Iron ligand speciation profiles analyzed by liquid chromatography-mass spectrometry from samples collected on the US GEOTRACES Pacific Meridional Transect (PMT) cruises (GP15, RR1814 & RR1815) on R/V Roger Revelle from September to November 2018

Website: https://www.bco-dmo.org/dataset/875210
Data Type: Cruise Results
Version: 1
Version Date: 2023-06-29

Project
» US GEOTRACES Pacific Meridional Transect (GP15) (U.S. GEOTRACES PMT)
» Trace Element Organic Speciation along the US GEOTRACES Pacific Meridional Transect (PMT Organic Speciation)

Program
» U.S. GEOTRACES (U.S. GEOTRACES)

Contributors	Affiliation	Role
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Abstract
This dataset includes iron ligand speciation profiles analyzed by liquid chromatography-mass spectrometry. Samples were collected on the US GEOTRACES Pacific Meridional Transect (PMT) cruises (GP15, RR1814 & RR1815) on R/V Roger Revelle from September to November 2018.

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Coverage

Temporal Extent: 2018-09 - 2018-11

Methods & Sampling

Sample collection and processing
Seawater samples were collected using a trace metal clean GTC rosette/Go-Flo bottle sampler. Each sample was filtered directly from the Go-Flo bottle through a 0.2 µm Pall Acropak-200 Supor cartridge into a trace metal grade acid-cleaned 4 L polycarbonate bottle. Samples were pumped at 20 mL/min through Bond-Elut ENV solid phase extraction (SPE) columns (1 g, 6 mL, Agilent Technologies) that had been previously activated by passing ~6 mL each of distilled methanol (MeOH, Optima LCMS grade, Fisher Scientific), pH 2 water (Optima HCl, Fisher Scientific), and ultrapure water (qH2O, 18.2 MΩ) through the column.

SPE columns were frozen (-20oC) immediately after sample collection and returned to the laboratory for processing. Columns were thawed and washed with 6 mL qH2O (to reduce salts) and the qH2O wash discarded. Ligands were then eluted with 6 mL distilled MeOH into acid-cleaned 10 mL falcon tubes. Process blanks were prepared in parallel by

eluting activated ENV columns with 6 mL qH2O followed by 6 mL MeOH. A 10 µL stock solution of 2.2 µM Ga-desferrioxamine-E (Ga-DFOE) was next added to each sample as an internal standard. The sample was concentrated to ~500 µL by vacuum centrifugation (SpeedVac, Thermo Scientific). A 100 µL aliquot of the sample was taken, mixed with 100 µL of qH2O, and analyzed by LC-MS.

To prepare the Ga-DOFE internal standard, 0.5 mg desferrioxamine-E (DFOE; Biophore Research) was dissolved with sonication in 1 mL distilled MeOH. Then, 10 µL of 200 mM gallium nitrate in qH2O adjusted to pH 1 with nitric acid (Optima grade, Fisher Scientific) was added to complex DFOE. The solution was diluted by adding 4 mL qH2O to make 5 mL of standard. To remove excess Ga, 500 µL of the solution was applied to a C18 SPE column (100 mg, 1 mL, Agilent Technologies), which had been previously activated with 2 mL each of distilled MeOH and qH2O. The cartridge was washed with 2 mL qH2O to remove excess Ga, and the Ga-DFOE eluted with 2 mL MeOH. The MeOH eluant was collected and then diluted with qH2O to a final volume of 20 mLs.

High pressure liquid chromatography-Inductively coupled plasma mass spectrometry
Chromatographic analyses were performed on a bioinert Dionex Ultimate 3000 LC system fitted with a loading pump, a nano pump, and a 10-port switching valve (Li et al 2021). During the loading phase, 200 µL of sample were withdrawn into the sample loop, then pushed onto a C18 trap column (3.5 µm, 0.5 mm x 35 mm, PN 5064-8260, Agilent Technologies) by the loading pump at 25 µL/min for 10 min. The loading solvent is a mixture of 95% solvent A (5 mM aqueous ammonium formate, Optima, Fisher Scientific) and 5% solvent B (5 mM methanolic ammonium formate). During the elution phase, the solvent was delivered by the nano pump at 10 µL/min, and the trap column outflow directed onto two C18 columns (3.5 µm, 0.5 mm x 150 mm, PN 5064-8262, Agilent Technologies) connected in series. Samples were separated with an 80 min linear gradient from 95% solvent A and 5% solvent B to 95% solvent B, followed by isocratic elution at 95% solvent B for 10 minutes. Meanwhile, the loading pump solvent was switched to 100% qH2O, increased to 35 µL/min and directed as a post column make-up flow, which was infused with the column eluant into the ICPMS. The high aqueous content of the combined flow serves to minimize the effect of changes in solvent composition (in this case increasing methanol content during the analysis) on the detector response to Fe, Ga, and Al.

