Total bacteria, including Archaea and Prochlorococcus, by flow cytometry from R/V Thomas G. Thompson cruise TN277 in the Eastern North Pacific Ocean in 2012 (POWOW project)

Website: https://www.bco-dmo.org/dataset/3900
Data Type: Cruise Results
Version: 2
Version Date: 2013-05-28

Project
» Seasonal and decadal changes in temperature drive Prochlorococcus ecotype distribution patterns (POWOW)

Contributors	Affiliation	Role
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Abstract
This dataset includes data on total bacteria, including Archaea and Prochlorococcus, by flow cytometry from R/V Thomas G. Thompson cruise TN277 in the Eastern North Pacific Ocean in 2012.

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Coverage

Spatial Extent: **N**:31.246 **E**:-120.6976 **S**:22.75 **W**:-158
Temporal Extent: 2012-03-01 - 2012-03-10

Dataset Description

Total bacterioplankton ("bacteria"), including Archaea and Prochlorococcus, determined by flow cytometry from the POWOW1 (TN277) cruise.

Methods & Sampling

Bacterioplankton (i.e. ‘bacteria’) were enumerated using a FACSCalibur flow cytometer (Becton Dickinson) and populations characterized as previously described (Johnson et al., 2010). Briefly, cells were excited with a 488 nm laser (15 mW Ar) and inelastic forward (<15°) scatter, inelastic side (90°) scatter (SSC), green (530 ± 30 nm) fluorescence, orange fluorescence (585 ± 42 nm), and red fluorescence (> 670 nm) emissions were measured. Bacterioplankton were quantified by staining the samples with the nucleic acid stain SYBR Green –I (Molecular Probes Inc.) (Marie et al., 1997).

References:

Johnson, Z.I., Shyam, R., Ritchie, A.E., Lin, Y., Mioni, C., Lance, V.P. et al. (2010) The effects of iron- and light-limitation on phytoplankton communities of deep chlorophyll maxima of the Western Pacific Ocean. Journal of Marine Research 68: 1-26. doi: 10.1357/002224010793721433

Marie, D., Partensky, F., Jacquet, S., and Vaulot, D. (1997) Enumeration and cell cycle analysis of natural populations of marine picoplankton by flow cytometry using the nucleic acid stain SYBR Green I. Applied and Environmental Microbiology 63: 186-193.

Data Processing Description

Cells counts were normalized to volume sampled to determined cells per mL.

BCO-DMO edits made:
- Parameter names have been changed to conform to BCO-DMO conventions.
- month_utc, day_utc, and year were added, based on the original date field.
- Original version of data (dated 22 March 2013) replaced with updated version 28 May 2013.

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Data Files

File
bacteria.csv (Comma Separated Values (.csv), 5.48 KB) MD5:409dcd3b993dbabb2ff4361b0195c06a Primary data file for dataset ID 3900

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Related Publications

Johnson, Z. I., Shyam, R., Ritchie, A. E., Mioni, C., Lance, V. P., Murray, J. W., & Zinser, E. R. (2010). The effect of iron- and light-limitation on phytoplankton communities of deep chlorophyll maxima of the western Pacific Ocean. Journal of Marine Research, 68(2), 283–308. doi:10.1357/002224010793721433
Methods

Marie, D., Partensky, F., Jacquet, S., & Vaulot, D. (1997). Enumeration and Cell Cycle Analysis of Natural Populations of Marine Picoplankton by Flow Cytometry Using the Nucleic Acid Stain SYBR Green I. Applied and Environmental Microbiology, 63(1), 186–193. doi:10.1128/aem.63.1.186-193.1997
Methods

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Parameters

Parameter	Description	Units
cruise_id	Cruise identifier (POWOW1 = TN277 = R/V Thomas G. Thompson cruise 277).	text
CTD_cast	Number of CTD cast.	unitless
lat	Latitude in decimal degrees. Positive = North.	decimal degrees
lon	Longitude in decimal degrees. Positive = East.	decimal degrees
month_utc	2-digit month of year, UTC.	mm (01 to 12)
day_utc	2-digit day of month, UTC.	dd (01 to 31)
year	4-digit year.	YYYY
depth	Sample depth.	meters
bot	Rosette position of the bottle.	unitless
bacteria	Bacteria (cells/mL) including Archaea and Prochlorococcus.	cells per milliliter

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Instruments

Dataset-specific Instrument Name	Flow Cytometer
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	A FACSCalibur flow cytometer (Becton Dickinson) was used to enumerate bacteria.
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. Description from: http://www.bio.umass.edu/micro/immunology/facs542/facswhat.htm

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Deployments

TN277

Website	https://www.bco-dmo.org/deployment/58867
Platform	R/V Thomas G. Thompson
Report	http://dmoserv3.whoi.edu/data_docs/POWOW/POWOW1-cruise_report.pdf
Start Date	2012-02-29
End Date	2012-03-11
Description	The POWOW#1 cruise was a trip of opportunity to sample along temperature gradients and test out new protocols. The primary goal of this cruise was to measure the abundance, diversity and activity of Prochlorococcus and associated bacterial and viral communities across temperature (and other environmental) gradients to understand how climate change may impact ocean ecology and biogeochemistry. There are many additional scientific and broader impact goals including characterizing oxidative stress and investigating nitrogen uptake/utilization molecular diversity. Cruise information and original data are available from the NSF R2R data catalog.

