Field temperature data from estuaries along the Atlantic coast of North America containing Nematostella vectensis from deployments between March of 2016 and January of 2017

Website: https://www.bco-dmo.org/dataset/752613
Data Type: Other Field Results
Version: 2
Version Date: 2019-01-11

Project
» Toxin expression and function by an estuarine model species in a dynamic seasonal community (Cnidarian Toxin Dynamics)

Contributors	Affiliation	Role
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Abstract
Field temperature data from estuaries along the Atlantic coast of North America containing Nematostella vectensis from deployments between March of 2016 and January of 2017.

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Coverage

Spatial Extent: **N**:43.54261 **E**:-70.34497 **S**:29.72642 **W**:-81.25772
Temporal Extent: 2016-03-11 - 2017-01-01

Methods & Sampling

HOBO temperature loggers where deployed in tidally restricted pools in estuaries along the Atlantic coast of North America. Loggers were fastened to pipes that were dug into these pools.

Problem report:
In this data set, the temperature logger for Maine failed to log temperature data after September 6th. All other locations have complete data sets from March 11 until December 31, 2016.

Locations:
St. Augustine, Florida: 29.72642,-81.25772
Georgetown, South Carolina: 33.33183,-79.19994
Ft. Fisher, North Carolina: 33.959,-77.93283
Sippewissett, Massachusetts: 41.58939,-70.63797
Pine Point, Maine: 43.54261,-70.34497

Data Processing Description

No processing performed, these are the raw data from the temperature logger.

BCO-DMO Data Manager Processing Notes:

Data version 1: 2019-01-08
* added a conventional header with dataset name, PI name, version date
* modified parameter names to conform with BCO-DMO naming conventions
* blank values in this dataset are displayed as "nd" for "no data." nd is the default missing data identifier in the BCO-DMO system.
* ISO_DateTime_UTC added from local date and time column.

Data version 2: 2019-01-11
* Five Temperature columns were unpivoted into one temperature columns with new column "Site" which contains the location specified in the original column name.

Temp_Florida,Temp_South_Carolina,Temp_North_Carolina,Temp_Massachusetts,Temp_Maine ->
37.384,24.738,29.652,15.76,2.624

to

Temp,Site
37.384,Florida
24.738,South_Carolina
...

* Lat and lon columns added to the dataset

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Data Files

File
temp.csv(Comma Separated Values (.csv), 7.68 MB) MD5:5aa76734edc45c9074d136eaaaa9ed83
Primary data file for dataset ID 752613

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Parameters

Parameter	Description	Units
Data_Point	Numeric identifier for data point	unitless
Date_Time	Date and Time (local,UTC-5) in format 'mm/dd/yyyy HH:MM'	unitless
ISO_DateTime_UTC	Timestamp with time zone (UTC) in standard ISO 8601:2004(E) format 'yyyy-mm-ddTHH:MMZ'	unitless
Site	Site of temperature deployment	unitless
Temp	Water temperature from HOBO logger	degrees Celsius (C)
lat	Latitude	decimal degrees (DD)
lon	Longitude	decimal degrees (DD)

Instruments

Dataset-specific Instrument Name	HOBO pendant temperature loggers (Onset, UA-002-64)
Generic Instrument Name	Temperature Logger
Generic Instrument Description	Records temperature data over a period of time.

Deployments

Reitzel_Estuarine_Temp

Website	https://www.bco-dmo.org/deployment/752704
Platform	shoreside Eastern United States
Start Date	2016-03-11
End Date	2017-01-01
Description	Locations: St. Augustine, Florida: 29.72642,-81.25772 Georgetown, South Carolina: 33.33183,-79.19994 Ft. Fisher, North Carolina: 33.959,-77.93283 Sippewissett, Massachusetts: 41.58939,-70.63797 Pine Point, Maine: 43.54261,-70.34497

Project Information

Toxin expression and function by an estuarine model species in a dynamic seasonal community (Cnidarian Toxin Dynamics)

Coverage: Georgetown, South Carolina; and Woods Hole, Massachusetts

Description from NSF award abstract:
Venomous animals such as cnidarians, scorpions, and snakes utilize their toxins for a diversity of functions including defense from predators and for capturing prey. Thus, venom plays a pivotal and central role in the ecology of the animal producing it. There are several major hypotheses regarding the ecological factors that

shape the diversity and expression of these molecules. A central hypothesis is that these toxins evolve rapidly due to their involvement in an evolutionary "arms race" between the organism and its potential predators and prey. Moreover, toxins are energetically expensive to produce so it is also hypothesized that their production is tightly regulated ("venom optimization hypothesis"), where individuals can module the amount and composition of their venom dependent on changes in diet and shifts in environmental factors such as temperature. Currently, there is a paucity of data to discern between these hypotheses. This research will provide an integrative approach to identify mechanisms that determine shifts in the quantity and composition of the venom essential for the feeding ecology of a model cnidarian specializing in estuarine habitats that are vulnerable to the ongoing climate change. This project will provide a synergistic international collaboration with Dr. Yehu Moran (The Hebrew University of Jerusalem, Israel) to connect environmental variation with the expression and potency of venom proteins. This research will provide mentoring and training for a postdoctoral fellow, graduate and undergraduate students at the University of North Carolina at Charlotte, and undergraduate students at Mitchell Community College in Statesville, NC. Additional research and educational opportunities will be provided for underrepresented students using PRODUCE, funded by the NSF through the NC Louis Stokes Alliance for Minority Participation to recruit, retain, and graduate students in STEM education. The PI will continue to involve high-school students in research through individual training, UNC Charlotte's outreach programs and the Burroughs Wellcome Science Enrichment program with the Olympic High School Biotechnology School.

Knowledge of the environmental, genetic, and molecular factors involved in modulating expression of toxin proteins is essential to understand and predict how venomous species will respond to changes in the composition of biological communities. The research team will rigorously test hypotheses in the expression of toxin peptides by studying the starlet sea anemone, Nematostella vectensis, a predator of ecological importance that lives in estuaries along the eastern coast of North America. N. vectensis has emerged as a model cnidarian for ecological genomics due to the availability of a genome, its central position in estuarine food webs, and the ease of field collection and laboratory manipulation; a combination rarely available for venomous animals. Expression of venom genes in field collected anemones will be correlated with ingested prey identified using microscopy and DNA barcodes. This analysis will be compared in three different seasons to identify impacts of seasonal changes in abiotic variables as well as prey availability. Differences in expression of these toxin genes in the field could be related to tuning of the toxin composition to the prey available, presence of predators, and/or the physiological condition of the individual determined by degree of abiotic stress. The research team will differentiate between these potential causal factors through controlled laboratory experiments where anemones are exposed to two common stressors (temperature, UV), individual prey items, and a predator. In order to better understand the selectivity of these toxins to particular prey, behavioral and in vitro assays test toxicity of each genetic variant will be compared when exposed to distinct animal prey groups to determine the relative potency. Finally, sequence analyses will be used to investigate the molecular targets of the toxins in the prey animals to determine if these targets are potentially adapted to toxin alleles restricted to different geographic locations. These data will help determine a potential causative link between toxin evolution of a venomous animal and its prey and whether toxins and their targets are involved in an "arms race". This project is expected to have a significant impact on the understanding of the evolution of toxins in the context of ecological interactions in natural environments and contribute to our knowledge about toxin pharmacology for future design of novel insecticides.

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1536530