Amplicon sequence variants (ASVs) and taxonomy of Pseudo-nitzschia spp. from Narragansett Bay in Rhode Island, USA and the Northeast U.S. Shelf (NES-LTER transect) from 2018-2023

Website: https://www.bco-dmo.org/dataset/936849
Data Type: experimental, Other Field Results
Version: 1
Version Date: 2024-10-11

Project
» Northeast U.S. Shelf Long Term Ecological Research site (NES LTER)
» RII Track-1: Rhode Island Consortium for Coastal Ecology Assessment, Innovation, and Modeling (C-AIM)
» Narragansett Bay Long-Term Plankton Time Series (NBPTS)

Program
» Long Term Ecological Research network (LTER)

Contributors	Affiliation	Role
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Abstract
This dataset includes amplicon sequence variants (ASVs) representing species of the harmful algal bloom diatom genus Pseudo-nitzschia that were sampled from various sites in Narragansett Bay, Rhode Island, including the Narragansett Bay Long Term Plankton Time Series site, and various stations along the Northeast U.S. Shelf Long Term Ecological Research program transect. These data correspond to an analysis of Pseudo-nitzschia species composition and domoic acid toxin production during winters and summers from 2018-2023 in Narragansett Bay and the Northeast U.S. Shelf, which was prepared for submission to Harmful Algae (Roche, et al.). ASVs are also available under NCBI GenBank Accession Numbers PQ002243 - PQ002350 and MW447658 - MW447770 and raw sequencing data is available under NCBI Sequence Read Archive Accession numbers associated with BioSample accessions SAMN42123204 - 42123391 within BioProject PRJNA1129077.

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Coverage

Location: Narragansett Bay in Rhode Island, USA and offshore Atlantic Ocean transect across the Northeast U.S. Shelf (NES).
Spatial Extent: **N**:41.57 **E**:-70.77 **S**:39.93 **W**:-71.42
Temporal Extent: 2018-01-31 - 2023-01-16

Dataset Description

Acknowledgement:

We acknowledge the NSF RI C-AIM EPSCoR Cooperative Agreement (OIA-1004057) for research support. Sequencing was performed at the University of Rhode Island Molecular Informatics Core supported by the Institutional Development Award (IDeA) Network for Biomedical Research Excellence from the National Institute of General Medical Sciences of the National Institutes of Health (P20GM103430).

Methods & Sampling

Samples were selected from the NES-LTER transect and various time series sites in Narragansett Bay, Rhode Island (NB) during winter and summer periods from January 2018 through February 2023 to compare seasonal and regional patterns of *Pseudo-nitzschia* species composition and DA, as well as environmental drivers. NB and NES will henceforth be referred to as subregions of the larger Northeast U.S. Continental Shelf region, with NES specifically referring to the area spanned by the NES-LTER transect. Samples were collected on NES-LTER cruises (*R/V* Endeavor, *R/V* Atlantis) from 11 stations along a 150 km transect (n=77) each winter (January-February) and summer (July-August). Samples from three to four stations per cruise were used in this dataset spanning innershelf (L1), midshelf (L3, L4) and outershelf (L7, L8, L10) sections of the transect. The northernmost station, L1, is about 50 km from the mouth of NB. To collect plankton biomass for nucleic acid isolation, CTD rosette seawater from the surface and subsurface chlorophyll maximum (SCM) were passed via peristaltic pump over 25 mm 5 µm pore size filters (Sterlitech, Kent, WA, USA). Biomass filters were either flash frozen in liquid nitrogen (2018-2022) or placed in DNA/RNA shield (winter 2023; Zymo Research, Irvine, CA, USA) and stored in a -80°C freezer. The SCM depth varied as observed by *in situ* chlorophyll fluorescence, with a median depth of 28 m for summer and 19 m for winter samples. In cases where the SCM was not well defined due to water column mixing that typically took place in winter at nearshore stations, a sampling depth between 20 and 30 m was targeted.

