Sample data for Lottia genomic samples

Website: https://www.bco-dmo.org/dataset/958640
Data Type: Other Field Results
Version: 1
Version Date: 2025-04-10

Project
» Evolutionary and ecological dynamics of a contemporary climate-driven range expansion (LottiaRangeExp)

Contributors	Affiliation	Role
Bay, Rachael	University of California-Davis (UC Davis)	Principal Investigator
Grosberg, Richard K.	University of California-Davis (UC Davis)	Co-Principal Investigator
Sanford, Eric	University of California-Davis (UC Davis)	Co-Principal Investigator
Cameron, Brenda	University of California-Davis (UC Davis)	Scientist
Fenberg, Philip	University of Southampton	Scientist
Nielsen, Erica	University of California-Davis (UC Davis)	Scientist
Sones, Jacqueline	University of California-Davis (UC Davis)	Scientist
Walkes, Sam	University of California-Davis (UC Davis)	Student
Mickle, Audrey	Woods Hole Oceanographic Institution (WHOI BCO-DMO)	BCO-DMO Data Manager

Abstract
As climatic variation re-shapes global biodiversity, understanding eco-evolutionary feedbacks during species range shifts is of increasing importance. Theory on range expansions distinguishes between two different forms: “pulled” and “pushed” waves. Pulled waves occur when the source of the expansion comes from low-density peripheral populations, while pushed waves occur when recruitment to the expanding edge is supplied by high-density populations closer to the species' core. How extreme events shape pushed/pulled wave expansion events, as well as trailing-edge declines/contractions, remains largely unexplored. We examined eco-evolutionary responses of a marine invertebrate (the owl limpet, Lottia gigantea) that increased in abundance during the 2014–2016 marine heatwaves near the poleward edge of its geographic range in the northeastern Pacific. We sampled Lottia gigantea from 19 populations across >11 degrees of latitude to characterize genomic variation, gene flow, and demographic histories across the species' range. This dataset includes sampling data for those individuals, including location, date, and size. Whole genomes were sequenced and raw genomic data can be found on NCBI (PRJNA1075458). Here we include summary statistics on whole genome data.

Table of Contents

Coverage

Location: Across the range of Lottia gigantea (Northern California to Baja)
Spatial Extent: **N**:38.591004548812 **E**:-114.245933 **S**:27.128191 **W**:-123.34527765215
Temporal Extent: 2020-11-12 - 2023-08-18

Methods & Sampling

We sampled 19 sites on the Pacific coast of North America, spanning most of the contemporary range of *L. gigantea.* We non-lethally excised a small piece of foot muscle tissue. For all locations except the four northern sites, we collected tissue from roughly 30 individuals per site, comprised of 10 individuals within each of the following size ranges: 10–25 mm (small), 30–40 mm (medium), and >40 mm (large). Sampling of the four northern sites (i.e., expanded range) also consisted of roughly 10 small, medium, and large individuals per site. However, as individual limpets at these four sites have been closely monitored over the past 8 years, these sites had known cohorts based on the estimated year of settlement. Size classes at sites for which we do not have monitoring data were chosen based on our data and previous growth curves (Kido & Murray, 2003) to approximately group individuals into those that settled during the MHWs, soon after the MHWs (late 2016 or late 2017), or well after the MHWs (late 2018 or late 2019). Tissue was stored in 90% ethanol at −20°C. We used the Qiagen DNAeasy extraction kit to perform DNA extractions following the manufacturer's protocols. DNA quantity and quality were assessed with Nanodrop, Qubit, and gel electrophoresis. Library preparation followed the Nextera Lite protocol, with adaptations following Rowan et al. (2019). Briefly, this consisted of normalizing samples, tagmentation, PCR, pooling samples, and bead size selection. The purified samples were run on a High Sensitivity DNA Bioanalyzer chip and then sent to BGI Genomics for whole-genome sequencing on the DNBSEQ-T7 PE150 platform on four lanes of sequencing.

Data Processing Description

The data included here are sample data taken directly in the field and summary data for whole genome data, before any processing or analysis.

[table of contents | back to top]

Related Publications

Kido, J., & Murray, S. (2003). Variation in owl limpetLottia giganteapopulation structures, growth rates, and gonadal production on southern California rocky shores. Marine Ecology Progress Series, 257, 111–124. https://doi.org/10.3354/meps257111
Methods

Nielsen, E. S., Walkes, S., Sones, J. L., Fenberg, P. B., Paz-García, D. A., Cameron, B. B., Grosberg, R. K., Sanford, E., & Bay, R. A. (2024). Pushed waves, trailing edges, and extreme events: Eco-evolutionary dynamics of a geographic range shift in the owl limpet, Lottia gigantea. Global Change Biology, 30(7). Portico. https://doi.org/10.1111/gcb.17414
Results

Rowan, B. A., Heavens, D., Feuerborn, T. R., Tock, A. J., Henderson, I. R., & Weigel, D. (2019). An Ultra High-DensityArabidopsis thalianaCrossover Map That Refines the Influences of Structural Variation and Epigenetic Features. Genetics, 213(3), 771–787. https://doi.org/10.1534/genetics.119.302406
Methods

[table of contents | back to top]

Parameters

Parameters for this dataset have not yet been identified

[table of contents | back to top]

Project Information

Evolutionary and ecological dynamics of a contemporary climate-driven range expansion (LottiaRangeExp)

Coverage: Coastal California intertidal

NSF abstract:
Anthropogenic climate change is shifting the distributions of species across the globe. Such contemporary shifts in species' ranges may have cascading effects on entire ecosystems. This project disentangles the mechanisms underlying climate-driven species range shifts in marine systems using the intertidal owl limpet as a case study. During the recent marine heatwaves off the Pacific coast of North America, populations at the northern range limit in northern California have expanded, with ongoing reproduction even after termination of the heatwave events. This is therefore an ideal system to explore the dynamics of natural selection that occur as species occupy new regions. Broadly, this project deepens understanding of how range shifts occur in marine systems and furthers the ability to predict future species distributions in response to climate change. The project provides research experiences for high school and undergraduate students from historically underrepresented groups by engaging with existing, demonstrably-effective programs. The investigators host leadership and skill-building workshops for senior female graduate students and engage the public in partnership with the California Academy of Sciences, Bodega Marine Lab, and San Francisco Exploratorium. Finally, the project provides training for a postdoctoral scholar and two graduate students.

Although phenomenological studies suggest that climate-associated range shifts are common in marine systems, to date, mechanistic studies of the climate-organism interactions that alter geographic distributions have largely focused on terrestrial systems. However, dispersal dynamics greatly differ in many marine systems, as currents may frequently transport planktonic larvae into new environmental regimes. This project integrates detailed demographic observations of the recent range expansion of the intertidal owl limpet, Lottia gigantea, with ecological, phenotypic, and genomic measurements of divergence across its range. Specifically, the work 1) documents phenotypic divergence in larval and juvenile traits across the zone of range expansion, 2) uses whole genome sequencing to estimate gene flow across the entire range, 3) identifies genomic patterns of selection across the zone of range expansion and through time, and 4) identifies drivers of variation in performance over latitudinal and microgeographic scales. The ability to monitor this range shift in real time, along with the suitability of this system for tracking individuals across multiple years, allows the investigators to examine the impact of selection in novel range-edge conditions at the phenotypic and genomic levels, and scale from individuals to species-level responses to ongoing environmental change.

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-2023297

[table of contents | back to top]