

# NCBI project accession and library information on each sample analyzed in upwelling experiments conducted on two phytoplankton species isolated from the California Upwelling Zone

**Website:** <https://www.bco-dmo.org/dataset/826494>

**Data Type:** experimental

**Version:** 1

**Version Date:** 2021-03-17

## 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
<a href="#">Marchetti, Adrian</a>	University of North Carolina at Chapel Hill (UNC-Chapel Hill)	Principal Investigator
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## Abstract

Two phytoplankton species, isolated from the California Upwelling Zone - *Chaetoceros decipiens* (UNC1416) and *Emiliana Huxleyi* (UNC1419) - were cultured at 12 degrees Celsius in artificial Aquil\* medium using trace metal clean (TMC) techniques. Upwelling conveyor belt cycle (UCBC) simulations were performed by transitioning the cultures to different nutrient and light regimes. RNA transcriptome libraries were created using the Illumina TruSeq Stranded mRNA Library Preparation Kit for *C. decipiens*, and the KAPA stranded mRNA-Seq kit for Illumina platforms for *E. huxleyi*. Samples were sequenced on an Illumina MiSeq. This dataset includes the NCBI project accession and library information on each sample analyzed in the upwelling experiments.

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## Coverage

**Temporal Extent:** 2017-01 - 2017-09

## Methods & Sampling

**Methodology:** (see related dataset for the discrete raw measurements from the experiment)

Two phytoplankton species, *Chaetoceros decipiens* (UNC1416) and *Emiliana huxleyi* (UNC1419), were cultured at 12 °C in artificial Aquil\* medium using trace metal clean (TMC) techniques. Macronutrients were supplied such that nitrate would become limiting for growth (50  $\mu\text{mol L}^{-1}$   $\text{NO}_3$ , 10  $\mu\text{mol L}^{-1}$   $\text{PO}_4$ , 200  $\mu\text{mol L}^{-1}$   $\text{H}_4\text{SiO}_4$ ) and two iron treatments were used (1370  $\text{nmol L}^{-1}$  and 3.1  $\text{nmol L}^{-1}$  total Fe). Upwelling conveyor belt cycle (UCBC) simulations were performed by transitioning the cultures to different nutrient and light regimes. They were grown by first growing the cultures with ample light (115  $\mu\text{mol photons m}^{-2}\text{s}^{-1}$ ) until nitrate depletion and stationary phase growth. Cultures were then moved to no light for 10 days to simulate the sinking out of the

euphotic zone. After this dark period, the cultures were subsequently transferred back to fresh medium under ambient light levels, and grown until stationary phase again. Samples were collected for six different time points associated with the different phases throughout the simulated upwelling cycle.

### **Sampling:**

Cell counts – 5 mL samples was preserved in 2% Lugol's solution in glass vials. Cells were then enumerated on an Olympus CKX41 inverted microscope using a 1 mL Sedgwick-Rafter counting chamber after allowing the cells to settle for five minutes and counting a minimum of 300 cells within 10-30 fields of view.

Chlorophyll – 50 mL of sample was filtered through 0.45 µm mixed cellulose ester filters under gentle vacuum pressure (< 100 mm Hg) and frozen at -80 °C immediately. Extraction was performed using 90% acetone at -20 °C for 24 hours and measured using a Turner 10-AU fluorometer (Parsons et al., 1984)

$F_v:F_m$  – The maximum photochemical yield of photosystem II ( $F_v:F_m$ ) was measured using the Satlantic FIRE (Gorbunov & Falkowski, 2005; Kolber et al., 1998). Samples were acclimated to low light for 20 minutes prior to the measurements. Data were blank corrected using microwave-sterilized Aquil medium. The resulting  $F_v:F_m$  was derived from the induction profile using a saturating pulse (Single Turnover Flash; 20,000 µmol photons  $m^{-2}s^{-1}$ ) for a duration of 100 µs. The gain was optimized for each sample (400, 600, or 800), and the average of 50 iterations was obtained.

