The Perspectives of the Pacific Salmon Stock Investigations in Russia

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The main goal of science associated with the fisheries industry is the exploitation and harvesting of fish populations without destroying them. It includes several important objectives: 1) to study the dynamics of populations and the mechanisms of their responses to environmental changes, 2) to forecast their responses and to estimate expected abundance in advance, and 3) to estimate the optimal size of future catches which stabilize population fluctuations and that will not destroy their ability to self-regulate. All of these objectives have one need in common – to determine the stock structure of exploited populations. The development of the "stock concept" of fish populations is especially important for the management of the salmon industry. This concept states that the whole species consists of reproductively isolated units – "stocks" or "Mendelian" populations that have their own genetically conserved specific traits and are organized into some kind of structure that allow them to maintain equilibrium for better adaptation and survival. Thus, the problem of revealing this structure and differentiation of fish populations is vitally important for salmon management.

In Russia such studies were started in the early 1970's by Yu. Altikhov and S. Konovalov. The main problem of these first studies of population structure was the lack of markers which could reveal differences between stocks and their responses to environmental influences. Now, 30 years later, the problem of good markers still stands before scientists studying population processes and micro-evolutionary changes. The first markers used were exterior morphological characteristics, but the genetic inheritance behind these characters was not understood. Some scientists used the bone structure of the skull, and this method was very useful for systematic studies. Other morphological method used more than 20 measurements of body composition such as the number of vertebra and gill rakers. There were significant morphological differences between populations, but they were not associated with interspecies structure on a permanent basis and varied from year to year. Parasite infestation was also used as a marker for some sockeye and pink stocks of Kamchatka and Sakhalin.

The most important technique involved the differences in scale structure. Scale analysis was first developed for determining the age of fish. However, it was discovered that there were differences between stocks in the structure of sclerites which formed in the first year at sea. Analysis of these differences resulted in successfully discriminating between some salmon stocks. In Russia this method was developed in the 1970's by M. Selifonov and V. Bugaev (sockeye), E. Nikolaeva (chum), J. Zorbidy (coho), N. Grachev (pink), Savvaitova (mykiss) and many others. Currently, using modern statistical procedures, stock identification by scale pattern analysis has been done by N. Antonov, A. Bugaev, O. Temnykh, N. Klovach, L. Zavarina, and others. However, scale analysis has its limitations. The main problem is that the scale structure is not genetically inherited and cannot be considered as a permanent population characteristic. Differences depend on the climate conditions of each particular year, and most importantly, reflect the specific environment of the estuaries and bays where juveniles spend their first summer and fall. Therefore, differences in scale structure reflect these particular environmental conditions and are not the result of genetic differences.

Protein polymorphism was the first set of markers which were able to reveal real genetic relationships between populations. In Russia we first studied the polymorphism of 2–5 markers which allowed us to determine many special traits of micro-evolutionary process, and to obtain important information on racial and spatial distributions of populations. Important studies in the 1980's were performed by the laboratories of population biology and genetics from Moscow Institute of General Genetics, Kamchatka Research Institute of Fisheries, TINRO-Center, Magadan Institute of Biological Problems of Arctic, Institute of Marine Biology, Vladivostok by Yu. Altukhov, E. Salmenkova, L. Jivotovsky, V. Omelchenko, V. Kirpichnikov, R. Victorovsky, A. Makoyedov, V. Kartavtcev, V. Efremov, N. Varnavskaya and others. The work of these scientists was very important, but the small number of markers used did not allow the use of reliable statistical procedures for discriminating individual populations.

Only when the ability to determine multi-loci genetic characteristics of populations was developed were we close to reaching the goal of identification by stock. The Laboratory of Population Biology and Genetics of KamchatNIRO, Petropavlovsk-Kamchatsky, began to collect data on multi-loci characteristics of salmon stocks throughout the Russian Far East. This data were analyzed by starch electrophoresis in co-operation with several North American agencies: Pacific Biological Station Nanaimo, Canada; NOAA Northwest Fisheries Center, Seattle;

