

## **Selective forces on individual reproductive success in a metapopulation of salmon**

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Morphological and behavioral variation within a species can be significant both as a starting point for speciation and as a reserve of pre-adaptation to novel stresses (Bock 1959). Selection and environmental gradients across species ranges can maintain this diversity even in the presence of significant gene flow, but the mechanisms by which microevolutionary forces effect genetic, phenotypic, and demographic changes within metapopulations remain poorly understood. As human effects on the environment intensify, the resilience of wild populations to shifting pressures has become a focal point for ecological researchers and guardians of natural resources. Previous studies, however, have focused on isolated populations, ignoring possible effects of genetic exchange within metapopulations, which could result in a significant misunderstanding of the manner in which wild populations endure environmental stresses (Hilborn *et al.* 2003).

A mechanistic approach to investigating the role of selection and migration in microevolutionary processes requires characterization of selective forces and reproductive success across multiple sub-populations with individual-level resolution. Fortunately, the advent of hypervariable genetic markers and high-throughput genotyping methods allows creation of complete pedigrees for relatively large wild populations, a technique that offers a direct view into the relationship between individual reproduction and population change (Kruuk & Hill 2008).

The goal of this project is to quantify the effects of selection pressures and inter-population migration on the morphology and productivity of creek-breeding Alaskan sockeye salmon (*Oncorhynchus nerka*). This model system is advantageous for my work because decades of life-history, behavioral and morphological data are available, fish maintain population structure by reliably homing to their natal site for spawning, and the limited size of the habitat (shallow creeks) allows exhaustive sampling of spawners. Tissue samples and life-history data are already available for six years of spawners in two distinct sub-populations, so with another two field seasons I will be able to match spawning pairs with their returning progeny for eight brood years. I propose to create full pedigrees for both sub-populations and associate individual reproductive success with environmental, morphological, population of origin, and mortality data to examine the following hypotheses:

1 – *Variation in predation intensity between creeks leads to distinct ideal reproductive sizes.* Bears hunt and kill large salmon preferentially, exerting a selective force on salmon body depth and length, but environmental factors also influence vulnerability to predation. I will attain a mechanistic model for the interaction of the stabilizing selection of predation and egg capacity (in females) or competitive fitness (in males) by examining mortality and reproductive rates of fish in each size class across creeks and years. This model will elucidate the maintenance of phenotypic and genetic variation between sub-populations that is known to be crucial to the resilience of the metapopulation to environmental change (Hilborn *et al.* 2003).

2 – *Exceptionally large brood years can be engendered by a few highly successful spawning pairs.* By comparing variation in individual reproductive success with expected total recruitment based on the total number of spawning adults, I will determine whether “super-spawners” have a disproportionate effect on the productivity of the

population. If so, predation and other forces that select against the largest individuals likely have a strong limiting effect on recruitment.

3 – *Immigrants exhibit lower reproductive success on average than locally spawned individuals.* Salmon that “stray” from their natal sites to spawn are likely to be maladapted to the local environment and suffer more strongly from local selection than fish that hatched locally (Hendry 2004). However, I also hypothesize that *in years of relatively weak selection, immigrants achieve higher reproductive success than they do in years of strong selection.* Salmon that exceed optimal body size under the normal selection regime may be well suited to take advantage of lulls in selection pressure, possibly even to the extent that they can outcompete local fish. Given the likely low effective sizes of these populations and their consequent susceptibility to genetic drift, prolonged periods of abnormally weak selection may allow immigrant fish to make considerable genetic contributions to the local population (Lin *et al.* 2008, Hedrick *et al.* 2000). I will examine this possibility by comparing reproductive success of immigrants with selection strength from predation across brood years.

**Anticipated Results:** I expect to find observable differences in average population morphology caused by variation in selection balances between the study creeks and between spawning years. I also anticipate that very productive brood years will be the result of a few highly successful mating pairs rather than evenly distributed reproductive success. The impact of immigrants on the genetic constitution of sub-populations is likely to be small, but I expect that it will increase in years of reduced selection. I hope to incorporate all of my results into a comprehensive mechanistic model of the interaction of microevolutionary forces on a phenotypically and genetically differentiated metapopulation that will be useful for basic ecological and evolutionary studies as well as immediately practical conservation applications.

**Broader Impacts:** This project will integrate learning and discovery by employing undergraduate students as field research assistants. Many of these students will be recruited from the local community of Native Alaskans, an ethnic group that is underrepresented in the sciences. I plan to disseminate the results and methodology of this project through publications in scientific journals, presentations at fisheries biology and natural resource conventions, and by partnering with local conservation groups. Middle and high school students will be reached through lectures and fieldwork demonstrations given at the Bristol Bay Salmon Camp, a local establishment that works with younger Native Alaskans. Society as a whole will benefit from this project because armed with a greater understanding of the ways in which wild fish populations respond to environmental stresses, natural resource and fishery managers will be better able to assure healthy stocks of these culturally and commercially important animals.

**Literature Cited:** 1. Bock WJ. 1959. *Evolution* 13(2): 194-211 2. Hedrick PW, Rashbrook VK, & Hedgecock D. 2000. *Can. J. Fish. Aquat. Sci.* 57(12): 2368–2373 3. Hendry AP. 2004. *Evolutionary Ecology Research* 6: 1219-1236 4. Hilborn R, Quinn TP, Schindler DE, Rogers DE. 2003. *Proc. Natl. Acad. Sci.* 100(11): 6564-6568. 5. Kruuk LEB, Hill WG. 2008. *Proc. R. Soc. Lond. B* 275: 593-596. 6. Lin J, Quinn TP, Hilborn R, Hauser L. 2008. *Heredity* 101: 341-350.