

# Dates and locations of Callinectes blue crab samples from the coastal Atlantic waters of north and south America, Gulf of Mexico and Caribbean from Massachusetts to Uruguay from 2017 to 2021

**Website:** <https://www.bco-dmo.org/dataset/785930>

**Data Type:** Other Field Results

**Version:** 2

**Version Date:** 2021-11-19

## Project

» [Collaborative research: Variation in life history and connectivity as drivers of pathogen-host dynamics and genetic structure in a trans-hemispheric pathosystem](#) (Blue Crab Connectivity)

Contributors	Affiliation	Role
<a href="#">Schott, Eric</a>	University of Maryland Center for Environmental Science (UMCES/IMET)	Principal Investigator
<a href="#">Behringer, Donald</a>	University of Florida (UF)	Co-Principal Investigator
<a href="#">Kough, Andrew</a>	Shedd Aquarium	Co-Principal Investigator
<a href="#">Plough, Louis V.</a>	University of Maryland Center for Environmental Science (UMCES/HPL)	Co-Principal Investigator
<a href="#">Biddle, Mathew</a>	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager
<a href="#">Rauch, Shannon</a>	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

## Abstract

Dates and locations of Callinectes blue crab samples from the coastal Atlantic waters of North and South America, the Gulf of Mexico, and the Caribbean from Massachusetts to Uruguay from 2017 through 2021. Crab populations were sampled using methods available to collaborating scientists, managers, and fishermen, as listed in the dataset.

## Table of Contents

- [Coverage](#)
- [Dataset Description](#)
  - [Methods & Sampling](#)
  - [Data Processing Description](#)
- [Related Publications](#)
- [Parameters](#)
- [Project Information](#)
- [Funding](#)

## Coverage

**Spatial Extent:** N:43.33487 E:-36.5267 S:-34.6285 W:-97.199

## Methods & Sampling

In 2017 to 2019, crab populations were sampled using methods available to collaborating scientists, managers, and fishermen, as listed in the table. Note: The location of Maldonado [UR\_Mal2018-09] crab collection is

approximate.

In 2020 and 2021, additional *Callinectes* spp. collections were made using baited traps in the San Juan Estuary; a few crabs were also collected from continental US coasts. These crabs were infected with CsRV1 and used in the genetic analysis of that virus.

## Data Processing Description

### BCO-DMO Processing Notes:

- added conventional header with dataset name, PI name, version date;
- modified parameter names to conform with BCO-DMO naming conventions;
- removed special characters;
- removed commas or replaced them with semi-colons;
- **2021-11-19**: appended additional data received on 2021-09-08; updated version number to v2.

[ [table of contents](#) | [back to top](#) ]

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## Related Publications

Zhao M, Behringer DC, Bojko J, Kough AS and others (2020) Climate and season are associated with prevalence and distribution of trans-hemispheric blue crab reovirus (*Callinectes sapidus* reovirus 1). *Mar Ecol Prog Ser* 647:123-133. <https://doi.org/10.3354/meps13405>  
*Results*

[ [table of contents](#) | [back to top](#) ]

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## Parameters

Parameter	Description	Units
sample_ID	unique identifier with place and year	unitless
Project_Identifier	identifier for the project	unitless
Geo_location_name	State or water body	unitless
lat_lon	approximate lat and lon within 10km	unitless
month_and_year	Collection month and year; higher resolution dates are presented in yyyy-mm-dd format	unitless
Collaborator	collaborating scientists; managers; and fishermen	unitless
Permitting_info	Authority under which collection is made	unitless
Collection_method	capture method	unitless
Sample_size	number of crabs in the collection	unitless
Latitude	latitude with negative values indicating South	decimal degrees
Longitude	longitude with negative values indicating West	decimal degrees

[ [table of contents](#) | [back to top](#) ]

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## Project Information

**Collaborative research: Variation in life history and connectivity as drivers of pathogen-host**

## dynamics and genetic structure in a trans-hemispheric pathosystem (Blue Crab Connectivity)

**Coverage:** Atlantic coast of north and south America from Massachusetts to Southern Brazil, Caribbean

### NSF Award Abstract:

Marine invertebrates use an array of strategies to survive, move, and reproduce across diverse and dynamic environmental conditions. This project investigates the intersection of these strategies and how they facilitate the persistence of blue crabs and a pathogenic virus along the Atlantic coast of North and South America. The widespread distribution of this crab-virus system makes it useful for investigating host-pathogen interactions. Blue crabs can reduce their activity level and induce winter dormancy in colder climates, but it is unclear how this alters progression and transmission of the pathogen. Conversely, year-round growth and reproduction of tropical blue crabs may be offset by higher pathogen abundance and activity. This project will use a combination of field and laboratory studies to reveal how crab life history and pathogen dynamics interact and adapt at the extremes of their range. Genetic sequencing, crab movement tracking and oceanographic models will be used to understand how crab-disease dynamics vary across temperate and tropical latitudes. The blue crab is an ecologically and economically important species and knowledge generated in this project will help provide management guidance to support sustainable fisheries. Best practices to avoid and limit disease will be communicated to commercial and artisanal harvesters through partnerships and workshops. Local high school and undergraduate students from underrepresented groups will be engaged through a variety of formal and informal educational programs. Public outreach will be implemented through a museum partnership with the Shedd Aquarium and will include the training of a science communication intern.

This collaborative project will combine empirical field and laboratory experiments, population genomics, and biophysical modeling to explore the consequences of latitude-driven changes in life history and oceanic connectivity on a trans-hemispheric pathosystem comprised of the blue crab, *Callinectes sapidus*, and the pathogenic virus, CsRV1. The virulence of the CsRV1 virus from tropical and temperate latitudes and the impact of overwintering will be studied by experimental virus challenges of crabs transplanted between high and low latitudes. The impact of infection and virulence on crab movement will be investigated in laboratory raceway experiments of healthy and infected crabs and in the field with acoustically tagged crabs deployed in temperate and tropical locations. Population genetic studies using thousands of genome-wide RAD sequencing markers for crabs and whole-genome sequencing for the virus will define genetic connectivity of crab and virus populations across their range, and will investigate the possible latitudinal, seascape, and life history-driven changes in blue crab and virus genomes. The two population genomic data sets are expected to provide different inferences and scales of connectivity because CsRV1 virus genotypes are transmitted only among post-larval crabs while blue crab genotypes also move by a potentially long-range dispersive larval stage. Finally, integrated biophysical models will be used to investigate the relative contributions of adult and larval dispersal on the population structure of the crab and the pathogen across a broad swath of habitat between New England and Argentina with a decade of simulations. An open-source Lagrangian stochastic model will estimate pelagic larval transport, and spatially explicit biased-correlated random walk models will estimate adult movement. Models will be informed by experimentally-derived movement and behavior data, as well as information on crab larval and adult behavior and overwintering duration available in the published literature. Under a series of scenarios in which crab behavior is affected by latitude and virus infection, statistical comparisons will be made between biophysical model-based predictions of connectivity and genetic estimates of connectivity. These analyses will advance our understanding of the physical, environmental, and biological factors that shape the dynamics of the blue crab CsRV1 pathosystem.

[ [table of contents](#) | [back to top](#) ]

## Funding

Funding Source	Award
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1658466</a>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1658396</a>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1658389</a>

[ [table of contents](#) | [back to top](#) ]