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Project Information

Seasonal and decadal changes in temperature drive Prochlorococcus ecotype distribution patterns (POWOW)

Website: http://oceanography.ml.duke.edu/johnson/research/powow/

Coverage: Eastern North Pacific Ocean

Project also known as '*Prochlorococcus* Of Warming Ocean Waters' (POWOW).

The two numerically-dominant ecotypes of the marine cyanobacterium *Prochlorococcus* partition the surface ocean niche latitudinally, with ecotype eMIT9312 dominant in the 30 degree N to 30 degree S region and eMED4 dominant at higher latitudes. These ecotypes may account for 25-50% of primary production in open ocean ecosystems, but this percentage is dependent on which ecotype dominates. The relative abundance of the two ecotypes follows a log-linear relationship with temperature, with the transition from eMIT9312 to eMED4 occurring at approx. 18 degrees C. From these descriptive data, it has been hypothesized that temperature is the primary driver of relative abundance. Their contribution to net primary production, however, appears to be independent of temperature, suggesting temperature regulates ecotype dominance through photosynthesis-independent mechanisms.

To test these hypotheses, the PIs are undertaking a series of field and lab studies to investigate the effect of temperature change on the distribution of these ecotypes. Two cruises in the North Pacific will trace the transitions from eMIT9312- to eMED4-dominated regions, with one cruise during the winter and the other during summer. They have hypothesized that the ratio of ecotype abundance will move latitudinally with the seasonal shift in temperature gradient: migration of the 18 degrees C isotherm northward in the summer will be matched by a similar migration of the 1:1 ecotype transition point. Multiple crossings of the 18 degrees C isotherm are proposed, and the summer cruise will also follow the isotherm to the Western US coast to gain insight on physical and geochemical influences. Environmental variables such as nutrient concentrations, light/mixing depths, and virus /grazing based mortality, which may impinge on the relationship between temperature and ecotype ratio, will be assessed through a series of multivariate analyses of the collected suite of physical, chemical and biological data. Seasonal comparisons will be complemented with on-deck incubations and lab competition assays (using existing and new isolates) that will establish, for the first time, how fitness coefficients of these ecotypes relate to temperature. As latitudinal shifts in temperature gradient and migration of ecotypes during seasonal warming likely share common features with high latitude warming as a consequence of climate change, the investigator's analyses will contribute important biological parameters

(e.g., abundances, production rates, temperature change coefficients) for modeling biological and biogeochemical responses to climate change. This research will be integrated with that of committed collaborators, generating data sufficient for ecosystem-scale characterizations of the contributions of temperature (relative to other forcing factors) in constraining the range and seasonal migration of these numerically dominant marine phototrophs.

Publications produced as result of this research:

Rowe, J.M., DeBruyn, J.M., Poorvin, L., LeCleir, G.R., Johnson, Z.I., Zinser, E.R., and Wilhelm, S.W. 2012. Viral and bacterial abundance and production in the Western Pacific Ocean and the relation to other oceanic realms. FEMS Microbiology Ecology, 72, p. 359. DOI: 10.1111/j.1574-6941.2011.01223.x

Morris, J.J., Lenski, R.E. and E.R. Zinser. 2012. The Black Queen Hypothesis: Evolution of Dependencies through Adaptive Gene Loss. mBio, 3, p. e00036-12. DOI: 10.1128/mBio.00036-12

Morris, J.J., Johnson, Z.I., Szul, M.J., Keller, M., and Zinser, E.R. 2011. Dependence of the cyanobacterium *Prochlorococcus* on hydrogen peroxide scavenging microbes for growth at the ocean's surface. PLoS One, 6(2), p. 16805. DOI:10.1371/journal.pone.0016805

Ringuet, S., Sassano, L., and Johnson, Z.I. 2011. A suite of microplate reader-based colorimetric methods to quantify ammonium, nitrate, orthophosphate and silicate concentrations for aquatic nutrient monitoring. Journal of Environmental Monitoring. DOI:10.1039/C0EM00290A

Ritchie, A.E. and Johnson, Z.I. 2012. Abundance and genetic diversity of aerobic anoxygenic phototrophic bacteria of coastal regions of the Pacific Ocean. Applied and Environmental Microbiology, 78, p. 2858. DOI: 10.1128/AEM.06268-11

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1031064

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