Auke Bay Laboratory, Juneau; U.S. Fish & Wildlife Service, Anchorage; Alaska Department of Fish & Game, Anchorage, USA. One of the main objectives of this project was to standardize allele mobilities and electrophoresis techniques, and to create comprehensive genetic baselines including all salmon populations throughout the Pacific Rim. The main species of study were pink salmon – *Oncorhynchus gorbuscha*, chum salmon – *O. keta*, sockeye salmon – *O. nerka*, and chinook salmon – *O. tshawytscha.*

The work consists of two parts: first is the conservation of natural populations; and secondly the identification of natural and artificial populations. It includes the determination of genetic population structure within species, the possible levels of interspecies hierarchy, and the estimation of their divergence using the random selection of enzymes-coding genes. The next step should be monitoring of genetic changes occurring as a result of human activities such as fishing and artificial propagation. Stock identification requires the use of techniques that will identify specific populations in mixed-stock aggregations throughout their habitats and different life stages. Practical applications of Genetic Stock Identification consist of: 1) estimations of contributions of particular local stocks to the fisheries, and therefore, the survival, stock composition and relative abundance of salmon in the ocean, and 2) to determine migration timing and routes for the adults and juveniles of local stocks in the Pacific Ocean, adjacent seas, estuaries, and freshwater basins.

During the last 15 years more than 20,000 individual fish were analyzed from natural populations from all over Russian Pacific coast, and more than 3,500 from the Pacific Ocean. Forty-three enzyme systems coding up to 100 loci were scored using starch gel electrophoresis. Variation at more than 30 polymorphic loci in stocks including those from the North America were analyzed, and significant differences between and within regional population complexes were detected. Cluster and multifactor analysis were performed for all main stocks throughout the Pacific Rim for four species. High levels of genetic divergence and characteristics of interspecies population hierarchy were obtained, and gene flow and migration were studied. Genetic data were used for detecting the mechanisms of micro-evolutionary changes such as natural selection, genetic drift, intensity of genetic migration, and reproductive isolation. The interactions of population dynamics and genetic structure were revealed. The relative abundance and biological characteristics of main regional population complexes throughout the Pacific Rim were summarized in comparison with interspecies structuring. Several sets of experiments were conducted revealing the mechanisms of natural selection influence on genetic polymorphism and its adaptive values. The international datasets on allozyme polymorphism were created, and a numerous studies on stock composition in mixed-stock fisheries in the Pacific Ocean were performed.

Enzyme polymorphism has been very useful for population genetic studies, but it has limitations. Many discriminating enzyme loci were found in chinook and chum salmon populations, but only a limited number in sockeye that have not allowed accurate stock discrimination. In pink salmon, many polymorphic loci were detected, but the spatial differention by population units was shown to be low, and regional groups of populations could not be satisfactorily identified. As a result, scientists are now investigating DNA polymorphism techniques for salmonid species.

In Russia, mitochondrial DNA polymorphism in salmon and other species is studied at the genetic laboratory of the Institute of Marine Biology since the early nineties under the supervision of Dr. V. Brykov. This work is conducted in association with University of Alaska, Juneau. They discovered polymorphism in haplotype variation in pink, chum, and coho salmon of Eastern Kamchatka, Sakhalin, Primorie and Kuril Islands. They found significant differences between pink salmon regional groups and significant differences between regional groups of Sakhalin and Primorie chum salmon. Within regional groups, they found no significant differences in both pink and chum salmon.

Variation in microsatellite nuclear DNA was shown to have some attributes that are useful in population analysis and stock identification. Alleles show co-dominant Mendelian inheritance, high levels of spatial variation, and no significant annual differences resulting in high levels of accuracy and precision for stock identification. Studies of microsatellite DNA in sockeye salmon of Asia were started recently in co-operation with the Pacific Biological Station, Nanaimo. Data for 25 local stocks were collected on variation of 13 microsatellite DNA loci: *Ots3*, *Ots100*, *Ots103*, *Ots107*, *Ots108*, *Omy77*, *Oki1a*, *Oki1b*, *Oki6*, *Oki10*, *Oki16*, *Oki29*, and *One8*. Stock identification studies in the Bering Sea were performed using microsatellite nuclear DNA variation in sockeye and the proportions of American and Russian stocks in that area during summer and fall were obtained.