

A Sea Change: Genetics in Conservation of the Rich and Strange

Ruth E. Withler, Kristina M. Miller, John R. Candy, and Terry D. Beacham

Fisheries and Oceans Canada, Pacific Biological Station
Nanaimo, British Columbia V9T 6N7, Canada



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Introduction of theoretical population genetics and practical molecular genetics to the biological sciences has wrought a sea-change to our understanding of species, their interactions with their environments and their potential for longterm stability, or at least persistence. Early 20th century genetic concepts envisioned environments as constant, or constantly variable, so that organisms evolved fixed, specialized adaptations to maximize fitness given their genetic potential. Much more recent is our understanding of environmental variability, both spatial and temporal, and its impact on resident organisms. This understanding led to the prediction that intraspecific genetic variation for all traits, including those directly affecting fitness, will persist both within and among populations of a species. Development of the quantitative and molecular genetic means to measure the genetic variation encompassed by species confirmed this view of species as connected but heterogeneous populations in which local adaptation has a major influence on the ability of organisms to not only survive, but to thrive over broad environmental spans. The ramifications of intraspecific ‘genetic structure’, as the distribution of genetic variation among organisms has come to be termed, have been enormous for ecological theory and for man’s efforts to manage and conserve organisms.

Few species exemplify local adaptation in a more spectacular fashion than anadromous salmonids, known for their proclivity to return to natal spawning grounds bounded in kilometers, if not meters, after trans-oceanic migrations themselves independently forged by population-specific interactions with the environment. Many studies have demonstrated the genetic basis for differences in growth, life history, reproduction, and mate choice among salmonids and some have even demonstrated a variable genetic basis for traits that are phenotypically identical among populations. Conservation must now be viewed in an entirely new light – no longer a Noah’s Ark type of proposition, in which minimal numbers ensure eternal, or even ephemeral, representation among earthly biota. Indeed, facing an era of environmental change that many believe will be the most rapid ever experienced on earth, Noah himself would be hard-pressed to identify populations with the genetic resources qualifying them as “most likely to succeed” over the next 100 years. In the absence of foresight, we choose to hedge our bets, attempting to first identify and then conserve in moderate abundance those segments of a species possessing unique genetic resources. Thus, we serve the future a banquet of evolutionary morsels - populations, ESUs or MUs - hoping that at least one will adapt throughout the upcoming environmental sea-change. In this manner, we are trying to preserve a status quo that evolution will certainly overthrow, but through which persistence may count as victory.

The finescale local adaptation characterizing Pacific salmonid species was recognized long before we had the means of quantifying it. Now that the molecular identification of population segments with at least the potential of unique evolutionary capacity has become a cottage industry for Pacific salmonid researchers, we enter an era in which genetic variation becomes simultaneously the resource to be conserved and the tool by which conservation is achieved. In Canada, modern molecular technologies have begun transformation of approaches to the management and conservation of Pacific salmon populations.

In the Molecular Genetics Lab at the Pacific Biological Station, salmonid research is most advanced for coho, chinook and sockeye salmon. For these species, molecular genetic data have been used to delineate management units for populations of conservation concern, manage mixed-stock fisheries to minimize harvest of vulnerable populations, provide forensic identification of illegally harvested and sold fish, provide otherwise unobtainable stock-specific ecological information including migration times and routes for both juvenile and adult fish and escapement estimates for remote populations. We have compared patterns of neutral and adaptive genetic variation in fish inhabiting complex, connected environments and identified the influence of selective forces that have both increased and decreased genetic variation within populations. Looking to the future, we are undertaking studies in which gene expression profiles, combined with genetic identification of fish sampled in the wild, will provide stock specific information on the physiological status of fish and insight into the mechanisms underlying environmental influences on growth and survival.

Genetic characterization of vulnerable population segments has been undertaken in coho salmon, for which sweeping fishery closures and restrictions were undertaken in 1998 and implemented based on the distinctiveness of the threatened Interior Fraser coho population. In sockeye salmon, management of the 2002 and 2003 Fraser River

commercial fishery, the most valuable fishery in BC, was based on conservation of the genetically defined Late Run stock grouping, which had been experiencing high pre-spawning mortality for the previous five years. Genetic identification of depressed west coast of Vancouver Island chinook salmon in the troll fishery conducted near the Queen Charlotte Islands enabled simultaneous conservation of target populations and exploitation of more numerically abundant populations.

Forensic identification of salmonid tissue to species and population of origin has been used in both the conviction and exoneration of individuals suspected of the illegal harvest and/or sale of salmon. The ability to identify fish sampled from high-class restaurants or from the tin after cannery processing has widened the scope of enforcement actions meant to stem the flow of illegal product. Species identification of juvenile and immature adult samples collected from freshwater and marine environments has revealed surprisingly frequent species mis-identification, sometimes with serious consequences for management decisions.

Finally, investigations of functional genes such as those in the major histocompatibility complex (MHC) form the basis of molecular studies investigating the geographic scale of natural selection on salmon populations. Surveys of existing functional variation reveal the footprint of past selection and indicate that closely related populations within a watershed have experienced different selective histories, leaving them with equally different prospects for future adaptation.

Genetic data have transformed our views of species and how they are influenced by their environments. Consequently our understanding of, and attempts to achieve, conservation are experiencing a sea-change. Genetic information, collected and implemented wisely into management, enforcement and conservation measures will continue to enrich the endeavour to sustain Pacific salmon, already rich and strange.