The combined flow from the LC was analyzed using a Thermo Scientific iCAP Q quadrupole mass spectrometer fitted with a perfluoroalkoxy micronebulizer (PFA-ST, Elemental Scientific), and a cyclonic spray chamber cooled to 4 °C (Boiteau and Repta, 2016). Measurements were made in kinetic energy discrimination (KED) mode, with a helium collision gas flow of 4-4.5 mL/min to minimize isobaric 40Ar16O+ interferences on 56Fe. Oxygen was introduced into the sample carrier gas at 25 mL/min to prevent the formation of reduced organic deposits onto the ICPMS skimmer and sampling cones. Isotopes monitored were 56Fe (integration time 0.05 s), 54Fe (0.02 s), 57Fe (0.02 s), 69Ga (0.05 s), 71Ga (0.02 s) and 27Al (0.02 s).

External and Internal Standards
The Fe detector response was calibrated using the siderophore ferrichrome which elutes at ~ 40 min in our chromatographic analysis. Stock solutions of 250 µM of ferrichrome were diluted to prepare standards with 2 nM, 5 nM, 10 nM, 20 nM, and 40 nM of the siderophore. Then, 5 µL of 2.2 µM Ga-DFOE was added to 995 µL of each standard. Next, a 100 µL aliquot was taken, mixed with 100 µL of qH2O, and analyzed by LC-ICPMS. A plot of the ratio of Fe-56 (ferrichrome):Ga-69 (Ga-DFOE) peak areas against ferrichrome/Ga-DFOE concentration yields a relationship (r2 ~0.999) between 0.2-4 pmole of ferrichrome. Calibrations and process blanks were made for every 10-20 samples analyzed, with only small changes (RSD~30%) in the slope of the calibration relationship observed over the course of the ~ 2 year of sample analysis. Concentrations of iron ligands in each sample were measured by plotting the FeL/Ga-DFOE peak area on the most appropriate calibration curve.

High pressure liquid chromatography-Electrospray ionization mass spectrometry
To verify the assignment of Fe-Ls to known siderophores, samples were analyzed by LC-ESIMS. The eluant from the LC, without qH2O infusion, was coupled to a Thermo Scientific Orbitrap Fusion mass spectrometer equipped with a heated electrospray ionization source. ESI source parameters were set to a capillary voltage of 3500 V, sheath, auxiliary and sweep gas flow rates of 5, 2, and 0 (arbitrary units), and ion transfer tube and vaporizer temperatures of 275°C and 20°C. MS1 scans for a m/z range of 150-1900 were collected in high resolution (450K) positive ion mode.

The LC-ESIMS data was converted from raw file format to mzXML (MSconvert, Chambers, Maclean, Burke et al 2012). The mzXML is imported to Matlab, and aligned with ICPMS data using the retention time of Ga-DFOE, which was obtained by monitoring m/z of 667.26 by ESIMS and 69Ga by ICPMS. Then, the m/z and intensity from each scan are extracted, and ordered by scan number into a scan number/mass (m/z)/intensity matrix, which is then interrogated by mass search algorithms (Boiteau and Repeta, 2016, Li et al 2021). The algorithms find pairs of co-eluting peaks with a difference of 1.995 amu in m/z and a ratio of 15.7 in intensity, which represent isotopologues of Fe containing complexes.

Instruments
We used a Gilson Aspec GX-271 to recover samples from solid phase extraction columns. Extracted samples were reduced in volume using a Thermo/Savant RVT 1505 vacuum centrifuge. Concentrated samples were analyzed by high pressure liquid chromatography using a Dionex Ultimate 3000 (liquid chromatograph) coupled to a Thermo iCap QC inductively coupled plasma mass spectrometer or a Thermo Orbitrap Fusion mass spectrometer fitted with a heated electrospray interface.

Additional Notes
Refer to Supplement Documents for a PDF containing the structure of the marinobactins and a table of masses used for identification.

