Metadata for RNASeq of green crabs collected in the northeast Pacific from Apr 2017 to Aug 2021

Website: https://www.bco-dmo.org/dataset/949682
Data Type: Other Field Results
Version: 1
Version Date: 2025-01-28

Project
» Collaborative Research: Tracking fine-scale selection to temperature at the invasion front of a highly dispersive marine predator (West Coast Carcinus)

Contributors	Affiliation	Role
Tepolt, Carolyn	Woods Hole Oceanographic Institution (WHOI)	Principal Investigator
Grason, Emily	Washington Sea Grant (WSG)	Co-Principal Investigator
McDonald, P. Sean	University of Washington (UW)	Co-Principal Investigator
Mickle, Audrey	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
This project explores genomic changes in the invasive European green crab (Carcinus maenas) in the northeast Pacific. It tracks the earliest stages of green crab invasion into a new environment where the species is predicted to have substantial ecological and economic impacts. Samples span time and space across the species range in the northeast Pacific, with a focus on areas where the species is currently expanding. This dataset includes individual metadata for 127 raw RNA-Seq reads, archived at GenBank's SRA under BioProject PRJNA1170986.

Table of Contents

Coverage

Location: Coastal northeastern Pacific in the range of Carcinus maenas, from California to British Columbia
Spatial Extent: **N**:50.698395 **E**:-122.45115 **S**:43.35635 **W**:-127.579577
Temporal Extent: 2017-04-29 - 2021-08-12

Methods & Sampling

Samples of *Carcinus maenas* (urn:lsid:marinespecies.org:taxname:107381) were collected by large network of collaborators, usually by trapping but approaches vary. Heart tissue was dissected from crabs after severing the ventral nerve cord, and hearts were preserved in RNALater and frozen at -80 prior to extraction. Total RNA extraction was conducted with TRI reagent and 1-bromo-3-chloropropane. mRNA libraries were prepared with Illumina TruSeq Stranded mRNA kits and individually single-indexed with Illumina index sets A and B. Samples were multiplexed 24 / lane of 150 bp pe Illumina HiSeq4000 sequencing at Azenta (formerly Genewiz; South Plainfield NJ).

Data Processing Description

Samples were demultiplexed by Azenta (formerly Genewiz; South Plainfield NJ), and are provided raw with no further processing.

BCO-DMO Processing Description

- Imported "BCO-DMO_RNASeq_metadata_NSF-1850996.csv" into the BCO-DMO system
- Converted date field to ISO UTC format YYYY-MM-DD
- Replaced non-standard character ”' with '"'
- Exported file as "949682_v1_green_crabs_rna_seq.csv"

Accepted species identifier confirmed on 2025-01-29.

Problem Description

Some latitude, longitude, and collector information was not reported. Those values are represented as blanks.

[table of contents | back to top]

Data Files

File
949682_v1_green_crabs_rna_seq.csv (Comma Separated Values (.csv), 19.13 KB) MD5:4152e99f120055e4ecdcfb96385d3513 Primary data file for dataset ID 949682, version 1

[table of contents | back to top]

Related Datasets

References

Woods Hole Oceanographic Instititíon. Carcinus maenas invasion in the northeast Pacific. 2024/10. 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/PRJNA1170986. NCBI:BioProject: PRJNA1170986.

[table of contents | back to top]

Parameters

Parameter	Description	Units
sample_name	Individual sample ID	unitless
SRA_accession	SRA accession number for individual sequence files	unitless
biosample_accession	Individual NCBI BioSample code	unitless
embayment	General coastal water body from which sample was collected	unitless
site	More specific data on collection location provided by collector	unitless
state	US state or Canadian province where samples was collected	unitless
sex	Sex (M=Male, F=Female, or U=Unknown)	unitless
size_CW	Carapace width of crab in mm	Millimeters (mm)
color	Color of ventral side of cephalothorax, as determined by collector	unitless
collection_date	Date of collection	unitless
latitude	Latitude of collection; positive values = North	decimal degrees
longitude	Longitude of collection; positive values = East	decimal degrees
collector	Person who collected the sample	unitless
collector_affiliation	Organization through which the sample was collected	unitless

[table of contents | back to top]

Instruments

Dataset-specific Instrument Name	Illumina HiSeq4000 sequencers
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Samples were sequenced using Illumina HiSeq4000 sequencers by Azenta (formerly Genewiz; South Plainfield NJ).
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

[table of contents | back to top]

Project Information

Collaborative Research: Tracking fine-scale selection to temperature at the invasion front of a highly dispersive marine predator (West Coast Carcinus)

Coverage: North American west coast: 36 N to 51 N. Emphasis on the Salish Sea

NSF Award Abstract:

Marine invasive species pose a serious and ongoing risk to ocean ecosystems and the economies that rely on them. Understanding how such species adapt rapidly to new environments is key to preventing and managing invasions. Traditionally, the focus has been on inherent traits and flexibility of an invasive species, ignoring the potential for evolutionary change after introduction. However, recent research has shown that some marine species may evolve specific genomic features which allow highly efficient selection over as little as a single generation. This project tests the importance of genomic traits in allowing marine invasive species to survive and thrive on new shores. Its focus is on the high-impact invasive European green crab, which has spread over 1,500 km of the West Coast of North America since 1989 and has very recently begun expanding into the Salish Sea. This project tracks the earliest stages of green crab invasion into a new environment where the species is predicted to have substantial ecological and economic impacts. Genetic differences are followed over time and space across the entire West Coast, with a focus on crabs found in the Salish Sea where the species is currently expanding. Genetic data is complemented by oceanographic modeling to predict the spread of green crabs into the Salish Sea and across the West Coast. Finally, targeted sequencing and prior sampling are used to probe the genomic traits underlying these changes and determine if the same traits have played a role in the species' invasive success on other shores. Sampling for this project is conducted by Washington Sea Grant's Crab Team, an expansive outreach and monitoring program powered largely by hundreds of volunteers who monitor green crabs across 3,000 miles of coastline in the Salish Sea. The results of this project are shared with these volunteers and other stakeholders and is used to inform trans-boundary green crab management and spread prediction on the West Coast.

Recent work has hypothesized that genomic architecture, which has been increasingly discovered to play a role in local adaptation, may also be key to a species' ability to adapt quickly when gene flow is high. This project integrates multiple approaches to track the speed and dynamics of adaptation-with-gene flow across a thermal gradient in an explicit oceanographic context using the invasive European green crab (Carcinus maenas). Prior work in this system identified a suite of genes that appear to constitute balanced polymorphisms whose allele frequencies correlate strongly with site temperature against a homogeneous neutral genetic background. This project has three main goals: 1) To examine fine-scale selection to temperature over a comprehensive spatial and temporal data set comprising most of the species' history on the West Coast, 2) To track the expanding range front in the Salish Sea, comparing the genetic trajectory of individuals at the range edge with oceanographic modeling of dispersal, and 3) To characterize the genomic regions surrounding putative balanced polymorphisms and examine the ubiquity of their association with temperature across globally replicated populations. This coupled evolutionary oceanography approach represents an unprecedented test of the speed and nature of rapid adaptation in a highly dynamic natural marine environment.

This award reflects NSF's statutory mission and has been deemed worthy of support through evaluation using the Foundation's intellectual merit and broader impacts review criteria.

[table of contents | back to top]

Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1850996
NSF Division of Ocean Sciences (NSF OCE)	OCE-1850945

[table of contents | back to top]