Diatom amplicon sequencing variants (ASVs) from Narragansett Bay, Rhode Island, USA from 2008-2014

Website: https://www.bco-dmo.org/dataset/911102
Data Type: Other Field Results
Version: 1
Version Date: 2023-11-09

Project
» Dimensions: Collaborative Research: Genetic, functional and phylogenetic diversity determines marine phytoplankton community responses to changing temperature and nutrients (Phytoplankton Community Responses)
» LTER: Linking Pelagic Community Structure with Ecosystem Dynamics and Production Regimes on the Changing Northeast US Shelf (NES LTER)
» Narragansett Bay Long-Term Plankton Time Series (NBPTS)

Programs
» Dimensions of Biodiversity (Dimensions of Biodiversity)
» Long Term Ecological Research network (LTER)

Contributors	Affiliation	Role
Rynearson, Tatiana A.	University of Rhode Island (URI-GSO)	Principal Investigator
Fontaine, Diana Nicole	University of Rhode Island (URI-GSO)	Student
Rauch, Shannon	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
These data include diatom composition information from a fixed sampling site in Narragansett, Bay, RI, USA over six years between dates 2008-12-09 and 2014-12-30. Sampling occurred monthly from 2008 to 2013 and twice per month in 2014. Diatom composition data, in the form of amplicon sequencing variants, were obtained via high throughput sequencing of filtered biomass samples. Diatoms are important contributors to marine primary production; however, their vast diversity makes species-level identification challenging. This dataset, collected over many years, includes diatom composition data at a more detailed level than ever before observed in Narragansett Bay and highlights the importance of time series for understanding phytoplankton dynamics in coastal systems. These data were collected by various students over the years with supervision from Dr. Tatiana Rynearson of URI's Graduate School of Oceanography. Diana Fontaine processed these data and together, Dr. Rynearson and her student Ms. Fontaine published their results in Limnology and Oceanography.

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Coverage

Spatial Extent: **Lat**:41.57 **Lon**:-71.39
Temporal Extent: 2008-12-09 - 2014-12-30

Methods & Sampling

The methods reported below are summarized from Rynearson et al. (2020) and Fontaine and Rynearson (2023), two publications that used this dataset.

Filtered biomass sample collection, processing, and sequencing
As part of the Narragansett Bay Plankton Time Series (NBPTS), weekly surface water samples (9 meters depth) were collected between December 2008 and December 2014 from the west passage of Narragansett Bay (41°34.2'N, 71°23.4'W), a partially mixed estuary in the northwest Atlantic. Sampling occurred at a fixed location (historically this station has been called 'Station II') with a small boat operated by the University of Rhode Island (Cap'n Bert).

Water samples were filtered in triplicate onto 0.22-micrometer (µm) pore size, 25-millimeter (mm) diameter ExpressPlus filters (MilliporeSigma, Burlington, Massachusetts, USA) and stored at -80° Celsius (C) for later DNA extraction. Filter volume was dependent on the in situ Secchi depth; 100 milliliters (mL) of water were filtered per 1 meter (m) of Secchi depth which ranged from 1- 6 m. Previously extracted DNA from 68 monthly surface water samples collected between December 2008 and December 2014 was used here (Canesi and Rynearson, 2020) in addition to extracted DNA from 12 monthly samples collected between January and December 2014 (Rynearson et al. 2020).