Relative retention time ranges are provided using codes in the 'Flag' columns in the dataset. Refer to the parameters section for definitions of each code. The different marinobactins (A-E) appear at different times during the analyses. However, the times that they appear may change slightly between analyses. For example, Marinobactin B might appear between 1.70 and 178 today, but between 1.72 and 1.80 in a month from now. When the marinobactins shift, they all shift together - that is if marinobactin B shifts, marinobactin C will also shift.

Data Processing Description

Data Processing:
Data were processed using MSconvert, Proteowizard, and: https://github.com/JingxuanJayLi/RepetaLab

BCO-DMO Processing Description

- renamed fields (column headers) to comply with BCO-DMO naming conventions.

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Data Files

File	
875210_v1_gp15_iron_ligands.csv	(Comma Separated Values (.csv), 17.69 KB) MD5:dd297f0b3286f60d2af46e7789bbd680
Primary data file for dataset ID 875210, version 1.	

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Supplemental Files

File	
marinobactin_structure_and_masses_20220608.pdf	(Portable Document Format (.pdf), 253.93 KB) MD5:14e5f1b9dfedaeeb6eeec91ea4ca6122
Diagrams of the structures of Marinobactins and table of masses used for identification in the datasets "GP15 Iron Ligands" (PI: Daniel Repeta).	

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Related Publications

Boiteau, R. M., & Repeta, D. J. (2015). An extended siderophore suite from Synechococcus sp. PCC 7002 revealed by LC-ICPMS-ESIMS. Metallomics, 7(5), 877–884. https://doi.org/10.1039/c5mt00005j
Methods

Chambers, M. C., Maclean, B., Burke, R., Amodei, D., Ruderman, D. L., Neumann, S., … Mallick, P. (2012). A cross-platform toolkit for mass spectrometry and proteomics. Nature Biotechnology, 30(10), 918–920. doi:10.1038/nbt.2377
Methods

Li, J., Boiteau, R. M., Babcock-Adams, L., Acker, M., Song, Z., McIlvin, M. R., & Repeta, D. J. (2021). Element-Selective Targeting of Nutrient Metabolites in Environmental Samples by Inductively Coupled Plasma Mass Spectrometry and Electrospray Ionization Mass Spectrometry. Frontiers in Marine Science, 8. https://doi.org/10.3389/fmars.2021.630494
Methods

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Parameters

Parameter	Description	Units
Station	Station number	unitless
GEOTRACES_ID	GEOTRACES GP-15 sample number	unitless
FeSiderophores_56_DSPEENV_CONC_BOTTLE	Total Fe-56 Siderophore_dissolved, recoverd by solid phase extraction using Agilent ENV resin (see metadata methods for details)	pmole/liter
FePolarligandA_56_DSPEENV_CONC_BOTTLE	Fe-56 PolarligandA_dissolved, recoverd by solid phase extraction using Agilent ENV resin (see metadata methods for details)	pmole/liter
Flag_FePolarligandA_56_DSPEENV_CONC_BOTTLE	Relative retention time range for Polar ligand A for this analysis. Code definitions: 1 = ; 2 = ; 3 = ; 4 = ; 5 = ; 6 = ; 7 = (1.28, 1.36)	unitless
FePolarligandB_56_DSPEENV_CONC_BOTTLE	Fe-56 PolarligandB_dissolved, recoverd by solid phase extraction using Agilent ENV resin (see metadata methods for details)	pmole/liter
Flag_FePolarligandB_56_DSPEENV_CONC_BOTTLE	Relative retention time range for Polar ligand B for this analysis. Code definitions: 1 = ; 2 = ; 3 = ; 4 = ; 5 = ; 6 = ; 7 = (1.36, 1.44)	unitless
FePolarligandC_56_DSPEENV_CONC_BOTTLE	Fe-56 PolarligandC_dissolved, recoverd by solid phase extraction using Agilent ENV resin (see metadata methods for details)	pmole/liter
Flag_FePolarligandC_56_DSPEENV_CONC_BOTTLE	Relative retention time range for Polar ligand C for this analysis. Code definitions: 1 = ; 2 = ; 3 = ; 4 = ; 5 = ; 6 = ; 7 = (1.44, 1.52)	unitless

