Rockfish microhaplotype sequence accessions from samples near Carmel and Monterey Bays, CA, 2013-2016 (Larval Dispersal in Kelp Rockfish project)

Website: https://www.bco-dmo.org/dataset/684944
Data Type: Other Field Results
Version: 1
Version Date: 2018-02-27

Project
» Integrative evaluation of larval dispersal and delivery in kelp rockfish using inter-generational genetic tagging, demography and oceanography (Larval Dispersal in Kelp Rockfish)

Program
» Partnership for Interdisciplinary Studies of Coastal Oceans (PISCO)

Contributors	Affiliation	Role
Carr, Mark	University of California-Santa Cruz (UCSC)	Principal Investigator
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Abstract
This dataset contains NCBI accessions and collection metadata for samples collected in September 2010 along the coast of Monterey and Carmel, California.

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Coverage

Spatial Extent: **N**:36.6405 **E**:-121.8946 **S**:36.3977 **W**:-121.9825
Temporal Extent: 2013-07-19 - 2015-10-01

Dataset Description

2018-02-21: The data are currently stored in the Dryad repository as the following two packages. The files may also be accessed here via the 'Get Data' button (above).

Dryad package: **Kelp-rockfish genotypes**, DOI: 10.5061/dryad.6cp14g8
Data from: "Larval dispersal connects marine reserves and replenishes fished populations along the central California coast." Baetscher DS, Anderson EC, Saarman E, Malone D, Carr MH, Garza JC (2018?) Molecular Ecology (in press).

NOTE: not all files are publicly available until the associated publication is published.

This data repository contains the following: Genotypes for 96 microhaplotypes - this file contains the genotypes for 6,108 kelp rockfish sequenced at 96 amplicon loci using paired-end Illumina sequencing. Genotypes were filtered for read depth (minimum 20 reads total per locus/individual) and allele balance (0.4 ratio of read depth for allele 1:allele 2 in a heterozygote). Samples with missing data at more than 10 percent of loci were excluded from this data set. Variant call format file generated using Freebayes software from 2,293 rockfish samples sequenced at 96 microhaplotype loci. Samples include four species of rockfishes: kelp (Sebastes atrovirens), copper (S. caurinus), black-and-yellow (S. chrysomelas), and gopher (S. carnatus). This file contains 1,495 variant sites across the 96 loci.

Dryad package: **Rockfish microhaplotype sequences,** DOI: 10.5061/dryad.5863d
Data from: Baetscher DS, Clemento AJ, Ng TC, Anderson EC, Garza JC (2017) Microhaplotypes provide increased power from short-read DNA sequences for relationship inference. Molecular Ecology Resources, https://doi.org/10.1111/1755-0998.12737
Consensus sequences and primer information for 192 targeted amplicons, the Binary Alignment/Map (BAM) files and variant call format (VCF) files for all retained regions genotype files for 144 kelp rockfish species and an R Notebook documenting all statistical analyses.

Methods & Sampling

Haplotype data from 150bp amplicon sequencing on an Illumina MiSeq. All loci used in the generation of haplotype sequence data will be submitted to GenBank (National Center for Biotechnology Information).

Genotype data are generated with high-throughput DNA sequencing on an Illumina MiSeq instrument. Amplicons are prepared through polymerase chain reaction with primers designed from either expressed sequence tags in publicly available databases (e.g., Cyverse) or from sequences generated by double digest Restriction-Site Associated DNA (RAD) sequencing. Amplicon sequencing is using the procedure described in Campbell et al. 2015 (Molecular Ecology Resources 15: 855-867) termed genotyping in thousands by sequencing (GT-seq). Data are filtered by quality score and genotypes called for all locus by individual combinations with read depth ≥20. Genotyping accuracy is evaluated by confirmation of Mendelian segregation in known families. Haplotypes are called from constituent SNPs using FreeBayes software.

Data Processing Description

Standard filtering for quality scores and read depth have been applied to the raw instrument output to call haplotypes.

