Transcriptomes of co-cultured marine microbes (Emiliania huxleyi, Thalassiosira pseudonana, and Synechococcus) and Ruegeria pomeroyi DSS-3

Website: https://www.bco-dmo.org/dataset/905306
Data Type: experimental
Version: 1
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Project
» Effects of Climate Change Variables on Microbial Autotroph-Heterotroph Carbon Flux (CC_Auto_Hetero_Fluxes)

Contributors	Affiliation	Role
Moran, Mary Ann	University of Georgia (UGA)	Principal Investigator
Olofsson, Malin	University of Georgia (UGA)	Scientist
Smith, Christa	University of Georgia (UGA)	Technician
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
These data are from three laboratory studies of co-cultured temperature-acclimated marine microbes and Ruegeria pomeroyi DSS-3. Model systems were established in which temperature-acclimated microbial strains were co-cultured with the heterotrophic bacterium Ruegeria pomeroyi. Cultures of the coccolithophore Emiliania huxleyi CCMP151 were pre-acclimated to three temperature treatments (15°, 20°, and 28° Celsius (C)). Cultures of the diatom Thalassiosira pseudonana CCMP1335 were pre-acclimated to 14°, 20°, and 28°C. Cultures of Synechococcus sp. WH8102 were pre-acclimated to 20°, 24°, and 28°C. The investigators characterized the transcriptomes of both the phytoplankter and heterotrophic bacterium at initial and late exponential growth at the three temperatures.

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Coverage

Temporal Extent: 2020-07-01 - 2021-05-28

Dataset Description

The CSV file available here describes the samples, methods, and fastq files for raw data available from the Joint Genome Institute (JGI) at https://data.jgi.doe.gov. The data in JGI can be found under the following project ID numbers: 1290093, 1290172, 1290174, 1317772, 1317774, 1317776, 1317778, and 1334780.

Methods & Sampling

Laboratory studies were carried out at the University of Georgia, Athens, GA, USA. The studies took place over the following dates:
Thalassiosira: 1-7th July 2020
Synechococcus: 16-23rd Feb 2021
Emiliania: 18-28th May 2021

Emiliania huxleyi CCMP151
A laboratory study was conducted using cultures of a marine coccolithophore (*Emiliania huxleyi* CCMP151) and heterotrophic bacterium, *Ruegeria pomeroyi*. Coccolithophore cultures were pre-acclimated to three temperature treatments (15°, 20°, and 28° Celsius) and grown co-cultures. The transcriptome treatments consisted of axenic coccolithophore, the coccolithophore with the bacterium, and the bacterium with the coccolithophore, and three replicates were analyzed at each sample point. Stranded RNA-Seq libraries were sequenced using an Illumina NovaSeq instrument. For co-cultures, *E. huxleyi* and bacterial cells were separated by filtration prior to RNA extraction.

Thalassiosira pseudonana CCMP1335
A laboratory study was conducted using cultures of a marine diatom (*Thalassiosira pseudonana* CCMP1335) and heterotrophic bacterium, *Ruegeria pomeroyi.* Diatom cultures were pre-acclimated to three temperature treatments (14°, 20°, and 28° Celsius) and grown as co-cultures. The transcriptome treatments consisted of axenic diatom, the diatom with the bacterium, and the bacterium with the diatom, and three replicates were analyzed at each sample point. Stranded RNA-Seq libraries were sequenced using an Illumina NovaSeq instrument. For co-cultures, diatom and bacterial cells were separated by filtration prior to RNA extraction.

Synechococcus sp. WH8102
A laboratory study was conducted using cultures of a marine cyanobacterium (*Synechococcus* sp. WH8102 and heterotrophic bacterium, *Ruegeria pomeroyi. Synechococcus* cultures were pre-acclimated to three temperature treatments (20°, 24°, and 28° Celsius) and grown as co-cultures. The transcriptome treatments consisted of axenic Synechococcus, Synechococcus with the heterotrophic bacterium, and the bacterium with the Synechococcus, and three replicates were analyzed at each sample point. Stranded RNA-Seq libraries were sequenced using an Illumina NovaSeq instrument. RNA extraction of co-cultures was carried out without prefiltration, and transcripts were separated at mapping.