To identify the diatoms present in each sample, a 420 base pair (bp) fragment within the variable V4 region of the 18S rDNA gene was amplified using primers D512 and D978rev (Zimmermann et al. 2011). Primers were modified by the addition of Illumina-specific adaptors: D512_illumina: 5' TCGTCGGCAGCGTCAGATGTGTATAAGAGACAGATT CCAGCTCCAATAGCG 3' and D978_illumina: 5' GTCTCGTGGGCTCGGAGATGTGTATAA GAGACAGGACTACGATGGTATCTAATC 3'. Ten microliter PCR reactions contained the following reagents: 1x Bio-x-Act Short Mix (Bioline USA Inc., Taunton, Massachusetts, USA), 0.5 micromolar (µM) each forward and reverse primer and approximately 0.3-2.7 nanograms (ng) DNA template. Reactions were amplified with a multi-step thermocycler protocol, consisting of a two-minute denaturing step at 94°C, followed by 20 cycles of 30 seconds each at 94°C, 49°C and 72°C, followed by 15 cycles of 30 seconds each at 94°C, 67°C and 72°C, followed by 10 minutes at 72°C. PCR amplicons were cleaned with Ampure XP beads (Beckman Coulter, Inc., Brea, California, USA), quantified with the Qubit High Sensitivity DNA Assay Kit (Thermo Fisher Scientific, Inc., Waltham, Massachusetts, USA), amplified for an additional five cycles to add Nextera indices and adaptors (Illumina, Inc., San Diego, California, USA) and cleaned again with Ampure XP beads. PCR products were pooled with the KAPA qPCR kit (Kapa Biosystems, Wilmington, Massachusetts, USA) and sequenced on the Illumina MiSeq platform with V2 chemistry (2x250bp reads; Illumina, Inc., San Diego, California, USA) at the University of Rhode Island Genomics and Sequencing Center.

Raw sequence data can be found on NCBI under BioProject number PRJNA327394 (https://www.ncbi.nlm.nih.gov/bioproject/327394).

Sampling Gaps:
Samples were not collected In February, March, April, and December 2012.

Data Processing Description

Sequence analysis and taxonomic assignment
To ultimately assign taxon identity to each read, paired-end sequencing reads were first processed using Cutadapt (Martin, 2011; version 2.10) to remove primers and Illumina adaptors. Reads were then processed and taxonomically assigned using the Divisive Amplicon Denoising Algorithm (DADA2) R package (Callahan et al. 2016; version 1.16). Forward (F) and reverse (R) reads were trimmed (F: 220 nucleotides (nt) and R: 210 nt), filtered (maxEE = F/ R: 2, truncQ = F/R: 2), denoised, and merged. Chimeras were removed using the consensus method in DADA2 (Callahan et al. 2016). Taxonomy was assigned to amplicon sequence variants (ASVs) using a naïve Bayesian classifier algorithm (Wang et al. 2007) with a minimum bootstrap confidence of 80% using the Protist Ribosomal Reference database (Guillou et al. 2013). ASVs that were identified to the same species were retained as separate ASVs here because the primers we used amplify a region of the 18S rRNA gene that has been shown to predominantly recover differences among species and not strains (Zimmermann et al. 2011). For ASVs where no species level information could be obtained, the species was reported as "Genus sp#" (e.g.,

"Chaetoceros sp1").

An additional taxonomic assignment step was performed using the assignSpecies function (Callahan et al. 2016) to allow for a single ASV to be assigned multiple species which resulted in some ASVs being classified as species groups because their sequences were not unique at the V4 region of the 18S rRNA gene. For *Skeletonema* and *Thalassiosira* ASVs, assignment of these sequences was performed upon manual examination of ASV sequences in Geneious (Kearse et al. 2012). The sequences were compared to a custom reference database for *Skeletonema* and *Thalassiosira* and taxonomies were assigned with 100% identity (Canesi and Rynearson 2016; Rynearson et al. 2020; accessible under DOI 10.5281/zenodo.10067598). The final dataset contained only ASVs that made up more than 0.075% of total sequence reads per sample, a threshold based on mock community analysis to determine spurious ASVs (Reitmeier et al. 2021).

BCO-DMO Processing Description

- Imported original file "Diatom_ASV_Table_V2.csv" into the BCO-DMO system.
- Flagged 'NA' as a missing data value. Missing data are blank/empty in the final CSV file.
- Created columns for Longitude and Latitude and filled in with the coordinates of the sampling locations provided in the metadata.
- Renamed the "Sample" column to "Sample_Date".
- Saved the final file as "911102_v1_diatom_asvs_narragansett.csv".

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Data Files

File	
911102_v1_diatom_asvs_narragansett.csv	(Comma Separated Values (.csv), 521.80 KB) MD5:f7f6736d0f4117342ca8332a477da061
Primary data file for dataset ID 911102, version 1.	

