

## DNA Analysis Increases the Utility of Other Stock Identification Methods in Sockeye Fisheries Management

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Fraser River sockeye return mainly as 4-year olds to coastal waters in one of four run-timing groups: Early Stuart, Early Summer run, Summer run, and Late run. The run-timing groups comprise many independently spawning populations of sockeye in the Fraser River. The characteristic run-timing of these populations relative to one another enables direction of higher exploitation rates toward healthy stocks and reduced fishing on weaker ones. Scale patterns reflect different growing conditions among lakes, and these patterns have been applied successfully to distinguish among Fraser sockeye stocks and runs in the past (Henry 1961). Scale patterns among some major Summer run and Late run stocks have converged recently, thereby reducing the utility of scales in stock identification. Compounding this problem is a concurrent reduction in the availability of scales from 3-year olds on the spawning grounds. In-season management on the basis of scale-based stock identification is therefore hindered because predictions of scale patterns are uncertain for returning 4-year olds. Post-season and in-season estimates of stock composition can differ considerably as a result.

Analysis of DNA provides accurate and precise estimates of stock composition. Because DNA-based analyses are not afflicted by the problems recently affecting scale-based analyses, DNA was used extensively for Fraser sockeye management in 2002 (Beacham et al. in press). Data provided via DNA are extremely informative but genetic analyses must be judiciously applied due to financial limitations. Scales are examined for purposes other than stock identification (such as estimation of age composition and evaluation of growing environments in lakes) and are not expensive to analyse, so we investigated the possibility of increasing their effectiveness in stock identification by the use of matched DNA analyses.

Our scale analysis procedure is outlined in Gable and Cox-Rogers (1993). Briefly, we examine the zone of freshwater growth of scales from sockeye sampled from mixed-stock fisheries and compare, via linear discriminant functions, four measured variables to standards based on equivalent data from scales sampled on the spawning grounds. Composition of the standards is influenced by run-strength forecasts. Genotypes of sampled fish were compared to a 47 population baseline including 15 genetic loci (see Beacham et al. in press). An individual sockeye's scale data were matched to its DNA-based stock of origin using GeneClass (Cornuet et al. 1999). Other data, including length, were also matched. Stock-specific lengths obtained from the spawning grounds are collected too late for in-season management, and they differ from lengths in fisheries because of wear and sexual maturation. We developed in-season scale standards from DNA-based identification of individuals and compared results to estimates that would otherwise have been available in-season. We compared marine lengths, scale resorption, and texture of gonads among stocks to evaluate the possibility of applying in-season DNA analyses to generate stock identification models using those variables.

Some stocks are not easily distinguished using scales and so the number of stocks included in the baseline for scale analyses is limited according to the strength and timing of runs. Stocks that rear in the same lake can have different migration timing and, whereas these are likely indistinguishable using scales, DNA analyses can resolve their relative abundances. Knowing proportions of these stocks allows better interpretation of scale results and can be used to describe run progression. For example, in-season estimation of the precise timing of the Summer run using only scale data and estimated abundance is difficult. Components of the Summer run are identifiable using DNA, however, and because these also have characteristic relative timing they can provide independent information on whether the Summer run is half or three quarters complete. This information can be used to predict appropriate baselines for scale analyses of samples in subsequent weeks.

Use of DNA can help scale analyses not only by suggesting the incorporation of appropriate stocks in baselines but also by improving the accuracy of the scale characteristics estimated for baseline stocks. Stock identification analyses based on scale standards generated using matched DNA were similar to post-season results generated using scale standards obtained from the spawning grounds. In contrast, scale standards from pre-season predictions yielded models whose results differed strongly from those obtained in the post-season. Only one season has been

examined, but the results observed indicate that updating scale standards via matching DNA samples collected in-season can potentially improve in-season results from scale models.

Length is another variable that could be estimated on an age- and stock-specific basis using in-season DNA analyses. In 2002, post-orbit to fork distance in Summer run sockeye was less than in Late run sockeye in general ( $P < 0.0001$  for both males and females), but the dominant stock groups in the Summer run and Late run did not differ greatly. Because males tend to be longer than females from the same stock (combined  $P < 0.0001$ ), separate discriminant function models should be constructed for males and females, which would unfortunately increase sample size requirements. Nevertheless, including length in stock identification models can apparently be useful in some years for discriminating some stocks.

We evaluated other characteristics that change over time which might distinguish Summer run and Late run sockeye, and we found significant differences in scale resorption ( $P < 0.001$ ) and gonad texture ( $P < 0.005$  for both males and females) among the dominant stocks in each run. Scale resorption appears particularly promising: over 80% of Summer run sockeye tested had resorbed scales, whereas only 50% of Late run sockeye from the same samples had scales that were significantly resorbed.

These results demonstrate how DNA-based stock identification can improve existing stock identification techniques and be used in the development of new ones. The benefits of such an approach are not limited to the management of Fraser River sockeye.

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