Data relating to RNA sequence accessions at NCBI from Ross Sea Dinoflagellates, Phaeocystis antarctica, Pyramimons tychotreta, and Micromonas polaris (CCMP 2099) (Kleptoplasty project)

Website: https://www.bco-dmo.org/dataset/728427
Data Type: experimental
Version: 1
Version Date: 2018-05-17

Project
» You are what you eat: The Role of Kleptoplasty in an Antarctic Dinoflagellate (Kleptoplasty)

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Coverage

Spatial Extent: **N**:76.2833 **E**:-74.75 **S**:-78 **W**:162
Temporal Extent: 1997-12 - 1998-04

Dataset Description

This dataset contains data related to RNA sequence genetic accessions at the National Center for Biotechnology Information (NCBI) including information about the host organism, collection location, and collection date.

The accessions are the unprocessed Illumina MiSeq reads for the Ross Sea Dinoflagellate RNA-Seq experiments, *Phaeocystis antarctica* RNA-Seq experiments, and *Pyramimons tychotreta* & *Micromonas polaris* (CCMP 2099) mixotrophy experiments.

Pyramimonas tychotreta & *Micromonas polaris* (CCMP 2099) mixotrophy RNA sequences are available through the NCBI Sequence Read Archive (SRA) under the SRA accession number SRP090401 (BioProject PRJNA342459)

Ross Sea Dinoflagellate RNA sequences are available through the NCBI Sequence Read Archive (SRA) under the accession number SRP132912 (BioProject PRJNA428208).

Phaeocystis antarctica RNA sequences are available through the NCBI Sequence Read Archive (SRA) under the accession number SRP133243 (BioProject PRJNA434497).

Methods & Sampling

Pyramimonas tychotreta and *Micromonas polaris* (CCMP 2099) mixotrophy RNA-Seq

Replicate cultures (n=4 for each isolate and treatment) were incubated under high- and reduced-nutrient conditions for a week. High-nutrient treatments were full strength f/2+Si (i.e., the maintenance media), while low-nutrient treatments were a 10-fold dilution of f/2 + Si culture media with filter-sterilized seawater. The low-nutrient conditions were previously found to elicit increases in ingestion by these two species.

Ross Sea Dinoflagellate and *Phaeocystis antarctica* RNA-Seq

The Ross Sea Dinoflagellate (RSD) was enriched away from the prey and grown in f/2 + Si at 0C under 14/10hr light dark cycle at 26.2 µmol/m2/sec. For the temperature experiment, flasks with approximately 450,000 cells each incubated at 0C (4 replicates) or 5C (4 replicates) for 5 days. For the different light conditions, flasks of approximately 450,000 cells each were incubated under constant illumination of 371 µmol/m2/sec (surface; 4 replicates), 48 µmol/m2/sec (DCM; 4 replicates) or darkness (4 replicates) at 0C for 5 days.

Phaeocystis antarctica was grown under the same experimental conditions with 4 replicates per treatment. Approximately 3.3 x 10^6 cells per replicate were used in the 0C incubation, 2.6 x 10^6 cells per replicate in the 5C incubation, and 1.4 x 10^7 cells per replicate in the different light exposure treatments.

Sampling and analytical procedures:

Pyramimonas and *Micromonas* were collected on 25mm 0.2 µm polycarbonate filters, frozen at -80°C, then extracted using the Qiagen Mini RNA kit, with confirmation of nucleic acid abundance and quality assessed by Bioanalyzer. Replicate samples were sent to the Sulzberger Genome Center at Columbia University for poly-A selection, library construction and sequencing by Illumina Mi-Seq (150bp paired-end reads, 30 million reads per sample).

RSD and *Phaeocystis* cultures were fixed with RNALater and harvested by filtration onto 0.8 micron pore size 25 mm polycarbonate filters. Cells were lysed using the Qiagen RNeasy Mini Kit. DNA was removed by DNase treatment on the purification column. mRNA was isolated using ribosomal depletion (Ribo-Zero™ rRNA Removal Kit for Plant Leaf). RNA quality was checked by Bioanalyzer and sent to Sulzberger Columbia Genome Center for library preparation and RNA-Seq (150bp paired-end reads, 30 million reads per sample).

