

Reviewing the Evidence that Adult Sockeye Salmon Strayed from the Fraser River and Spawned in Other Rivers in 1997

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During the summer and autumn of 1997, sea surface temperatures (SSTs) along the British Columbia coast and in the Gulf of Alaska were the warmest on record, and the return migration of sockeye salmon to the Fraser River was unusually protracted (McKinnell, 1997). Some sockeye salmon had developed secondary sexual characteristics in the sea. From northern California (Smith River) to northern Vancouver Island, sockeye salmon were observed in unusual abundance in rivers and streams where they are not normally seen. Two hypotheses were developed to explain these observations: (1) there had been good survival of small local sea- and river-type populations that had largely gone unnoticed by biologists, and/or (2) an unusually high number of the abundant Fraser River sockeye salmon had strayed. Samples of sockeye salmon (whole fish and/or tissues) were collected from 30 locations on Vancouver Island (~450 fish) and 4 locations in Oregon (45 fish) to investigate their origin. Of the whole fish collected on Vancouver Island, most were spawned out.

Mitochondrial DNA (mtDNA) variation in sockeye salmon has been surveyed throughout the species' range and baseline haplotype frequencies were available from all major populations (36 sample sites) spanning the region of interest from Queen Charlotte Sound to the Columbia River (Wood, un-

published data). Genetically similar populations were pooled to form 11 "stocks", the maximum number that could be resolved with the 11 haplotypes observed in this region. Simulations with mixtures of sockeye salmon of known origin were conducted to determine the reliability of stock composition estimates based on mtDNA variation among the 11 stocks. Haplotype frequencies in samples collected from rivers on the west coast of Vancouver Island (WCVI), the east coast of Vancouver Island (ECVI), and Oregon were compared with corresponding frequencies in the baseline to determine first, whether non-Fraser sockeye salmon haplotypes were present, and second, to estimate the most likely contributions by each of the 11 stocks using Statistical Program for Analyzing Mixtures (SPAM). Where haplotype frequencies were consistent with significant contributions from Fraser River fish, scale patterns were used to estimate contributions by individual populations within the Fraser River using the baseline developed by the Pacific Salmon Commission. Estimates of stock composition from mtDNA and scale patterns were then assessed for consistency with information on age composition, run timing and parasites carried by the sockeye.

Analyses of mtDNA (Figure 1) and scale patterns (Figure 2) of sockeye salmon sampled from rivers

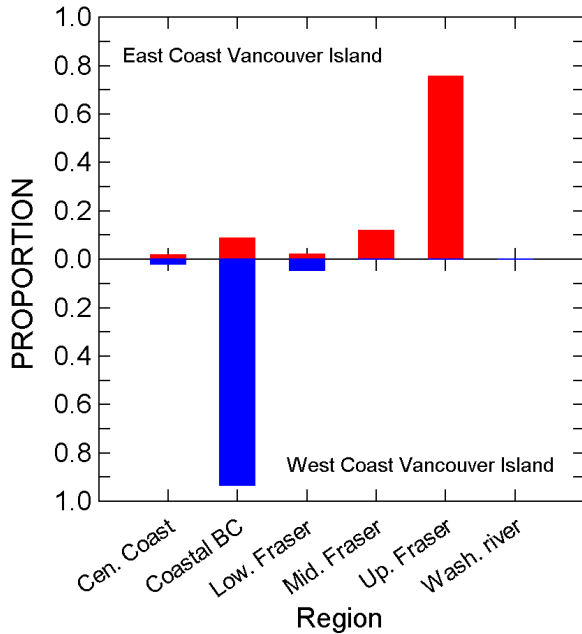


Figure 1. Maximum likelihood estimates of sockeye salmon population origin based on mtDNA haplotypes for samples taken on the east and west coasts of Vancouver Island, B.C.

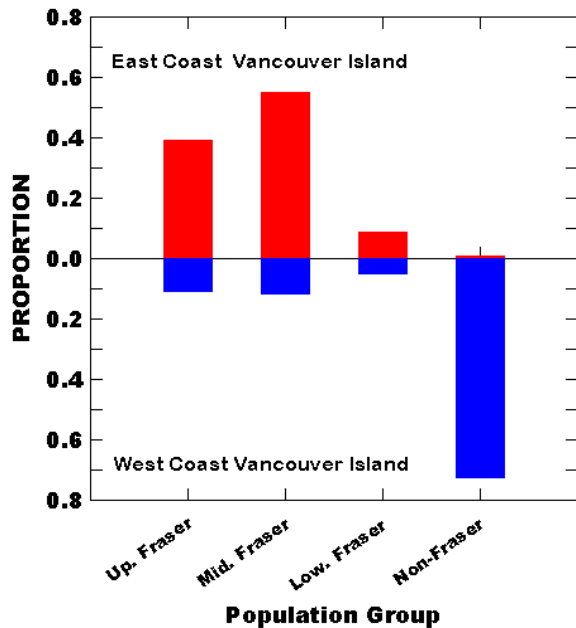


Figure 2. Maximum likelihood estimates of sockeye salmon population origin based on scale patterns for samples taken on the east and west coasts of Vancouver Island, B.C.

along the ECVI are consistent with the hypothesis of straying Fraser River sockeye salmon; however, there was also evidence of non-Fraser haplotypes in these samples suggesting that a small fraction of the sockeye salmon were of local origin. Age composition (mostly age 1.2) and *Myxobolus* and *Philonema* parasite incidence were consistent with sockeye of Fraser River origin. On the other hand, analyses of mtDNA haplotypes and scale patterns of sockeye salmon sampled from rivers on the WCVI are not consistent with the hypothesis of straying Fraser River fish, suggesting an unusual recruitment to local populations. Age composition data were similar to Fraser River and other southern sockeye populations. Parasite data were not available for these samples.

The mtDNA haplotypes sampled from the Deschutes River, Oregon ($n = 33$) were those typically found in many southern sockeye salmon populations such as the Columbia and Fraser rivers. The haplotype frequencies, however, were not typical of populations sampled to date from either of these rivers, with the possible exception of some small populations in the lower Fraser River. The date of sample collection in the Deschutes River (mid-August) was earlier than would be expected for sockeye salmon from the lower Fraser River. Of two sockeye salmon sampled from the Rogue River, Oregon, one contained a haplotype that is not found in the Fraser River but is common in river-type populations on the west coast of North America and north of central British Columbia. Four fish from the Clackamas and two from the Klaskanine rivers had haplotypes that are common in southern populations and little can be said of their origin.

At least some Fraser River sockeye strayed. These fish may have (1) begun their migration from a location that was more distant than normal, or (2) started their migration from a normal location but took a longer route homeward, or (3) encountered anomalous ocean currents that made their migration more arduous, or (4) some combination of the above. Homeward migration was likely abandoned in favour of a more convenient river due to advancing sexual maturation.

References

- McKinnell, S. 1997. An unusual ocean climate in the Gulf of Alaska during the spring of 1997 and its effect on coastal migration of Fraser River sockeye. (*NPAFC Doc. 282*) 10 pp. Fisheries and Oceans Canada, Ocean Science and Productivity Division, Pacific Biological Station, Nanaimo, B.C. V9R 5K6.