Data Processing Description

Raw reads, mapped read counts, and quality control checks were performed at JGI and are available on the JGI Data portal.

BCO-DMO Processing Description

- imported three original data files into the BCO-DMO system: Ehux.txt, Tpseudo.txt, Syn.txt.
- concatenated the three files into one data file.
- renamed fields to comply with BCO-DMO naming conventions.
- named the final data file "905306_v1_transcriptomes.csv".

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Data Files

File	
905306_v1_transcriptomes.csv	(Comma Separated Values (.csv), 20.93 KB) MD5:0c8ef4fe3a055c5308aace16b1275cc4
Primary data file for dataset ID 905306, version 1.	

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Parameters

Parameter	Description	Units
Taxon	name of strain	unitless
JGI_Project_Name	name of sequencing project at the Joint Genome Institute Data portal (https://data.jgi.doe.gov)	unitless
JGI_Project_ID	ID number of sequencing project at the Joint Genome Institute Data portal (https://data.jgi.doe.gov)	unitless
Library_Name	sample identifier	unitless
Sample_Name	sample name	unitless
Replicate	replicate number	unitless
Sample_condition	treatment conditions (temperature of acclimation in degrees C, co-culture or axenic)	unitless
Filtered_Raw_Data_file	name of fastq sequence file at the Joint Genome Institute Data portal (https://data.jgi.doe.gov)	unitless

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Instruments

Dataset-specific Instrument Name	Illumina NovaSeq
Generic Instrument Name	Automated DNA Sequencer
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

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Project Information

Effects of Climate Change Variables on Microbial Autotroph-Heterotroph Carbon Flux (CC_Auto_Hetero_Fluxes)

Coverage: Laboratory in Athens, GA, USA, and waters around Sapelo Island, GA, USA

NSF Award Abstract:
Phytoplankton in the surface ocean are responsible for roughly half of all photosynthesis on the planet. Much of the organic material created by these photosynthetic organisms is ultimately consumed by diverse marine bacteria with differing preferences for specific types of chemical compounds. This project investigates how climate change (temperature and CO2) might alter the types and amounts of organic compounds produced by different species of marine phytoplankton and the types and amounts of compounds transferred from phytoplankton to marine bacteria. Shifts in organic compounds transferred to bacteria could alter the

distribution of bacterial species in the ocean, their growth rates and efficiencies, and flows of energy through the global ocean. This project helps scientists better understand the effects of climate change on marine ecosystems. Two graduate students and a postdoctoral researcher are supported by the project, receiving interdisciplinary training in biology, chemistry, and ocean sciences. Summer research internships in the PIs' laboratories are offered to AP Biology students enrolled at Cedar Shoals High School in Athens, GA, a school that serves a diverse social and economic community.

Much of the bacterial secondary production in the surface ocean is supported by rapid uptake of labile metabolites released from phytoplankton, either directly through excretion and diffusion or indirectly through lysis and predation. This project investigates the effects of two climate change variables (temperature and CO2) on the metabolite pools produced and released by three model phytoplankton species (a diatom, a coccolithophore, and a cyanobacterium) and assesses changes in the composition and fate of metabolites transferred to bacteria. Phytoplankton species are being grown axenically at two different temperatures and CO2 concentrations in a factorial design and endo- and exometabolite composition is determined using NMR. A suite of phytoplankton physiological characteristics is measured and evaluated in the context of metabolite composition. Experiments with heterotrophic bacteria (either model bacteria or natural bacterial communities) are being conducted to assess the effects of climate change variables on metabolite transfer from phytoplankton to marine bacteria. In the first experiment type, bacteria are co-cultured with the phytoplankton at different temperatures and CO2 concentrations, and changes in bacterial gene expression and metabolite concentrations are used to assess shifts in the composition of metabolites transferred. In the second type, bacteria are grown on phytoplankton metabolite pools produced at different temperatures and CO2 concentrations in high-throughput bioassays, and changes in bacterial traits (growth rate, carrying capacity, growth efficiency) resulting from the different climate scenarios are used to indicate changes in metabolite quality. Knowledge of how the heterotrophic processing of phytoplankton metabolites might shift in response to climate change allows better prediction of Earth's future carbon cycle.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1948104
US Department of Energy - Joint Genome Institute (DOE-JGI)	JGI Proposal 50689

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