# Chlorophyll a and flow cytometry data from bi-weekly vertical profiles in Resurrection Bay, AK from January to March of 2023 from bi-weekly vertical profiles in Resurrection Bay, AK from January to March of 2023

**Website**: https://www.bco-dmo.org/dataset/954173
**Version**: 1
**Version Date**: 2025-02-21

**Project**
» Collaborative Research: Zooplankton restarts in a high-latitude marine ecosystem: species-specific recruitment and development in early spring (Zooplankton recruitment)



| Contributors | Affiliation | Role |
|---|---|---|
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**Abstract**
The Gulf of Alaska is a highly seasonal environment that is characterized by an order-of-magnitude increase in copepod biomass in the photic zone between winter and spring. The study focused on copepod recruitment to characterize species-specific naupliar production. Concurrent environmental monitoring included measurements of chlorophyll α and flow cytometry as indicators of prey field. Bi-weekly vertical profiles of temperature, salinity and fluorescence were recorded at an established station (RES2.5) in Resurrection Bay, AK. Discrete water samples were obtained for size-fractionated chlorophyll α samples and cell counts using flow cytometry. The water column was stratified by salinity with the lowest salinities recorded in the surface layer. A moderate increase in chlorophyll α concentrations occurred during March prior to the spring phytoplankton bloom.

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## Coverage

**Location**: Gulf of Alaska, sub-arctic Pacific
**Spatial Extent**: **Lat**:60.025 **Lon**:-149.3583
**Temporal Extent**: 2023-01-05 - 2023-03-24

### Methods & Sampling

Samples were collected in Resurrection Bay within the inner basin at RES2.5 (60° 1.5' N, 149° 21.5' W; 298 m deep) at approximately biweekly intervals aboard the R/V Nanuq between January 5th and March 24th, 2023. Collection and sample processing are described in detail in Block (2024). Water was collected at discrete

depths (surface, 10, 20, 30, 40, 50, 150, and 280 m) using 4-L Niskin Bottles. Two casts were required to collect all water samples, since only six Niskin bottles were mounted on an SBE55 rosette. Water samples were stored in dark Nalgene bottles in a cooler.

Chlorophyll α samples were size fractionated to estimate the chlorophyll α contribution of pico- and nano-phytoplankton (< 20 µm size fraction) and larger phytoplankton (including diatoms plus larger photosynthetic dinoflagellates) (> 20 µm size fraction) at 10-m intervals from the surface to 50 m for each sample time point. Polycarbonate (47-mm diameter, 20-µm pore size) and glass fiber (25-mm diameter, 0.7-µm pore size) filters were used to size fractionate 250 mL samples using a serial filtration vacuum manifold system (Strom et al., 2016). Filters were extracted in 90% acetone for 24 hours in the dark at -20°C. Fluorescence was measured using a Turner 10-AU fluorometer using the acidification method (Strom et al., 2016). Fluorescence measurements were converted to estimated chlorophyll α concentrations (µg/L) (Lorenzen, 1966). Integrated chlorophyll α (mg/m2) was calculated using trapezoidal integration (Strom et al., 2016).

Synechococcus, photosynthetic picoeukaryotes, and heterotrophic bacterial abundances were measured using flow cytometry at 8 depths (surface, 10, 20, 30, 40, 50, 150, and 280 m). Samples (1 ml) from each depth were preserved with paraformaldehyde to a final concentration of 0.5%, frozen initially at -40°C, and later transferred to -80°C until batch analysis. Samples were thawed, stained with Hoechst 34580 (1 µg/mL final concentration), and analyzed with a Beckman Coulter CytoFLEX S flow cytometer (Selph, 2021). Data were processed using FlowJo software (version 10.8.2). Synechococcus and picoeukaryote abundances were converted to carbon biomass using cellular carbon content estimates appropriate for the region (200 and 1,490 fg C per cell, respectively) (Strom et al., 2016).

