Pfam differential expression data for mixotrophs from an iron incubation experiment during the PUPCYCLE II R/V Sally Ride cruise within the California Current System in May and June of 2023

Website: https://www.bco-dmo.org/dataset/1004659
Data Type: Cruise Results, experimental
Version: 1
Version Date: 2026-08-12

Project
» CAREER: An integrated molecular and physiological approach to examining the dynamics of upwelled phytoplankton in current and changing oceans (Upwelled Phytoplankton Dynamics)

Contributors	Affiliation	Role
Marchetti, Adrian	University of North Carolina at Chapel Hill (UNC-Chapel Hill)	Principal Investigator
Cohen, Natalie	University of Georgia (UGA)	Scientist
Schnetzer, Astrid	North Carolina State University (NCSU)	Scientist
Cook, Claire	University of Georgia (UGA)	Student
Jeong, Yubeen	University of North Carolina at Chapel Hill (UNC-Chapel Hill)	Student
Lim, Prisca	University of North Carolina at Chapel Hill (UNC-Chapel Hill)	Student
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Speciale, Emily	University of North Carolina at Chapel Hill (UNC-Chapel Hill)	Student
Gerlach, Dana Stuart	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
This dataset includes RNA-seq differential expression results of Pfam domains within mixotrophs from an iron incubation experiment using upwelled waters sampled in the California Current System (CCS) during the PUPCYCLE II cruise with Chief Scientist Adrian Marchetti. PUPCYCLE II (Phytoplankton response to the UPwelling CYCLE) took place onboard the R/V Sally Ride from May 29th to June 10th, 2023. Freshly upwelled seawater for the incubation experiment was collected within the northern CCS and placed into designated cubitainers. Three cubitainers were immediately harvested for the initial timepoint (T0). The remaining twenty-seven cubitainers were assigned treatments: nine were unamended (Ctrl), nine were amended with 5 nM FeCl2 (Fe), and nine were amended with 200 nM Desferrioxamine B, a strong iron chelator (DFB). Three cubitainers from each treatment were harvested for each of the three subsequent timepoints: 48 hours (T1), 168 hours (T2), and 264 hours (T3) after incubation. Approximately 4 liters of each sample was harvested for RNA-seq of the natural phytoplankton community, or metatranscriptomics. The dataset provides differential expression results of Pfam domains within mixotrophs (and which genera they map to), specifically comparing expression levels between +Fe and DFB at T1 and T2. This data includes domains that significantly differ in expression between treatments in mixotrophs, and results were used to understand phagotrophic versus phototrophic gene expression based on iron bioavailability.

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Coverage

Location: California Current System, off the southern coast of Oregon at 43°02'42.7"N, 124°33'07.2"W, depth 55m
Spatial Extent: **Lat**:43.045194 **Lon**:-124.552
Temporal Extent: 2023-05-29 - 2023-06-10

Dataset Description

This dataset is one of many generated from an iron incubation experiment conducted as part of the PUPCYCLE II cruise in May and June 2023. The different analyses are listed here, with links to other datasets from this study in the Related Datasets section.

Analyses include:

- Physiology (dataset 994607)
  - Dissolved inorganic nutrients
  - Size-fractionated chlorophyll a
  - Size-fractionated isotope uptake rates
  - Flow cytometry
  - FlowCAM analysis
  - FLP experiments for mixotroph grazing
- RNA taxonomy data (dataset 1003525)
- Differential expression: Pfam
  - **Mixotroph Pfam (this dataset 1004659)**
  - Diatom Pfam (dataset 1004674)
- Differential expression: KEGG gene (dataset 1004689)
- Differential expression: KEGG pathways (dataset1004704)
- Dissolved iron concentrations (dataset 1004007)

See Related Datasets section below for links to above mentioned datasets.