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Related Publications

Callahan, B. J., McMurdie, P. J., Rosen, M. J., Han, A. W., Johnson, A. J. A., & Holmes, S. P. (2016). DADA2: High-resolution sample inference from Illumina amplicon data. Nature Methods, 13(7), 581–583. doi:10.1038/nmeth.3869
Methods

Canesi, K., & Rynearson, T. (2016). Temporal variation of Skeletonema community composition from a long-term time series in Narragansett Bay identified using high-throughput DNA sequencing. Marine Ecology Progress Series, 556, 1–16. doi:10.3354/meps11843
Methods

Diana Fontaine. (2023). difontaine/Fontaine_Rynearson_2023: Zenodo DOI (Version Zenodo_v1) [Computer software]. Zenodo. https://doi.org/10.5281/ZENODO.10067598
Software

Fontaine, D. N., & Rynearson, T. A. (2023). Multi-year time series reveals temporally synchronous diatom communities with annual frequency of recurrence in a temperate estuary. Limnology and Oceanography, 68(9), 1982–1994. Portico. https://doi.org/10.1002/lno.12400
Results

Guillou, L., Bachar, D., Audic, S., Bass, D., Berney, C., Bittner, L., ... & Christen, R. (2012). The Protist Ribosomal Reference database (PR2): a catalog of unicellular eukaryote small sub-unit rRNA sequences with curated taxonomy. Nucleic acids research, 41(D1), D597-D604. https://doi.org/10.1093/nar/gks1160
Methods

Kearse, M., Moir, R., Wilson, A., Stones-Havas, S., Cheung, M., Sturrock, S., ... Drummond, A. (2012). Geneious Basic: An integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics, 28(12), 1647–1649. doi:10.1093/bioinformatics/bts199
Methods

Martin, M. (2011). Cutadapt removes adapter sequences from high-throughput sequencing reads. EMBnet.journal, 17(1), 10. doi:10.14806/ej.17.1.200
Methods

Reitmeier, S., Hitch, T. C. A., Treichel, N., Fikas, N., Hausmann, B., Ramer-Tait, A. E., Neuhaus, K., Berry, D., Haller, D., Lagkouvardos, I., & Clavel, T. (2021). Handling of spurious sequences affects the outcome of high-throughput 16S rRNA gene amplicon profiling. ISME Communications, 1(1). https://doi.org/10.1038/s43705-021-00033-z
Methods

Rynearson, T. A., Flickinger, S. A., & Fontaine, D. N. (2020). Metabarcoding Reveals Temporal Patterns of Community Composition and Realized Thermal Niches of Thalassiosira Spp. (Bacillariophyceae) from the Narragansett Bay Long-Term Plankton Time Series. Biology, 9(1), 19. https://doi.org/10.3390/biology9010019
Methods

Wang, Q., Garrity, G. M., Tiedje, J. M., & Cole, J. R. (2007). Naïve Bayesian Classifier for Rapid Assignment of rRNA Sequences into the New Bacterial Taxonomy. Applied and Environmental Microbiology, 73(16), 5261–5267. https://doi.org/10.1128/aem.00062-07 https://doi.org/10.1128/AEM.00062-07
Methods

Zimmermann, J., Jahn, R., & Gemeinholzer, B. (2011). Barcoding diatoms: evaluation of the V4 subregion on the 18S rRNA gene, including new primers and protocols. Organisms Diversity & Evolution, 11(3), 173–192. https://doi.org/10.1007/s13127-011-0050-6
Methods

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Related Datasets

IsRelatedTo

Thibodeau, P., Rynearson, T. A. (2022) **Weekly surface water quality measurements in Narragansett Bay from 1959-2019.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2022-07-28 doi:10.26008/1912/bco-dmo.874956.1 [view at BCO-DMO]

University of Rhode Island. Thalassiosira spp., Community composition of diatom genus Thalassiosira in Narragansett Bay. 2016/06. In: BioProject [Internet]. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; 2011-. Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA327394. NCBI:BioProject: PRJNA327394.