Data Processing Description

BCO-DMO Data Manager Processing Notes:
* added a conventional header with dataset name, PI name, version date
* modified parameter names to conform with BCO-DMO naming conventions
* blank values replaced with no data value 'nd' for "no data" so they are recognized in our system
* metadata for runs obtained with sra run selector results at NCBI to download files that have the biosample, bioproject, sra project and sample info in them.
* split lat_lon into lat,lon in decimal degrees
* commas replaced with ;
* added link to each BioProject at NCBI

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Data Files

File
SRA_toplevel.csv (Comma Separated Values (.csv), 16.59 KB) MD5:8823c26aad1ff1af15dfdfefb1566409
Primary data file for dataset ID 728427

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Parameters

Parameter	Description	Units
BioProject_descrip	Brief description of BioProject	unitless
SRA_Study	SRA Study accession number	unitless
BioProject	NCBI BioProject number. A BioProject is a collection of biological data related to a single initiative originating from a single organization or from a consortium	unitless
BioProject_link	Link to the NCBI BioProject page	unitless
Experiment	Experiment identifier	unitless
Library_Name	Library name	unitless
Sample_Name	Sample name	unitless
Assay_Type	Assay type	unitless
LibrarySelection	Library Selection	unitless
replicate	Replicate name	unitless
BioSample	Biosample accession number at NCBI (stores descriptive information about the physical biological materials)	unitless
Organism	Organism sampled	unitless
collection_date	Date sample was collected (various formats)	unitless
geo_loc_name	Geographical origin of the sample	unitless
isolate	Identification or description of the specific individual from which this sample was obtained	unitless
sample_type	Sample type, such as cell culture, mixed culture, tissue sample, whole organism, single cell, metagenomic assembly	unitless
collected_by	Name of persons or institute who collected the sample	unitless
culture_collection	Institution code and identifier for the culture from which the nucleic acid sequenced was obtained (see http://www.insdc.org/controlled-vocabulary-culturecollection-qualifier)	unitless
depth	Depth (vertical distance below surface)	unitless
identified_by	Name of the taxonomist who identified the specimen	unitless
lat	Collection latitude of sampled organism	decimal degrees
lon	Collection longitude of sampled organism	decimal degrees
temp	Water temperature at organism collection location	degrees Celsius

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Instruments

Dataset-specific Instrument Name	Illumina Mi-Seq
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

You are what you eat: The Role of Kleptoplasty in an Antarctic Dinoflagellate (Kleptoplasty)

Coverage: Ross Sea, Antarctica

Description from NSF award abstract:
Kleptoplasty, the temporary acquisition and use of functional chloroplasts derived from algal prey, is viewed as an important model for the early evolution of the permanent, endosymbiotically-derived chloroplasts found in all permanently photosynthetic eukaryotes. This project will study the evolutionary history and expression of plastid-targeted genes in an abundant Antarctic dinoflagellate that steals chloroplasts from an ecologically important alga, the haptophyte Phaeocystis. Algae play an important role in the fixation and export of CO2 in the Southern Ocean, and this project will explore the genetic basis for the function of these chimeric cells with regard to their functional adaptation to extreme environments and will study the evolutionary history and expression of plastid-targeted genes in both the host and recipient. The project seeks to determine whether the kleptoplastidic dinoflagellate utilizes ancestral plastid proteins to regulate its stolen plastid, and how their transcription is related to environmental factors that are relevant to the Southern Ocean environment (temperature and light). To accomplish these goals, the project will utilize high throughput transcriptome analysis and RNA-sequencing experiments with the dinoflagellate and Phaeocystis.

This work will help biologists understand the environmental success of this alternative nutritional strategy, and to assess the potential impact of anthropogenic climate change on the organism. The project will also contribute to the maintenance of a culture collection of heterotrophic, phototrophic and mixotrophic Antarctic protists that are available to the scientific community, and it will support the mentoring of a graduate student and a postdoctoral fellow. The work is being accomplished as an international collaboration between US and Canadian scientists, and in addition to publishing results in peer-reviewed journals, the investigators will incorporate aspects of this work into public outreach activities. These include field data analysis opportunities for middle school students and science-based art projects with local schools and museums.

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Funding

Funding Source	Award
NSF Office of Polar Programs (formerly NSF PLR) (NSF OPP)	PLR-1341362

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