Methods & Sampling

Data collection took place on the R/V Sally Ride from May 29th to June 10th, 2023. To simulate upwelling conditions under different iron treatments, an onboard incubation experiment was conducted. Seawater for the incubation experiment was collected within the northern CCS, off the southern coast of Oregon at 43°02'42.7"N, 124°33'07.2"W. The collected seawater was deemed as freshly upwelled water and taken from a depth of 55 meters – which corresponds to a depth slightly below the euphotic zone receiving less than 1% irradiance – using trace-metal clean techniques on May 30th, 2023, 13:30 GMT. The seawater was pumped and homogenized using trace metal clean techniques, then transferred into a total of thirty 20 L low-density polyethylene cubitainers. Three cubitainers were immediately harvested for the initial timepoint (T0). The remaining twenty-seven cubitainers were assigned treatments: nine were unamended (Ctrl), nine were amended with 5 nM $FeCl_2$ (+Fe), and nine were amended with 200 nM desferrioxamine B, a strong iron chelator that inhibits dissolved iron uptake (DFB). The cubitainers were placed in an on-deck incubator covered with two layers of neutral density screening to simulate 26% of incidence irradiance supplied with flow-through surface seawater to maintain ambient surface temperature. Three cubitainers from each treatment were harvested for each of the three subsequent timepoints: 48 hours (T1), 168 hours (T2), and 264 hours (T3) after incubation.

RNA Collection and Metatranscriptomics. Cubitainers were harvested for RNA by collecting and filtering approximately 2.5 to 4 L of each sample onto 0.8 µm Pall Supor filters (142 mm) using a peristaltic pump; samples were then immediately flash frozen in liquid nitrogen and stored at -80°C. RNA was extracted using the RNAqueous-4PCR kit, per instructions from the manufacturer with few modifications – filters were cut up due to their large size, 200 µL of glass beads were added, and 3 mL of lysis buffer was added. RNA samples were sent to GENEWIZ for library preparation and sequencing with PolyA tail selection. Sequencing was

performed on an Illumina HiSeq 4000 with a 2x150 bp configuration. GENEWIZ provided raw paired-end read sequences for each sample.

Raw reads were trimmed using Trim Galore v0.6.10 (Krueger, 2015) and quality control was assessed through FastQC (Martin, 2011). A *de novo* metatranscriptome assembly was conducted using rnaSPAdes v3.15.5 for individual assemblies (Bushmanova et al., 2019) and CD-HIT v4.8.1 for a grand assembly (Li & Godzik, 2006). TransDecoder v5.7.1 was used to determine the most likely open reading frame (ORF) for each contig (Haas, 2023). ORFs were annotated using the Marine Functional Eukaryotic Reference Taxa (MarFERReT) database v1.1.1 (e-value < $1e^{-06}$) (Groussman et al., 2023) for NCBI taxonomies (Federhen, 2012), PR^2 taxonomies (Guillou et al., 2012) and Pfam 34.0 functions (Mistry et al., 2021). To remove any potential bacterial contamination, ORFs were also annotated against the PhyloDB v1076 database using EUKulele (e-value < $1e^{-06}$) (Krinos et al., 2020). Any ORF with a higher bitscore for a bacteria or virus compared to its MarFERReT annotation was removed (resulting in < 3% of ORFs removed). To maximize functional annotation coverage, ORFs were annotated using eggNOG-mapper v2.1.12 (Cantalapiedra et al., 2021) to obtain annotations from the Kyoto Encyclopedia of Genes and Genomes (KEGG) (Kanehisa, 2000). Trimmed samples were then aligned to the grand assembly using Salmon v1.10.3 (Patro et al., 2017) and exported into a comprehensive counts table using tximport (Soneson et al., 2016). Reads not mapping to a protist group as defined by MarFERReT annotations were removed before downstream analysis.

