Genetic Stock Identification and Full Parental Genotyping for Management of California's Chinook Salmon Fisheries

John Carlos Garza, Eric Anderson
Southwest Fisheries Science Center, 110 Shaffer Road Santa Cruz, CA 95062
carlos.garza@noaa.gov; Tel. 831-420-3903

Genetic tools have a long history in fishery management, with the use of genetic "tags" to distinguish hatchery and wild trout described more than 20 years ago (Taggart and Ferguson 1984). More recently, the use of genetic stock identification (GSI) techniques have been used to elucidate ocean migration patterns and to estimate stock proportions in a mixed stock fishery context (e.g. Teel et al. 2004). Such GSI for estimation of stock proportions can occur either post-season or in-season. An in-season GSI system requires a facility with dedicated staff and can typically produce stock proportion estimates from fishery or port samples within approximately one day of delivery (Beacham et al. 2004). Such stock composition estimates can then be used to adaptively focus fishery effort to avoid stocks of conservation concern, or to best target abundant stocks.

Because of the current and potential future utility of GSI methods to assist in fishery management, the Pacific Salmon Commission has recently funded a collaborative effort to develop a coastwide genetic database for GSI of Chinook salmon. This $1.1 million effort has resulted in an unprecedented database of 13 microsatellite loci, which have been standardized across most major Pacific salmon genetics labs, typed in over 105 Chinook salmon populations (~120 fish per population) from Alaska to California and is capable of accurately distinguishing most major stocks of Chinook salmon in the northeast Pacific. The Southwest Fisheries Science Center in Santa Cruz is the California representative to this consortium of collaborating salmon genetics labs.

The ability of the coastwide genetic database to distinguish Chinook salmon from the different basins and ESUs in California is straightforward and relatively trivial with this database, due to substantial genetic differences between CA Chinook salmon populations (Figure 1). These differences are also reflected in the performance of individual assignment tests, which correctly identify nearly every fish to basin/stock/ESU of origin. This is particularly true with salmon from the Klamath/Trinity basin, which are correctly distinguished from other California ESUs with near-perfect accuracy, because of their substantial genetic divergence from all other California Chinook salmon stocks (Figure 1; Waples et al. 2004). The coastwide GSI database can also identify individual fish to tributary of origin more than 80% of the time. Additional microsatellite genes in use by our lab can increase that accuracy to above 95%.

The existence of this database for GSI thus provides a powerful tool for determining and minimizing fishery impacts on salmon stocks of conservation concern. For example, a well-designed GSI program can be used to distinguish salmon from the Klamath/Trinity basin from those of the Central Valley and Coastal ESUs in fishery catches. Such information can be used to directly measure fishery impacts on fish from the Klamath ESU, as well as provide a much clearer picture of ocean migration/distribution patterns of all California Chinook salmon stocks. We believe that such information could be used to design fishing regimes that minimize impacts on Klamath/Trinity Chinook salmon, while allowing maximum exploitation of abundant stocks, such as the Central Valley Fall run.

The current fishery management regime for Chinook salmon is based on cohort reconstruction, and therefore requires more information than just the stock of origin provided by traditional GSI. Traditionally, genetic methods have not been able to provide cohort/broodyear information for salmonids. However, we have developed a novel genetic technique that provides both stock and cohort of origin for individual salmonids from hatcheries: precisely the same information provided by a traditional coded wire tag (CWT) system. This method, termed full parental genotyping (FPG; Anderson and Garza 2005), actually provides more information than just stock and cohort of origin; it identifies the specific parent pair for a sampled fish.

The basic idea behind FPG is that DNA is an individual-specific "fingerprint" which is transmitted from one generation to the next in reproduction. Therefore, by collecting genotype data from all broodstock adults at a hatchery (or theoretically, but not practically, in-stream), one can identify offspring of particular matings through parentage analysis on fishery samples. By identifying the particular parent pair, the stock and cohort of origin are then known. Anderson and Garza (2006) have shown how this can be done essentially without error using a surprisingly modest amount of genetic information.