FePolarligandD_56_DSPEENV_CONC_BOTTLE	Fe-56 PolarligandD_dissolved, recoverd by solid phase extraction using Agilent ENV resin (see metadata methods for details)	pmole/liter
Flag_FePolarligandD_56_DSPEENV_CONC_BOTTLE	Relative retention time range for Polar ligand D for this analysis. Code definitions: 1 = ; 2 = ; 3 = ; 4 = ; 5 = ; 6 = ; 7 = (1.52, 1.60)	unitless
FePolarligandE_56_DSPEENV_CONC_BOTTLE	Fe-56 PolarligandE_dissolved, recoverd by solid phase extraction using Agilent ENV resin (see metadata methods for details)	pmole/liter
Flag_FePolarligandE_56_DSPEENV_CONC_BOTTLE	Relative retention time range for Polar ligand E for this analysis. Code definitions: 1 = ; 2 = ; 3 = ; 4 = ; 5 = ; 6 = ; 7 = (1.60, 1.68)	unitless
FeMarinobactinA_56_DSPEENV_CONC_BOTTLE	Fe-56 Marinobactin A_dissolved, recoverd by solid phase extraction using Agilent ENV resin (see metadata methods for details)	pmole/liter
Flag_FeMarinobactinA_56_DSPEENV_CONC_BOTTLE	Relative retention time range for Marinobactin A for this analysis. Code definitions: 1 = ; 2 = (1.62, 1.70); 3 = (1.65, 1.75); 4 = (1.70, 1.78); 5 = (1.68, 1.76); 6 = (1.68, 1.76); 7 = (1.68, 1.76)	unitless
FeMarinobactinB_56_DSPEENV_CONC_BOTTLE	Fe-56 Marinobactin B_dissolved, recoverd by solid phase extraction using Agilent ENV resin (see metadata methods for details)	pmole/liter
Flag_FeMarinobactinB_56_DSPEENV_CONC_BOTTLE	Relative retention time range for Marinobactin B for this analysis. Code definitions: 1 = (1.70, 1.78); 2 = (1.70, 1.78); 3 = (1.75, 1.85); 4 = (1.78, 1.86); 5 = (1.76, 1.84); 6 = (1.76, 1.84); 7 = (1.76, 1.84)	unitless

FeMarinobactinC_56_DSPEENV_CONC_BOTTLE	Fe-56 Marinobactin C_dissolved, recoverd by solid phase extraction using Agilent ENV resin (see metadata methods for details)	pmole/liter
Flag_FeMarinobactinC_56_DSPEENV_CONC_BOTTLE	Relative retention time range for Marinobactin C for this analysis. Code definitions: 1 = (1.78, 1.86); 2 = (1.78, 1.86); 3 = (1.85, 1.95) ; 4 = (1.86, 1.94); 5 = (1.84, 1.92); 6 = (1.84, 1.92); 7 = (1.84, 1.92)	unitless
FeMarinobactinD_56_DSPEENV_CONC_BOTTLE	Fe-56 Marinobactin D_dissolved, recoverd by solid phase extraction using Agilent ENV resin (see metadata methods for details)	pmole/liter
Flag_FeMarinobactinD_56_DSPEENV_CONC_BOTTLE	Relative retention time range for Marinobactin D for this analysis. Code definitions: 1 = (1.86, 1.94); 2 = (1.86, 1.94); 3 = (1.95, 2.05) ; 4 = (1.94, 2.02); 5 = (1.92, 2.00); 6 = (1.92, 2.00); 7 = (1.92, 2.00)	unitless
FeMarinobactinE_56_DSPEENV_CONC_BOTTLE	Fe-56 Marinobactin E_dissolved, recoverd by solid phase extraction using Agilent ENV resin (see metadata methods for details)	pmole/liter
Flag_FeMarinobactinE_56_DSPEENV_CONC_BOTTLE	Relative retention time range for Marinobactin E for this analysis. Code definitions: 1 = (1.94, 2.02); 2 = (1.94, 2.02); 3 = ? ; 4 = (2.02, 2.10); 5 = (2.00, 2.08); 6 = ?; 7 = (2.00, 2.08)	unitless

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Instruments

Dataset-specific Instrument Name	Dionex Ultimate 3000
Generic Instrument Name	High-Performance Liquid Chromatograph
Generic Instrument Description	A High-performance liquid chromatograph (HPLC) is a type of liquid chromatography used to separate compounds that are dissolved in solution. HPLC instruments consist of a reservoir of the mobile phase, a pump, an injector, a separation column, and a detector. Compounds are separated by high pressure pumping of the sample mixture onto a column packed with microspheres coated with the stationary phase. The different components in the mixture pass through the column at different rates due to differences in their partitioning behavior between the mobile liquid phase and the stationary phase.

