

# Determining Accuracy of a Bayesian Approach to Estimate Individual Identification to Stock-of-Origin for Pacific Salmon in Marine Fisheries Using Microsatellite and MHC Loci

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Successful identification of individual sockeye to stock-of-origin remains one of the most useful and most challenging problems for mixed stock analysis. Capability to correctly identify individuals on the high-seas provides new research opportunities to study numerous biological and behavioural traits of Pacific salmon. A number of applications which employ Bayesian analysis for individual identification are available and work with varying degrees of success. The accuracy of individual identification is best evaluated using known mixture samples. The most convincing evidence for the success of individual identification requires “blind sample testing” where the laboratory provides estimates without knowing the true stock-of-origin for the sample.

Genomic DNA was extracted from liver, scales, operculum punches, muscle tissue, or fin clips from over 46,000 sockeye salmon collected between 1983 and 2002 representing 261 Pacific Rim populations spanning Washington, British Columbia, Alaska, Russia, and Japan. PCR products at 14 microsatellite loci: *Ots2*, *Ots3* (Banks et al. 1999), *Ots100*, *Ots103*, *Ots107*, and *Ots108* (Small et al. 1998; Nelson and Beacham 1999), *Oki1a*, *Oki1b*, *Oki6*, *Oki10*, *Oki16*, and *Oki29* (Smith et al. 1998 and unpub.), *One8* (Scribner et al. 1996), and *Omy77* (Morris et al. 1996) were size fractionated on denaturing polyacrylamide gels and allele sizes determined with the ABI 377 automated DNA sequencer. Genetic variation at the MHC class II *DAB-β1* locus was surveyed by denaturing gradient gel electrophoresis (DGGE) using methods of Miller et al. (2000, 2001). Four different “blind” mixture samples were collected from locations near or on the spawning grounds in the Fraser River, Nass/Skeena rivers, and populations from the West Coast of Vancouver Island and S.E. Alaska. The mixture samples were screened for the same 14 microsatellite and 1 MHC loci used for the baseline. Individual multi-locus genotypes in the mixture were assigned to population using the Pacific Rim baseline allele frequencies and a Bayesian mixture model (Pella and Masuda 2001). Stock assignments of the mixture individuals were determined by the greatest posterior probability. Once assignments were made, the estimated stock-of-origin was verified against the known sample location determining if individuals were correctly assigned to population, run-timing (where applicable), and region.

The first sample was a mixture of 140 fish consisting of 10 Fraser River populations collected in 1999. Accuracy of individual identification was 82% correct to population, 91% correct to run timing (Early Stuart, Early Summer, Summer, Late) and 100% correct to the Fraser River (Table 1). The second sample was collected from three geographically proximate populations in Barkley Sound (Henderson, Great Central, and Sproat), on the west coast of Vancouver Island. For the 91 fish sample, individual identification was 90% correct to population and 100% correct to Barkley Sound, again using the Pacific Rim baseline. In the third sample a blind mixture was provided by the Alaska Department of Fish and Game (ADFG) composed of SE Alaska, Skeena, and Nass populations. Since population specific populations was not known for the Nass and Skeena Rivers (sample taken from lower river fish wheel), estimates of population specific accuracy was only available for S.E. Alaska (Table 1). However, individual identification to region was 93% accurate. In the fourth sample, approximately 800 sockeye salmon returning to the Fraser River were radio-tagged in near-shore areas. Prior to reaching the spawning grounds, each tagged fish was individually identified. Of the 275 fish that were tracked to the spawning grounds 85% were correctly identified to population, 92% were identified to run time, and 100% were correctly identified to the Fraser River.

Analysis of these known samples highlights the high level of accuracy to stock-of-origin obtained from Bayesian analysis for individual assignments using a microsatellite/MHC genetic markers and extensive Pacific Rim baseline. Levels of accuracy expected from any high-seas collections of sockeye salmon should be ~90% correct to population and ~100% correct to region given an extensive Pacific Rim baseline.

**Table 1.** Accuracy of known sockeye salmon mixture samples analyzed with a Pacific Rim baseline consisting of 261 populations ranging from Japan to Washington State. \*indicates accuracy to S.E. Alaska where mixture sample contains only those Alaskan populations in the baseline.

Mixture Sample	N	%toPopulation	%toRun Time	%toRegion
99PSCBlind	140	86%	91%	100%
02BarkleySndBlind	91	90%	n/a	100%
02AlaskaBlind	525	91%*	n/a	93%
02LGLTagging	275	85%	92%	100%

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