Considering genetics in salmon restoration: insights from functional markers

Melissa Evans*, Samuel Shry, Nicholas Sard, Dave Jacobson, and Kathleen O'Malley

Oregon State University, Department of Fisheries and Wildlife
Coastal Oregon Marine Experiment Station, Hatfield Marine Science Center
2030 SE Marine Science Drive, Newport, Oregon 97365
melissa.evans@oregonstate.edu

For at-risk populations, reintroductions to historical habitats are often implemented in conservation efforts. Establishing a demographically viable population is of primary concern during early stages of a reintroduction program. However, over the longer-term, population persistence will depend on the ability of individuals to adapt to stochastic environmental change. Adaptation depends on genetic variation underlying functionally-important traits i.e. traits that influence phenotype and the fitness of individuals. Reintroduction operations or strategies may inadvertently influence genetic variation exhibited by a restored population; for instance, the source, number, sex ratio, or relatedness of individuals used in reintroductions may alter founding population genetic diversity. Indeed, many studies have attributed reduced genetic diversity in reintroduced compared to "source" populations as a result of such "founder effects".

Since dam construction on Willamette River tributaries during the 1960s, spring Chinook salmon (*Oncorhynchus tshawytscha*) populations have been primarily supported using hatcheries. In the 1990s, the Oregon Department of Fish and Wildlife initiated reintroductions of Chinook salmon above Willamette basin dams with the goal of re-establishing natural spawning activity in historical habitats. We are currently investigating genetic diversity at genes associated with functionally-important traits including the timing of migration and immunity in reintroduced Chinook salmon.

Our findings indicate that diversity at genes linked to the circadian rhythm mechanism (*OtsClock1b* and *OmyFbxw11*), candidate genes associated with migration timing, in reintroduced Chinook salmon from the South Santiam and South Fork McKenzie rivers are similar to those found in other extant North American populations. Hatchery programs established following dam construction and the more recent reintroduction efforts therefore appear to have maintained diversity at these genes. We found evidence of temporal (between run years) and spatial (between populations) differentiation at the three genes, though little support for adaptation influencing patterns of genetic differentiation. However, we observed a strong relationship between variation at the *OmyFbxw11* gene and arrival time to the spawning grounds. Reintroduced salmon may therefore be capable of an evolutionary response to ecological shifts that alter the adaptive landscape between fitness and arrival timing to the spawning grounds.

Analyses of major histocompatibility complex (MHC) genes involved in parasite recognition and the initiation of the immune response are ongoing and some preliminary results will be discussed.