

# Isolate information on genes found in samples collected on the Gould (LMG1411) cruise in the Western Antarctica Peninsula in 2014 (Polar Transcriptomes project).

Website: <https://www.bco-dmo.org/dataset/665288>

Data Type: experimental

Version: 1

Version Date: 2016-11-18

## Project

» [Iron and Light Limitation in Ecologically Important Polar Diatoms: Comparative Transcriptomics and Development of Molecular Indicators](#) (Polar\_Transcriptomes)

Contributors	Affiliation	Role
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## Abstract

Isolate information on genes found in samples collected on the Gould (LMG1411) cruise in the Western Antarctica Peninsula in 2014 (Polar Transcriptomes project).

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## Coverage

**Spatial Extent:** N:-66.254 E:-67.337 S:-68.112 W:-72.739

**Temporal Extent:** 2014 - 2014

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## Dataset Description

Isolate information on genes found in samples collected on LMG1411.

Diatom isolates were obtained from the Western Antarctic Peninsula surface waters.

## Acquisition Description

Nine species of diatoms were isolated from the Western Antarctic Peninsula along the Palmer LTER sampling grid in 2013 and 2014. Isolations were performed using an Olympus CKX41 inverted microscope by single cell isolation with a micropipette (Anderson 2005). Diatom species were identified by morphological characterization and 18S rRNA gene (rDNA) sequencing. DNA was extracted with the DNeasy Plant Mini Kit according to the manufacturer's protocols (Qiagen). Amplification of the nuclear 18S rDNA region was achieved with standard PCR protocols using eukaryotic-specific, universal 18S forward and reverse primers. Primer sequences were obtained from Medlin et al. (1982). The length of the region amplified is approximately 1800 base pairs (bp). Pseudo-nitzschia species are often difficult to identify by their 18S rDNA sequence, therefore, additional support of the taxonomic identification of *P. subcurvata* was provided through sequencing of the 18S-ITS1-5.8S regions. Amplification of this region was performed with the 18SF-euk and 5.8SR\_euk primers of Hubbard et al. (2008). PCR products were purified using either QIAquick PCR Purification Kit (Qiagen) or ExoSAP-IT (Affymetrix) and sequenced by Sanger DNA sequencing (Genewiz). Sequences were edited using Geneious Pro software (<http://www.geneious.com>, Kearse et al., 2012) and BLASTn sequence homology searches were performed against the NCBI nucleotide non-redundant (nr) database to determine species with a cutoff identity of 98%.

Diatom phylogenetic analysis was performed with Geneious Pro and included 71 additional diatom 18S rDNA sequences from publically available genomes and transcriptomes, including those in the MMETSP database. Diatom sequences were trimmed to the same length and aligned with MUSCLE (Edgar 2004). A phylogenetic tree was created in Mega with the Maximum-likelihood method of tree reconstruction, the Jukes-Cantor genetic distance model (Jukes and Cantor 1969), and 100 bootstrap replicates.

Isolates were maintained at 4 deg C in constant irradiance at intensities of either 10  $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$  (low light) or 90  $\mu\text{mol photons m}^{-2} \text{ s}^{-1}$  (growth saturating light) and with media containing high and low iron concentrations. Cultures were grown in the synthetic seawater medium, AQUIL, enriched with filter sterilized vitamin and trace metal ion buffer containing 100  $\mu\text{mol L}^{-1}$  EDTA. The growth media also contained 300  $\mu\text{mol L}^{-1}$  nitrate, 200  $\mu\text{mol L}^{-1}$  silicic acid and 20  $\mu\text{mol L}^{-1}$  phosphate. Premixed Fe-EDTA (1:1) was added separately for total iron concentrations of either 1370  $\text{nmol L}^{-1}$  or 3.1  $\text{nmol L}^{-1}$ . Cultures were grown in acid-washed 28 mL polycarbonate centrifuge tubes (Nalgene) and maintained in exponential phase by dilution. Specific growth rates of successive transfers were calculated from the linear regression of the natural log of in vivo chlorophyll a fluorescence using a Turner 10-AU fluorometer (Brand et al. 1981).