In NB, surface seawater samples were collected from various sites in the East and West Passages including the Narragansett Bay Long-Term Plankton Time Series (NBPTS) site, Whale Rock (WR), Castle Hill Beach (CHB), East Passage (EP), and University of Rhode Island Graduate School of Oceanography (GSO) dock. Seawater was transported back to the laboratory and passed over 25 mm 5 µm pore size filters (Sterlitech, Kent, WA, USA) using a peristaltic pump before flash freezing in liquid nitrogen and storage at -80°C. To fill in several missing dates from this time series, six samples collected separately in the NBPTS (https://web.uri.edu/gso/research/plankton/) sampling program were used. These samples differed in collection methodology only by the filter pore size used (0.22 µm, Express Plus, Millipore Sigma) and vacuum as opposed to peristaltic filtration.

DNA was extracted from most NB and NES samples (n=219) using a modified version of the DNeasy Plant Kit (Qiagen, Germantown, MD, USA) that included a 1-minute bead beating step (0.1 mm and 0.5

mm Zirconia/Silica beads, BioSpec Products, Bartlesville, OK, USA) and two part elution into a total of 45 µL Buffer AE. Similarly, the six NBPTS samples were extracted using a modified version of the DNeasy Blood & Tissue kit (Qiagen, Germantown, MD, USA) with a 1-minute bead beating step and final elution into 50 µL Buffer AE. Some NES samples (n=18) were extracted using the Quick-DNA/RNA Miniprep Plus Kit (Zymo Research, Irvine, CA, USA) with a 1-minute bead beating step (0.4 mm Zirconium Beads, OPS Diagnostics, Lebanon, NJ, USA) and final elution into 50 µL nuclease-free water. DNA from each sample was amplified with a primer set that targets the eukaryotic internal transcribed spacer region 1 (ITS1) and effectively distinguishes *Pseudo-nitzschia* species (White et al., 1990; Sterling et al., 2022). Briefly, DNA was diluted to 1-4 ng/µL and 2 µL of template was added to 25 µL PCR reactions with Phusion Hot Start High-Fidelity Master Mix (Thermo Fisher Scientific Inc., Waltham, MA, USA) and HPLC-purified forward and reverse primers at 0.5 µM concentration with Illumina MiSeq adapters (Integrated DNA Technologies, Coralville, IA, USA). A stepwise thermocycle was used as described in Sterling et al. (2022).

DNA amplicons were sequenced at the Rhode Island-INBRE Molecular Informatics Core on the Illumina MiSeq platform (Illumina, Inc., San Diego, CA, USA). There, libraries were prepared by cleaning ITS1 PCR products with KAPA pure beads (KAPA Biosystems, Woburn, MA, USA) and attaching sequencing indices and adapters using PCR. This amplification was performed with the Illumina Nextera XT Index Kit (Illumina, San Diego, CA, USA) and Phusion High Fidelity Master Mix, followed by a second round of cleaning with KAPA pure beads and visualization with gel electrophoresis. The quality of select samples was assessed on a Bioanalyzer DNA1000 chip (Agilent Technologies, Santa Clara, CA, USA) and all samples were quantified on a Qubit fluorometer (Invitrogen, Carlsbad, CA, USA). The final library was pooled, quantified with qPCR on a LightCycler480 (Roche, Pleasanton, CA, USA) using a KAPA Biosystems Illumina Kit (KAPA Biosystems, Woburn, MA, USA), and sequenced on the Illumina MiSeq using v3 chemistry and 2x250 paired-end reads. Samples were sequenced across five separate MiSeq runs using identical methods and negative controls.

Sampling Locations

Narragansett Bay sites:

Narragansett Bay Long Term Plankton Time Series (41.57 N -71.39 W)

Whale Rock (41.43 N -71.42 W)

East Passage (41.45 N -71.38 W)

Castle Hill Beach (41.46 N -71.36 W)

Graduate School of Oceanography dock (41.49 N -71.42 W)

NES stations:

L1 (41.20 N -70.88 W), L3 (40.86 N -70.88 W), L4 (40.70 N -70.88 W), L7 (40.23 N -70.88 W), L8 (40.14 N -70.77 W), L10 (39.93 N -70.88 W)

