Metadata for targeted genotyping of green crabs collected in the northeast Pacific from Aug 2016 to Oct 2022

Website: https://www.bco-dmo.org/dataset/949610
Data Type: Other Field Results
Version: 1
Version Date: 2025-01-27

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
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Abstract
This project explores genetic changes in the invasive European green crab (Carcinus maenas) in the northeast Pacific, using targeted genotyping of SNPs identified in prior high-resolution population genomics in the region. It tracks the early stages of green crab invasion into a new environment, particularly through repeated sampling of multiple size-classes of crabs from the same sites over multiple years. Samples span time and space across the species range in the northeast Pacific, with a focus on the coast of Washington and Oregon. This dataset includes individual collection and accession metadata for 1,662 crabs, for which raw demultiplexed reads are archived at GenBank's SRA under BioProject PRJNA1177418.

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Coverage

Location: Coastal northeastern Pacific in the range of Carcinus maenas, from California to British Columbia.
Spatial Extent: **N**:49.606306 **E**:-122.422437 **S**:43.347281 **W**:-124.323273
Temporal Extent: 2016-08-17 - 2022-10-12

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. Crabs were first frozen at -20C, then muscle or gill tissue was dissected out, preserved in 95% ethanol, and archived at -80C. Genomic DNA was extracted with Chelex 100 resin. Targeted genotyping of ~200 SNPs was conducted following the approach of Campbell et al. 2015; target SNPs were identified in prior population genomics analysis in the region based on RNA-Seq data. Samples were prepared in two groups, with overlapping but not identical targets; some samples were normalized using SequalPrep plates and others were not, following results of replicate sequencing with ("norm" in sequence names) and without normalization showing that this step did not improve genotyping success. Libraries were individually dual-indexed with plate and well barcodes, and multiplexed 800-1500 / lane on two lanes of 150 bp paired-end Illumina NovaSeq X 10B sequencing at the University of California at Berkeley's QB3 Genomics Core lab. Some samples were re-run across multiple plates / lanes as technical replicates ("repA" and "repB" in sequence names).

Data Processing Description

Samples were demultiplexed by UC Berkeley's QB3 Genomics Core lab, and are provided raw with no further processing.

BCO-DMO Processing Description

- Imported "BCO-DMO_GTSeq_metadata_NSF-1850996.csv" into BCO-DMO system
- Replaced "â€™" with """ in collector_affiliation field
- Replaced "10-2018-11" with "2018-11" in collection_date field
- Exported file as "949610_v1_green_crab_collection"

Accepted species identifier confirmed on 2025-01-29.

Problem Description

Some dates, latitude, longitude, and collector information was not reported. Those values are represented as blanks. Sampling coordinates are withheld for samples collected in Makah tribal waters. To request coordinates for these samples, please contact Adrianne Akmajian (marine.ecologist@makah.com).

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Data Files

File
949610_v1_green_crab_targeted_genotyping.csv (Comma Separated Values (.csv), 237.63 KB) MD5:bf186b66ef6c1f40eb269afc29891faf
Primary data file for dataset ID 949610, version 1

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Related Publications

Campbell, N. R., Harmon, S. A., & Narum, S. R. (2014). Genotyping-in-Thousands by sequencing (GT-seq): A cost effective SNP genotyping method based on custom amplicon sequencing. Molecular Ecology Resources, 15(4), 855–867. Portico. https://doi.org/10.1111/1755-0998.12357
Methods

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Related Datasets

References

Woods Hole Oceanographic Instittion. Targeted genotyping of Carcinus maenas spread 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/PRJNA1177418. NCBI:BioProject: PRJNA1177418.

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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 to the level of specificity available	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

Instruments

Dataset-specific Instrument Name	Illumina NovaSeq X 10B
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Illumina NovaSeq X 10B sequencing (150 bp paired-end), conducted at University of California at Berkeley's QB3 Genomics Core lab
Generic Instrument Description	A DNA sequencer is an instrument that determines the order of deoxynucleotides in deoxyribonucleic acid sequences.

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.

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Funding

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

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