Wirewalker data

Website: https://www.bco-dmo.org/dataset/732091
Data Type: Cruise Results
Version:

Project
» Collaborative Research: EAGER: Particle-specific DNA sequencing to directly observe ecological mechanisms of the biological pump (EAGER DNA BioPump)

Contributors	Affiliation	Role
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Dataset Description

This dataset includes data from Wirewalker deployments during the R/V Falkor cruise FK170124 as part of the Sea to Space Particle Investigation project (see https://schmidtocean.org/cruises/).

These data were utilized in the following publication (Omand et al., 2017).

Methods & Sampling

The data was acquired from a Wirewalker platform. The Wirewalker uses wave energy to propel an instrument package vertically along a wire suspended from a buoy at the sea surface. A more detailed description of the Wirewalker can be found in Rainville and PInkel, (2001) “Wirewalker: An Autonomous Wave-Powered Vertical Profiler”. The average descent rate of the Wirewalker was about 0.4 m/s and the ascent was 0.7 m/s, quickly reaching a terminal velocity determined by a combination of buoyancy and drag. The time required to make a complete round-trip to 120 m varied from 7-10 minutes. Temperature, salinity, and depth were measured with a Maestro CTD system (Richard Branker Research), and an integrated WET Labs Ecotriplet measured chlorophyll a fluorescence (FL), chromophoric dissolved organic matter (CDOM), and backscatter at λ = 700 nm. Downwelling solar irradiance was measured with a JFE Advantech cosine miniature photo- synthetically active radiation (PAR) sensor. Beam attenuation was measured with a WET Labs C-Star (λ = 650 nm) mounted vertically with brackets that allowed a minimally interrupted flow past the sensing volume during ascent. The Wirewalker also had a Rinko dissolved oxygen sensor, but the sensor appears to have gotten bleached and was not useable. The CTD sampled a 6 Hz. The bio-optical and PAR sensors sampled at 1 Hz. Individual profiles were isolated and the downcast data was discarded. The upcast data was interpolated onto 2m vertical bins.

Data Processing Description

RBR Ruskin software was used to download data and export as a text file.

MatLab was used for all subsequent data processing.

QUALITY CONTROL STEPS:

Minimal QC was required for this dataset. The raw temp, sal, PAR were in good shape. The bio-optics required minor adjustment as described below.

FL contained spurious negative values (0.1% of the total). These were modified with a criteria that set values < 50 (lowest dark counts) to 50.

bbp contained spurious negative values (0.08% of the total). These were modified with a criteria that set values < 50 (lowest dark counts) to 50.

CDOM contained spurious high points (0.18% of the total) and negative values (3.2% of the total). These were modified with a criteria that set values < 41 (lowest dark counts) to 41, and values > 55 to 44 (median value).

CORRECTION FOR NON-PHOTOCHEMICAL QUENCHING

The FL data show a clear diel pattern in the upper 30 m, correlated with PAR. This quenching during high light is attributed to NPQ of fluorescence. Therefore as a first steps toward getting values useful for calibration to mgChl/m^3, the data was corrected for this signal. The correction was obtained from a linear regression between the PAR and raw FL values at each depth bin. These regressions show a relatively linear relationship over the course of each 24 hour period, with the highest FL observed at night and quenching during higher light conditions. The daytime quenching is adjusted based on the slope and intercept at each depth to approximately match the night-time values.

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Related Publications

Omand, M., Cetinić, I., & Lucas, A. (2017). Using Bio-Optics to Reveal Phytoplankton Physiology from a Wirewalker Autonomous Platform. Oceanography, 30(2), 128–131. doi:10.5670/oceanog.2017.233
Results

Rainville, L., & Pinkel, R. (2001). Wirewalker: An Autonomous Wave-Powered Vertical Profiler. Journal of Atmospheric and Oceanic Technology, 18(6), 1048–1051. doi:10.1175/1520-0426(2001)018<1048:waawpv>2.0.co;2 https://doi.org/10.1175/1520-0426(2001)018<1048:WAAWPV>2.0.CO;2
Methods