**Data Processing Description**

Flow cytometry data were processed using FlowJo software (version 10.8.2). Synechococcus and picoeukaryote abundances were converted to carbon biomass using cellular carbon content estimates appropriate for the region (200 and 1,490 fg C per cell, respectively) (O'Hara, 2023, Strom et al. 2016).

**BCO-DMO Processing Description**

* Sheet 1 of submitted file "NaupProj2023_chla_flowc_BCODMO.csv
" was imported into the BCO-DMO data system for this dataset. Values "NA" imported as missing data values.
Table will appear as Data File: 954173_v1_chl-a-flow-cyto.csv (along with other download format options).

Missing Data Identifiers:
* In the BCO-DMO data system missing data identifiers are displayed according to the format of data you access. For example, in csv files it will be blank (null) values. In Matlab .mat files it will be NaN values. When viewing data online at BCO-DMO, the missing value will be shown as blank (null) values.

**Problem Description**

On January 20th, chlorophyll and flow cytometry samples were not collected at 0, 20, and 40 m depths due to abbreviated sampling.
January 20th 0 m chlorophyll-a sample was not size fractionated due to filter malfunction.
No chlorophyll samples were collected on January 27th. Only flow cytometry samples.
February 7th 20 m Niskin bottle misfired, therefore there is no sample for chlorophyll or flow cytometry.

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## Related Publications

Block, L. N. (2024). Evaluating Species-Specific Naupliar Recruitment During the Winter-to-Spring Transition in the Northern Gulf of Alaska Using Molecular Tools (Master's thesis, University of Hawai'i at Manoa). Available from https://hdl.handle.net/10125/108679
*Results*

FlowJo, LLC (n.d.) FlowJo™ Software Version 10.8 [software application] Becton, Dickinson and Company. https://docs.flowjo.com/flowjo/getting-acquainted/10-8-release-notes/10-8-exhaustive-release-notes/
*Software*

FlowJo, LLC. (2023) FlowJo™ Software Version 10.6 [software application] Becton, Dickinson and Company. https://docs.flowjo.com/flowjo/getting-acquainted/10-6-release-notes/10-6-exhaustive-release-notes/
*Software*

Lorenzen, C. J. (1966). A method for the continuous measurement of in vivo chlorophyll concentration. Deep Sea Research and Oceanographic Abstracts, 13(2), 223–227. doi:10.1016/0011-7471(66)91102-8
*Methods*

O'Hara, Megan, "Distribution and Mixotrophy of Cryptophyte Phytoplankton in the Northern Gulf of Alaska" (2023). WWU Graduate School Collection. 1152. https://cedar.wwu.edu/wwuet/1152
*Methods*

Selph, K. E. (2021). Enumeration of marine microbial organisms by flow cytometry using near-UV excitation of Hoechst 34580-stained DNA. Limnology and Oceanography: Methods, 19(10), 692–701. Portico. https://doi.org/10.1002/lom3.10454
*Methods*

Strom, S. L., Fredrickson, K. A., & Bright, K. J. (2016). Spring phytoplankton in the eastern coastal Gulf of Alaska: Photosynthesis and production during high and low bloom years. Deep Sea Research Part II: Topical Studies in Oceanography, 132, 107–121. https://doi.org/10.1016/j.dsr2.2015.05.003
*Methods*

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## Related Datasets

### IsRelatedTo

Block, L. N., Lenz, P. H. (2025) **CTD (temperature, salinity and fluorescence) from bi-weekly vertical profiles in Resurrection Bay, AK from January to March of 2023.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2025-02-21 http://lod.bco-dmo.org/id/dataset/954156 [view at BCO-DMO]
*Relationship Description: Related data collected as part of the same study published in Block, L. N. (2024, https://hdl.handle.net/10125/108679).*

Block, L. N., Lenz, P. H. (2025) **Microplankton microscopy and biovolume analysis from Lugol's samples collected in Resurrection Bay, AK from January to March of 2023.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2025-02-21 http://lod.bco-dmo.org/id/dataset/954189 [view at BCO-DMO]
*Relationship Description: Related data collected as part of the same study published in Block, L. N. (2024, https://hdl.handle.net/10125/108679).*

