Physiochemical data from samples collected along the coast of Louisiana, USA during 2018

Website: https://www.bco-dmo.org/dataset/745449
Data Type: Other Field Results
Version: 2
Version Date: 2020-02-13

Project
» Collaborative Research: EAGER: Salinity-based selection between sister clades of abundant coastal bacterioplankton (CoastalSAR11)

Contributors	Affiliation	Role
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Abstract
Physiochemical data from samples collected along the coast of Louisiana, USA during 2018.

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Coverage

Spatial Extent: **N**:29.867989 **E**:-89.676029 **S**:29.243342 **W**:-93.340714
Temporal Extent: 2018-01-27 - 2018-11-16

Dataset Description

Physiochemical data from samples collected along the coast of Louisiana in the Gulf of Mexico.

Methods & Sampling

Samples were collected manually by filling an acid-washed and autoclaved 20L carboy after three rinses. Temperature, pH, and salinity were taken using a handheld YSI. Cell counts were obtained by filtering water through a 2.7 µm Whatman GF/D filter, fixing with 10% formaldehyde, placing on ice, and then counting using flow cytometry (Thrash et al., 2015, Hydrocarbon and Lipid Microbiology Protocols). Inorganic nutrients were measured at the University of Washington Marine Chemistry Laboratory after sequential filtration through 2.7 Whatman GF/D and 0.22 µm Sterivex filters. Samples were initially placed on ice in the field, and then refrigerated until shipment with ice packs.

Data Processing Description

Data Problem Report:
pH is not reported for the first time points because a crack was noticed in the housing of the YSI cable that seemed to be associated with calibration. This was subsequently replaced and all values were also checked in the lab with a Fisherbrand pH meter.

Sample ARD 9/19/18 was not filtered on site because of bad weather. Therefore, the filtration steps for nutrients were conducted back at the lab after a 2.5 hour transit time

Sample ARD 11/16/18 was filtered for nutrients after a 3 hour delay at site CJ because of power supply issues at the ARD site.

BCO-DMO Data Processing Notes:
-Reformatted column names to comply with BCO-DMO standards;
-Replaced blank cells with nd;
-Reformatted dates;
-Added ISO DateTime column.

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Data Files

File
sar11.csv (Comma Separated Values (.csv), 5.24 KB) MD5:2f6bdc881504dd1c018dbb14e1a0e26a Primary data file for dataset ID 745449

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Related Publications

Thrash, J. Cameron, Jessica Lee Weckhorst, and David M. Pitre. 2015. Cultivating Fastidious Microbes. In Hydrocarbon and Lipid Microbiology Protocols, vol. 4 (Cultivation). Edited by Terry J. McGenity, Kenneth N. Timmis and Balbina Nogales.
Methods

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Parameters

Parameter	Description	Units
Site	Sampling site designation	unitless
Lat	Latitude of site	decimal degrees
Lon	Longitude of site	decimal degrees
Date	Date of sampling; format: yyyy-mm-dd	unitless
Time_Central	Time of sampling in the Central Time Zone, USA; format: HH:MM	unitless
Offset	Universal time coordinated (UTC) offset, corrected for daylight savings	unitless
Time_UTC	Universal Time Coordinated (UTC) subtracting Central Time from the UTC offset; format: HH:MM	unitless
Temp	Temperature measured via YSI at the sampling site	degrees Celsius
Cond	Conductivity measured via YSI at the sampling site	ms/cm
Salinity	Calculated salinity based on the conductivity measurement from the YSI	unitless
pH	pH of the seawater at the sampling site	unitless
Cell_counts	Number of cells passing through a 2.7 µm filter (Whatman GF/D) determined via flow cytometry	cells/mL
PO4	Concentration of phosphate in seawater from the site	umol/L
SiOH4	Concentration of silicate in seawater from the site	umol/L
NO3	Concentration of nitrate in seawater from the site	umol/L
NO2	Concentration of nitrite in seawater from the site	umol/L
NH4	Concentration of ammonium in seawater from the site	umol/L
ISO_DateTime_UTC	Date and time of sampling (UTC) formatted to ISO 8601 standard; format: yyyy-mm-ddTHH:MMZ	unitless

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Instruments

Dataset-specific Instrument Name	Millipore Guava 5HT HPL benchtop flow cytometer
Generic Instrument Name	Flow Cytometer
Dataset-specific Description	Used for sampling
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	YSI 556 MPS handheld meter
Generic Instrument Name	Multi Parameter Portable Meter
Dataset-specific Description	YSI 556 MPS handheld meter, calibrated with salinity and pH standards immediately prior to use
Generic Instrument Description	An analytical instrument that can measure multiple parameters, such as pH, EC, TDS, DO and temperature with one device and is portable or hand-held.

