

# Wild adult and recruit *Kelletia kelletii* samples from 2015 to 2017 (KW connectivity project)

**Website:** <https://www.bco-dmo.org/dataset/874458>

**Data Type:** Other Field Results

**Version:** 1

**Version Date:** 2022-05-17

## Project

» [Collaborative Research: RUI: Combined spatial and temporal analyses of population connectivity during a northern range expansion](#) (KW connectivity)

Contributors	Affiliation	Role
<a href="#">White, Crow</a>	California Polytechnic State University San Luis Obispo (Cal Poly)	Principal Investigator, Contact
<a href="#">Christie, Mark</a>	Purdue University	Co-Principal Investigator
<a href="#">Toonen, Robert J.</a>	Hawaii Institute of Marine Biology	Co-Principal Investigator
<a href="#">Newman, Sawyer</a>	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

## Abstract

Tissue samples of the North American west coast subtidal marine gastropod Kellet's whelk, *Kelletia kelletii*, were collected by Crow White and colleagues to support population genomics research. A total of 6,900 samples from 36 sites across the species' geographic range (Monterey, California, USA to Isla Asunsion, Baja California, Mexico) were collected during the summer months of June, July, and August in 2015, 2016, and 2017. Samples were collected by hand at sub-tidal reefs using SCUBA. Adult samples (n=4,624) represent ~60-100 mg tissue removed from the foot of the organism with a modified scalpel. All sampled adults were at least 60 mm in shell length. Adult samples at each site were stored together in a single 15-ml tube. Recruit samples (n=2,276) represent the entire organism. All recruit samples were a maximum of ~30 mm shell length. Recruit samples at each site were stored together in a ziplock bag. All samples were frozen in the field in a cooler with dry ice and/or container with liquid nitrogen, then transported to California Polytechnic State University and stored long-term in a minus ~70C freezer in the Biological Sciences Department.

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## Coverage

**Spatial Extent:** N:36.6182 E:-114.362 S:27.1533 W:-121.939

**Temporal Extent:** 2015 - 2017

## Methods & Sampling

### Methodology:

Samples (n=6900) were collected during the summer months (June, July, August) of each year (2015, 2016, 2017). Samples were collected by hand at sub-tidal reefs using SCUBA. Adult samples (n=4624) represent

~60-100 mg tissue removed from the foot of the organism with a modified scalpel. All sampled adults were at least 60 mm in shell length. Adult samples at each site are stored together in a single 15-ml tube. Recruit samples (n=2276) represent the entire organism. All recruit samples were a maximum of 30 mm shell length. Recruit samples at each site are stored together in a ziplock bag. All samples were frozen in the field in a cooler with dry ice and/or container with liquid nitrogen, then transported to California Polytechnic State University and stored long-term in a minus ~70C freezer in the Biological Sciences Department.

## Data Processing Description

### BCO-DMO Processing Notes

- Removed apostrophes from Site\_description column
- Renamed column headers by replacing any spaces with underscores (\_)

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## Data Files

File
<b>bcodmo_kw_2015-17_wildsamples_dataset_bco_dmo_reformatted-1.csv</b> (Comma Separated Values (.csv), 5.79 KB) MD5:413bec994d8706fa1566d9bf4b335978
Primary data file for dataset ID 874458

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## Parameters

Parameter	Description	Units
Year	Year of recruit collection; format: YYYY	unitless
Site_description	Local name of site	unitless
site_CODE	Unique site code name	unitless
Latitude	Latitude of site; Positive indicates North	degrees North
Longitude	Longitude of site; Negative indicates West	degrees West
Adult_tissues	Adult tissues collected	count
Recruits	Whole recruits collected	count

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## Project Information

**Collaborative Research: RUI: Combined spatial and temporal analyses of population connectivity during a northern range expansion (KW connectivity)**

**Coverage:** California, USA and Baja, Mexico coast

NSF Award Abstract:

Where do young marine fish and shellfish come from? This project aims to improve our understanding of how coastal marine populations are connected in space and time. Coastal populations are replenished through the arrival of minuscule larvae that have been dispersed for weeks to months in the open ocean after spawning at

remote sites. The combination of the long dispersal period of marine fish and shellfish larvae and the varying ocean currents results in complex patterns of "connectivity" among populations near and far. Identifying these patterns of connectivity is fundamental to marine science and critical for effective fisheries management and conservation, yet it remains an unresolved component of marine ecology. The study species is currently expanding its biogeographic range up the U.S. west coast. By genetically analyzing individuals from across the species' range, including offspring spawned in the laboratory by experimentally-crossed individuals collected in the field from throughout the species historical and expanded range, certain genes can serve to differentiate populations along the coast. The team leverages the statistical power of these geographically-informative genes to assign thousands of young collected in the field to the source populations that spawned them (across the species' range and over multiple years). The team then quantifies patterns of connectivity over multiple years, and tests fundamental hypotheses on the spatial scale, temporal variability, biogeographic patterns, and biophysical drivers of population connectivity. The project trains approximately two dozen U.S. university students in molecular ecology and marine science, as well as creating intellectual linkages among Ph.D.-granting and non-Ph.D.-granting universities. The project also supports further development of a K-12 education program that uses SCUBA diving and videography to teach elementary school students Next Generation Science Standards and train them for careers in science, technology, engineering and mathematics.

Using a kelp forest gastropod and fisheries species (Kellet's whelk, *Kelletia kelletii*), this project combines genome-wide Restriction site Associated DNA (RAD) loci with transcriptomic loci identified from common-garden laboratory crosses of individuals from the species' historical and expanded range to identify geographically-informative loci that maximize power for individual assignment testing. Leveraging the combined power of these loci, genetic assignment of approximately three thousand recruit samples to 20 putative source populations allows the team to construct three independent years of connectivity matrices and test some of the most fundamental questions in marine ecology, including: 1) Are marine populations open or closed and at what scales? 2) To what degree is the evolutionary pattern of gene flow represented by single versus multiple generations of connectivity events? And, 3) How spatially heterogeneous and temporally variable is population connectivity? Can one year of connectivity data predict anything about the next? Additionally, by focusing on a range-expanding species with common life history traits, the team addresses a number of questions with broad applicability and significant ecological and societal implications: 4) How much is population connectivity influenced by post-recruitment demographic and evolutionary processes? 5) How well-connected are historic- and expanded-range populations? And, of particular relevance to climate change, 6) Are El Nino oceanographic conditions, which are predicted to increase in frequency and intensity this century, driving the poleward range expansion of this coastal marine species? By coupling common-garden experimental crosses to identify maximally-informative transcriptomic loci with genomic RAD analysis of field samples, this project aims to accurately and precisely quantify marine population connectivity in high gene flow species with large population sizes.

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
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1924537</a>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1924505</a>
<a href="#">NSF Division of Ocean Sciences (NSF OCE)</a>	<a href="#">OCE-1924604</a>

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