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Parameters

Parameter	Description	Units
Sample_Date	Sample date	unitless
Year	Sample year	unitless
Month	Sample month	unitless
Week	Sample week. Week number can be used to cross-reference the environmental data in the "Narragansett Bay Plankton Time Series" dataset (https://www.bco-dmo.org/dataset/874956)	unitless
Latitude	Latitude of sample collection location. Positive values = North.	decimal degrees
Longitude	Longitude of sample collection location. Negative values = West.	decimal degrees
ASV	Amplicon Sequence Variant (ASV) obtained from sequence processing	unitless
Kingdom	Taxonomic kingdom	unitless
Supergroup	Taxonomic supergroup	unitless
Division	Taxonomic division	unitless
Class	Taxonomic class	unitless
Order	Taxonomic order	unitless
Family	Taxonomic family	unitless
Genus	Taxonomic genus	unitless
Species	Taxonomic species	unitless

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Instruments

Dataset-specific Instrument Name	Niskin bottle
Generic Instrument Name	Niskin bottle
Dataset-specific Description	A Niskin bottle was used to collect surface water in the field.
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.

Dataset-specific Instrument Name	Illumina MiSeq platform
Generic Instrument Name	Automated DNA Sequencer
Generic Instrument Description	General term for a laboratory instrument used for deciphering the order of bases in a strand of DNA. Sanger sequencers detect fluorescence from different dyes that are used to identify the A, C, G, and T extension reactions. Contemporary or Pyrosequencer methods are based on detecting the activity of DNA polymerase (a DNA synthesizing enzyme) with another chemoluminescent enzyme. Essentially, the method allows sequencing of a single strand of DNA by synthesizing the complementary strand along it, one base pair at a time, and detecting which base was actually added at each step.

Dataset-specific Instrument Name	Eppendorf Mastercycler EP Gradient
Generic Instrument Name	PCR Thermal Cycler
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Project Information

Dimensions: Collaborative Research: Genetic, functional and phylogenetic diversity determines marine phytoplankton community responses to changing temperature and nutrients (Phytoplankton Community Responses)

Coverage: Narragansett Bay, RI and Bermuda, Bermuda Atlantic Time-series Study (BATS)

NSF Award Abstract:
Photosynthetic marine microbes, phytoplankton, contribute half of global primary production, form the base of most aquatic food webs and are major players in global biogeochemical cycles. Understanding their community composition is important because it affects higher trophic levels, the cycling of energy and elements and is sensitive to global environmental change. This project will investigate how phytoplankton communities respond to two major global change stressors in aquatic systems: warming and changes in nutrient availability. The researchers will work in two marine systems with a long history of environmental monitoring, the temperate Narragansett Bay estuary in Rhode Island and a subtropical North Atlantic site near Bermuda. They will use field sampling and laboratory experiments with multiple species and varieties of phytoplankton to assess the diversity in their responses to different temperatures under high and low nutrient concentrations. If the diversity of responses is high within species, then that species may have a better chance to adapt to rising temperatures and persist in the future. Some species may already be able to grow at high temperatures; consequently, they may become more abundant as the ocean warms. The researchers will incorporate this response information in mathematical models to predict how phytoplankton assemblages would reorganize under future climate scenarios. Graduate students and postdoctoral associates will be trained in diverse scientific approaches and techniques such as shipboard sampling, laboratory experiments, genomic analyses and mathematical modeling. The results of the project will be incorporated into K-12 teaching, including an advanced placement

environmental science class for underrepresented minorities in Los Angeles, data exercises for rural schools in Michigan and disseminated to the public through an environmental journalism institute based in Rhode Island.