## Processing Description

### **BCO-DMO Data Processing Notes:**

- reformatted column names to comply with BCO-DMO standards
- added a column to accession number links
- replaced spaces with underscores

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## Parameters

<b>Parameter</b>	<b>Description</b>	<b>Units</b>
polar_diatoms	Species names	unitless
strain_ID	Strain ID number	unitless
PalmerLTER_station	Palmer LTER station number	unitless
lat	Latitude; N is positive	decimal degrees
lon	Longitude; E is positive	decimal degrees
GenBank_bestHit	Accession number of best hit in GenBank	unitless
percentSimilarity_bestHit	Percent similarity of sequence to the best hit	percent
accession_number	NBII Accession number	unitless
accession_link	Accession link	unitless

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## **Instruments**

<b>Dataset-specific Instrument Name</b>	Olympus CKX41
<b>Generic Instrument Name</b>	Inverted Microscope
<b>Dataset-specific Description</b>	Used to perform isolations
<b>Generic Instrument Description</b>	<p>An inverted microscope is a microscope with its light source and condenser on the top, above the stage pointing down, while the objectives and turret are below the stage pointing up. It was invented in 1850 by J. Lawrence Smith, a faculty member of Tulane University (then named the Medical College of Louisiana). Inverted microscopes are useful for observing living cells or organisms at the bottom of a large container (e.g. a tissue culture flask) under more natural conditions than on a glass slide, as is the case with a conventional microscope. Inverted microscopes are also used in micromanipulation applications where space above the specimen is required for manipulator mechanisms and the microtools they hold, and in metallurgical applications where polished samples can be placed on top of the stage and viewed from underneath using reflecting objectives. The stage on an inverted microscope is usually fixed, and focus is adjusted by moving the objective lens along a vertical axis to bring it closer to or further from the specimen. The focus mechanism typically has a dual concentric knob for coarse and fine adjustment. Depending on the size of the microscope, four to six objective lenses of different magnifications may be fitted to a rotating turret known as a nosepiece. These microscopes may also be fitted with accessories for fitting still and video cameras, fluorescence illumination, confocal scanning and many other applications.</p>

## Deployments

### LMG1401

<b>Website</b>	<a href="https://www.bco-dmo.org/deployment/675566">https://www.bco-dmo.org/deployment/675566</a>
<b>Platform</b>	ARSV Laurence M. Gould
<b>Start Date</b>	2014-11-27
<b>End Date</b>	2014-12-21

## Project Information

### **Iron and Light Limitation in Ecologically Important Polar Diatoms: Comparative Transcriptomics and Development of Molecular Indicators (Polar\_Transcriptomes)**

**Website:** [http://www.nsf.gov/awardsearch/showAward?AWD\\_ID=1341479](http://www.nsf.gov/awardsearch/showAward?AWD_ID=1341479)

**Coverage:** Antarctica

The Southern Ocean surrounding Antarctica is changing rapidly in response to Earth's warming climate. These changes will undoubtedly influence communities of primary producers (the organisms at the base of the food chain, particularly plant-like organisms using sunlight for energy) by altering conditions that influence their growth and composition. Because primary producers such as phytoplankton play an important role in global biogeochemical cycling, it is essential to understand how they will respond to changes in their environment. The growth of phytoplankton in certain regions of the Southern Ocean is constrained by steep gradients in chemical and physical properties that vary in both space and time. Light and iron have been identified as key variables influencing phytoplankton abundance and distribution within Antarctic waters. Microscopic algae known as diatoms are dominant members of the phytoplankton and sea ice communities, accounting for significant proportions of primary production. The overall objective of this project is to identify the

molecular bases for the physiological responses of polar diatoms to varying light and iron conditions. The project should provide a means of evaluating the extent these factors regulate diatom growth and influence net community productivity in Antarctic waters. The project will also further the NSF goals of making scientific discoveries available to the general public and of training new generations of scientists. It will facilitate the teaching and learning of polar-related topics by translating the research objectives into readily accessible educational materials for middle-school students. This project will also provide funding to enable a graduate student and several undergraduate students to be trained in the techniques and perspectives of modern biology. Although numerous studies have investigated how polar diatoms are affected by varying light and iron, the cellular mechanisms leading to their distinct physiological responses remain unknown. Using comparative transcriptomics, the expression patterns of key genes and metabolic pathways in several ecologically important polar diatoms recently isolated from Antarctic waters and grown under varying iron and irradiance conditions will be examined. In addition, molecular indicators for iron and light limitation will be developed within these polar diatoms through the identification of iron- and light-responsive genes -- the expression patterns of which can be used to determine their physiological status. Upon verification in laboratory cultures, these indicators will be utilized by way of metatranscriptomic sequencing to examine iron and light limitation in natural diatom assemblages collected along environmental gradients in Western Antarctic Peninsula waters. In order to fully understand the role phytoplankton play in Southern Ocean biogeochemical cycles, dependable methods that provide a means of elucidating the physiological status of phytoplankton at any given time and location are essential.

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## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">PLR-1341479</a>

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