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SALMONID GENETICS: STATUS AND ROLE IN AQUACULTURE

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GENETIC DELINEATION OF SALMONID POPULATIONS BASED ON ELECTROPHORETIC DATA

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The capability of managing a fishery on the basis of its component populations is an objective that has generally eluded salmonid biologists until recently because of the difficulties involved in defining these populations. Tagging and marking studies have provided useful information concerning originsand degrees of straying of fish but have been limited by the need for handling all treated individuals. Natural features such as scale characters and relative mineral composition have also proven actually or potentially useful for identification of areas of origin through reflections of natal environments. None of the above approaches are capable of genetically defining population structures, however, and such definitions are necessary if management is to be based on population structures.

A method has matured during the past decade through which definition of salmonid populations has been achieved in much greater detail and clarity than had previously been possible. This method is starch gel electrophoresis coupled with histochemical staining. The method is based on the separation of protein solutions in an electric field, and on the subsequent use of the specific activity of the protein (enzyme) in the staining process. Electrophoretic data are particularly useful for providing genetic information on populations because:

1. Properly selected variants reflect simply inherited traits that are constantly expressed throughout the life cycle of an individual, and are not directly affected by environmental variables.
2. This kind of variation permits actual counting of frequencies of different genes in collections taken from different areas; significantly different frequencies of genes from different areas are positive data that samples from these areas are genetically different. Data are also useful for estimating relationships among populations and amounts of inbreeding within them.
3. Frequencies of variants in a given population are stable attributes of that population and tend to persist at the same levels over many generations.
4. The methodology allows collection of relatively large amounts of data in a given period of time.

Our group has been actively engaged in the electrophoretic study of salmonid populations over the past 10 years. This summary reviews some applications of electrophoretic data in the study of fish populations from the perspective of these studies.

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The power of electrophoretic data for genetically defining populations has been demonstrated in studies of salmonid populations of the Pacific Northwest. Previously unrecognized major population units have been identified that are rather surprising in some instances. Although geography plays a major role in the structuring of these units, it is not necessarily true that geographically proximal populations are genetically the most similar. Genetic structuring of some populations is also less closely tied to time of return and anadromy than had previously been thought. Below are some examples of major population units defined through electrophoretic studies carried out by our group and other laboratories of the Pacific Northwest.

A major genetic division of rainbow trout populations occurs east and west of the Cascade Crest. Both anadromous and landlocked populations east of the Crest in both the Fraser and Columbia River drainages are more similar to one another than to any populations of west slope drainages of the Cascades. Similarly, west slope populations are genetically more similar to one another than to those of the east, regardless of whether they return in the summer or the winter. This separation presumably dates back to the last period of glaciation, which receded about 10,000 years ago. The inland populations are probably descendents of rainbow trout that populated large inland lakes formed by Columbia and Fraser River drainages impounded behind the glaciers. The coastal populations appear to have descended from another source.

Major population units of coho salmon are distinctly defined over the entire drainages of the Columbia and Fraser Rivers where a single type of the serum protein - transferrin (Tfn AA) is found in well over 90% of the fish. All other drainages between and on either side of these large river systems (including those directly adjacent to, but not joining the Columbia River) have frequencies of AA types of less than 10%. This abrupt discontinuity may reflect selective factors favoring the AA transferrin type in the large river systems.

Fall chinook salmon populations from streams of both Washington and Oregon entering the Pacific Ocean are genetically distinct from populations of Puget Sound or Columbia River tributaries. Both of these population units, in turn, are genetically different from spring run chinook salmon of the Columbia River.

Estimation of component populations of mixed fisheries for two populations and a single variant genetic system is a simple matter of direct proportionality. Analysis becomes more complex as the numbers of populations and variant systems increase. Computer analysis involving maximum likelihood methods is a feasible approach to this problem that is being developed and applied by personnel of our group.

Hatchery Populations

Determining the effects of plantings of hatchery fish on native salmonids of the same species is a major concern to management biologists. Native fish are a valuable reservoir of genetic variation and provide a useful supplement to the fishery even in stocks that are largely maintained through hatcheries. Although native fish may be more adapted to a particular area than hatchery fish, they are potentially endangered through hatchery plantings by factors including (1) competition for spawning and rearing ground resulting from large hatchery releases, (2) possible earlier hatching of progeny of hatchery fish resulting in a competitive advantage, and (3) hybridization of native and hatchery fish resulting in disruption of adaptive gene pools.

Biochemical genetic markers are very useful for studying the effects of hatchery plantings on native fish provided there are differences in gene frequencies between the two groups. Genetically marked hatchery fish require no special handling prior to release, and long-term effects of plantings can be measured because genetic markers are passed on to subsequent generations.

The population of summer run steelhead from the Skamania hatchery of the Washington State Department of Game has a variant form of the enzyme alpha glycerophosphate dehydrogenase (AGPD) which occurs with a frequency of about 0.15. This variant is absent from native steelhead of the Kalama River (Washington) and from winter run steelhead of the Game Department's South Tacoma hatchery that have been planted in the Kalama River; the variant is therefore useful for following the effects of plantings of Skamania hatchery fish on other steelhead stocks of the Kalama River. The data indicate that Skamania hatchery fish planted in the main stream tend to enter tributaries prior to their seaward migration. Adult fish from hatchery plantings return near the point of release and many of them spawn successfully. Descendents of these fish apparently hatch earlier than those other stocks based on their larger size in a given sampling area. Almost all of the residualized steelhead of the Kalama River appear to be from the Skamania hatchery.

Genetic Marking

The potential value of a genetic marker for the identification of populations increases as the differences in its frequency increase between populations. The sample size needed to demonstrate differences between two populations decreases to the point where individual fish can be identified if different alleles for a particular protein are fixed in the two populations. Such a situation rarely occurs naturally within a species--particularly among populations where gene flow is possible--but can be straightforwardly created through artificial propagation.

We are presently working with the Washington State Department of Game to create genetically marked stocks for maximizing genetic differences between these stocks and native fish in areas where the stocks are to be planted. One such stock is being bred from Skamania hatchery fish for introduction into previously unplanted tributaries of the Kalama River. Selection is based on the AGPD variant. In the first generation, males carrying twodoses of the variant gene (i.e. homozygous--about 2% of those screened) are mated with randomly selected females. In the next generation there are sufficient individuals of both sexes that are homozygous for the variant for the derivative population to be brought to fixation at this time.

Two potential pitfalls that must be kept in mind during the development of projects of this kind are inbreeding and differential selection (i.e., nonrandom survival of different genetic types) against alternate forms of a given protein. Effects of inbreeding can be minimized through the selection of an adequate number of breeders during early phases of the program. The possibility of differential selection emphasizes the need to continually seek evidence of differential environmental effects on parent and selected progeny stocks.

We foresee artificial genetic marking of hatchery stocks becoming a very useful management tool. The fate of hatchery and wild fish presently is of more than biological interest in salmonid fisheries of the Pacific Northwest. Recent Washington State court decisions have indicated that native Americans may be entitled by treaty to 50% of the natural spawning salmonids returning to rivers of ancestral fisheries but to a lesser share of hatchery fish. Sea ranching is a concept being developed currently in which privately reared salmon are released to grow naturally in the marine environment, and are then harvested by the releasing organization upon their return. Genetically marked stocks have obvious management implications in both of these instances.

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