Two other important elements of an FPG tagging system are that its implementation provides a 100% tagging rate for those hatcheries where it is practiced and that the tagging costs are much lower than with CWTs or any other tagging system with which we are familiar. Tag recovery, through determination of the genotype of a fish sampled in the fishery or at escapement, is currently more expensive than recovery of a CWT, but the overall cost of the two systems should be roughly similar. Moreover, substantial cost-savings are possible with genetic-based tagging methods; the cost of such work in the human genetics area is several times less than it is in fishery and wildlife genetics. Implementation of an FPG tagging program at the Trinity River and Iron Gate Hatcheries could be achieved at modest cost and provide the ability to identify every fish from these facilities in a mixed fisheries context. This would provide a potentially important improvement to the data used in stock assessment and forecasting for Klamath Chinook salmon.

One of the greatest advantages of an FPG tagging system is that it is easily and economically integrated with a GSI system (Anderson and Garza 2005). This allows a staged genetic analysis to be employed on both marked (adipose fin clipped) and unmarked fish, with GSI yielding stock of origin for every sampled fish. Those fish that are assigned to "stocks" that are hatcheries where FPG is performed would then be subjected to additional genetic analysis yielding cohort of origin. Such an integrated system can also easily accommodate samples from released sub-legals and strays from stocks that normally are not detected in fishery sampling.

We suggest that management agencies charged with determining salmon fishery regulations support a pilot study to evaluate the utility of genetic based methods to help further define ocean distribution of California's Chinook salmon stocks and possibly replace CWTs for stock assessment. We also recommend that they consider whether an in-season rapid response GSI system might help to best meet both conservation and fishery access goals for California's salmon fisheries.

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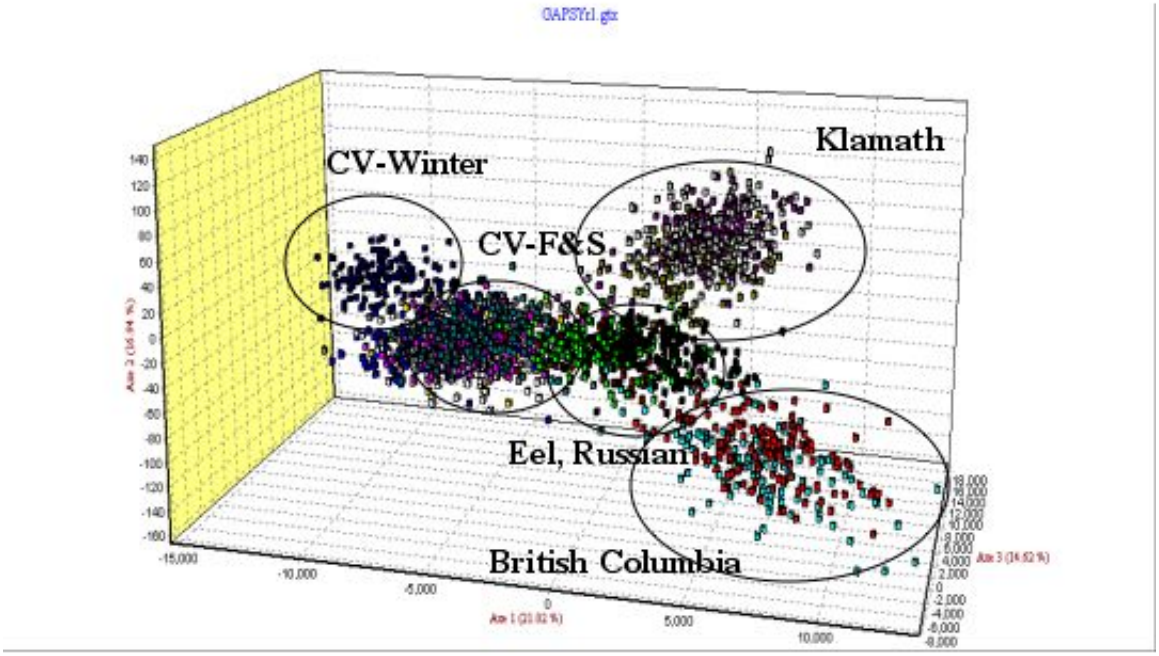

Figure 1: Factorial Correspondence Analysis of individual genotypes for Chinook salmon from California and three populations from Canada. The ability to easily distinguish Central Valley, Coastal and Klamath/Trinity salmon is evident from the lack of overlap in the distribution of genotypes.