DESeq2 was used to obtain normalized counts and conduct differential expression analyses (Love et al., 2014). Differential expression analysis for Pfam protein domains was performed for reads mapping to mixotrophs. Reads not mapping to mixotrophs were removed prior to normalization and statistical testing. Mixotrophs were identified based on constitutive mixotroph genera within the Mixoplankton Database (MDB) (Mitra et al., 2023). Reads were summed based on annotation ID prior to entering DESeq2 analysis; if a contig annotated to multiple IDs, its reads were evenly distributed between the mapped annotations. The differential expression analyses only focused on comparing +Fe vs DFB at T1 and T2. Normalized counts for each Pfam protein domain were also obtained to determine relative contributions of each mixotroph genera to the annotation ID.

Data Processing Description

The metatranscriptomic pipeline code used for this project is publicly available at https://github.com/emilyspeciale/Speciale-Metatranscriptomics.

The following software was used:

Trim Galore v0.6.10
CD-HIT v4.8.1
TransDecoder v5.7.1
Marine Functional Eukaryotic Reference Taxa (MarFERReT) database v1.1.1
PhyloDB v1076 database using EUKulele
eggNOG-mapper v2.1.12
Salmon v1.10.3
tximport
DESeq2

BCO-DMO Processing Description

CURATION ACTIONS PERFORMED ON DATA
- Loaded source file "BCO_DMO_PUPCYCLEII_MixoPfamDE.csv" into the BCO-DMO system converting missing data identifier NA to empty cell
- Set data types for mixotroph columns as number, others to string
- Exported final file as "1004659_v1_mixotroph_pfam.csv"

CURATION ACTIONS PERFORMED ON METADATA
- Changed in-line citations to have format of (author, year) replacing number references.
- Added details to the parameter description for log2FoldChange -->Base-2 logarithm of the ratio of normalized read abundance under the iron-amended (+Fe) treatment to normalized read abundance under the desferrioxamine B (DFB) treatment, calculated for each Pfam domain
- Corrected minor typos and punctuation

ISSUES POTENTIALLY IMPACTING REUSE
N/A

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Related Publications

Bushmanova, E., Antipov, D., Lapidus, A., & Prjibelski, A. D. (2019). rnaSPAdes: a de novo transcriptome assembler and its application to RNA-Seq data. GigaScience, 8(9). https://doi.org/10.1093/gigascience/giz100
Software

Cantalapiedra, C. P., Hernández-Plaza, A., Letunic, I., Bork, P., & Huerta-Cepas, J. (2021). eggNOG-mapper v2: Functional Annotation, Orthology Assignments, and Domain Prediction at the Metagenomic Scale. Molecular Biology and Evolution, 38(12), 5825–5829. https://doi.org/10.1093/molbev/msab293
Software

Cook, C. C. Z., Ewton, E. M., Marchetti, A., Menden-Deuer, S., Millette, N. C., Slomka, S., Speciale, E. V., Wilken, S., & Cohen, N. R. (2025). Evaluating acidotropic dyes for detecting mixotrophy in protists: Insights from cultures and field communities. https://doi.org/10.1101/2025.09.29.679303
Methods

Federhen, S. (2011). The NCBI Taxonomy database. Nucleic Acids Research, 40(D1), D136–D143. https://doi.org/10.1093/nar/gkr1178
Related Research

Groussman, R. D., Blaskowski, S., Coesel, S. N., & Armbrust, E. V. (2023). MarFERReT, an open-source, version-controlled reference library of marine microbial eukaryote functional genes. Scientific Data, 10(1). https://doi.org/10.1038/s41597-023-02842-4
Software

Guillou, L., Bachar, D., Audic, S., Bass, D., Berney, C., Bittner, L., ... & Christen, R. (2012). The Protist Ribosomal Reference database (PR2): a catalog of unicellular eukaryote small sub-unit rRNA sequences with curated taxonomy. Nucleic acids research, 41(D1), D597-D604. https://doi.org/10.1093/nar/gks1160
General