BCO-DMO Processing Notes:
- created table of files downloaded from Dryad
- added conventional header with dataset name, PI name, version date

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Data Files

File
Dryad package: Kelp-rockfish genotypes, DOI: 10.5061/dryad.6cp14g8 filename: doi_10.5061_dryad.vq3rg55__v1.zip　　　　　　(ZIP Archive (ZIP), 47.55 MB) MD5:d90e22185e4542e088f59b2e1c564799 Zip file containing two files: Genotype data (CSV) and the variant call format (VCF) file used to generate genotypes for all kelp rockfish.
rockfish_microhaplotype_dryad.csv　　　(Comma Separated Values (.csv), 4.40 KB) MD5:ed4a92f7c1bcff4f6a6e0421030bf8e2 Primary data file for dataset ID 684944

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Related Publications

Baetscher, D. S., Anderson, E. C., Gilbert-Horvath, E. A., Malone, D. P., Saarman, E. T., Carr, M. H., & Garza, J. C. (2019). Dispersal of a nearshore marine fish connects marine reserves and adjacent fished areas along an open coast. Molecular Ecology, 28(7), 1611–1623. doi:[10.1111/mec.15044](10.1111/mec.15044)
Results

Baetscher, D. S., Clemento, A. J., Ng, T. C., Anderson, E. C., & Garza, J. C. (2017). Microhaplotypes provide increased power from short-read DNA sequences for relationship inference. Molecular Ecology Resources, 18(2), 296–305. doi:[10.1111/1755-0998.12737](10.1111/1755-0998.12737)
Results

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Related Datasets

IsRelatedTo

Carr, M., Edwards, C., Garza, J. C. (2021) **Species, sample date, location individual size and sample disposition of adult fish surveyed near Carmel and Monterey Bays, CA, 2013-2016 (Larval Dispersal in Kelp Rockfish project).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 2) Version Date 2017-08-15 doi:10.26008/1912/bco-dmo.684426.2 [[view at BCO-DMO](#)]

Carr, M., Edwards, C., Garza, J. C. (2021) **Survey of fish species, number and size from transects near Carmel and Monterey Bays, CA, 1999-2015 (Larval Dispersal in Kelp Rockfish project).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2017-03-17 doi:10.26008/1912/bco-dmo.684484.1 [[view at BCO-DMO](#)]

IsSupplementedBy

Carr, M., Edwards, C., Garza, J. C. (2021) **Fish species code key for data collected along the shore of Monterey and Carmel from 1999-2015 (Larval Dispersal in Kelp Rockfish project).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2017-03-17 doi:10.26008/1912/bco-dmo.684512.1 [[view at BCO-DMO](#)]

Carr, M., Edwards, C., Garza, J. C. (2021) **Locations of fish surveys in the Monterey and Carmel nearshore from 1999-2015 (Larval Dispersal in Kelp Rockfish project).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2017-08-16 doi:10.26008/1912/bco-dmo.712843.1 [[view at BCO-DMO](#)]

Carr, M., Tinker, T. (2021) **Site code key for kelp forest community data collected along the coast of Monterey and Carmel, CA from 1999-2015 (Kelp Forest Resilience project).** Biological and Chemical Oceanography Data Management Office (BCO-DMO). (Version 1) Version Date 2017-08-16 doi:10.26008/1912/bco-dmo.661175.1 [[view at BCO-DMO](#)]

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Parameters

Parameter	Description	Units
file_link	hyperlink to downloadable file	unitless
file_size	file size	kilobytes to gigabytes
publication	publication that used the data	unitless
Dryad_DOI	dryad.org DOI	unitless
description	description of file contents	unitless
file_name	file name	unitless

Instruments

Dataset-specific Instrument Name	Illumina MiSeq
Generic Instrument Name	Automated DNA Sequencer
Dataset-specific Description	Used to sequence genomes
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.

Dataset-specific Instrument Name	
Generic Instrument Name	Thermal Cycler
Generic Instrument Description	A thermal cycler or "thermocycler" is a general term for a type of laboratory apparatus, commonly used for performing polymerase chain reaction (PCR), that is capable of repeatedly altering and maintaining specific temperatures for defined periods of time. The device has a thermal block with holes where tubes with the PCR reaction mixtures can be inserted. The cycler then raises and lowers the temperature of the block in discrete, pre-programmed steps. They can also be used to facilitate other temperature-sensitive reactions, including restriction enzyme digestion or rapid diagnostics. (adapted from http://serc.carleton.edu/microbelife/research_methods/genomics/pcr.html)

Deployments

Carr_1999

Website	https://www.bco-dmo.org/deployment/661099
Platform	Long Marine Lab UCSC
Start Date	1999-09-22
End Date	2015-07-24
Description	Sites of Kelp Forest Resilience project. Nearshore waters of southern Monterey Bay and Carmel Bay, California. 36 N, 121 W.