Data Processing Description

Raw sequencing read quality was assessed using FastQC and MultiQC (v.0.11.9, v1.11) before and after primer and adapter trimming in Cutadapt (v3.2). The Divisive Amplicon Denoising Algorithm (DADA2) was used in R to estimate sequencing error and identify distinct amplicon sequence variants (ASVs) (v1.20.0). DADA2 was run separately for each sequencing run because it is designed to account for run-specific error. Taxonomy was assigned to ASVs from all sequencing runs using a dual approach to maximize the number of ASVs identified to the species level and enhance confidence. First, the scikit-learn naïve Bayes machine learning classifier in QIIME2 (v2022.11) and a curated reference database were used to assign taxonomy with a confidence threshold of 0.8. This curated database from Roche et al. (2022) included 302 unique *Pseudo-nitzschia* spp. ITS1 sequences from the National Center for Biotechnology Information (NCBI) GenBank with 51 different species represented (retrieved June 1, 2021). Next, to ensure that relevant *Pseudo-nitzschia* spp. ITS1 taxonomy was not omitted from the curated database, a megablast search was performed using the entire BLAST nt database. Additional ASVs classified by megablast were retained if there was >99% identity and >99% query cover to NCBI *Pseudo-nitzschia* species. If QIIME2 and megablast taxonomic assignment did not match for a particular ASV, no species-level taxonomy was assigned. Samples containing no reads identified to the *Pseudo-nitzschia* species level were removed from the analysis (n=15). To avoid potentially falsely detected taxa, ASVs classified as a species that appeared in only one sample across the dataset were discarded (n=6).

BCO-DMO Processing Description

1) Processed the submitted data file DATASET01_PN_ASVs_taxonomy.csv with the BCO-DMO tool Laminar.

Added a version number of 1 to the accession values in the column NCBI_GenBank_Accession_Numbe so that it is a GenBank accession value (which includes a version number).

Added a column named BioProject containing the BioProject accession number PRJNA1129077.

Saved the modified dataset to the file 936849_v1_pseudo_nitzschia_amplicon_seq_variant.csv.

2) Created a taxonomy table using the species names in the dataset and getting taxonomy values using the World Register of Marine Species (WoRMS) website and saved it to the file species_taxonomy.csv.

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Data Files

File
936849_v1_pseudo_nitzschia_amplicon_seq_variant.csv (Comma Separated Values (.csv), 64.46 KB) MD5:d2c2d4c168a2030dec5a1e0b25e89a41 Primary data file for dataset ID 936849, version 1

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Supplemental Files

File
Species taxonomy filename: species_taxonomy.csv (Comma Separated Values (.csv), 4.61 KB) MD5:b71fe109919c3fcab434fab08c771763 Species taxonomy from WoRMS with columns: ScientificName, AphiaID, LSID, Kingdom, Phylum, Class, Order, Family, Genus, Species

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Related Publications

Andrews S. (2010). FastQC: a quality control tool for high throughput sequence data. Available online at: http://www.bioinformatics.babraham.ac.uk/projects/fastqc
Software

Bolyen, E., Rideout, J. R., Dillon, M. R., Bokulich, N. A., Abnet, C. C., Al-Ghalith, G. A., … Asnicar, F. (2019). Reproducible, interactive, scalable and extensible microbiome data science using QIIME 2. Nature Biotechnology, 37(8), 852–857. doi:10.1038/s41587-019-0209-9
Software

Ewels, P., Magnusson, M., Lundin, S., & Käller, M. (2016). MultiQC: summarize analysis results for multiple tools and samples in a single report. Bioinformatics, 32(19), 3047–3048.

doi:10.1093/bioinformatics/btw354
Software

FastQC (2015), FastQC [Online]. Available online at: https://qubeshub.org/resources/fastqc.
Software

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

R Core Team (2023). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL https://www.R-project.org/
Software

Roche, K. M., Sterling, A. R., Rynearson, T. A., Bertin, M. J., & Jenkins, B. D. (2022). A Decade of Time Series Sampling Reveals Thermal Variation and Shifts in Pseudo-nitzschia Species Composition That Contribute to Harmful Algal Blooms in an Eastern US Estuary. Frontiers in Marine Science, 9. https://doi.org/10.3389/fmars.2022.889840
Methods

