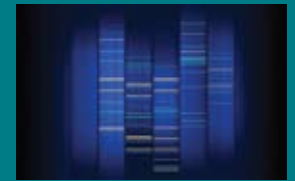


Report from the Ad Hoc Working Group on Stock Identification



The total biomass of Pacific salmon has shown significant fluctuations over the last decades, and the pattern of these fluctuations differs among species as well as local stocks. Recent attention has focused on climate change and how the ocean environment and variable marine ecosystems affect these fluctuations and the abundance and distribution of salmon stocks. Information on the oceanic migration pattern and marine survival of individual stocks is essential for understanding the population dynamics of these species.

Stock-specific biological information has been provided by various stock identification techniques including tags, parasites, scale patterns, and genetic marks. In 2000, the North Pacific Anadromous Fish Commission established an *ad hoc* Working Group on Stock Identification with the intent to: 1) develop, standardize, and disseminate genetic and other databases among the Parties; 2) encourage the development of new genetic technologies; and 3) facilitate the dissemination of statistical techniques. The focus of the working group has been on the various types of genetic markers as genetic stock identification studies have become a central part of NPAFC research activities supporting BASIS and other programs across the Pacific Rim.

Genetic analyses of salmon in international waters require large, comprehensive datasets of genetic information developed cooperatively by multiple parties across international boundaries. Multi-party, multi-national datasets require robust methods that are both transparent and transportable because all NPAFC Parties are contributing to a common set of data that can be accessed

and used by each for analyses. Initially, protein or allozyme marker were used, but they are now rapidly being replaced by DNA markers such as microsatellites, and, more recently, single nucleotide polymorphisms (SNPs).

However, the large data set of allozyme allele frequencies from chum salmon originating from the Pacific Rim has been widely used by multiple research laboratories. Most recently, the database has been used by NPAFC scientists to track the stock-specific migration of chum salmon in the North Pacific Ocean and Bering Sea (Fig. 1).

Concurrently with the application of the allozyme databases, genetic markers based on DNA fragment variation (e.g. microsatellites) were shared among the NPAFC Parties. Although more difficult to transfer between laboratories than many other genetic markers, large databases exist for microsatellites across the Pacific Rim. Canadian researchers at the Department of Fisheries and Oceans have developed extensive microsatellites baselines with greater than 40,000 individuals for the five main species. They have shared these databases with other NPAFC Parties for collaborative stock identification research projects.

Recent efforts in United States and Japan have centered on developing DNA databases using single nucleotide polymorphism (SNPs). SNPs are assayed through high-throughput technologies and are particularly appropriate for NPAFC applications (Fig. 2). Unlike marker types based on fragment size, SNPs are based on the actual DNA sequence and require relatively little inter-laboratory standardization. SNP data can be easily transferred

