

International Data Bases Help Resolve Migration and Survival of Pacific Salmon in the North Pacific Ocean and Bering Sea

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Keywords: Allozyme, allele standardization, microsatellite, SNP, stock identification

In the summer of 2003, the United States completed its fifth decade of research into the distribution and migration of salmonids in the North Pacific Ocean and Bering Sea. These basins provide major feeding habitats for various salmon stocks originating from both Asia and North America (e.g., Kaeriyama 1998; Seeb et al. in press). Information from tags, parasites, or scale patterns provides important insights (Wood et al. 1989; Patton et al. 1998; Urawa et al. 2000); here we review the emergence of genotyping approaches used by United States laboratories that have led to finer resolution in stock identification studies.

Unanticipated fluctuations in the productivity of some regional aggregations of stocks (see Anon. 1998) increased interest into the effects of environmental variables. We anticipate that stock identification using gene markers will provide a better understanding of migration patterns that, when coupled with existing ecological studies, may clarify mechanisms that cause variable production in the patchy marine environment (see Sukhanova et al. 1999). Pertinent hypotheses include: stocks are segregated both geographically and temporally, stocks utilize similar geographic areas, but are temporally segregated, stocks overlap both geographically and temporally but respond differently to existing environmental conditions, competition of wild fish with larger hatchery fish, or interceptions in near-shore fisheries (Brannon 1984, cf. Welch et al. 2003).

The usefulness of gene markers, initially in the form of allozyme data developed by the NOAA Fisheries laboratory in Seattle, emerged in the 1970s (Utter et al. 1976). During the 1980s several laboratories, ranging from University of California Davis to the NOAA Fisheries Auke Bay Laboratory in Alaska, started their own stock identification programs using allozymes. It was soon realized that the synergy provided by laboratory to laboratory standardization could generate huge and enormously valuable databases for gene markers from populations throughout the species range (see Shaklee and Phelps 1990). The laboratories named above, along with laboratories from the States of Washington and Alaska, formed a consortium of cooperating agencies who met frequently to run allele comparisons and merge data sets from their respective jurisdictions. Cooperation and support by laboratories from Japan and Russia yielded some of the largest data sets of this kind for any organism (chinook salmon data maintained by NOAA Fisheries, Seattle [Teel et al. 1999]; sockeye salmon data maintained by NOAA Fisheries, Auke Bay [Habicht et al. 2001]; and chum salmon data maintained by Alaska Department of Fish and Game [Kondzela et al. 2002]).

During the 1980s and 1990s laboratories began comparing various DNA techniques to improve the accuracy offered by allozyme data and to streamline the sample collection procedures (allozyme analysis requires frozen tissue and organs while DNA can be extracted from fins stored at room temperature; interesting comparisons may be seen in Park et al. 1994; Scribner et al. 1998; Allendorf and Seeb 2000). Numerous techniques were developed and evaluated including detection of (1) DNA sequences (Park et al. 1993), (2) restriction fragment length polymorphisms (RFLPs) of mitochondrial and nuclear DNA (Cronin et al. 1993), (3) randomly amplified polymorphic DNA (RAPDs; e.g., Allendorf and Seeb 2000), and (4) length polymorphisms of minisatellite and microsatellite DNA (Beacham 1996; Beacham and Wood 1999; Allendorf and Seeb 2000). Each offered some advantages over allozyme techniques, but data from highly polymorphic microsatellite loci emerged as the favored technique of many laboratories. However, various issues such as slow throughput or the non-transportability of data from laboratory to laboratory retarded the general application of these DNA approaches for most high-seas studies.

The NPAFC Science Plan 2001-2005 (<http://www.npafc.org>) renewed the mandate for expanded stock identification research and increased at-sea research on the effects of anomalous ocean conditions. Consortium agencies are now collaborating to replace the allozyme data bases by (1) standardizing an inter-agency database for microsatellite DNA for chinook salmon and (2) shifting to analysis of single nucleotide polymorphisms (SNP DNA) whose attributes lend themselves to high throughput and easy standardization among laboratories and among nations (see Brumfield et al. 2003; Melton 2003).

Standardizing data from microsatellite DNA across laboratories and analysis platforms has proven to be extremely difficult. An attempt to standardize microsatellite data for chinook salmon was begun in 1999, but that effort was dropped, and to date no interagency databases exist for any Pacific salmon. Recently, a large and costly

program to standardize microsatellite loci for chinook salmon was funded by the Pacific Salmon Commission. This program shows substantial promise, but the standard data set will be limited to those populations inhabiting the eastern Pacific Ocean.

In contrast, the various SNP assays now available all produce genotype data that is automatically standardized across laboratories. Additionally, the SNP techniques capture some of the same genetic data that was collected by slower-throughput sequencing and RFLP techniques used in the past. For chum salmon, for example, historical sequence data (Park *et al.* 1993), RFLP data (Cronin *et al.* 1993), contemporary sequence data collected by different techniques (Abe *et al.* 2002) or microarray analysis (Moriya *et al.* 2002) are all captured by the high-throughput SNP techniques of Smith *et al.* (2003). In some organisms, SNPs have demonstrated diagnostic differences between populations that could not be differentiated by microsatellites (Bensch *et al.* 2002). Several United States laboratories are developing SNP assays for chum, chinook, and sockeye salmon, anticipating that issues such as data quality and transportability will make these the markers of choice for the study of these migratory species (*cf.* Morin *et al.* in press).

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