Project Information

Integrative evaluation of larval dispersal and delivery in kelp rockfish using inter-generational genetic tagging, demography and oceanography (Larval Dispersal in Kelp Rockfish)

Website: http://research.pbsci.ucsc.edu/eeb/rclab/kelp-rockfish-pbt-project/

Coverage: Monterey Bay and vicinity

Description from NSF award abstract:
The spatial structure and dynamics of coastal marine fish populations are strongly influenced by the transport and recruitment of larvae. However, the scale and patterns of larval dispersal are among the most difficult demographic parameters to quantify in marine systems, due to the inability to tag and track the movement of larvae. In particular, the extent of local retention of larvae versus regional dispersal to other locations and populations is currently a hotly debated topic in the field of marine ecology and has profound implications for the design and effectiveness of Marine Protected Areas (MPAs). The research will identify patterns of larval dispersal and use those patterns to test predictions of dispersal generated by state-of-the-art circulation models.

The PI team brings together ecologists, geneticists, statisticians, and oceanographers with expertise in population demography and field sampling, mark/recapture data from genetic tags, and empirical and model-based evaluation of oceanographic processes to answer the following questions:
1. Do observed patterns of dispersal and connectivity of larval kelp rockfish correspond to patterns predicted by high spatial resolution regional ocean circulation models? Model predictions will be tested empirically using larval settlement samples. Parentage analysis will be used to verify the occurrence of larvae derived from genetically tagged source populations.
2. Is there evidence for local retention of larval kelp rockfish within the study area? To test the hypothesis that local retention of juvenile kelp rockfish from source populations is greater than expected by existing larval transport models, the PIs will compare the proportion of recruits that are genetically identified to have been produced from within three focal sites with the proportion of larval production that was tagged in those sites.
3. Is the relative recruitment of recently settled kelp rockfish to focal sites in the study region proportionate to the relative larval production of those focal sites? The PIs will compare the proportion of tagged recruits with the proportion of larval production generated from tagged adults at varying spatial scales. They will use goodness of fit models to compare expected and observed connectivity matrices under varying hypotheses of larval dispersal. Alternatively, if the relative contribution of focal sites to larval replenishment of themselves, one another, and more distant populations is disproportionate to their relative production, can this discrepancy be explained by oceanographic processes that could facilitate particular trajectories of larval dispersal?

To determine if differences in self recruitment and connectivity can be attributed to local oceanographic features, the PIs will examine spatial and temporal correlations between these features and the spatial distribution and timing of recruitment.

Related websites:
http://piscoweb.org
http://research.pbsci.ucsc.edu/eeb/rclab/kelp-rockfish-pbt-project/ (broken link)
http://rockfish.ucsc.edu/
http://oceanmodeling.ucsc.edu

Program Information

Partnership for Interdisciplinary Studies of Coastal Oceans (PISCO)

Website: http://www.piscoweb.org/

Coverage: West coast of North America from Mexico to Alaska

The Partnership for Interdisciplinary Studies of Coastal Oceans is a long-term ecosystem research and monitoring program established with the goals of:

- understanding dynamics of the coastal ocean ecosystem along the U.S. west coast
- sharing that knowledge so ocean managers and policy makers can make science based decisions regarding coastal and marine stewardship
- producing a new generation of scientists trained in interdisciplinary collaborative approaches

Over the last 10 years, PISCO has successfully built a unique research program that combines complementary disciplines to answer critical environmental questions and inform management and policy. Activities are conducted at the latitudinal scale of the California Current Large Marine Ecosystem along the west coast of North America, but anchored around the dynamics of coastal, hardbottom habitats and the oceanography of the nearshore ocean – among the most productive and diverse components of this ecosystem. The program integrates studies of changes in the ocean environment through ecological monitoring and experiments. Scientists examine the causes and consequences of ecosystem changes over spatial scales that are the most relevant to marine species and management, but largely unstudied elsewhere.

Findings are linked to solutions through a growing portfolio of tools for policy and management decisions. The time from scientific discovery to policy change is greatly reduced by coordinated, efficient links between scientists and key decision makers.

Core elements of PISCO are:

- Interdisciplinary ecosystem science
- Data archiving and sharing
- Outreach to public and decision-making user groups
- Interdisciplinary training
- Coordination of distributed research team

Established in 1999 with funding from The David and Lucile Packard Foundation, PISCO is led by scientists from core campuses Oregon State University (OSU); Stanford University's Hopkins Marine Station; University of California, Santa Cruz (UCSC); and University of California, Santa Barbara (UCSB). Collaborators from other institutions also contribute to leadership and development of PISCO programs. As of 2005, core PISCO activities are funded by collaborative grants from The David and Lucile Packard Foundation and the Gordon and Betty Moore Foundation. Core support, along with additional funding from diverse public and private sources, make this unique partnership possible.

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Funding

Funding Source	Award
NSF Division of Ocean Sciences (NSF OCE)	OCE-1260693

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