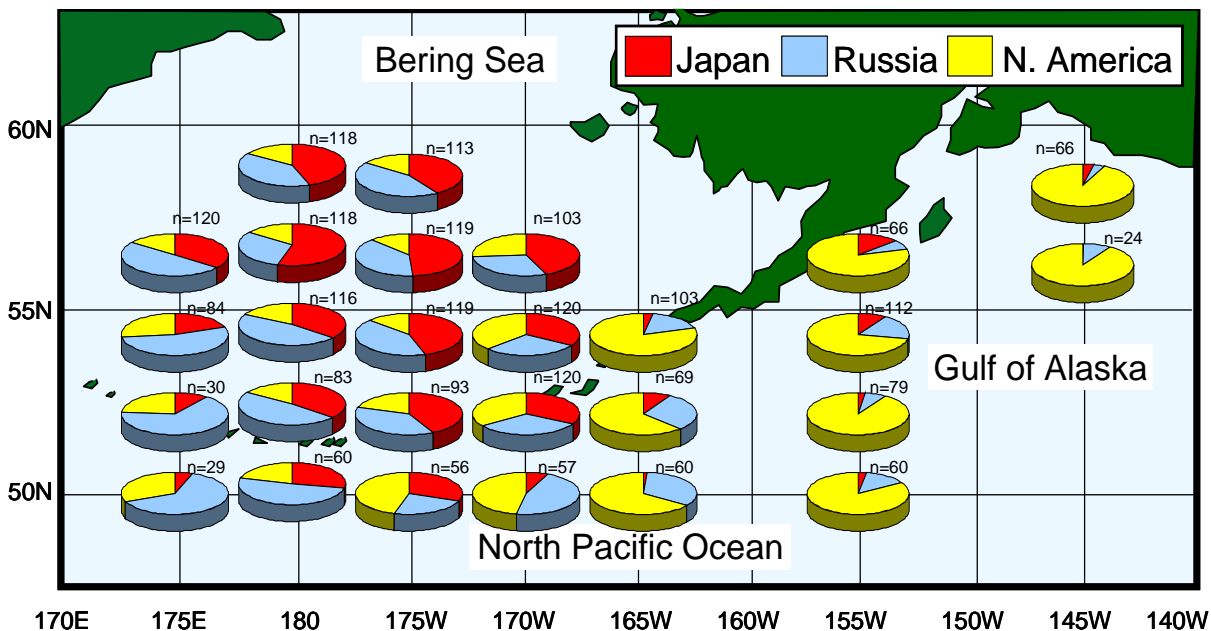


Fig. 1. The stock composition of immature chum salmon in the Bering Sea and North Pacific Ocean, estimated by 20 allozyme loci (Urawa et al. 2005. NPAFC Doc. 896).

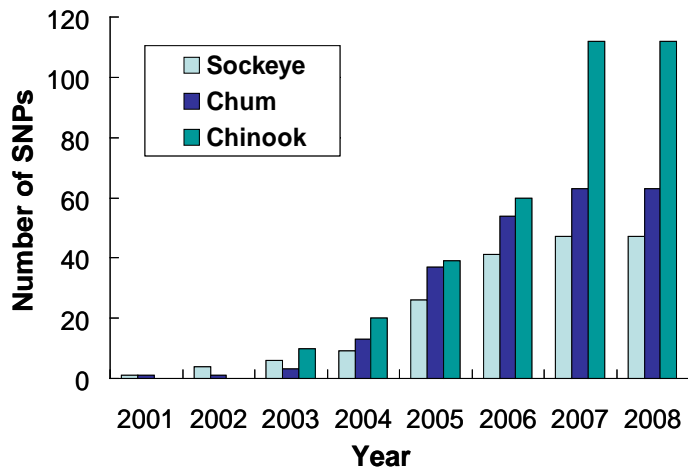


Fig. 2. Annual changes in number of SNPs found in sockeye, chum and Chinook salmon.

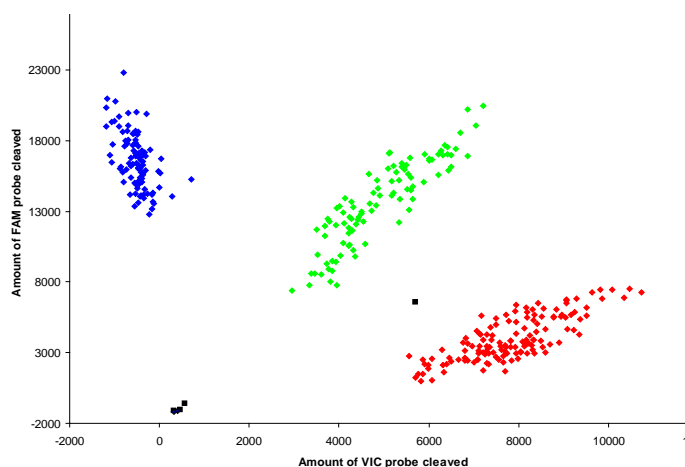


Fig. 3. Scatter plot of 380 individuals assayed for an A/T SNP. Units on the Y axis are fluorescence probes designed to detect the A allele; units on the X axis are fluorescence of the probes designed to detect the T allele. Four no-template controls cluster near the origin on the bottom left. AA homozygotes cluster on the Y axis and TT homozygotes cluster on the X axis. Heterozygotes (green) are intermediate.

between laboratories and instrument platforms (Fig. 3). United States and Japanese researchers met at the National Salmon Resources Center in Sapporo, Japan, for a 2-day meeting, October 15-16, 2008, hosted by the University of Washington with a grant from the Moore Foundation (Fig. 4). The goal of the meeting was to discuss progress and development of a shared database for chum salmon. The participants informally adopted the name



Fig. 4. Eleven scientists and students from Japan, Korea, and United States participated in the PacSNP meeting in Sapporo, Japan. (from left to right: (front row) K. Warheit, J.-N. Yu, J. Stevens, and N. Azuma; (back row) S. Abe, Y. Kogura, B. Templin, J. Seeb, L. Seeb, S. Sato, and S. Urawa)

PacSNP for the initiative. Following the meeting in Sapporo, graduate students and researchers from Russia, Korea, and Japan visited the University of Washington in Seattle for one to two weeks of hands-on training in SNP discovery and genotyping. Work on other SNP databases are progressing on both sockeye and Chinook salmon lead by efforts at Alaska Department of Fish and Game.

Within the next year, the *ad hoc* Stock Identification Working Group anticipates continuing research and development of DNA-level databases and markers in all species. Easily accessible on-line databases to archive and disseminate the data are also a high priority for future efforts to support these highly valuable multi-party, multi-national datasets.



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