducted in November of 2018

Website: https://www.bco-dmo.org/dataset/783873
Data Type: experimental
Version: 1
Version Date: 2019-12-10

Project
» New technology for high resolution analysis of proteins and other organic materials produced by marine microorganisms (MM Proteins and Organics Tech)
» Marine Microbial Investigator Award: Investigator Mak Saito (MM Saito)

Program
» Marine Microbiology Initiative (MMI)

Contributors	Affiliation	Role
Saito, Mak A.	Woods Hole Oceanographic Institution (WHOI)	Principal Investigator
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Abstract
Diel proteomes of cultured Trichodesmium erythraeum sp. IMS101 from laboratory experiments conducted in November of 2018.

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Coverage

Temporal Extent: 2018-11

Dataset Description

Diel proteomes of cultured *Trichodesmium erythraeum* sp. IMS101 from laboratory experiments conducted in November of 2018.

The mass spectrometry proteomics data have been deposited to the ProteomeXchange Consortium via the PRIDE [1] partner repository with the dataset identifier PXD016332 and 10.6019/PXD016332 but are not yet public.

Project Name: Trichodesmium erythraeum sp. IMS101 Diel proteomes
Project accession: PXD016332
Project DOI: 10.6019/PXD016332

The format of these data in the BCO-DMO data system is tabular. For a version formatted as a matrix, see the "Data Files" section.

Methods & Sampling

A batch culture (1.5L) of *Trichodesmium erythraeum* sp. IMS101 was grown in a 27°C incubator with a 14:10 light cycle that ramps up and down mimicking dawn and dusk. Sampling occurred every 1-3 hours with concentrated sampling at dawn and dusk. 70mL of the culture was sterically subsampled and collected on 0.2mm Supor filters, then frozen at -80°C. 10mL was collected and filtered on combusted GFF filters for CHN analysis.

Proteins were extracted in sodium dodecyl sulfate and digested in gel similar to Saito et al., 2014 (Science). Peptides were analyzed by LC-MS/MS on a Thermo Orbitrap Fusion using LC x LC/MS chromatography with high and low pH reversed phase chromatography.

Data Processing Description

Peptide to spectrum matching was performed in SEQUEST implemented in Proteome Discoverer 2.2 using the *Trichodesmium erythraem* sp. IMS101 genome. Statistical validation was performed at the 1% protein and peptide FD levels calculated in Scaffold (Proteome Software).

BCO-DMO Data Manager Processing Notes:
* originally submitted file "dielproteindata.csv" in matrix format added to "Data Files" section.
* a tabular version of dielproteindata.csv was created and imported into the BCO-DMO data system. Data was unpivoted to transform from the matrix into a table with columns for hours_post_dawn,cnratio,relative_protein_abundance.
* added a conventional header with dataset name, PI name, version date
* modified parameter names to conform with BCO-DMO naming conventions (spaces, +, and - changed to underscores). Units in parentheses removed and added to Parameter Description metadata section.
* blank values in this dataset are displayed as "nd" for "no data." nd is the default missing data identifier in the BCO-DMO system

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Data Files

File	
diel_proteins.csv	(Comma Separated Values (.csv), 3.52 MB) MD5:ee506aaba0a12e64b3b705a4f7d4d15c
Primary data file for dataset ID 783873	
dielproteindata.csv	(Comma Separated Values (.csv), 398.85 KB) MD5:5d6ee8ebc660a58d8816f1823db02066
Diel proteomes Tricho IMS101 data. This file contains relative protein abundance, normalized spectral counts formatted as a matrix. This is the format originally submitted to BCO-DMO which was unpivoted into a tabular version in the BCO-DMO data system. row 1: hourspostdawn, hours after incubator light is on row 2: cnratio, POC:PON ratio of culture column 1 (rows 3-2392): protein name columns 2-14 (rows 3-2392): Relative protein abundance, normalized spectral counts	

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Related Publications

ProteomeXchange dataset. (n.d.). doi:10.6019/pxd016332 https://doi.org/10.6019/PXD016332
Related Research

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Parameters

Parameter	Description	Units
protein_name	Protein name	unitless
hours_post_dawn	Hours post dawn. Hours after incubator light is on	hours
cnratio	POC:PON ratio of culture. Ratio of particulate organic carbon to particulate organic nitrogen	dimensionless
relative_protein_abundance	Relative protein abundance. Normalized spectral counts.	unitless

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Instruments

Dataset-specific Instrument Name	Thermo Orbitrap Fusion mass spectrometer
Generic Instrument Name	Mass Spectrometer
Generic Instrument Description	General term for instruments used to measure the mass-to-charge ratio of ions; generally used to find the composition of a sample by generating a mass spectrum representing the masses of sample components.