Dataset-specific Instrument Name	Thermo Orbitrap Fusion
Generic Instrument Name	Mass Spectrometer
Generic Instrument Description	General term for instruments used to measure the mass-to-charge ratio of ions; generally used to find the composition of a sample by generating a mass spectrum representing the masses of sample components.

Dataset-specific Instrument Name	Thermo/Savant RVT 1505
Generic Instrument Name	Vacuum centrifuge concentrator
Generic Instrument Description	A centrifuge that includes a vacuum chamber within which a centrifuge rotord is rotatably mounted for spinning a plurality of vials containing a solution at high speed while subjecting the solution to a vacuum condition for concentration and evaporation. Alternative names: sample concentrator; speed vacuum; speed vac.

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Deployments

RR1814

Website	https://www.bco-dmo.org/deployment/776913
Platform	R/V Roger Revelle
Report	https://datadocs.bco-dmo.org/docs/geotraces/GEOTRACES_PMT/casciotti/data_docs/GP15_Cruise_Report_with_ODF_Report.pdf
Start Date	2018-09-18
End Date	2018-10-21
Description	Additional cruise information is available from the Rolling Deck to Repository (R2R): https://www.rvdata.us/search/cruise/RR1814

RR1815

Website	https://www.bco-dmo.org/deployment/776917
Platform	R/V Roger Revelle
Report	https://datadocs.bco-dmo.org/docs/geotraces/GEOTRACES_PMT/casciotti/data_docs/GP15_Cruise_Report_with_ODF_Report.pdf
Start Date	2018-10-24
End Date	2018-11-24
Description	Additional cruise information is available from the Rolling Deck to Repository (R2R): https://www.rvdata.us/search/cruise/RR1815

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Project Information

US GEOTRACES Pacific Meridional Transect (GP15) (U.S. GEOTRACES PMT)

Website: http://www.geotraces.org/

Coverage: Pacific Meridional Transect along 152W (GP15)

A 60-day research cruise took place in 2018 along a transect form Alaska to Tahiti at 152° W. A description of the project titled "*Collaborative Research: Management and implementation of the US GEOTRACES Pacific Meridional Transect*", funded by NSF, is below. Further project information is available on the US GEOTRACES website and on the cruise blog. A detailed cruise report is also available as a PDF.

Description from NSF award abstract:
GEOTRACES is a global effort in the field of Chemical Oceanography in which the United States plays a major role. The goal of the GEOTRACES program is to understand the distributions of many elements and their isotopes in the ocean. Until quite recently, these elements could not be measured at a global scale. Understanding the distributions of these elements and isotopes will increase the understanding of processes that shape their distributions and also the processes that depend on these elements. For example, many "trace elements" (elements that are present in very low amounts) are also important for life, and their presence or absence can play a vital role in the population of marine ecosystems. This project will launch the next major U.S. GEOTRACES expedition in the Pacific Ocean between Alaska and Tahiti. The award made here would support all of the major infrastructure for this expedition, including the research vessel, the sampling equipment, and some of the core oceanographic measurements. This project will also support the personnel needed to lead the expedition and collect the samples.

This project would support the essential sampling operations and infrastructure for the U.S. GEOTRACES Pacific Meridional Transect along 152° W to support a large variety of individual science projects on trace element and isotope (TEI) biogeochemistry that will follow. Thus, the major objectives of this management proposal are: (1) plan and coordinate a 60 day research cruise in 2018; (2) obtain representative samples for a wide variety of TEIs using a conventional CTD/rosette, GEOTRACES Trace Element Sampling Systems, and in situ pumps; (3) acquire conventional CTD hydrographic data along with discrete samples for salinity, dissolved oxygen, algal pigments, and dissolved nutrients at micro- and nanomolar levels; (4) ensure that proper QA/QC protocols are followed and reported, as well as fulfilling all GEOTRACES intercalibration protocols; (5) prepare and deliver all hydrographic data to the GEOTRACES Data Assembly Centre (via the US BCO-DMO data center); and (6) coordinate all cruise communications between investigators, including preparation of a hydrographic report/publication. This project would also provide baseline measurements of TEIs in the Clarion-Clipperton fracture zone (~7.5°N-17°N, ~155°W-115°W) where large-scale deep sea mining is planned. Environmental impact assessments are underway in partnership with the mining industry, but the effect of mining activities on TEIs in the water column is one that could be uniquely assessed by the GEOTRACES community. In support of efforts to communicate the science to a wide audience the investigators will recruit an early career freelance science journalist with interests in marine science and oceanography to participate on the cruise and do public outreach, photography and/or videography, and social media from the ship, as well as to submit articles about the research to national media. The project would also support several graduate students.