Particulate carbon and nitrogen – 50 mL of sample was vacuum-filtered onto pre-combusted GF/F filters. Filters were then immediately stored in Petri dishes at -20 °C, and dried at 65 °C for 24 hours before being pelleted. Total nitrogen and carbon were quantified with a Costech 4010 CHNOS Elemental Combustion system according to U.S. Environmental Protection Agency Method 440.0 (Zimmermann et al., 1997). Three blanks were run alongside the samples and were all below the detection limits (0.005 mg N and 0.071 mg C). Carbon and nitrogen per cell were calculated by dividing particulate carbon and nitrogen concentration by cell concentration.

Dissolved nitrate and nitrite – Filtrate from the 0.45 µm filters used for RNA was transferred to polypropylene tubes and immediately frozen at -80 °C. Dissolved nitrate + nitrite ( $NO_3 + NO_2$ ) concentrations were quantified with an OI Analytical Flow Solutions IV auto analyzer according to EPA method 353.4 (Zhang et al., 1997). The detection limit for  $NO_3 + NO_2$  was 0.2 µmol  $L^{-1}$ .

RNA Extraction – 300 mL of sample was filtered onto 0.45 µm Pall Supor polyethersulfone filters (47 mm) filters using gentle vacuum pressure and immediately frozen and stored at -80 °C. Total RNA was extracted using RNAqueous-4PCR Total RNA Isolation Kit for

*Chaetoceros* cultures, and TRIzol reagent for *E. huxleyi* cultures. RNA was then purified and examined for quality and quantity using a Nanodrop spectrophotometer.

### **Analysis:**

RNA libraries were constructed using a custom protocol for 3' poly-A-directed mRNA-seq (also known as TagSeq) based on Meyer et al. (2011) and adapted for Illumina HiSeq based on Lohman et al. (2016) and Strader et al. (2016). For most samples 1 µg but as low as 250 ng of total RNA were fragmented by incubating at 95 °C for 15 min.

First strand cDNA was synthesized with SMARTScribe Reverse Transcriptase (Takara Bio, Mountain View, CA, USA), an oligo-dT primer, and template switching to attach known sequences to each end of the poly-A mRNA fragments. cDNA was then amplified with a PCR reaction consisting of 32 µL sterile  $H_2O$ , 5 µL dNTPs (2.5 mM each), 5 µL 10X Titanium Taq Buffer (Takara Bio), 1 µL of each primer (10 µM) designed amplify the sequences attached during cDNA synthesis, and 1 µL of Titanium Taq DNA Polymerase (Takara Bio). The PCR was run with an initial denaturing step at 95 °C for 5 min, then 17 cycles consisting of 95 °C for 1 min, 63 °C for 2 min, and 72 °C for 2 min. cDNA amplification was then verified on a 1% agarose gel and purified with the QiaQuick PCR Purification Kit (Qiagen). cDNA was quantified with the Quant-iT dsDNA High-Sensitivity Assay (Invitrogen) and cDNA concentrations were then normalized to the same volume.

Samples were then barcoded with a PCR reaction consisting of 11 µL sterile  $H_2O$ , 3 µL dNTPs (2.5 mM each), 3 µL 10X Titanium Taq Buffer (Takara Bio), 0.6 µL TruSeq Universal Primer (10 µM), 6 µL barcoding primer (1 µM), Titanium Taq Polymerase (Takara Bio), and 6 µL of purified cDNA with an initial denaturing step at 95 °C for 5 min, then 5 cycles consisting of 95 °C for 40 s, 63 °C for 2 min, and 72 °C for 1 min. Samples were barcoded from both ends using unique combinations of 6 bp sequences on both the TruSeq universal primer and barcoding primers. Products were then again confirmed on a 2% agarose gel and combined into small pools of 6-8 samples. The 400-500 bp region of these pools was extracted with the QIAquick Gel Extraction Kit (Qiagen), quantified with the Quant-iT dsDNA High-Sensitive Assay, and then mixed in equal proportions. The

library was sequenced at the University of Texas at Austin Genomic Sequencing and Analysis Facility on Illumina HiSeq 2500 (three lanes, single-end 50bp reads) with a 15% PhiX spike-in to target approximately 8 million reads per sample.