Predicting how ecological communities will respond to a changing environment requires knowledge of genetic, phylogenetic and functional diversity within and across species. This project will investigate how the interaction of phylogenetic, genetic and functional diversity in thermal traits within and across a broad range of species determines the responses of marine phytoplankton communities to rising temperature and changing nutrient regimes. High genetic and functional diversity within a species may allow evolutionary adaptation of that species to warming. If the phylogenetic and functional diversity is higher across species, species sorting and ecological community reorganization is likely. Different marine sites may have a different balance of genetic and functional diversity within and across species and, thus, different contribution of evolutionary and ecological responses to changing climate. The research will be conducted at two long-term time series sites in the Atlantic Ocean, the Narragansett Bay Long-Term Plankton Time Series and the Bermuda Atlantic Time Series (BATS) station. The goal is to assess intra- and inter-specific genetic and functional diversity in thermal responses at contrasting nutrient concentrations for a representative range of species in communities at the two sites in different seasons, and use this information to parameterize eco-evolutionary models embedded into biogeochemical ocean models to predict responses of phytoplankton communities to projected rising temperatures under realistic nutrient conditions. Model predictions will be informed by and tested with field data, including the long-term data series available for both sites and in community temperature manipulation experiments. This project will provide novel information on existing intraspecific genetic and functional thermal diversity for many ecologically and biogeochemically important phytoplankton species, estimate generation of new genetic and functional diversity in evolution experiments, and develop and parameterize novel eco-evolutionary models interfaced with ocean biogeochemical models to predict future phytoplankton community structure. The project will also characterize the interaction of two major global change stressors, warming and changing nutrient concentrations, as they affect phytoplankton diversity at functional, genetic, and phylogenetic levels. In addition, the project will develop novel modeling methodology that will be broadly applicable to understanding how other types of complex ecological communities may adapt to a rapidly warming world.

LTER: Linking Pelagic Community Structure with Ecosystem Dynamics and Production Regimes on the Changing Northeast US Shelf (NES LTER)

Website: https://nes-lter.whoi.edu/

Coverage: Northeast U.S. Continental Shelf Large Marine Ecosystem: 35.2019 to 46.0906 latitude, -77.3492 to -63.3608 longitude

NSF Award Abstract:

The northwest Atlantic is renowned for productive fisheries that depend upon a complex food web of planktonic organisms that provide them energy. In these waters -- as in coastal waters around the globe -- human activities, environmental variability, and decadal-scale change intersect to have diverse effects on the planktonic food web. It is crucial to understand the structure of this web, how it functions, and how it responds to seasonal environmental change, in order to respond appropriately to long-term trends that are accelerating in this region. Our understanding, however, has been limited by a lack of systematic and detailed measurements over a sufficient length of time so that we can observe the responses of these webs to environmental perturbations and uncover the underlying causes and implications. The Northeast US Shelf (NES) Long-Term Ecological Research (LTER) project will provide such observations, analyze them with a variety of models, and improve our ability to predict how planktonic food webs change through space and time, and how those changes impact the productivity of higher trophic levels including commercially important fish. In addition, the NES-LTER project will have multifaceted broader impacts, including collaboration with the National Oceanic and Atmospheric Administration's (NOAA), Northeast Fisheries Science Center to support multispecies, ecosystem-based management on the NES. The project includes an education plan that will provide opportunities to a broad range of learners and a far-reaching public outreach component will be developed through NOAA's international Science-On-a-Sphere network.

While patterns of ecosystem change over seasons to decades have already been documented in this region, the key mechanisms linking changes in the physical environment, planktonic food webs, and higher trophic levels remain poorly understood. For this reason, predictive capability is limited and management strategies are largely reactive. To address these needs, the NES-LTER strategy combines observations that provide regional-scale context, process cruises along a high gradient cross-shelf transect, high-frequency time series at inner- and outer-shelf locations, coupled biological-physical food web models, and targeted population models. The research plan is guided by an overarching science question: How is long-term environmental change impacting the pelagic NES ecosystem and, in particular, affecting the relationship between compositional (e.g., species diversity and size structure) and aggregate (e.g., rates of primary production, and transfer of energy to important forage fish species) variability? By capitalizing on high levels of seasonal and interannual variability in the NES, the research will study short-term responses to change in the environment to a) characterize low and high export food webs, b) understand the linkages and transfer of energy from the phytoplankton to pelagic fish, and c) identify the mechanisms that underlie shifts between high and low export communities. Ultimately, mechanistic knowledge will be scaled up to understand and predict the impacts and feedbacks associated with trends in decadal-scale forcing in the ecosystem.

Additional Information:

The NES-LTER project includes collaboration with the National Marine Fisheries Service / Northeast Fisheries Science Center [NMFS/NEFSC] in particular for sharing data related to Project EcoMon Zooplankton https://www.bco-dmo.org/project/2106.

