

## **Why Fin Clips?**

### **Genetics: a Tool in Fishery Management and Stocking**

Long before the recent advances in molecular genetic techniques, fishery managers had observed that different management strategies could affect the population structure of a species that was being exploited. For example, a harvest focused primarily on fish that returned early in a spawning run could eventually result in a reduction of those early spawners and their genetic characteristics. In addition, in some populations harvest of only the largest fish has been observed to result in a downward trend in size at age, resulting in smaller fish. The mechanisms at work in these types of changes are not well understood but may well be the result of genetic changes in the fish populations. In order to preserve the genetic fitness of a population, managers have to balance harvest against conservation. Managers also have to consider not only morphological or developmental changes in the fish but also any changes in genetic diversity that may result from the overfishing. This is also true for any project that would consider stocking fish into the wild. All types of management actions require, as a prerequisite, understanding the genetic characteristics of the target population so that steps can be taken to avoid loss of fitness.

Fortunately in the case of red drum, there have been numerous investigations into the population structure along its entire historic range from Massachusetts to the northern coast of Mexico. In general, geneticists have found evidence of little population genetic structure. The data show that the red drum population in the south Atlantic is genetically similar to that found in the Gulf of Mexico.

Using these same genetic markers that were used to determine population structure, researchers can identify individual fish and trace cultured fish back to their known broodstock parents. The Peach State Reds Initiative will use genetic “fingerprinting” as a method of evaluating the fate of fish stocked into the wild. One major advantage of this technique is that the fish do not have to be sacrificed; a fin clip provides sufficient DNA to do the analyses. We have begun the program by working with anglers to collect fin clips for the genetic analysis. Data from these fish will be used for several purposes: to add to the baseline of information about the wild red drum population in our state, to determine the wild or cultivated status of the fish, to determine the effectiveness of the stocking programs, and to assess the impacts of stocking on the wild populations. We will continue these collections through 2006 and 2007, as fish are stocked. By using this approach we can determine whether stocking fish is a cost effective way of increasing red drum abundance and a wise use of public money.

The genetic analysis techniques are relatively simple. The fin clip is collected and stored in a solution that will preserve the DNA and denature the rest of the tissue. (Alcohol works as a preservative, too.) Once in the laboratory, researchers isolate DNA from the fin clip. The researchers will look at several different genes; the most useful ones for this purpose are known as microsatellites. The analyses take advantage of the fact that each fish carries two copies of each gene: one inherited from each parent. Genes from the parents and the offspring are compared and matched. If there are no matches, we conclude that the fish is of wild origin. By looking at several different genes, we can assign offspring to parents with a very high degree of certainty: greater than a million to one. These data tell us not only whether or not the fish was cultured or

wild, but also which parents produced most of the offspring that survived after release.

All these results help to determine the effectiveness of stocking, what proportion of fish caught are of stocked origin, and if there is any impact on the wild gene pool.