## Data Processing Description

### The following were used for data processing:

Trimmomatic v0.36  
Trinity v2.5.1  
CD-HIT-EST v4.7  
KEGG (Release 86.0)  
UniProt (Release 2018\_03)  
PhyloDB (v1.076)  
BLASTP v2.7.1  
Pfam 31.0  
HMMER v3.1b2

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## Data Files

File
<b>SRA.csv</b> (Comma Separated Values (.csv), 12.55 KB) MD5:30bf9a91b6f4b89b43d0176041f2d637 Primary data file for dataset ID 826494

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## Related Publications

Barwell-Clarke, J. & Whitney, Frank. (1996). IOS nutrient methods and analysis. Can Tech Rep Hydrog Ocean Sci. 182. 1-43.

*Methods*

Bertrand, E. M., McCrow, J. P., Moustafa, A., Zheng, H., McQuaid, J. B., Delmont, T. O., ... Allen, A. E. (2015). Phytoplankton-bacterial interactions mediate micronutrient colimitation at the coastal Antarctic sea ice edge. Proceedings of the National Academy of Sciences, 112(32), 9938-9943. doi:[10.1073/pnas.1501615112](https://doi.org/10.1073/pnas.1501615112)

*Methods*

Bolger, A. M., Lohse, M., & Usadel, B. (2014). Trimmomatic: a flexible trimmer for Illumina sequence data. Bioinformatics, 30(15), 2114-2120. doi:[10.1093/bioinformatics/btu170](https://doi.org/10.1093/bioinformatics/btu170)

*Methods*

Dixon, G. B., Davies, S. W., Aglyamova, G. V., Meyer, E., Bay, L. K., & Matz, M. V. (2015). Genomic determinants of coral heat tolerance across latitudes. Science, 348(6242), 1460-1462.

doi:[10.1126/science.1261224](https://doi.org/10.1126/science.1261224)

*Methods*

El-Gebali, S., Mistry, J., Bateman, A., Eddy, S. R., Luciani, A., Potter, S. C., ... Finn, R. D. (2018). The Pfam protein families database in 2019. Nucleic Acids Research, 47(D1), D427-D432. doi:[10.1093/nar/gky995](https://doi.org/10.1093/nar/gky995)

*Methods*

Fu, L., Niu, B., Zhu, Z., Wu, S., & Li, W. (2012). CD-HIT: accelerated for clustering the next-generation sequencing data. Bioinformatics, 28(23), 3150-3152. doi:[10.1093/bioinformatics/bts565](https://doi.org/10.1093/bioinformatics/bts565)

*Methods*

Gorbunov, M. Y., & Falkowski, P. G. (2004, August). Fluorescence induction and relaxation (FIRE) technique and instrumentation for monitoring photosynthetic processes and primary production in aquatic ecosystems. In 13th International Congress of Photosynthesis (Vol. 2, pp. 1029-1031). Montreal, QC: Allen Press.

*Methods*

Grabherr, M. G., Haas, B. J., Yassour, M., Levin, J. Z., Thompson, D. A., Amit, I., ... Regev, A. (2011). Full-length transcriptome assembly from RNA-Seq data without a reference genome. *Nature Biotechnology*, 29(7), 644–652. doi:[10.1038/nbt.1883](https://doi.org/10.1038/nbt.1883)

*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](https://doi.org/10.1093/nar/28.1.27)

*Methods*

Kolber, Z. S., Prášil, O., & Falkowski, P. G. (1998). Measurements of variable chlorophyll fluorescence using fast repetition rate techniques: defining methodology and experimental protocols. *Biochimica et Biophysica Acta (BBA) - Bioenergetics*, 1367(1-3), 88–106. doi:[10.1016/s0005-2728\(98\)00135-2](https://doi.org/10.1016/s0005-2728(98)00135-2)

*General*

Lampe, R. H., Hernandez, G., Lin, Y. Y., & Marchetti, A. (2020). Representative diatom and coccolithophore species exhibit divergent responses throughout simulated upwelling cycles. doi:[10.1101/2020.04.30.071480](https://doi.org/10.1101/2020.04.30.071480)

*Results*

Lohman, B. K., Weber, J. N., & Bolnick, D. I. (2016). Evaluation of TagSeq, a reliable low-cost alternative for RNAseq. *Molecular Ecology Resources*, 16(6), 1315–1321. doi:[10.1111/1755-0998.12529](https://doi.org/10.1111/1755-0998.12529)

