
Workshop Review

Over the past several decades the biomass of Pacific salmon has shown significant fluctuations, and the pattern of these fluctuations differs among species as well as local stocks. Recent attention has focused on 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. Further, despite hatchery releases over the last decades, biological interactions between wild and hatchery fish in the ocean are poorly understood.

Stock-specific biological information has been provided by various stock identification techniques including tags, parasites, scale patterns, and genetic marks. The Workshop explored where and how these techniques are applied, what types of information are being generated, and what directions are desirable in the future. A consistent theme of the Workshop was the need for cooperation and collaboration to develop comprehensive and transferable methods and maximize research opportunities.

Contributed papers were organized around species. A synopsis of the presented work by species follows:

Chum salmon

Significant efforts have been directed towards gathering stock-specific information on chum salmon. Genetic databases have been particularly useful in this species. An extensive allozyme baseline was cooperatively developed and shared by the NPAFC Parties to determine stock components of mixtures of stocks at various life stages in coastal and high seas areas of the Bering Sea and Pacific Ocean. The oceanic migration pattern of Japanese chum salmon throughout their entire marine life cycle was estimated using this baseline. Stock-specific distribution and migration of juvenile and adult chum salmon of North American stocks in the shelf of eastern Bering Sea and Gulf of Alaska were also investigated using the allozyme baseline. Variation in the mtDNA control region and microsatellite loci are also under investigation. Japanese and United States laboratories are investigating DNA microarray and analysis of single nucleotide polymorphisms (SNPs) as rapid and easily-standardized methods of stock identification. In addition, mass otolith marking has been useful to determine hatchery origins, and a combination of genetic and otolith marks has been used in understanding biological interactions between hatchery and wild fish.

Chinook salmon

Historically scale pattern analyses were used extensively to estimate the composition of mixed-stock fisheries for chinook salmon in the Pacific Northwest and Bering Sea. More recently an extensive allozyme baseline was developed cooperatively among the NPAFC Parties. The allozyme baseline has been used extensively to monitor nearshore migration patterns of juvenile and adult chinook salmon. Currently multiple laboratories are developing comprehensive microsatellite and SNP databases for populations around the Pacific Rim. A large effort is currently being coordinated by the Pacific Salmon Commission to standardize a set of microsatellite loci and develop a comprehensive baseline within the Commission's area of interest.

Coho salmon

Coho salmon have recently been surveyed for MHC and microsatellite loci. These genetic analyses suggest that there are clear stock-specific differences in the migratory behavior of the species. Development of standardized and comprehensive genetic databases for coho salmon has not yet become a priority among laboratories.

Sockeye salmon

Scale pattern analysis has been used extensively to separate eastern and western Kamchatka stocks of sockeye salmon in mixture fisheries within the Russian EEZ as well as stocks in freshwater. Expansion of these analyses to determine the continental origins of high-seas fish has not been successful because of similar scale structures among Asian and North American stocks. Baselines of allozyme, microsatellite, and SNP markers are under development to determine the composition of sockeye stock mixtures caught in the Bering Sea. The current baseline, composed of Alaskan and Russian stocks, can precisely estimate the stock origins among and within major regions of the Pacific Rim.

Pink salmon

Pink salmon is the most abundant species among Pacific salmon and is essential to North Pacific ecosystems. Although extensive allozyme data have been collected for pink salmon across the Pacific Rim, standardized baselines have not been used extensively as has occurred in chum, sockeye and chinook salmon. The rigid two-year life cycle has produced reproductively isolated brood lines with large genetic differences, essentially requiring two independent baselines and analyses for this species. North American and Asian stocks are currently being examined for allozyme loci, and simulations are being done on even- and odd-year data sets to determine the regional groupings for mixed-stock analyses of coastal and high-seas pink salmon.

Statistical Analysis

For genetic data, various statistical analyses have recently been developed that are particularly appropriate for hypervariable microsatellite data with large numbers of alleles. These analyses are targeted at improving compositional estimates, dealing with incomplete baseline coverage, evaluating the relative information content among loci, and assessing the ability of the database to identify individuals to stock-of-origin. For scale data, probabilistic neural networks have been developed for handling difficult classification problems and as a tool for developing new scale analyses for stock separation.

Discussion

During the panel discussion a number of points emerged including the following:

- Significant information on migration patterns of Pacific salmon is emerging from the stock identification work to identify such factors as feeding areas, migration of juveniles, and extent of seasonal feeding competition. However, winter patterns are still poorly understood.
- It is important for future studies to examine the ocean carrying capacity and the interactions between hatchery and wild fish on the high-seas.
- Molecular techniques must be coordinated and standardized to develop comprehensive baselines, to extend research funds, and to maximize limited high-seas research opportunities.
- The question under consideration must first be identified before an appropriate method for stock identification is chosen.
- Sampling opportunities exist in the bycatch fisheries, and the composition of the bycatch can potentially be used as a forecasting tool.
- Significant resources have been spent on salmonid research in the last fifty years, but the legacy of that research is unclear. In the future, effort may be placed on developing mega-databases with emphasis on other species in addition to salmonids.
- Korea has recently joined the NPAFC and looks forward to future collaborations and assistance from the other NPAFC Parties.
- Collaboration of NPAFC scientists is an excellent example of international cooperation, and NPAFC successes should be communicated to policy-makers throughout the Pacific Rim.

Conclusions

The workshop demonstrated that information on stock identification is essential to our understanding to the marine ecosystem, potential effects of global warming, as well as the roles of hatchery releases. Significant progress has been made in stock identification, and techniques are changing rapidly with the emergence of new technologies in genetics, tagging, and microchemistry. Coordination and scientific exchanges among Pacific Rim nations is essential to insure continued progress, reduce unnecessary duplication, and maximize research opportunities.

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