Narragansett Bay Long-Term Plankton Time Series (NBPTS)

Website: https://web.uri.edu/gso/research/plankton/

The Narragansett Bay Long-Term Plankton Time Series is one of the world's longest-running plankton surveys. Beginning in 1957, weekly samples have been collected to assess the phytoplankton community and characterize the physical parameters of Narragansett Bay.

Samples are collected once per week -regardless of tidal stage- for temperature, salinity, turbidity, size-fractionated chlorophyll a and nutrients. Microplankton community composition (size range >10µm, both species identification and abundance) is determined using a light microscope to quantify live samples. The species list for the >10µm size fraction includes 246 different species or species complexes of protists. Samples are also collected for the determination of copepod and ctenophore concentrations.

Funding for the time series has come from the University of Rhode Island since 1999. Ship time is frequently provided by the U.S. Department of Fish and Wildlife.

This Time Series is related to the following projects at BCO-DMO:

- Connecting local, regional and global scales of gene flow in planktonic marine diatoms (https://www.bco-dmo.org/project/511708)
- Dimensions: Collaborative Research: Genetic, functional and phylogenetic diversity determines marine phytoplankton community responses to changing temperature and nutrients (https://www.bco-dmo.org/project/712787)
- LTER: Linking Pelagic Community Structure with Ecosystem Dynamics and Production Regimes on the Changing Northeast US Shelf (https://www.bco-dmo.org/project/747769)
- Quantifying Temperature Dependence In Growth & Grazing Rates of Planktonic Herbivores (https://www.bco-dmo.org/project/739232)
- RII Track-1: Rhode Island Consortium for Coastal Ecology Assessment, Innovation, and Modeling (https://www.bco-dmo.org/project/836631)

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Program Information

Dimensions of Biodiversity (Dimensions of Biodiversity)

Website: http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=503446

Coverage: global

(adapted from the NSF Synopsis of Program)

Dimensions of Biodiversity is a program solicitation from the NSF Directorate for Biological Sciences. FY 2010 was year one of the program. [MORE from NSF]

The NSF Dimensions of Biodiversity program seeks to characterize biodiversity on Earth by using integrative, innovative approaches to fill rapidly the most substantial gaps in our understanding. The program will take a broad view of biodiversity, and in its initial phase will focus on the integration of genetic, taxonomic, and functional dimensions of biodiversity. Project investigators are encouraged to integrate these three dimensions to understand the interactions and feedbacks among them. While this focus complements several core NSF programs, it differs by requiring that multiple dimensions of biodiversity be addressed simultaneously, to understand the roles of biodiversity in critical ecological and evolutionary processes.