*Methods*

Meyer, E., Aglyamova, G. V., & Matz, M. V. (2011). Profiling gene expression responses of coral larvae (*Acropora millepora*) to elevated temperature and settlement inducers using a novel RNA-Seq procedure. *Molecular Ecology*. doi:10.1111/j.1365-294x.2011.05205.x <https://doi.org/10.1111/j.1365-294X.2011.05205.x>

*Methods*

Parsons, T. R., Y. Maita, and C. M. Lalli. "A Manual of Chemical and Biological Methods of Seawater Analysis", Pergamon Press (1984). ISBN: [9780080302874](https://doi.org/9780080302874)

*Methods*

Strader, M. E., Aglyamova, G. V., & Matz, M. V. (2016). Red fluorescence in coral larvae is associated with a diapause-like state. *Molecular Ecology*, 25(2), 559–569. doi:[10.1111/mec.13488](https://doi.org/10.1111/mec.13488)

*Methods*

Tang, S., Lomsadze, A., & Borodovsky, M. (2015). Identification of protein coding regions in RNA transcripts. *Nucleic Acids Research*, 43(12), e78–e78. doi:[10.1093/nar/gkv227](https://doi.org/10.1093/nar/gkv227)

*Methods*

The UniProt Consortium (2016). UniProt: the universal protein knowledgebase. *Nucleic Acids Research*, 45(D1), D158–D169. doi:[10.1093/nar/gkw1099](https://doi.org/10.1093/nar/gkw1099)

*Methods*

Zhang J., Ortner P. B., Fischer C. J. (1997). Determination of Nitrate and Nitrite in Estuarine and Coastal Waters by Gas Segmented Continuous Flow Colorimetric Analysis. National Exposure Research Laboratory Office of Research and Development US Environmental Protection Agency Cincinnati. Method 353.4. URL: <https://nepis.epa.gov/Exe/ZyPURL.cgi?Dockkey=P100PDOG.txt>

*Methods*

Zimmerman, C. F., C. W. Keefe, & J. Bashe. (1997). Method 440.0 Determination of Carbon and Nitrogen in Sediments and Particulates of Estuarine/Coastal Waters Using Elemental Analysis. U.S. Environmental Protection Agency, Washington, DC, EPA/600/R-15/009.

*Methods*

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## Related Datasets

### Is Supplement To

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Marchetti, A. (2021) **Discrete raw measurements from upwelling experiments conducted on two phytoplankton species isolated from the California Upwelling Zone**. Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2020-10-13  
doi:10.26008/1912/bco-dmo.826448.1 [[view at BCO-DMO](#)]

*Relationship Description: Both datasets are the result of the same upwelling experiment.*

University of North Carolina at Chapel Hill. Simulated upwelling conveyer belt cycle experiments with *Chaetoceros decipiens*. 2019/01. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: <http://www.ncbi.nlm.nih.gov/bioproject/PRJNA513340>. NCBI:BioProject: PRJNA513340.

University of North Carolina at Chapel Hill. Simulated upwelling conveyer belt cycle experiments with *Emiliana huxleyi*. 2019/01. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: <http://www.ncbi.nlm.nih.gov/bioproject/PRJNA514092>. NCBI:BioProject: PRJNA514092.

## References

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Lampe, R., & Marchetti, A. (2020). *Chaetoceros decipiens* (UNC1416) reference transcriptome [Data set]. Zenodo. <https://doi.org/10.5281/ZENODO.3747717> <https://doi.org/10.5281/zenodo.3747717>

Lampe, R., & Marchetti, A. (2020). *Emiliana huxleyi* (UNC1419) reference transcriptome [Data set]. Zenodo. <https://doi.org/10.5281/ZENODO.3747989> <https://doi.org/10.5281/zenodo.3747989>

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## Parameters

Parameter	Description	Units
bioproject_accession	NCBI BioProject Accession; typically of the form PRJNA[number].	unitless
sample_name	NCBI BioSample name.	unitless
library_ID	Short unique identifier for the sequencing library.	unitless
title	Short description	unitless
library_strategy	Library strategy; RNA-Seq = Random sequencing of whole transcriptome	unitless
library_source	Library source; TRANSCRIPTOMIC = Transcription products or non genomic DNA (EST, cDNA, RT-PCR, screened libraries)	unitless
library_selection	Library selection; other = see design_description	unitless
library_layout	Paired-end or single.	unitless
platform	Platform	unitless
instrument_model	Instrument model	unitless
design_description	Free-form description of the methods used to create the sequencing library; a brief 'materials and methods' section.	unitless
filetype	Type of file	unitless
filename	Name of the fastq file	unitless