Haas, B. J. (2023). TransDecoder (Version 5.7.1) [Computer software]. GitHub. https://github.com/TransDecoder/TransDecoder/releases/tag/TransDecoder-v5.7.1
Software

Kanehisa, M. (2000). KEGG: Kyoto Encyclopedia of Genes and Genomes. Nucleic Acids Research, 28(1), 27–30. doi:10.1093/nar/28.1.27
Methods

Krinos, A. I., Hu, S. K., Cohen, N. R., & Alexander, H. (2020). EUKulele: Taxonomic annotation of the unsung eukaryotic microbes (Version 1). arXiv. https://doi.org/10.48550/ARXIV.2011.00089
Software

Krueger, F. (2015). Trim Galore!: A wrapper around Cutadapt and FastQC to consistently apply adapter and quality trimming to FastQ files, with extra functionality for RRBS data. Babraham bioinformatics - trim galore! https://www.bioinformatics.babraham.ac.uk/projects/trim_galore/
Software

Li, W., & Godzik, A. (2006). Cd-hit: a fast program for clustering and comparing large sets of protein or nucleotide sequences. Bioinformatics, 22(13), 1658–1659. https://doi.org/10.1093/bioinformatics/btl158
Software

Love, M. I., Huber, W., & Anders, S. (2014). Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biology, 15(12). https://doi.org/10.1186/s13059-014-0550-8
Software

Martin, M. (2011). Cutadapt removes adapter sequences from high-throughput sequencing reads. EMBnet.journal, 17(1), 10. doi:10.14806/ej.17.1.200
Software

Mistry, J., Chuguransky, S., Williams, L., Qureshi, M., Salazar, G. A., Sonnhammer, E. L. L., Tosatto, S. C. E., Paladin, L., Raj, S., Richardson, L. J., Finn, R. D., & Bateman, A. (2020). Pfam: The protein families database in 2021. Nucleic Acids Research, 49(D1), D412–D419. https://doi.org/10.1093/nar/gkaa913

Methods

Mitra, A., Caron, D. A., Faure, E., Flynn, K. J., Leles, S. G., Hansen, P. J., McManus, G. B., Not, F., do Rosario Gomes, H., Santoferrara, L. F., Stoecker, D. K., & Tillmann, U. (2023). The Mixoplankton Database (MDB): Diversity of photo-phago-trophic plankton in form, function, and distribution across the global ocean. Journal of Eukaryotic Microbiology, 70(4). Portico. https://doi.org/10.1111/jeu.12972
Methods

Patro, R., Duggal, G., Love, M. I., Irizarry, R. A., & Kingsford, C. (2017). Salmon provides fast and bias-aware quantification of transcript expression. Nature Methods, 14(4), 417–419. doi:10.1038/nmeth.4197
Software

Pierce, E., Torano, O., Lin, Y., Schnetzer, A., & Marchetti, A. (2023). Comparison of advanced methodologies for diatom identification within dynamic coastal communities. Limnology and Oceanography: Methods, 21(11), 687–702. Portico. https://doi.org/10.1002/lom3.10575
Methods

Soneson, C., Love, M. I., & Robinson, M. D. (2016). Differential analyses for RNA-seq: transcript-level estimates improve gene-level inferences. F1000Research, 4, 1521. doi:10.12688/f1000research.7563.2
Methods

Speciale, E. V. (2026). Speciale-Metatranscriptomics [Computer software]. GitHub. https://github.com/emilyspeciale/Speciale-Metatranscriptomics
Methods

,
Software

Speciale, Emily. (2025). THE MOLECULAR PHYSIOLOGY OF MIXOTROPHIC PHYTOPLANKTON UNDER IRON-LIMITED UPWELLING CONDITIONS. The University of North Carolina at Chapel Hill University Libraries. https://doi.org/10.17615/C0G7-RP52 https://doi.org/10.17615/c0g7-rp52
Results