Block, L. N., Lenz, P. H. (2025) **Molecular identification of genetic variants of Neocalanus flemingeri in the Gulf of Alaska from samples collected from 2015 to 2023.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2025-02-21 http://lod.bco-dmo.org/id/dataset/954181 [view at BCO-DMO]
*Relationship Description: Related data collected as part of the same study published in Block, L. N. (2024, https://hdl.handle.net/10125/108679).*

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## Parameters

| Parameter | Description | Units |
|---|---|---|
| cruise | description | unitless |
| date | Date (Local time) in ISO 8601 format yyyy-mm-dd | unitless |
| station | Station ID | unitless |
| latitude | Station latitude, north is positive | decimal degrees |
| longitude | Station latitude, west is negative | decimal degrees |
| cast | Sequential cast number per cruise | unitless |
| niskin | Niskin bottle used for sample collection | unitless |
| depth | Target water collection depth | Meters (m) |
| chla_gt_20 | Size fractionated chlorophyll-a concentration greater than 20 um | Micrograms per liter (ug/L) |
| chla_lt_20 | Size fractionated chlorophyll-a concentration less than 20 um | Micrograms per liter (ug/L) |
| chla_total | Total chlorophyll-a concentration (>20 um + <20 um) | Micrograms per liter (ug/L) |
| phaeo_gt_20 | Size fractionated phaeopigment concentration greater than 20 um | Micrograms per liter (ug/L) |
| phaeo_lt_20 | Size fractionated phaeopigment concentration less than 20 um | Micrograms per liter (ug/L) |
| phaeo_total | Total phaeopigment concentration (>20 um + <20 um) | Micrograms per liter (ug/L) |
| hbact | Heterotrophic bacterial abundance | Number per milliliter (#/mL) |
| syn | Synechococcus abundance | Number per milliliter (#/mL) |
| peuk | Photosynthetic eukaryote abundance | Number per milliliter (#/mL) |

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## Instruments

| | |
|---|---|
| **Dataset-specific Instrument Name** | SBE55 |
| **Generic Instrument Name** | CTD - profiler |
| **Dataset-specific Description** | SBE55 rosette with 6 4-L Niskin Bottles |
| **Generic Instrument Description** | The Conductivity, Temperature, Depth (CTD) unit is an integrated instrument package designed to measure the conductivity, temperature, and pressure (depth) of the water column. The instrument is lowered via cable through the water column. It permits scientists to observe the physical properties in real-time via a conducting cable, which is typically connected to a CTD to a deck unit and computer on a ship. The CTD is often configured with additional optional sensors including fluorometers, transmissometers and/or radiometers. It is often combined with a Rosette of water sampling bottles (e.g. Niskin, GO-FLO) for collecting discrete water samples during the cast. This term applies to profiling CTDs. For fixed CTDs, see https://www.bco-dmo.org/instrument/869934. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | Beckman Coulter CytoFLEX S flow cytometer |
| **Generic Instrument Name** | Flow Cytometer |
| **Generic Instrument Description** | Flow cytometers (FC or FCM) are automated instruments that quantitate properties of single cells, one cell at a time. They can measure cell size, cell granularity, the amounts of cell components such as total DNA, newly synthesized DNA, gene expression as the amount messenger RNA for a particular gene, amounts of specific surface receptors, amounts of intracellular proteins, or transient signalling events in living cells. (from: http://www.bio.umass.edu/micro/immunology/facs542/facswhat.htm) |

| | |
|---|---|
| **Dataset-specific Instrument Name** | |
| **Generic Instrument Name** | Niskin bottle |
| **Dataset-specific Description** | SBE55 rosette with 6 4-L Niskin Bottles |
| **Generic Instrument Description** | A Niskin bottle (a next generation water sampler based on the Nansen bottle) is a cylindrical, non-metallic water collection device with stoppers at both ends. The bottles can be attached individually on a hydrowire or deployed in 12, 24, or 36 bottle Rosette systems mounted on a frame and combined with a CTD. Niskin bottles are used to collect discrete water samples for a range of measurements including pigments, nutrients, plankton, etc. |

| | |
|---|---|
| **Dataset-specific Instrument Name** | |
| **Generic Instrument Name** | Turner Designs Fluorometer 10-AU |
| **Generic Instrument Description** | 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