Roche, K.M., Church, I.N., Sterling, A.R., Rynearson, T.A., Bertin, M.J., Kim, A.M., Kirk, R.D., Jenkins, B.D. (2024). Connectivity of toxigenic Pseudo-nitzschia species assemblages between the Northeast U.S. continental shelf and an adjacent estuary. Manuscript submitted for publication.
Results

Sterling, A. R., Kirk, R. D., Bertin, M. J., Rynearson, T. A., Borkman, D. G., Caponi, M. C., Carney, J., Hubbard, K. A., King, M. A., Maranda, L., McDermith, E. J., Santos, N. R., Strock, J. P., Tully, E. M., Vaverka, S. B., Wilson, P. D., & Jenkins, B. D. (2022). Emerging harmful algal blooms caused by distinct seasonal assemblages of a toxic diatom. Limnology and Oceanography, 67(11), 2341–2359. Portico. https://doi.org/10.1002/lno.12189
Methods

White, T. J., Bruns, T., Lee, S., & Taylor, J. (1990). AMPLIFICATION AND DIRECT SEQUENCING OF FUNGAL RIBOSOMAL RNA GENES FOR PHYLOGENETICS. PCR Protocols, 315–322. https://doi.org/10.1016/b978-0-12-372180-8.50042-1 https://doi.org/10.1016/B978-0-12-372180-8.50042-1
Methods

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Related Datasets

IsRelatedTo

Roche, K. M., Church, I., Sterling, A., Rynearson, T. A., Bertin, M., Kim, A., Kirk, R., Jenkins, B. D. (2024) **Pseudo-nitzschia spp. presence-absence and environmental data in Narragansett Bay in Rhode Island, USA and the Northeast U.S. Shelf (NES-LTER transect) from 2018-2023.** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2024-10-14 doi:10.26008/1912/bco-dmo.936856.1 [view at BCO-DMO]

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Parameters

Parameter	Description	Units
Species	Taxonomic assignment of Pseudo-nitzschia species	unitless
Assignment_method	Method used for taxonomic assignment. QIIME2 indicates the QIIME2 scikit-learn naïve Bayes machine learning classifier was used with a curated Pseudo-nitzschia species database to assign taxonomy. Megablast means that an Amplicon Sequence Variant (ASV) was assigned using a megablast search of NCBI's nr database with a threshold of >99% percent identity and >99% query coverage.	unitless
NCBI_GenBank_Accession_Number	GenBank accession number associated with an Amplicon Sequence Variant (ASV)	unitless
Genbank_ASV_number	Amplicon Sequence Variant (ASV) number assigned during GenBank submission	unitless
ASV_seq	DNA sequence of Amplicon Sequence Variant (ASV)	unitless
BioProject	NCBI BioProject accession number	unitless

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Instruments

Dataset-specific Instrument Name	Illumina MiSeq Next Generation Sequencing
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Manufactured by Illumina, Inc., San Diego, CA, USA
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	CTD rosette
Generic Instrument Name	CTD - profiler
Generic Instrument Description	The Conductivity, Temperature, Depth (CTD) unit is an integrated instrument package designed to measure the conductivity, temperature, and pressure (depth) of the water column. The instrument is lowered via cable through the water column. It permits scientists to observe the physical properties in real-time via a conducting cable, which is typically connected to a CTD to a deck unit and computer on a ship. The CTD is often configured with additional optional sensors including fluorometers, transmissometers and/or radiometers. It is often combined with a Rosette of water sampling bottles (e.g. Niskin, GO-FLO) for collecting discrete water samples during the cast. This term applies to profiling CTDs. For fixed CTDs, see https://www.bco-dmo.org/instrument/869934.

Dataset-specific Instrument Name	peristaltic pump
Generic Instrument Name	Pump
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

Dataset-specific Instrument Name	LightCycler480
Generic Instrument Name	qPCR Thermal Cycler
Dataset-specific Description	Benchtop instrument. The LightCycler® 480 System features a versatile, plate-based, real-time PCR device that supports mono- or multicolor applications. Manufactured by Roche, Pleasanton, CA, USA
Generic Instrument Description	An instrument for quantitative polymerase chain reaction (qPCR), also known as real-time polymerase chain reaction (Real-Time PCR).