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Related Datasets

IsRelatedTo

Speciale, E., Marchetti, A., Lim, P., Jeong, Y., Cook, C., Cohen, N., McClure, W., Schnetzer, A. (2026) **KEGG gene differential expression data for mixotrophs and diatoms.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2026-08-13 http://lod.bco-dmo.org/id/dataset/1004689 [view at BCO-DMO]

Speciale, E., Marchetti, A., Lim, P., Jeong, Y., Cook, C., Cohen, N., McClure, W., Schnetzer, A. (2026) **KEGG pathway differential expression data for mixotrophs and diatoms.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2026-08-14 http://lod.bco-dmo.org/id/dataset/1004704 [view at BCO-DMO]

Speciale, E., Marchetti, A., Lim, P., Jeong, Y., Cook, C., Cohen, N., McClure, W., Schnetzer, A. (2026) **Pfam differential expression data for diatoms from an iron incubation experiment during the PUPCYCLE II R/V Sally Ride cruise within the California Current System in May and June of 2023.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2026-08-13 http://lod.bco-dmo.org/id/dataset/1004674 [view at BCO-DMO]

Speciale, E., Marchetti, A., Lim, P., Jeong, Y., Cook, C., Cohen, N., McClure, W., Schnetzer, A. (2026) **Physiological measurements from iron incubation experiment using upwelled waters in the California Current System during the PUPCYCLE II cruise in May and June 2023.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2026-08-11 http://lod.bco-dmo.org/id/dataset/994607 [view at BCO-DMO]

Speciale, E., Marchetti, A., Lim, P., Jeong, Y., Cook, C., Cohen, N., McClure, W., Schnetzer, A. (2026) **RNA taxonomy data from an iron incubation experiment during the PUPCYCLE II cruise (R/V Sally Ride) within the California Current System in May and June of 2023.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2026-08-12 http://lod.bco-dmo.org/id/dataset/1003525 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
Taxa_Group	Taxa group being targeted for differential expression analysis. All reads not mapping to the targeted taxa group were removed prior to analysis.	unitless
Timepoint	Timepoint identification (T1 or T2)	unitless
DE_Comparison	Treatments being targeted for differential expression analysis. This will always be +FevsDFB, representing the iron-replete vs iron-limited treatments.	unitless
Pfam_ID	Number ID of Pfam domain.	unitless
Pfam_Name	Short name of Pfam domain.	unitless
Pfam_Description	Long name of Pfam domain.	unitless
baseMean	The average expression level of the Pfam domain across all samples (normalized).	number of normalized reads
log2FoldChange	Base-2 logarithm of the ratio of normalized read abundance under the iron-amended (+Fe) treatment to normalized read abundance under the desferrioxamine B (DFB) treatment, calculated for each Pfam domain; log2(number of normalized reads in +Fe / number of normalized reads in DFB).	unitless
lfcSE	Standard error of log2FoldChange estimate.	unitless
stat	Test statistic used in Wald test to determine significance.	unitless
pvalue	Raw p-value from Wald test.	unitless
padj	The False Discovery Rate adjusted p-value using the Benjamini-Hochberg correction.	unitless
Gonyaulax	The number of normalized reads that the mixotroph genera Gonyaulax contributes to the Pfam domain.	number of normalized reads
Ochromonas	The number of normalized reads that the mixotroph genera Ochromonas contributes to the Pfam domain.	number of normalized reads