Dataset-specific Instrument Name	Masterflex I/P peristaltic pump
Generic Instrument Name	Pump
Dataset-specific Description	Used for sampling
Generic Instrument Description	A pump is a device that moves fluids (liquids or gases), or sometimes slurries, by mechanical action. Pumps can be classified into three major groups according to the method they use to move the fluid: direct lift, displacement, and gravity pumps

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Deployments

Coastal_SAR11

Website	https://www.bco-dmo.org/deployment/745476
Platform	shoreside Gulf of Mexico
Start Date	2018-01-27
End Date	2018-11-16

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Project Information

Collaborative Research: EAGER: Salinity-based selection between sister clades of abundant coastal bacterioplankton (CoastalSAR11)

Coverage: Coastal Louisiana, northern Gulf of Mexico

NSF award abstract:
Adaptation to new environments is a fundamental challenge for organisms, including microbes, in expanding their habitat range. It is important to investigate the cellular mechanisms underlying salinity tolerance in coastal bacterioplankton and their different responses to salinity in nature because (i) it will provide fundamental understanding for how microorganisms evolve to inhabit environments with different salinities, and (ii) alterations in coastal salinity are connected to climate change, so the way these alterations affect abundant coastal microorganisms also alters the biogeochemical cycling of, e.g., carbon. The project will examine microbial adaptations to salinity and determine how changes in salinity affect microbial metabolism using two

closely related groups of abundant coastal bacterioplankton as model taxa. In addition, the research will continue and expand microbiology Course-based Undergraduate Research Experiences (mCUREs) in high-throughput cultivation and microbial characterization at the Lousiana State University. Sections of freshman biology laboratories will learn how to isolate, characterize, and molecularly identify microorganisms from local aquatic systems. mCURE sections will lead to newly isolated strains, genome sequences, and physiological data, these results will be published with the contributing students as co-authors. The relative success of mCURE sections will be assessed compared to traditional freshman biology sections. mCURE sections will offer unique opportunities for LSU students by creating excitement about research through discovery of new organisms and generating knowledge of the coastal habitats that are essential to the livelihood of the Gulf Coast.

The evolutionary transition between salt- and freshwater environments occurs rarely in microorganisms. In one of the most abundant aquatic groups, SAR11, the transition between salt- and freshwater environments has happened only once: all freshwater SAR11 belong to subclade IIIb/LD12, which has also been found to inhabit coastal environments where salinity varies widely. The first reported isolates of the SAR11 freshwater clade LD12 and a member of the sister clade IIIa from the same region are now available. These pure culture representatives provide a powerful model for experimentally investigating adaptations to new environments in microorganisms, specifically (i) the genomic pathway and regulatory distinctions that arise during the evolutionary transition from marine to freshwater environments, and (ii) the physiological mechanisms that underlie the ecological restrictions imposed on microorganisms by ionic strength in coastal and freshwater environments. Furthermore, because these organisms have distinct differences in metabolic potential, the isolates facilitate testing (iii) the effects of changing coastal salinity on microbial contributions to other biogeochemical cycles, such as that for carbon. The project will test the hypothesis that the relative ionic strength tolerances between the sister lineages (LD12, IIIa) result from fundamental differences in metabolic flexibility at a genomic and regulatory level. To do so it will assess transcriptional and metabolic responses to varied ionic strength for both taxa and measure the distribution and activity of both groups in nature to translate laboratory findings to the field. The research will provide new understanding of LD12 habitat range and insights into how the "freshwater" lineage evolved from a SAR11 common ancestor. The project will also more generally provide important information on microbial responses to salinity changes in coastal systems and the evolutionary paths separating freshwater and marine microorganisms.

This award is co-funded by Biological Oceanography, Division of Ocean Sciences in the Directorate for Geosciences and by Systems and Synthetic Biology, Division of Molecular and Cellular Biosciences in the Directorate for Biological Sciences.

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Funding

Funding Source	Award
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