



Decoding Cryptic Population Structures using Stable Isotope Markers

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Life-history diversity has been shown to contribute to the resilience of species but can be challenging to quantify, particularly where intra-population genetic structure is lacking. Such is the case for salmon within many fisheries of the North American Pacific Northwest, where the resolution of genetic markers is variable and limited. For Sockeye salmon (*Oncorhynchus nerka*) within the U.S.-Canada transboundary Taku Watershed, for example, single-nucleotide polymorphisms have successfully distinguished populations associated with specific inland lakes but allocates many individuals to an undifferentiated “River Type” stock. The extent and dynamics of geographic structure within this stock, and thus its potential contribution to the fishery’s resilience, remain unresolved.

In such cases, intrinsic non-genetic markers that record key aspects of life history, such as the isotope ratios of body tissues, can provide valuable information on population structure and diversity. We combined a recently published stream network model for strontium stable isotopes ($^{87}\text{Sr}/^{86}\text{Sr}$) with otolith (ear stone) microchemistry data to infer the geographic natal origins of 45 adult fish captured during the 2019 run. Our analysis was implemented in a Bayesian framework and leveraged radio tag data as a source of prior information. We distinguish 4 previously undifferentiated sub-populations within the River Type stock, characterized by groups of fish with distinct natal $^{87}\text{Sr}/^{86}\text{Sr}$ values and, by inference, natal habitat locations. Although data from additional years will be needed to assess the persistence of these patterns, the result implies potential for previously unrecognized geographic structure within the River Type stock as a contributor to resilience within the population. The lack of genetic differentiation among the subpopulations may suggest that plasticity of habitat use is prevalent and contributes to adaptation. Alternatively, individuals may exhibit strong site fidelity, but differentiation of these sub-populations may be relatively recent or obscured by gene flow. Distinction between these hypotheses should be resolvable by applying the Sr-isotope method to fish recovered across multiple years.