Alexandrium	The number of normalized reads that the mixotroph genera Alexandrium contributes to the Pfam domain.	number of normalized reads
Amphidinium	The number of normalized reads that the mixotroph genera Amphidinium contributes to the Pfam domain.	number of normalized reads
Calcidiscus	The number of normalized reads that the mixotroph genera Calcidiscus contributes to the Pfam domain.	number of normalized reads
Chattonella	The number of normalized reads that the mixotroph genera Chattonella contributes to the Pfam domain.	number of normalized reads
Chrysochromulina	The number of normalized reads that the mixotroph genera Chrysochromulina contributes to the Pfam domain.	number of normalized reads
Dinobryon	The number of normalized reads that the mixotroph genera Dinobryon contributes to the Pfam domain.	number of normalized reads
Emiliania	The number of normalized reads that the mixotroph genera Emiliania contributes to the Pfam domain.	number of normalized reads
Florenciella	The number of normalized reads that the mixotroph genera Florenciella contributes to the Pfam domain.	number of normalized reads
Gambierdiscus	The number of normalized reads that the mixotroph genera Gambierdiscus contributes to the Pfam domain.	number of normalized reads
Geminigera	The number of normalized reads that the mixotroph genera Geminigera contributes to the Pfam domain.	number of normalized reads
Gymnodinium	The number of normalized reads that the mixotroph genera Gymnodinium contributes to the Pfam domain.	number of normalized reads
Haptolina	The number of normalized reads that the mixotroph genera Haptolina contributes to the Pfam domain.	number of normalized reads
Heterocapsa	The number of normalized reads that the mixotroph genera Heterocapsa contributes to the Pfam domain.	number of normalized reads
Isochrysis	The number of normalized reads that the mixotroph genera Isochrysis contributes to the Pfam domain.	number of normalized reads

Karenia	The number of normalized reads that the mixotroph genera Karenia contributes to the Pfam domain.	number of normalized reads
Lingulodinium	The number of normalized reads that the mixotroph genera Lingulodinium contributes to the Pfam domain.	number of normalized reads
Micromonas	The number of normalized reads that the mixotroph genera Micromonas contributes to the Pfam domain.	number of normalized reads
Nephroselmis	The number of normalized reads that the mixotroph genera Nephroselmis contributes to the Pfam domain.	number of normalized reads
Pelagodinium	The number of normalized reads that the mixotroph genera Pelagodinium contributes to the Pfam domain.	number of normalized reads
Phaeocystis	The number of normalized reads that the mixotroph genera Phaeocystis contributes to the Pfam domain.	number of normalized reads
Prorocentrum	The number of normalized reads that the mixotroph genera Prorocentrum contributes to the Pfam domain.	number of normalized reads
Prymnesium	The number of normalized reads that the mixotroph genera Prymnesium contributes to the Pfam domain.	number of normalized reads
Pyramimonas	The number of normalized reads that the mixotroph genera Pyramimonas contributes to the Pfam domain.	number of normalized reads
Rhizochromulina	The number of normalized reads that the mixotroph genera Rhizochromulina contributes to the Pfam domain.	number of normalized reads
Scrippsiella	The number of normalized reads that the mixotroph genera Scrippsiella contributes to the Pfam domain.	number of normalized reads
Symbiodinium	The number of normalized reads that the mixotroph genera Symbiodinium contributes to the Pfam domain.	number of normalized reads
Triparma	The number of normalized reads that the mixotroph genera Triparma contributes to the Pfam domain.	number of normalized reads
Tripos	The number of normalized reads that the mixotroph genera Tripos contributes to the Pfam domain.	number of normalized reads
Mantoniella	The number of normalized reads that the mixotroph genera Mantoniella contributes to the Pfam domain.	number of normalized reads

Protoceratium	The number of normalized reads that the mixotroph genera Protoceratium contributes to the Pfam domain.	number of normalized reads
Pterosperma	The number of normalized reads that the mixotroph genera Pterosperma contributes to the Pfam domain.	number of normalized reads
Synchroma	The number of normalized reads that the mixotroph genera Synchroma contributes to the Pfam domain.	number of normalized reads
Fibrocapsa	The number of normalized reads that the mixotroph genera Fibrocapsa contributes to the Pfam domain.	number of normalized reads

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Instruments

Dataset-specific Instrument Name	Illumina HiSeq 4000
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Sequencing was performed on an Illumina HiSeq 4000 with a 2x150 bp configuration.
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