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Parameters

Parameters for this dataset have not yet been identified

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Deployments

FK170124

Website	https://www.bco-dmo.org/deployment/732225
Platform	R/V Falkor
Report	https://datadocs.bco-dmo.org/docs/302/EAGER_DNA_BioPump/data_docs/DurkinOmandEstapa_Cruise_report.pdf
Start Date	2017-01-24
End Date	2017-02-20
Description	Station 1: 01/28/2017 17:45 to 02/02/2017 05:43 (GMT) Station2: 02/05/2017 16:06 to 02/08/2017 17:20 (GMT) Station3_dep1: 02/12/2017 04:23 to 02/13/2017 16:42 (GMT) Station3_dep2: 02/13/2017 17:48 to 02/14/2017 18:46 (GMT)

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Project Information

Collaborative Research: EAGER: Particle-specific DNA sequencing to directly observe ecological mechanisms of the biological pump (EAGER DNA BioPump)

Coverage: Eastern Pacific

NSF Award Abstract:
Carbon is fixed into organic matter by phytoplankton growing in the surface ocean, and is naturally sequestered in the ocean interior when particles and organisms sink: a process called the "biological pump." Because of its recognized influence on the global carbon cycle, ocean scientists have studied the biological pump for decades. However, we still do not have a sufficient understanding of the underlying processes to accurately quantify and predict carbon cycling. Much of this uncertainty stems from an inability to directly link specific plankton in the surface ocean with the types of particles sinking out of the surface ocean. To address this missing link in biological pump research, this work will directly observe how plankton are transported out of the surface ocean using novel, particle-specific observational approaches embedded within an interdisciplinary field program that will finely resolve upper ocean plankton groups and the resulting amount of sinking carbon across space and in time. The genetic identity of organisms within different types of sinking particles will be determined by sequencing the genetic contents of individually collected particles. This new application of a molecular method will definitively link surface plankton with sinking particles at five locations across the Pacific Ocean. This work has the potential to transform our understanding of the biological pump by identifying previously unknown links between surface ecosystems and sinking carbon particles. Because this work is embedded within an interdisciplinary field program, including biogeochemical modelers and remote sensing scientists, these data will feed directly into new models of the biological pump, improving our ability to quantify and predict carbon uptake by the ocean. This project will train 1 graduate student and at least 2 undergraduate researchers. Findings will be communicated to the non-scientific public through blogs, videos, and the public communication channels of participating institutions.

Accurate prediction of the global carbon cycle requires an understanding of the specific processes that link surface plankton communities and sinking particulate carbon flux (export) out of the surface ocean, but current methodological paradigms in biological pump research do not directly observe these processes. This project will comprehensively determine who is exported from the surface ocean and how using new, particle-resolving optical and molecular techniques embedded within a sampling scheme that characterizes export events at high time and space resolution. The investigation suggests that different plankton types in the surface waters are transported out of the surface ocean by distinct export pathways, and that an understanding of these connections is critical knowledge for global carbon cycle modeling. If successful, this work has the potential to transform our conceptual understanding of the biological pump by directly identifying mechanisms that link surface plankton with particle export, without relying on bulk sampling schemes and large-scale correlation analysis. Particle export environments will be studied at five open ocean locations during a cruise from Hawaii to Seattle in January-February 2017. The surface plankton communities will be characterized by a combination of satellite observations, sensors attached to a free-drifting, continuously profiling WireWalker, an in situ holographic camera, microscopy, and by sequencing 18S and 16S rRNA gene fragments. Exported particles will simultaneously be captured by various specialized sediment traps and their

characteristics will be directly related to their sources in the surface community by identifying the genetic contents of individual particle types. Individual particles will be isolated from gel layers and the 16S and 18S rRNA gene fragments will be amplified and sequenced. This work would, for the first time, combine molecular approaches with particle-specific observations to enable simultaneous identification of both which organisms are exported and the processes responsible for their export.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1703336

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