

Genetic Mixed Stock Analysis of Juvenile Chinook Salmon in Coastal Areas of Western North America

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Genetic mixed-stock analysis has been used routinely for over two decades to estimate the origins of ocean-caught Pacific salmon. However, nearly all of these applications have focused on the study of maturing adult fish taken in fisheries. Recently, genetic stock identification efforts are also being directed at the study of juvenile mixtures (e.g., Teel et al. 2003; Brodeur et al. 2004). This shift is due in part to the recent availability of samples taken in surveys along the coast of North America in large-scale programs to study juvenile salmonids during their ocean phase (e.g., Brodeur et al. 2000). The genetic analysis of juveniles is also motivated by a lack of available information on the initial marine movements of many stocks, particularly of untagged natural spawning populations. The purpose of this paper is to use results from allozyme analyses of juvenile chinook salmon (*Oncorhynchus tshawytscha*) sampled in nearshore areas of the U.S. Pacific Northwest to illustrate examples of genetically distinct stocks with contrasting migration patterns.

Fish were captured during the summers of 1998–2001 in surveys of nearshore coastal areas ranging from central Oregon to northern Washington (Emmett and Brodeur, 2000). Trawls consisted of one-half-hour long surface tows with a 264 Nordic rope trawl along nine transects perpendicular to shore ranging from La Push, Washington (47°55'N) to Cape Perpetua, Oregon (44°15'N). Sampling stations began 1–5 nautical miles offshore and continued, in about 5 nautical-mile increments, to about 30 nautical miles offshore. Cruises, of about one week duration, were conducted in May, June, and September each year. Tissues were dissected from approximately 2,600 juveniles which were genotyped at 32 allozyme loci. Allele frequencies from 150 chinook salmon spawning populations in California and the Pacific Northwest were used as baseline data (Teel et al. 1999). Estimates of stock composition were made using maximum likelihood procedures and weighted by catch to estimate the numbers of fish sampled from a particular stock group. Additional details on methods are given in Teel et al. (2003).

Stock compositions of marine samples varied greatly by month and location reflecting the juvenile movements of genetically distinct populations of chinook salmon. Spring-run (season of adult migration to freshwater) fish from the interior Columbia River basin were the most abundant population group off northern Oregon and Washington throughout the early summer (58% of the marine catches) and were nearly absent in September. The estimated number of interior spring-run fish caught in May and June cruises illustrated the rapid northward movement of these juveniles (Fig. 1). In May, most of the fish captured near the mouth of the Columbia River (Columbia region) were spring-run chinook salmon from upstream sources. In June, nearly all of the interior spring-run individuals were sampled further north (Washington region).

In contrast to interior spring-run juveniles, Columbia Basin fall-run chinook salmon were evident throughout summer sampling, and predominate in September (45% to 89%). Two ecotypes of fall-run populations identified by genetic and life history differences (“brights” and “tules”) showed distinct juvenile migration patterns after sea entry (Fig. 2). Brights were mostly caught in southern sampling areas (Oregon and Columbia regions) and tules were more abundant further north (Washington region).

Fig. 1. Estimated number of juvenile chinook salmon from three stock groups captured in two regions along the Oregon and Washington coasts during early summer trawls during 1998–2001. Regions are Columbia River (CR) and Washington Coast (WA).

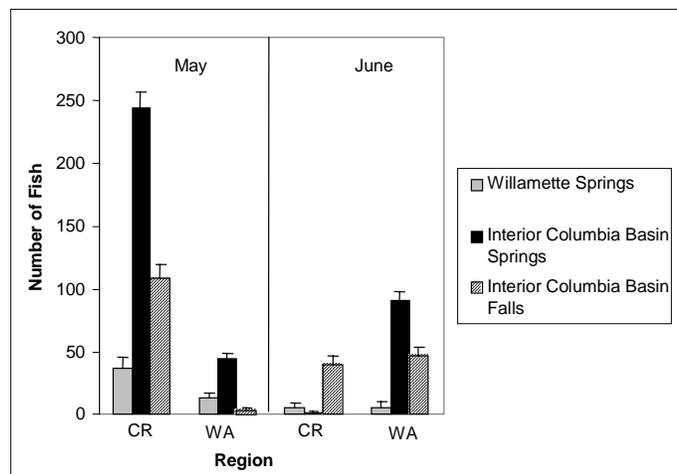
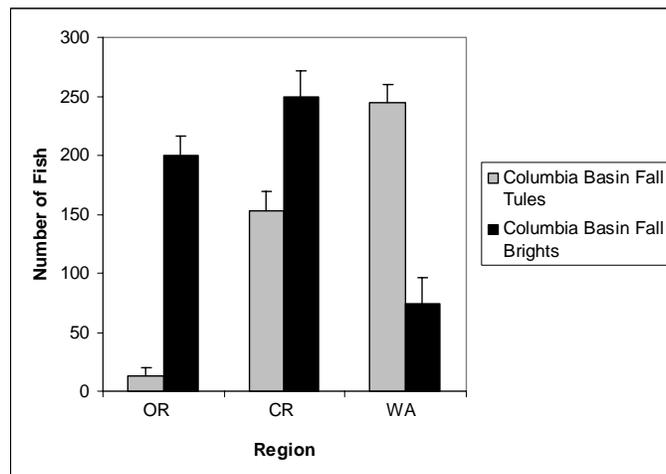


Fig. 2. Estimated number of juvenile chinook salmon from two stock groups captured in three regions along the Oregon and Washington coasts during September trawls during 1998–2001. Regions are Oregon coast (OR), Columbia River (CR), and Washington Coast (WA).



The contrasting juvenile migration patterns of interior Columbia Basin spring- and fall-run populations are consistent with the chinook salmon population structure recently described by Waples et al. (in press.) That study jointly considered genetic and life-history variation, including patterns of adult ocean migration, and revealed distinct evolutionary lineages within the Columbia Basin. The genetic analysis presented here suggests that differing initial juvenile marine migrations also provide an important source of diversity among these populations of chinook salmon.

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