

GTseq KW 2025-2017

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Project

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

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Parameters

Parameters for this dataset have not yet been identified

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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 |
|--|-----------------------------|
| NSF Division of Ocean Sciences (NSF OCE) | OCE-1924537 |
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| NSF Division of Ocean Sciences (NSF OCE) | OCE-1924604 |

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