Nucleotide sequences of CsRV1 virus amplified from blue crabs (Callinectes sapidus) from coastal waters and estuaries in North and South America, including the Caribbean and Gulf of Mexico from 2006 to 2020

Website: https://www.bco-dmo.org/dataset/890835
Data Type: Other Field Results
Version: 1
Version Date: 2023-02-28

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
Schott, Eric	University of Maryland Center for Environmental Science (UMCES/IMET)	Principal Investigator
Plough, Louis V.	University of Maryland Center for Environmental Science (UMCES/IMET)	Co-Principal Investigator
Zhao, Mingli	University of Maryland at Baltimore	Scientist
York, Amber D.	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
This record contains nucleotide sequences of CsRV1 virus amplified from blue crabs (Callinectes sapidus) across the study region. RNA from crabs identified as infected using a sensitive Rt-qPCR assay was amplified using primers specific to segment and segment 9 of the virus genome. A subset of CsRV1-positive RNA preparations were amplified using a full-genome amplification set of primers to amplify the entire CsRV1 genome. (http://primal.zibraproject.org; Quick et al. 2017). The segment-specific data: seg9 (960 nt amplicon) and seg8 (807 nt amplicon) were trimmed and used to create maximum likelihood trees. Similarly, the full genome sequences were used for a maximum likelihood tree. In total, 22 complete or near-complete genomes, 42 seg8 ORF sequences, and 96 seg9 ORF sequences of CsRV1 were collected from 15 geographic locations along the US Atlantic coast, Gulf of Mexico, Caribbean Sea and S. America between 2006 – 2021. Sequence generation and tree building was accomplished by Mingli Zhao with input from coauthors Plough and Kough. Pairwise analyses and ML trees can be found in the Supplemental Materials of results publication Zhao et al. (2023). The sequences generated in this study are deposited in NCBI GenBank, with accession numbers OP067244-OP067635 and are accessible under BioProject PRJNA939818.

Table of Contents

Coverage

Spatial Extent: **N**:41.5118 **E**:-54.2921 **S**:-34.6285 **W**:-71.0929

Temporal Extent: 2006 - 2020

Methods & Sampling

Location:
Coastal waters and estuaries N. America and S. America, including the Caribbean and Gulf of Mexico. Collections from trapping, dredging, and netting by commercial and recreational fishers, and scientific collections by resource managers.

Methods & Sampling:
Crabs were obtained by collaborating partners in the Caribbean and South America using mixed methods of baited traps and line, nets, and dredges.

DNA sequencing was conducted using both Sanger sequencing (Big Dye terminator) of PCR amplicons at the BioAnalytical Lab in IMET (https://www.umces.edu/baslab).

Illumina-based sequencing of full virus genome amplifications used Illumina MiSeq platform at GENEWIZ (South Plainfield, NJ, USA) with a MiSeq Reagent kit v3 (Illumina, San Diego, CA, USA).

Instruments:
No lab-specific environmental equipment was used to record metadata at the time of crab collection.

For sequence analysis, equipment was 3130 XL Genetic Analyzer from Life Technologies at IMET and contracted Illumina MiSeq platform at GENEWIZ (South Plainfield, NJ, USA) with a MiSeq Reagent kit v3 (Illumina, San Diego, CA, USA).

Taxonomic identifiers:
blue crabs, Callinectes sapidus, urn:lsid:marinespecies.org:taxname:107379

Data Processing Description

BCO-DMO dataset processing notes:
* lat lons formatted as decimal degrees (W and S are negative)
* empty depth column removed
* upon request from the submitter all "host" values filled in as Callinectes sapidus. And VA site coordinates were corrected from 38.0214,-76.3524 to 37.1477,-76.1573

.

[table of contents | back to top]

Data Files

File
CsRV1 alignment and trees filename: Concatenated_ORF_genome_alignment_3_30_2021.1.fa (FASTA, 434.37 KB) MD5:99b2a140cee3b7a52645e00e4764ecf4 This file is a list of the concatenated sequences the protein coding regions each of the 12 segments of CsRV1. There are 22 individual genomes from different locations and dates. CsRV1 alignment and trees. Concatenated CsRV1 segments used for alignments in fasta format. Pairwise analyses and ML trees. These sequences are truncated relative to the full sequences in Genbank accessions KU311708 - KU311719.
Sample and Accession information filename: samples_and_accessions.csv (Comma Separated Values (.csv), 33.29 KB) MD5:c59a8183fe17ce967be2196a7ce69190 Sample and Accession information for nucleotide sequences of CsRV1 virus amplified from blue crabs (Callinectes sapidus). Parameters (Column name, description, units): Genbank_accession, NCBI Genbank accession identifier for the sequence collection_date, Date of collection in ISO 8601 format yyyy lat, Sample latitude, decimal degrees lon, Sample longitude, decimal degrees site, Site code (state or island) sample_name, Sample name mol_type, type (genomic RNA) virus_genome_segment, Virus genome segment number organism, organism host, Host taxon definition, accession definition

[table of contents | back to top]

Supplemental Files

File
Site List filename: site_list.csv (Comma Separated Values (.csv), 612 bytes) MD5:dd0fcc5d118dc5f47ba0a40604e9c0f0 Site list containing the site code (State or Island), name of the location, and lat,lon in decimal degrees.

[table of contents | back to top]

Related Publications

Quick, J., Grubaugh, N. D., Pullan, S. T., Claro, I. M., Smith, A. D., Gangavarapu, K., Oliveira, G., Robles-Sikisaka, R., Rogers, T. F., Beutler, N. A., Burton, D. R., Lewis-Ximenez, L. L., de Jesus, J. G., Giovanetti, M., Hill, S. C., Black, A., Bedford, T., Carroll, M. W., Nunes, M., … Loman, N. J. (2017). Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. Nature Protocols, 12(6), 1261–1276. https://doi.org/10.1038/nprot.2017.066
Methods

Zhao, M., Plough, L. V., Behringer, D. C., Bojko, J., Kough, A. S., Alper, N. W., Xu, L., & Schott, E. J. (2023). Cross-Hemispheric Genetic Diversity and Spatial Genetic Structure of Callinectes sapidus Reovirus 1 (CsRV1). Viruses, 15(2), 563. https://doi.org/10.3390/v15020563
Results

Zhao, M., Xu, L., Bowers, H., & Schott, E. J. (2022). Characterization of Two Novel Toti-Like Viruses Co-infecting the Atlantic Blue Crab, Callinectes sapidus, in Its Northern Range of the United States. Frontiers in Microbiology, 13. https://doi.org/10.3389/fmicb.2022.855750
Results

[table of contents | back to top]

Related Datasets

IsRelatedTo

University of Maryland Center for Environmental Science. Callinectes sapidus reovirus 1. (2023). In: NCBI:BioProject: PRJNA939818. Bethesda, MD: National Library of Medicine (US), National Center for Biotechnology Information; Available from: http://www.ncbi.nlm.nih.gov/bioproject/PRJNA939818.

[table of contents | back to top]

Parameters

Parameters for this dataset have not yet been identified

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Illumina MiSeq
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.

[table of contents | back to top]

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
NSF Division of Ocean Sciences (NSF OCE)	OCE-1658466
NSF Division of Ocean Sciences (NSF OCE)	OCE-1658396
NSF Division of Ocean Sciences (NSF OCE)	OCE-1658389

[table of contents | back to top]