Dataset-specific Instrument Name	Sea Bird SBE 9 plus CTD
Generic Instrument Name	Sea-Bird SBE 9plus CTD
Generic Instrument Description	High precision and accuracy CTD comprising an SBE 9plus underwater unit (SBE 3plus temperature, SBE 4C conductivity, and Paroscientific Digiquartz pressure sensors, and an SBE 5T submersible pump). Can be used for either real-time data acquisition or for autonomous operations at a sampling speed of up to 24 Hz. The instrument package also includes a TC duct, to reduce salinity spiking caused by ship heave for improved resolution of water column features, and to ensure that temperature and conductivity measurements are made on the same parcel of water. Supplied with both an aluminium and titanium main housing, allowing for use up to 6800 and 10,500 metre depths respectively. Also capable of measuring from eight auxiliary sensors.

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Deployments

SR2311

Website	https://www.bco-dmo.org/deployment/994610
Platform	R/V Sally Ride
Start Date	2023-05-29
End Date	2023-06-10
Description	California Current System, off the southern coast of Oregon at 43°02'42.7"N, 124°33'07.2"W, depth 55m

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Project Information

CAREER: An integrated molecular and physiological approach to examining the dynamics of upwelled phytoplankton in current and changing oceans (Upwelled Phytoplankton Dynamics)

Coverage: California Upwelling Zone

NSF Award Abstract:
Upwelling zones are hotspots of photosynthesis that are very dynamic in space and time. Microsocopic algae, known as phytoplankton, bloom when deep, nutrient-rich waters are upwelled into sunlit surface layers of the ocean, providing nourishment that supports productive food webs and draws down carbon dioxide (CO2) from the atmosphere to the deep ocean. Photosynthetic microbes in these regions must constantly adapt to changes in their chemical and physical environments. For example, subsurface populations respond to changes in light as they approach the surface. When upwelled waters move offshore, cells sink out of the illuminated zone, establishing seed populations that remain inactive until the next upwelling event. This process is called the upwelling conveyor belt cycle (UCBC). How phytoplankton respond to these changes in environmental conditions and how they may influence their nutrient requirements remains unknown. With future ocean changes predicted to alter seawater chemistry, including ocean acidification and decreased iron availability, some phytoplankton groups may be more vulnerable than others. Accompanying educational activities provide learning experiences to enhance understanding and awareness of marine microbes. The development of a research hub at UNC aims to provide infrastructure and support for scientists and students conducting research on environmental genomics. A laboratory component for an upper-level undergraduate course focused on marine phytoplankton is being developed. Educational outreach activities to broader communities include creation of a lesson plan on phytoplankton in upwelling zones and a virtual research cruise experience for middle-school students, as well as a hands-on lab activity for a local museum focused on marine phytoplankton and the important roles they play in shaping our planet.

The project examines how phytoplankton respond at the molecular and physiological level to the different UCBC stages, which seed populations (i.e., surface versus subsurface) contribute most to phytoplankton blooms during upwelling events of varying intensity, how phytoplankton elemental compositions are altered throughout UCBC stages, and how future predicted ocean conditions will affect the phytoplankton responses to UCBC conditions. This project contains both laboratory and fieldwork. In the laboratory, phytoplankton isolates recently obtained from upwelling regions are exposed to simulated UCBC conditions to examine changes in gene expression, growth and photosynthetic characteristics and elemental composition. Cultures are subjected to both current and future ocean conditions, including reduced iron availability and higher CO2. In the field, research cruises within upwelling regions study the dynamics of natural phytoplankton communities (both surface and subsurface) experiencing upwelling and relaxation and within simulated upwelling incubation experiments. Knowledge of how phytoplankton are affected by UCBC conditions at an integrated molecular, physiological and elemental level under both current and future scenarios is imperative for the proper conservation and management of these critically important ecosystems.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1751805

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