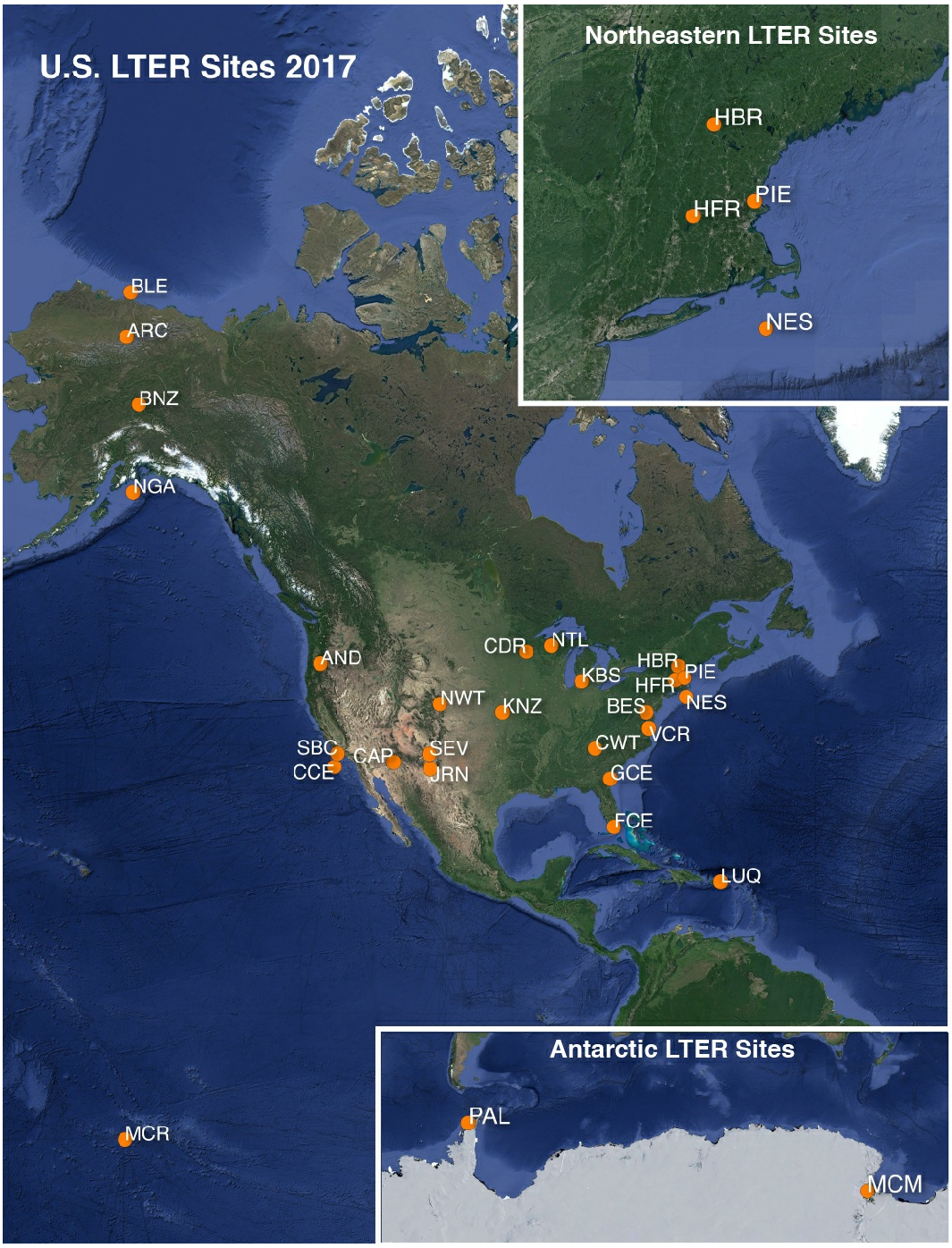
Long Term Ecological Research network (LTER)

Website: http://www.lternet.edu/

Coverage: United States

adapted from http://www.lternet.edu/

The National Science Foundation established the LTER program in 1980 to support research on long-term ecological phenomena in the United States. The Long Term Ecological Research (LTER) Network is a collaborative effort involving more than 1800 scientists and students investigating ecological processes over long temporal and broad spatial scales. The LTER Network promotes synthesis and comparative research across sites and ecosystems and among other related national and international research programs. The LTER research sites represent diverse ecosystems with emphasis on different research themes, and cross-site communication, network publications, and research-planning activities are coordinated through the LTER Network Office.



Site Codes

AND	Andrews Forest LTER
ARC	Arctic LTER
BES	Baltimore Ecosystem Stu
BLE	Beaufort Lagoon Ecosystems LTER
BNZ	Bonanza Creek LTER
CCE	California Current Ecosystem LTER
CDR	Cedar Creek Ecosystem Science Reserve
CAP	Central Arizona-Phoenix LTER
CWT	Coweeta LTER
FCE	Florida Coastal Everglades LTER
GCE	Georgia Coastal Ecosystems LTER
HFR	Harvard Forest LTER
HBR	Hubbard Brook LTER
JRN	Jornada Basin LTER
KBS	Kellogg Biological Station LTER
KNZ	Konza Prairie LTER
LUQ	Luquillo LTER
MCM	McMurdo Dry Valleys LT
MCR	Moorea Coral Reef LTEF
NWT	Niwot Ridge LTER
NTL	North Temperate Lakes I
NES	Northeast U.S. Shelf LTE
NGA	Northern Gulf of Alaska I
PAL	Palmer Antarctica LTER
PIE	Plum Island Ecosystems LTER
SBC	Santa Barbara Coastal L
SEV	Sevilleta LTER
VCR	Virginia Coast Reserve L

2017 LTER research site map obtained from https://lternet.edu/site/lter-network/

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1638834
NSF Division of Ocean Sciences (NSF OCE)	OCE-1655686

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