Dataset-specific Instrument Name	Qubit fluorometer
Generic Instrument Name	Qubit fluorometer
Dataset-specific Description	Manufactured by Invitrogen, Carlsbad, CA, USA
Generic Instrument Description	Benchtop fluorometer. The Invitrogen Qubit Fluorometer accurately and quickly measures the concentration of DNA, RNA, or protein in a single sample. It can also be used to assess RNA integrity and quality. Manufactured by Invitrogen, Carlsbad, CA, USA (Invitrogen is one of several brands under the Thermo Fisher Scientific corporation.)

Dataset-specific Instrument Name	Eppendorf Mastercycler EP Thermal Cycler Series
Generic Instrument Name	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. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

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Deployments

EN608

Website	https://www.bco-dmo.org/deployment/848016
Platform	R/V Endeavor
Start Date	2018-01-31
End Date	2018-02-06
Description	C-AIM project

EN617

Website	https://www.bco-dmo.org/deployment/848018
Platform	R/V Endeavor
Start Date	2018-07-20
End Date	2018-07-25

EN627

Website	https://www.bco-dmo.org/deployment/848056
Platform	R/V Endeavor
Start Date	2019-02-01
End Date	2019-02-06

EN644

Website	https://www.bco-dmo.org/deployment/848020
Platform	R/V Endeavor
Start Date	2019-08-20
End Date	2019-08-25

EN649

Website	https://www.bco-dmo.org/deployment/940001
Platform	R/V Endeavor
Start Date	2020-02-01
End Date	2020-02-06
Description	Project: NES-LTER # 4

EN655

Website	https://www.bco-dmo.org/deployment/940004
Platform	R/V Endeavor
Start Date	2020-07-25
End Date	2020-07-28
Description	Project: NES-LTER

EN661

Website	https://www.bco-dmo.org/deployment/940007
Platform	R/V Endeavor
Start Date	2021-02-03
End Date	2021-02-08
Description	Project: NES-LTER transect #8

EN668

Website	https://www.bco-dmo.org/deployment/940010
Platform	R/V Endeavor
Start Date	2021-07-16
End Date	2021-07-21
Description	Project: NES-LTER transect #9

EN687

Website	https://www.bco-dmo.org/deployment/940013
Platform	R/V Endeavor
Start Date	2022-07-29
End Date	2022-08-03
Description	Project: NES - LTER Summer 2022

EN695

Website	https://www.bco-dmo.org/deployment/940016
Platform	R/V Endeavor
Start Date	2023-01-11
End Date	2023-01-16
Description	Project: NES-LTER 2023-01

AT46

Website	https://www.bco-dmo.org/deployment/940019
Platform	R/V Atlantis
Start Date	2022-02-16
End Date	2022-02-21
Description	Project: LTER: Linking Pelagic Community Structure with Ecosystem Dynamics and Production Regimes on the Changing Northeast US Shelf

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Project Information

Northeast U.S. Shelf Long Term Ecological Research site (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

Continuing Award OCE-2322676
Sep 2023 to Aug 2028 (estimated)
LTER: Scales of Variability in Ecosystem Dynamics and Production on the Changing Northeast U.S. Shelf (NES II)
NSF Award Abstract:

The Northeast U.S. Shelf (NES) is the region of the Northwest Atlantic Ocean that overlies the continental shelf from North Carolina to Maine. The NES has a long history of intense human utilization and provides an array of ecosystem services including shipping, recreation, conservation, and energy development. The NES also comprises a seasonally dynamic and productive ecosystem, supporting renowned fisheries, whose integrity is critical to the health of the Northeast U.S. economy. The NES ecosystem's productivity is fueled by planktonic organisms that interact with each other in complex food webs whose structure depends on environmental conditions (e.g., temperature, light, and nutrient levels). These conditions are rapidly changing because of climate-change-related warming and human utilization. For example, the NES is seeing the largest development of coastal wind farms in the U.S. to date. Phase II of the Northeast U.S. Shelf Long-Term Ecological Research program (NES-LTER II) advances our ability to predict how anthropogenic impacts will affect the dynamics of the shelf's planktonic food webs and their ability to support the productivity of higher trophic levels, from fish to whales and humans. Because the NES is subject to long-term challenges that will impact many people, the project emphasizes an active education component for helping to train the next generation of marine scientists and outreach activities to increase public understanding of marine science and technology. The project team conducts education and outreach via three main components: (1) training and mentoring for early career researchers from undergraduates to postdoctoral researchers in LTER research; (2) an LTER Schoolyard program that engages middle and high school teachers and students; and (3) public outreach through targeted events, the project website, and social media channels.

