NCBI accession numbers and related metadata for an SRA archive of the Pacific oyster, Magallana gigas

Website: https://www.bco-dmo.org/dataset/958631
Data Type: Other Field Results
Version: 1
Version Date: 2025-04-10

Project
» The genetic legacy of an Asian oyster introduction and its disease-causing parasite (Oyster historical genetics)

Contributors	Affiliation	Role
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Abstract
The massive geographic expansion of terrestrial plant crops, livestock, and marine aquacultured species during the 19th and 20th centuries provided local economic benefits, stabilized food demands, and altered local ecosystems. The invasion history of these translocations remains uncertain for most species, limiting our understanding of their future adaptive potential and historical roles as vectors for co-invaded species. We provide a framework for filling this gap in invasion biology using the widely transplanted Pacific oyster (Magallana gigas) as a case study. A two-dimensional summary of population-level variation in single nucleotide polymorphisms (SNPs) in native Japan reflected the geographical map of Japan and allowed identification of the source regions for the worldwide expansion. Pacific oysters proliferate in non-native areas with environmental temperatures similar to those areas where native lineages evolved.

Table of Contents

Coverage

Spatial Extent: **N**:58.8684 **E**:175.11 **S**:-40.5394 **W**:-124.023696
Temporal Extent: 2005-07 - 2021-11

Methods & Sampling

Sampling was conducted at several locations: South Korea, Japan, USA, European coastlines, Argentina, and Chile.

At each site, we collected approximately 20 individuals at least 1 meter apart from natural and artificial substrata outside of obvious aquacultural infrastructure to target naturally-settled spat. The two exceptions were in Chile, which were a mix of aquacultural (n=17) and feral (n=3) samples collected from the same estuary (Estero Tongoy), and New Zealand, where oysters were naturally settled within aquaculture farms.

Shells were pulled by hand off of hard substrata. Whole or mantle tissue was preserved in 95% ethanol and shipped to Charleston, South Carolina (USA) for DNA extraction using Macherey-Nagel Nucleospin Tissue kits, using the manufacturer's instructions.

To generate libraries for RADseq (restriction-site associated DNA sequencing), we digested gDNA with two restriction enzymes, EcoRI and MseI, and ligated adaptors containing unique 8 to 10 bp barcodes to the digested DNA of each individual. The products were then PCR amplified in two independent reactions with standard Illumina primers. All amplicons were pooled and shipped to the University of Texas Genomic Sequencing and Analysis Facility or the Tufts University Core Facility, which used Pippin Prep® to isolate the 300 – 450 bp fraction. This fraction was then single-read sequenced (100 or 150 basepairs) with Illumina Novaseq, HiSeq 2500 and/or HiSeq 4000 machines. We used custom scripts to demultiplex into sample-specific FASTQ-formatted files.

Data Processing Description

These data are the demultiplexed files from Illumina sequencing.

BCO-DMO Processing Description

- Imported original file "meta_forBIODMO.csv" into the BCO-DMO system.
- Created column for collection date in YYYY-MM format.
- Saved final file as "958631_v1_m_gigas_sra.csv".

[table of contents | back to top]

Data Files

File	
958631_v1_m_gigas_sra.csv	(Comma Separated Values (.csv), 103.72 KB) MD5:29a2dd3cafb5ab51306a100768bf7d36
Primary data file for dataset ID 958631, version 1	

[table of contents | back to top]

Related Publications

Sotka, E. E., Carnegie, R. B., Carlton, J. T., Couceiro, L., Crooks, J. A., Endo, H., Hayford, H., Hori, M., Kamiya, M., Kanaya, G., Kochmann, J., Lee, K.-S., Lees, L., Miller, H., Nakaoka, M., Pante, E., Ruesink, J. L., Schwindt, E., Strand, Å., … Strand, A. E. (2025). The genetic legacy of a global marine invader. Proceedings of the National Academy of Sciences, 122(15). https://doi.org/10.1073/pnas.2418730122
Results

[table of contents | back to top]

Related Datasets

IsRelatedTo

Erik Sotka, & Strand, A. (2025). esotka/gigas-popgen: 3.0.0 (Version 3.0.0) [Computer software]. Zenodo. https://doi.org/10.5281/ZENODO.13381622 https://doi.org/10.5281/zenodo.13381622