Trace Element Organic Speciation along the US GEOTRACES Pacific Meridional Transect (PMT Organic Speciation)

Website: https://www2.whoi.edu/site/repetagroup/

Coverage: North Pacific Ocean

NSF Abstract:

In many areas of the ocean microbes live in an environment that has very little of the nutrients they need to grow and thrive. In particular, nutrients with nitrogen (N), phosphorus (P), and iron (Fe), needed for the synthesis of proteins and nucleic acids, are in short supply. Iron is supplied to the ocean by dust blowing off the continents, and in areas remote from land, microbial life is limited by the very low concentrations of iron dissolved in seawater. To extract iron from their surroundings, some microbes synthesize and release organic compounds called siderophores into their environment. Siderophores are specifically designed to bind iron and transport it back into the cell. But only recently have we had the technology to measure siderophores in seawater, and we do not know where or when they are used, or which microbes are making and using them. The study proposed here is designed to address all of these questions. We will measure siderophores in the Pacific Ocean along a track from Alaska to Tahiti. The distribution of siderophores will be compared with data from other measurements (nutrients, cell numbers, genomics) to understand how microbes are able to live in very low iron environments, and how they can use organic compounds to extract metals from seawater. The study will also allow us test and improve the technology of measuring iron and other metals (mercury, copper, and cadmium, for example) bonded to organic compounds in other environmental samples, such as ground-waters, lakes and rivers, which is important for monitoring the toxicity of metal contaminants.

Nearly all iron dissolved in the ocean is complexed by strong organic ligands of unknown composition. The effect of ligand composition on microbial iron acquisition is poorly understood, but amendment experiments using model ligands show they can facilitate or impede iron uptake depending on their identity. Here we propose to measure the molecular speciation of a suite of bioactive trace element (iron, copper, cobalt, nickel, and zinc) ligands (TE-Ls) in particulate and dissolved organic matter across the US GEOTRACES Pacific Meridional Transect (PMT). We will use high pressure liquid chromatography coupled to inductively coupled plasma mass spectrometry to detect and quantify TE-Ls, and companion electrospray ionization mass spectra to identify and characterize organic ligands. The PMT will cross five different biogeochemical provinces: shelf/slope, subarctic high nutrient/low chlorophyll (HNLC), North Pacific oligotrophic gyre, equatorial HNLC, and South Pacific oligotrophic gyre. The cruise track further intersects at least three different subsurface features, the subarctic and equatorial particle veils, oxygen deficient waters, and mid depth hydrothermal plumes. We expect the unique physical, chemical, and biological properties that characterize these regimes and features will lead to very different TE-L distributions across and down the water column. TE-L molecular speciation measurements will enable us to better integrate datasets of trace element distribution with metagenomic datasets of nutrient-driven changes in microbial metabolism across some of the Earth's major biomes.

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Program Information

U.S. GEOTRACES (U.S. GEOTRACES)

Website: http://www.geotraces.org/

Coverage: Global

GEOTRACES is a SCOR sponsored program; and funding for program infrastructure development is provided by the U.S. National Science Foundation.

GEOTRACES gained momentum following a special symposium, S02: Biogeochemical cycling of trace elements and isotopes in the ocean and applications to constrain contemporary marine processes (GEOSECS II), at a 2003 Goldschmidt meeting convened in Japan. The GEOSECS II acronym referred to the Geochemical Ocean Section Studies To determine full water column distributions of selected trace elements and isotopes, including their concentration, chemical speciation, and physical form, along a sufficient number of sections in each ocean basin to establish the principal relationships between these distributions and with more traditional hydrographic parameters;

* To evaluate the sources, sinks, and internal cycling of these species and thereby characterize more completely the physical, chemical and biological processes regulating their distributions, and the sensitivity of these processes to global change; and

* To understand the processes that control the concentrations of geochemical species used for proxies of the past environment, both in the water column and in the substrates that reflect the water column.

GEOTRACES will be global in scope, consisting of ocean sections complemented by regional process studies. Sections and process studies will combine fieldwork, laboratory experiments and modelling. Beyond realizing the scientific objectives identified above, a natural outcome of this work will be to build a community of marine scientists who understand the processes regulating trace element cycles sufficiently well to exploit this knowledge reliably in future interdisciplinary studies.

Expand "Projects" below for information about and data resulting from individual US GEOTRACES research projects.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1736280

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