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## Instruments

<b>Dataset-specific Instrument Name</b>	Illumina MiSeq
<b>Generic Instrument Name</b>	Automated DNA Sequencer
<b>Dataset-specific Description</b>	Samples were sequenced on an Illumina MiSeq.
<b>Generic Instrument Description</b>	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

<b>Dataset-specific Instrument Name</b>	Costech 4010
<b>Generic Instrument Name</b>	Costech International Elemental Combustion System (ECS) 4010
<b>Dataset-specific Description</b>	Total nitrogen and carbon were quantified with a Costech 4010 CHNOS Elemental Combustion system according to U.S. Environmental Protection Agency Method 440.0 (Zimmermann et al., 1997).
<b>Generic Instrument Description</b>	The ECS 4010 Nitrogen / Protein Analyzer is an elemental combustion analyser for CHNSO elemental analysis and Nitrogen / Protein determination. The GC oven and separation column have a temperature range of 30-110 degC, with control of +/- 0.1 degC.

<b>Dataset-specific Instrument Name</b>	Olympus CKX41 inverted microscope
<b>Generic Instrument Name</b>	Inverted Microscope
<b>Dataset-specific Description</b>	Cells were enumerated using a Sedgwick-Rafter counting chamber on an Olympus CKX41 inverted microscope.
<b>Generic Instrument Description</b>	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.

<b>Dataset-specific Instrument Name</b>	Astoria Analyzer
<b>Generic Instrument Name</b>	Nutrient Autoanalyzer
<b>Dataset-specific Description</b>	Dissolved nitrate and nitrite was quantified with an Astoria Analyzer.
<b>Generic Instrument Description</b>	Nutrient Autoanalyzer is a generic term used when specific type, make and model were not specified. In general, a Nutrient Autoanalyzer is an automated flow-thru system for doing nutrient analysis (nitrate, ammonium, orthophosphate, and silicate) on seawater samples.

<b>Dataset-specific Instrument Name</b>	Satlantic FIRE
<b>Generic Instrument Name</b>	Satlantic Fluorescence Induction and Relaxation of Emission Spectrometer
<b>Dataset-specific Description</b>	Fv:Fm was measured by the Satlantic FIRE (Fluorescence Induction and Relaxation System).
<b>Generic Instrument Description</b>	The Satlantic FIRE (Fluorescence Induction and Relaxation) System is a bio-optical technology used to measure variable chlorophyll fluorescence in photosynthetic organisms. Based on the Fast Repetition Rate Fluorometry (FRRF) technique, the FIRE was developed in collaboration with Dr. Maxim Gorbunov and Dr. Paul Falkowski from Rutgers University. More information on FIRE (PDF).

<b>Dataset-specific Instrument Name</b>	Nanodrop 2000
<b>Generic Instrument Name</b>	Spectrophotometer
<b>Dataset-specific Description</b>	RNA was purified and examined for quality and quantity using a Nanodrop 2000 spectrophotometer (Thermo Fisher Scientific, Waltham, MA, USA).
<b>Generic Instrument Description</b>	An instrument used to measure the relative absorption of electromagnetic radiation of different wavelengths in the near infra-red, visible and ultraviolet wavebands by samples.

<b>Dataset-specific Instrument Name</b>	Turner 10-AU fluorometer
<b>Generic Instrument Name</b>	Turner Designs Fluorometer 10-AU
<b>Dataset-specific Description</b>	Chlorophyll was measured using a Turner 10-AU fluorometer.
<b>Generic Instrument Description</b>	The Turner Designs 10-AU Field Fluorometer is used to measure Chlorophyll fluorescence. The 10AU Fluorometer can be set up for continuous-flow monitoring or discrete sample analyses. A variety of compounds can be measured using application-specific optical filters available from the manufacturer (read more from Turner Designs, turnerdesigns.com, Sunnyvale, CA, USA).

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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. Microscopic 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 (CO<sub>2</sub>) 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 CO<sub>2</sub>. 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
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1751805</a>

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