Reproductive Isolation

A review of published accounts indicates that homing fidelity in coho salmon is generally strong, with low levels of straying (about 1 percent) estimated for most natural populations that have been studied. On the other hand, coho salmon habitat typically includes small tributaries that experience relatively frequent, temporary blockages, and there are a number of examples in which coho salmon have rapidly recolonized vacant habitat that had only recently become accessible to anadromous fish. Because ESU determinations focus on units that are strongly isolated over evolutionarily important time frames, NMFS concludes that, in general, local spawning populations of coho salmon are unlikely to meet the criterion of reproductive isolation. However, groups of local populations among tributaries within a river drainage may experience substantial, long-term isolation from other such groups.

Genetic data provide useful indirect information on reproductive isolation because they integrate information about migration and gene flow over evolutionarily important time frames. The Genetics Project within the NWFSC is developing a coastwide database of protein electrophoretic data for coho salmon, and the database now includes information for 53 polymorphic gene loci in samples from over 100 populations covering a geographic range from the Trinity River, CA, to Bristol Bay, AK. Published results from several other studies of genetic characteristics of coho salmon populations were also considered. These included additional studies based on protein electrophoresis (Olin 1984, Solazzi 1986, Reisenbichler and Phelps 1987, Wehrhahn and Powell 1987, Bartley 1987, Gall 1991), an agglomerative approach based on data from life history, morphology, and protein electrophoresis (Hjort and Schreck 1982), and two recent studies of variation at the DNA level (Currens and Farnsworth 1993, who examined variation at mitochondrial DNA (mtDNA) and Forbes et al. 1993, who examined variation in nuclear DNA).

Although collectively these studies show that the pattern of relationships among populations is complex, there is a strong geographic component to the observed population structure, and several major stock groupings can be identified. While a few individual samples proved to be exceptions to the general patterns, possible explanations for these results include true ancestral relationships, stock transfers, and random variation in an analysis involving a large number of samples. Major stock groupings resulting from NMFS' analysis are described below.

Southern Oregon/California—Because the NMFS data set included only a single sample from California, the analysis was supplemented with published data from Olin (1984), Bartley (1987), and Gall (1991). This resulted in data for 13 polymorphic gene loci for 26 samples from southern Oregon (south of Cape Blanco) and California, including 4 from the NMFS data set. Limitations of this analysis are that many sample sizes were small, and data were not available for some of the most variable gene loci. Nevertheless, results clearly show two major geographic clusters in this region, separated by a relatively large genetic distance. The northern (and primarily large-river) group includes 12 samples ranging from the Elk River (just south of Cape Blanco) to the Eel River (just north of Cape Mendocino). The southern (and primarily small-river) group includes 11 samples, spanning a geographic range from Fort Bragg to Tomales Bay. There is considerable genetic diversity within both groups, particularly the northern. Three small-river samples from the southern region (Scott, Cottoneva, and Pudding Creeks) are outliers to both of the major groups, and Huckleberry Creek (Eel River Basin) is only loosely allied to the northern group.

Oregon coast—The NMFS study shows that samples of coho salmon from the Oregon coast are genetically distinct from other coastal and Columbia River populations. In addition, there is evidence for genetic differentiation within this group. Samples from four hatcheries on the northern Oregon coast form a group that is well differentiated from other samples. It is not known how accurately these samples reflect genetic characteristics of coho salmon native to this area. Most samples from the Oregon coast are part of a large genetic cluster. This cluster includes both natural and hatchery populations. A third cluster within the Oregon coastal group consists of wild and hatchery samples from the Elk and Umpqua Rivers that also share some degree of similarity with a hatchery sample from the Rogue River.

Hjort and Schreck (1982) also found that a group of hatchery populations from northern Oregon was distinct from other hatchery and natural populations along the Oregon coast. Their study further indicated that Oregon coastal populations of coho salmon differed from those in other regions, including the Columbia River Basin, California, and Washington. Results obtained by Olin (1984) and Solazzi (1986) are generally consistent with the patterns described above. In addition, Solazzi (1986) found that two wild populations from the north coast of Oregon, which were not included in the NMFS data set, clustered with hatchery samples from northern Oregon.

Recent DNA data for Oregon coho salmon are largely consistent with results based on protein electrophoretic analyses. Currens and Farnsworth (1993) identified three major groups within Oregon: (1) North and central Oregon coastal populations, (2) Columbia River populations, and (3) south Oregon coastal populations and two unusual Columbia River populations—the Clatskanie and Clackamas Rivers. Forbes et al. (1993) reported highly significant differences between Columbia River and Oregon coastal coho salmon, but only marginal differences among stocks within these regions.

Lower Columbia River—Another major cluster in the NMFS analysis includes all of the lower Columbia River samples, as well as samples from the southwest Washington coast. Within this larger group, several smaller clusters can be identified. Two of the subclusters, one dominated by samples from Washington and the other by samples from Oregon, include most of the samples from the lower Columbia River. Another subcluster contains three samples from Willapa Bay on the southwest Washington coast. A final subcluster includes samples from the Clackamas and Clatskanie Rivers in the lower Columbia River and samples from the Humptulips and Simpson Hatcheries on the southwest Washington coast. As noted above, Currens and Farnsworth also found a genetic similarity between samples from the Clackamas and Clatskanie Rivers, based on mtDNA markers.

Puget Sound, Strait of Georgia, and Olympic Peninsula—The few samples NMFS examined from Alaska and the upper Fraser River, Canada, are substantially different genetically from all U.S. populations and are not considered further here. In contrast, samples NMFS has examined from Puget Sound and the Strait of Georgia form a coherent genetic cluster. Closely allied to this Puget Sound/Strait of Georgia group is a group of populations from the northwestern Olympic Peninsula (northern coast of Washington and the western end of the Strait of Juan de Fuca). In earlier studies, Reisenbichler and Phelps (1987) found little geographic structure among samples of coho salmon from the northern coast of Washington, whereas Wehrhahn and Powell (1987) found