[table of contents | back to top]

Parameters

Parameter	Description	Units
sample_name	Individual ID (3 letter pop name and 3-digit identifier)	unitless
accession	GenBank SRA accession number	unitless
bioproject_accession	GenBank BioProject number	unitless
biosample_accession	GenBank BioSample number	unitless
pop	3 letter Population abbreviation	unitless
Population	Full population name	unitless
Region	shorted region name	unitless
Region2	region name	unitless
NatNon	Native (nat) and non-native (non)	unitless
Collection_Date	Population collection date (Year-Month)	unitless
CollectionMonth	Population collection Month (when available)	unitless
CollectionYear	Population collection Year	unitless
Latitude	Latitude of population collection site	decimal degrees
Longitude	Longitude of opulation collection site	decimal degrees
Collector	Scientist that collected the dataset	unitless

[table of contents | back to top]

Project Information

The genetic legacy of an Asian oyster introduction and its disease-causing parasite (Oyster historical genetics)

Coverage: Global

NSF abstract:

During the 20th century, the Pacific oyster *Crassostrea gigas* was deliberately introduced from its native range of coastal Asia to the estuaries of six continents. While the introduced Pacific oysters are widely aquacultured and thus can generate local economic wealth, they sometimes outcompete native oysters, and can carry microbial, animal and plant hitchhikers that negatively impact local economies and the ecological functioning of local estuaries. This study comprehensively assesses the pathways and sources of Pacific oyster introductions using a worldwide, population genetic survey. Simultaneously, the study also assesses the pathways and source of one hitchhiking protist (*Haplosporidium nelsoni*) that causes the disease MSX (multinucleated sphere X) in the Virginia oyster (*Crassostrea virginica*) along the eastern seaboard of the United States. One goal of this research is to generate management strategies that combat the negative impacts of the Pacific oyster and its associated invaders, and minimize future invasions. A second goal is to minimize some uncertainty about the population biology of the devastating Haplosporidium parasite, and thus, increase confidence of policy makers who are managing shellfish health, restoration and commerce. By quantifying the pathways and sources of *C. gigas*, this project may inform strategies to combat negative impacts of *C. gigas* and its associated invaders, as well as minimize future invasions. Moreover, quantifying dispersal within and among populations of *H. nelsoni* along the US East Coast will provide perspective on the effectiveness of regional biosecurity measures in preventing the ongoing dispersal of this destructive pathogen via aquaculture. In addition, the project lends itself well to programs that foster critical thinking and research experience among both undergraduate and K-12 students. The project provides opportunities for 6-9 undergraduates to perform research, includes a 2-day workshop on bioinformatics for the wider undergraduate community, and facilitates ongoing opportunities for K-12 students to participate in citizen-science research.

There is a wealth of information on the source, pathways and vectors of *C. gigas* based largely on historical documents but no study has comprehensively tested whether these historical accounts are correct using a worldwide, population genetic survey. Using >14K single-nucleotide polymorphisms (SNPs) from 41 populations across five continents a high level of spatial genetic differentiation was found within the native range and differences in source populations among non-native regions. Preliminary genetic data indicated that the parasitic protist, *Haplosporidium nelsoni* arrived with C. gigas imports to the US Atlantic coastline and then infected the native C. virginica, however the native source populations, the pathways and vector from which *H. nelsoni* arrived remain unknown. This project couples high-throughput sequencing technologies and Approximate Bayesian Computing (ABC)-based models to answer the following: What are the population genomic patterns among *C. gigas* from native and non-native regions? What are the population genomic patterns of *Haplosporidium nelsoni* among Asian and North American Crassostrea gigas and eastern North American *C. virginica*? What were the source populations and invasion pathways of *C. gigas* and *H. nelsoni*? Identifying source locations, pathways and vectors of introduction of C. gigas will provide researchers with a null-model of invasion history for dozens of other non-native species that were transported with *C. gigas*. Currently, there are no verified 'vector maps' for historical shipments of *C. gigas* that are similar to those generated from modern-day or historical shipping records.

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-1924599

[table of contents | back to top]