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Project Information

New technology for high resolution analysis of proteins and other organic materials produced by marine microorganisms (MM Proteins and Organics Tech)

Website: https://www.moore.org/grant-detail?grantId=GBMF3934

In support of acquiring a high resolution mass spectrometer that incorporates the latest technologies for analyzing proteins and other organic materials.

Marine Microbial Investigator Award: Investigator Mak Saito (MM Saito)

In support of obtaining deeper knowledge of major biogeochemically relevant proteins to inform a mechanistic understanding of global marine biogeochemical cycles.

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Program Information

Marine Microbiology Initiative (MMI)

Website: https://www.moore.org/initiative-strategy-detail?initiativeId=marine-microbiology-initiative

A Gordon and Betty Moore Foundation Program.

Forging a new paradigm in marine microbial ecology:

Microbes in the ocean produce half of the oxygen on the planet and remove vast amounts of carbon dioxide, a greenhouse gas, from the atmosphere. Yet, we have known surprisingly little about these microscopic organisms. As we discover answers to some long-standing puzzles about the roles that marine microorganisms play in supporting the ocean's food webs and driving global elemental cycles, we realized that we still need to learn much more about what these organisms do and how they do it—including how they evolved and contribute to our ocean's health and productivity.

The Marine Microbiology Initiative seeks to gain a comprehensive understanding of marine microbial communities, including their diversity, functions and behaviors; their ecological roles; and their origins and evolution. Our focus has been to enable researchers to uncover the principles that govern the interactions among microbes and that govern microbially mediated nutrient flow in the sea. To address these opportunities, we support leaders in the field through investigator awards, multidisciplinary team research projects, and efforts to create resources of broad use to the research community. We also support development of new instrumentation, tools, technologies and genetic approaches.

Through the efforts of many scientists from around the world, the initiative has been catalyzing new science through advances in methods and technology, and to reduce interdisciplinary barriers slowing progress. With our support, researchers are quantifying nutrient pools in the ocean, deciphering the genetic and biochemical bases of microbial metabolism, and understanding how microbes interact with one another. The initiative has five grant portfolios:

Individual investigator awards for current and emerging leaders in the field.
Multidisciplinary projects that support collaboration across disciplines.
New instrumentation, tools and technology that enable scientists to ask new questions in ways previously not possible.
Community resource efforts that fund the creation and sharing of data and the development of tools, methods and infrastructure of widespread utility.
Projects that advance genetic tools to enable development of experimental model systems in marine microbial ecology.
We also bring together scientists to discuss timely subjects and to facilitate scientific exchange.

Our path to marine microbial ecology was a confluence of new technology that could accelerate science and an opportunity to support a field that was not well funded relative to potential impact. Around the time we began this work in 2004, the life sciences were entering a new era of DNA sequencing and genomics, expanding possibilities for scientific research – including the nascent field of marine microbial ecology. Through conversations with pioneers inside and outside the field, an opportunity was identified: to apply these new sequencing tools to advance knowledge of marine microbial communities and reveal how they support and influence ocean systems.

After many years of success, we will wind down this effort and close the initiative in 2021. We will have invested more than $250 million over 17 years to deepen understanding of the diversity, ecological activities and evolution of marine microbial communities. Thanks to the work of hundreds of scientists and others involved with the initiative, the goals have been achieved and the field has been profoundly enriched; it is now positioned to address new scientific questions using innovative technologies and methods.

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Funding

Funding Source	Award
Gordon and Betty Moore Foundation: Marine Microbiology Initiative (MMI)	GBMF3934
Gordon and Betty Moore Foundation: Marine Microbiology Initiative (MMI)	GBMF3782

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