Patterns of ecosystem change over seasons to decades have been documented in the NES, but the key mechanisms linking changes in the physical environment, planktonic food webs, and higher trophic levels remain poorly understood. As a result, predictive capability is limited and management strategies are largely reactive. To address these needs, NES II is targeting a mechanistic understanding of how food web structure and function responds to environmental conditions, natural variability and human induced changes. NES II combines observations that provide regional-scale context, process cruises along a high gradient cross-shelf transect, high-frequency time series at an inner-shelf location, coupled biological-physical food web models, and targeted population models. In addition, the research team is investigating how community structure and trophic transfer are impacted by disturbances including (i) the increasing prevalence of heat waves, (ii) intrusions of offshore water associated with increasing instability in the Gulf Stream, and (iii) offshore wind farms now under construction on the NES. The long-term research plan is guided by the overarching science question: "How is climate 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 higher trophic levels) variability?" The investigators are assessing the extent to which the NES ecosystem possesses a biodiversity reservoir that is resilient to dramatic changes in the environment and that will allow the ecosystem to maintain overall productivity.

Prior Award
Sep 2017 to Feb 2024
LTER: Linking Pelagic Community Structure with Ecosystem Dynamics and Production Regimes on the Changing Northeast US Shelf
Summary information including abstract, PIs, and other award details are included in the Funding History PDF in the Files section below.

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.

This project is supported by continuing grants with slight name variations:

- LTER: Linking Pelagic Community Structure with Ecosystem Dynamics and Production Regimes on the Changing Northeast US Shelf
- LTER: Scales of Variability in Ecosystem Dynamics and Production on the Changing Northeast U.S. Shelf (NES II)

RII Track-1: Rhode Island Consortium for Coastal Ecology Assessment, Innovation, and Modeling (C-AIM)

Coverage: Narragansett Bay, Rhode Island

NSF Award Abstract:

Non-technical Description
The University of Rhode Island (URI) will establish the Consortium for Coastal Ecology Assessment, Innovation, and Modeling (C-AIM) to coordinate research, education, and workforce development across Rhode Island (RI) in coastal marine science and ecology. C-AIM addresses fundamental research questions using observations, computational methods, and technology development applied to Narraganset Bay (NB), the largest estuary in New England and home to important ecosystem services including fisheries, recreation, and tourism. The research will improve understanding of the microorganisms in NB, develop new models to predict pollution and harmful algal bloom events in NB, build new sensors for nutrients and pollutants, and provide data and tools for stakeholders in the state. Observational capabilities will be coordinated in an open platform for researchers across RI; it will provide real-time physical, chemical, and biological observations ? including live streaming to mobile devices. C-AIM will also establish the RI STEAM (STEM + Art) Imaging Consortium to foster collaboration between artists, designers, engineers, and scientists. Research internships will be offered to undergraduate students throughout the state and seed funding for research projects will be competitively awarded to Primarily Undergraduate Institution partners.

Technical Description
C-AIM will employ observations and modeling to assess interactions between organisms and ecosystem function in NB and investigate ecological responses to environmental events, such as hypoxia and algal blooms. Observations of the circulation, biogeochemistry, and ecosystem will be made using existing and new instrument platforms. The Bay Observatory ? a network of observational platforms around NB - will be networked to trigger enhanced water sampling and sensing during specific environmental events, such as hypoxic conditions or phytoplankton blooms. Biogeochemical, ecological, and coastal circulation models will be integrated and coupled to focus on eutrophication and pollutant loading. Data and models will be integrated on multiple scales, from individual organisms and trophic interactions to food-web responses, and from turbulence to the regional ocean circulation. New sensing technologies for nutrients and pollutants will be developed, including affordable, micro-fluidic (Lab-on-a-Chip) devices with antifouling capabilities. The results will be synthesized and communicated to stakeholders.