**Collaborative Research: Zooplankton restarts in a high-latitude marine ecosystem: species-specific recruitment and development in early spring (Zooplankton recruitment)**

**Coverage**: Sub-arctic marine ecosystem, Gulf of Alaska

**NSF Award Abstract**
Global climate change and associated extreme weather events are increasingly impacting marine communities at all trophic levels and leading to shifts in the timing of life history events. This project is investigating the annual restart of the spring zooplankton community in the Gulf of Alaska in order to determine the timing of species-specific recruitment and growth. Zooplankton are small pelagic animals that are a critical link between microalgae and protozoans and higher levels in the food web including economically important fishes, birds and marine mammals. While their abundances and species composition have been documented over part of the annual cycle between late spring and fall, this project focuses on winter and early spring. The project integrates traditional methods with modern molecular approaches to characterize the diversity, development, feeding and physiology of zooplankton, especially the early developmental stages of copepods (small crustaceans). The goal is to determine which species are there, how many are present and where they are in the water column, and to reveal indicators of their health. Broader impacts include research training for three graduate students and at least four undergraduates in biological oceanography and physiological ecology. Outreach activities are focusing on broadening the public's understanding of plankton ecology. An illustrated zooplankton guide for the Gulf of Alaska and plankton module for school teachers and students is being produced in collaboration with the Center for Alaskan Coastal Studies. Other plans include sponsorship of nature-drawing workshops on zooplankton and the production of an Art & Science traveling exhibit.

This project is tracking zooplankton population abundances, species composition and developmental stages through the spring restart in a high-latitude fjord in the northern Gulf of Alaska. While the entire zooplankton community is being characterized, the main focus is on the difficult-to-assess early developmental stages of copepods, which dominate the late spring biomass in the region. Three central hypotheses guide the research: 1) high abundances of copepod nauplii are present before any measurable increases in food in surface waters; 2) species diversity increases between winter and spring, with nauplii from large lipid-rich capital-breeding species appearing first, followed by those from income- and hybrid-strategy species and finally nauplii that emerge from dormant eggs; 3) prior to the appearance of food resources, nauplii from capital-breeding species conserve resources by delaying development and entering a state of dormancy in the second and third naupliar stages. The project entails intensive depth-stratified field sampling to characterize the wild community, in combination with laboratory experiments on nauplii to determine their responsiveness to food. The prey are being characterized by measuring chlorophyll a, dietary and prey community DNA sequencing and flow cytometry to establish diversity and abundances. Size-fractionated zooplankton samples are being analyzed using microscopy and community DNA sequencing to ascertain species diversity, developmental stage distribution and abundances. Feeding activity is being measured using dietary DNA sequencing of nauplii followed by comparisons with the prey field. Dormancy in nauplii is being determined by differential gene expression of target genes (RT-qPCR) and high-throughput sequencing of mRNA of individuals (transcriptomics) and community samples (meta-transcriptomics). Short-term and long-term effects of food availability on dormancy, development and growth are being quantified in laboratory experiments. Broader

impacts are focused on training of students in interdisciplinary research and state-of-art techniques, and public outreach to introduce plankton ecology to broader audiences.

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## Funding


| Funding Source | Award |
|---|---|
| NSF Office of Polar Programs (formerly NSF PLR) (NSF OPP) | OCE-2222376 |
| NSF Office of Polar Programs (formerly NSF PLR) (NSF OPP) | OCE-2222592 |
| NSF Office of Polar Programs (formerly NSF PLR) (NSF OPP) | OCE-2222558 |


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