

CAUSES AND CONSEQUENCES OF BIOCOMPLEXITY

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Conspecific populations often differ in important fitness-related traits. Why might this be? One mechanism driving population differentiation is divergent natural selection, wherein spatial variation in selection drives divergence of populations. Such phenotypic diversity among proximate populations [hereafter “biocomplexity” (1)] is important for the long-term sustainability of the larger population complex because the relative contribution to total production may shift among different life histories depending on the prevailing environmental conditions (1). Despite the intuitive appeal of these ideas, the causes and consequences of biocomplexity are rarely studied.

Variation in natural selection is the presumed mechanism generating biocomplexity. For instance, spatial variation in selection has been shown to drive divergence in age-at-maturity of Trinidadian guppies (2). Similarly, temporal variation can drive evolution of phenotypic traits, as evidenced by microevolution of beak size in Darwin’s finches in response to short-term climate perturbations (3). Yet, studies quantifying spatio-temporal variation in selection are exceedingly rare and the ecological circumstances driving selection are rarely understood.

The overarching goal of my study is to examine the causes and consequences of biocomplexity among proximate salmon populations. Pacific salmon are an excellent system in which to test these ideas because they form discrete breeding populations, which are then subject to local selection pressures. Reproductive isolation combined with spatially varying selection pressures result in adaptation to local conditions and, ultimately, a diversity of phenotypes among populations. Furthermore, fine-scale variation in environmental conditions also leads to ecologically-driven variation among proximate populations (i.e., phenotypic plasticity). Herein, I propose to study coho salmon (*Oncorhynchus kisutch*) during their freshwater-rearing (juvenile) stage across multiple sites within the Lagunitas Creek watershed (California).

Goal 1: Determine the causes of biocomplexity

Hypothesis 1: Physical habitat attributes drive variation in fitness-related traits. Variation in local conditions can lead to phenotypic variation among salmon populations (4). Indeed, recent work has demonstrated that when habitat diversity is lost, specific salmon life history components are also lost (5). I will quantify seasonal variation in stream temperature and flow among ten tributaries of Lagunitas Creek across 3 years using standard methods (6). At each site, I will mark individual fish to monitor their size and growth through time. I will use a formal model comparison approach (7) to determine the physical habitat attributes contributing to phenotypic diversity among these proximate salmon populations.

Hypothesis 2: Food web structure drives variation in fitness-related traits. Variation in stream flows has been shown to have a strong impact on food web structure among years (8). Moreover, variation in food-web structure can influence fitness-related traits in fish consumers (9). To investigate the role of food web structure as a driver of biocomplexity among salmon populations, I will characterize variation in food web structure among three tributaries spanning a gradient of stream size. Specifically, I will sample tissues from multiple trophic levels and quantify stable isotopes of carbon and nitrogen to illuminate food web structure (10). I will again use a formal model comparison approach to test the drivers of variation in food web structure among sites using data collected as part of *Hypothesis 1*, as well as the consequences of variation in food web structure to size and growth of salmon across sites.

Hypothesis 3: Spatio-temporal variation in natural selection drives variation in body size. After determining the drivers of variation in size and growth, I plan to quantify natural selection acting

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on these traits. I will use data collected on individual fish across multiple seasons to relate phenotypic traits to survival across focal intervals (e.g., winter). I will use standard approaches (11) for quantifying natural selection across sites and years.

Goal 2: Determine the consequences of biocomplexity

Hypothesis 4: Variation in smolt size and production differs among sites and years. Many studies have demonstrated the importance of size-at-smolt migration to ocean survival, with larger smolts presumed to survive at higher rates than relatively smaller smolts (12). I propose to determine the consequences of biocomplexity in juvenile growth rates and survival by quantifying variation in smolt size and production among sites by trapping out-migrating smolts from each site, measuring body size, and estimating site-specific smolt production. Analysis of these data will allow me to determine the consequences of variation in the ecological circumstances experienced during the juvenile-rearing stage to smolt size and production, which then influence adult production. This will then allow me to identify production “hotspots” within the system and to distinguish factors that lead to high smolt production in those areas.

Anticipated Results: I anticipate that variation among sites of abiotic conditions and food web structure drives biocomplexity among proximate salmon populations. I also expect to find evidence of spatio-temporal variation in the strength and form of selection acting on body size. With the above factors potentially driving biocomplexity, I expect smolt size and production to vary among sites. This underscores the importance of maintaining a diversity of freshwater habitats to maintain biocomplexity among salmon populations as a buffer for future changes.

Intellectual Merit and Broader Impacts: With the recent collapse of California salmon stocks, investigations regarding the link between biocomplexity and sustainability are becoming increasingly important. My research seeks to provide insight into the causes and consequences of biocomplexity and may help create more robust management practices that maintain the full diversity of phenotypes in proximate populations, thus ensuring some resilience to future perturbations. To communicate the significance of my original research, I plan to disseminate the findings of this study through various modes including via 1) peer-reviewed, published literature; 2) the Ecological Society of America conference (where I am a student member); and 3) to interested citizens via, for instance, the Point Reyes National Parks Service Podcast.

Additionally, I plan to work closely with a local community-based group, the Salmon Protection and Watershed Network (SPAWN), in order to convey my findings to the local community. Finally, as a Burmese-American student in the environmental sciences, I am aware of the lack of ethnic diversity in my field. U.C. Berkeley has an incredibly diverse undergraduate body and I will strive to incorporate students from diverse backgrounds into all aspects of my research.

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