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

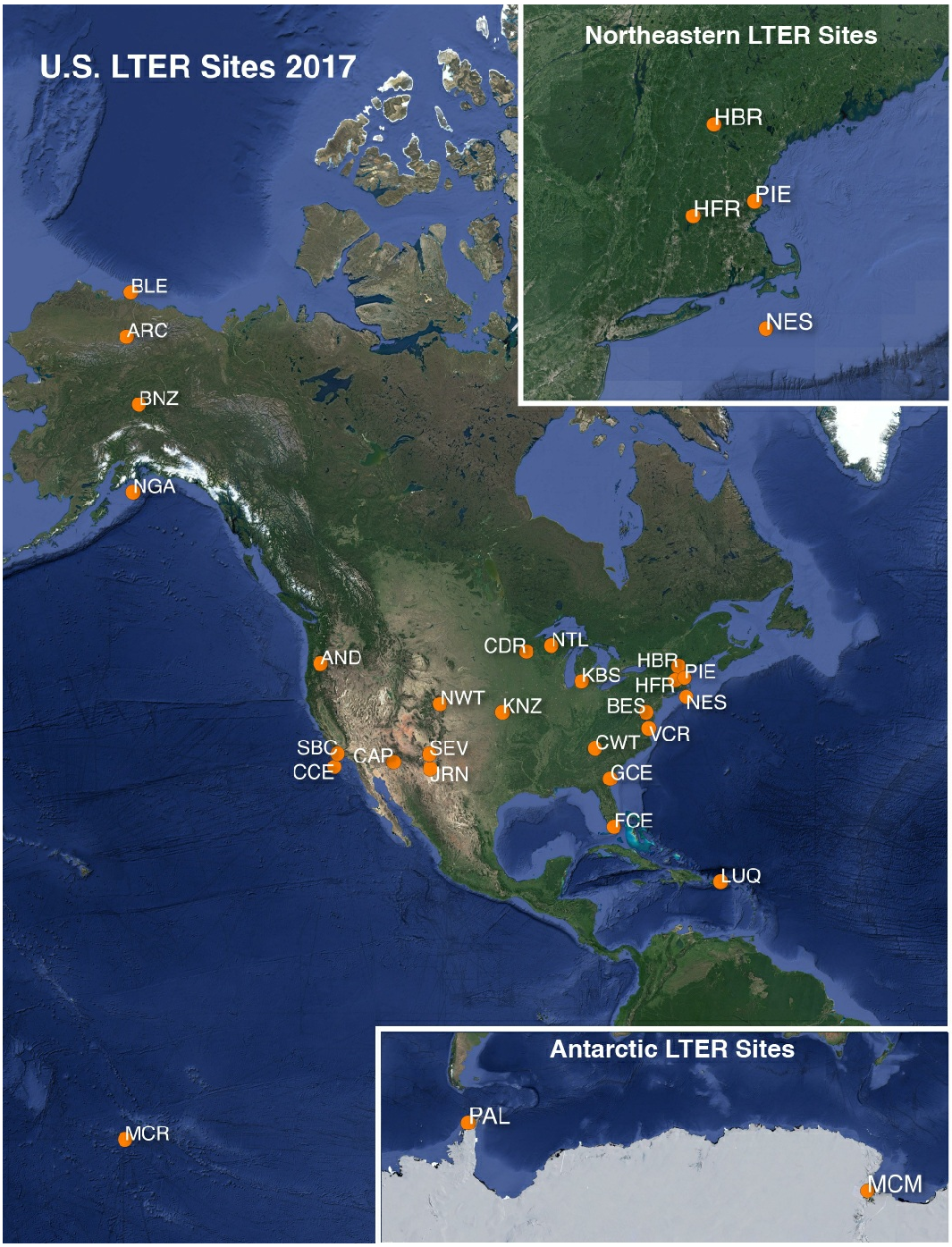
Long Term Ecological Research network (LTER)

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.



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

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

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Funding

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NSF Division of Ocean Sciences (NSF OCE)	OCE-1655686
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NSF Division of Ocean Sciences (NSF OCE)	OCE-2322676

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