# Link to published bacterial cDNA sequences from the Bermuda Atlantic Time Series (BATS) Station, Sargasso Sea, 2008 (En-Gen DMSP Cycling project)

**Website**: https://www.bco-dmo.org/dataset/3793
**Version**: 26 April 2018
**Version Date**: 2018-04-26

**Project**
» En-Gen: A Functional Genomics Approach to Organic Sulfur Cycling in the Ocean (En-Gen DMSP Cycling )


| Contributors | Affiliation | Role |
|---|---|---|
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## Coverage

**Spatial Extent**: **Lat**:31.668 **Lon**:-64.132

## Dataset Description

A link is provided to published bacterial cDNA sequences from samples from the Bermuda Atlantic Time Series (BATS) station. Metatranscriptomic sequencing was used to analyze the gene expression profiles of the bacterial assemblage with and without short-term enrichment of dimethylsulfoniopropionate (DMSP).

**Experimental design, methods, and results are further described in:**
**Vila-Costa**, M., J. M. Rinta-Kanto, S. Sun, S. Sharma, R. Poretsky, and M. A. Moran. (2010). Transcriptomic analysis of a marine bacterial community enriched with dimethylsulfoniopropionate. ISME Journal, vol. 4, p. 1410. doi: 10.1038/ismej.2010.62

### Methods & Sampling

See Vila-Costa et al. (2010) for detailed methodology, which is paraphrased below:

"Sampling was carried out on 15 April 2008 at the Bermuda Atlantic Time-series Study (BATS) station at a depth of 10m using 10-L Niskin bottles. A 2 L subsample of unfiltered water was collected to measure in situ concentrations of Chl-a and total DMSP. The remaining seawater was prefiltered by gravity through 3 mm pore-size polycarbonate filters (142mm, Millipore, Billerica, MA, USA) to exclude eukaryotes and large particles. Water was dispensed into 20 L polycarbonate carboys and maintained in a temperature-controlled room in the

dark at in situ temperature for 3 h before beginning the experiment to allow time for adaptation to any DMSP released from the cells during filtration.

DMSP was added to experimental carboys to a final concentration of 25 nM. Control carboys remained untreated. Bacterial cells were collected after 30 minutes by filtering the water through 0.2 um pore-size polycarbonate filter. Filters were placed in 15 ml RNAse-free tubes containing 2 ml of Buffer RLT (RNeasy kit, Qiagen, Valencia, CA, USA) plus 10 ml of b-mercaptoethanol per ml. Messenger RNA (mRNA) extraction, enrichment, amplification, and conversion to complementary DNA was performed as described by Poretsky et al. (2009) with few modifications (see Supplementary Material in Vila-Costa et al. 2010). Only one replicate from the experimental and control treatments yielded RNA of sufficient quality for processing.

Complementary DNA libraries were sequenced with Roche GS FLX sequencing (Branford, CT, USA), yielding 606 286 reads (209-bp average length). The sequences were deposited in the Community Cyberinfrastructure for Advanced Marine Microbial Ecology Research and Analysis (CAMERA) database with the Genome Project ID CAM_PROJ_SargassoSea."

**References:**

**Poretsky**, R.S., Hewson, I., Sun, S.L., Allen, A.E., Zehr, J.P., and Moran, M.A. (2009) Comparative day/night metatranscriptomic analysis of microbial communities in the North Pacific subtropical gyre. Environ Microbiol 11: 1358–1375. DOI: 10.1002/9781118010518.ch63

### Data Processing Description

2018.04.26: Updated the link and repository location for sequences: CAMERA data has been migrated to iMicrobe.

BCO-DMO added coordinates of the BATS station and the sampling date from Vila-Costa et al. (2010).

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## Data Files

| File | |
|---|---|
| **BATS_cDNA_sequences.csv** | (Comma Separated Values (.csv), 234 bytes) MD5:4457806f375ff88d6fe2f217df15b83a |
| Primary data file for dataset ID 3793 | |

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## Parameters

| Parameter | Description | Units |
|---|---|---|
| taxon | Description of the taxonomic group of study. | text |
| site_desc | Description of the sampling site. | text |
| lat | Latitude of sampling site. North = positive. | decimal degrees |
| lon | Longitude of the sampling site. East = positive. | decimal degrees |
| day | 2-digit day of month when field sampling occurred. | dd (01 to 31) |
| month | 2-digit month of year when field sampling occurred. | mm (01 to 12) |
| year | 4-digit year when field sampling occurred. | YYYY |
| project_id | The identifier assigned to the project in the repository. | text |
| repository | Name of and link to the repository where sequences can be accessed. | text |

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## Instruments

| | |
|---|---|
| **Dataset-specific Instrument Name** | Niskin bottle |
| **Generic Instrument Name** | Niskin bottle |
| **Dataset-specific Description** | Samples were collected in 10-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. |

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## Deployments

### DMSP_Sargasso_Sea

| | |
|---|---|
| **Website** | https://www.bco-dmo.org/deployment/58890 |
| **Platform** | Bermuda Atlantic Time Series Vessel |
| **Start Date** | 2008-04-15 |
| **End Date** | 2008-04-15 |
| **Description** | Sampling for the project "En-Gen: A Functional Genomics Approach to Organic Sulfur Cycling in the Ocean" was carried out at the Bermuda Atlantic Time-series Study (BATS) station (31 40.1N, 64 7.9W) at a depth of 10m using 10-l Niskin bottles on 15 April 2008. |

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## Project Information

**En-Gen: A Functional Genomics Approach to Organic Sulfur Cycling in the Ocean (En-Gen DMSP Cycling )**

**Coverage**: Sapelo Island, GA, USA, 31.4° N Lat, 81.3° W Lon / Dauphin Island, AL, USA, 30.3 ° N Lat, 88.1° W Lon

The recent discovery of key genes that mediate competing pathways at a critical juncture in the marine sulfur cycle has allowed biogeochemists to make rapid advances in understanding where and when sulfur transformations occur in the ocean, and most importantly, what factors regulate them. This project describes an environmental functional genomics project that will rapidly increase our knowledge of the role that bacterioplankton play in dimethylsulfoniopropionate (DMSP) cycling in ocean surface waters, focusing particularly on biological controls of volatile sulfur exchange across the ocean/atmosphere boundary.

The investigators have asked three critical hypotheses to explain the regulation of bacterial DMSP degradation: that involve investigations on the energy constraints of DMSP cycling, the role that DMSP concentration in the oceans plays, and the sulfur requirements for bacterial growth. These research areas serve as the focus for hypothesis-driven laboratory and field studies using functional genomics approaches that will track patterns in gene expression in relation to sulfur metabolism. The hypotheses will be tested with:
1) chemostat systems with a model marine bacterium Silicibacter pomeroyi;
2) microcosm experiments with Gulf of Mexico seawater; and
3) field studies at various sites in the Gulf of Mexico. Marine bacterioplankton play a key role in regulating the flux of DMSP-derived sulfur to the atmosphere, a process of great importance for global climate regulation and marine productivity.

The investigators will also be involved in graduate and undergraduate student education, and two post-doctoral associates will be trained to address multidisciplinary challenges in environmental microbiology. High school biology students in Athens, GA will participate in marine microbial biology research that includes bacterial diversity and discovery studies in coastal Georgia, follow-up training in molecular tools and bioinformatics in their own classroom, and summer internships at the University of Georgia and Dauphin Island Sea Laboratory.

(The description above is from the NSF Award Abstract).

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## Funding

| Funding Source | Award |
|---|---|
| NSF Division of Ocean Sciences (NSF OCE) | OCE-0724017 |

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