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Genetic Markers for Detecting Population Structure of West Coast Chinook Salmon

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SUMMARY

Scientists have identified 117 new single nucleotide polymorphisms (SNPs) for detecting the genetic relatedness of Chinook salmon.

The most basic genetic variation possible, a SNP (pronounced “snip”) refers to a single difference in one base pair of a nucleotide. The major outcome of this project is the identification of an optimal panel of 96 SNPs that is capable of detecting both the parentage of hatchery-born Chinook and the origin (i.e., stock) of Chinook caught off California and Oregon.

SNPs are fast becoming the tool of choice for population genetics studies of nonmodel organisms such as Pacific salmon, because of their low rates of error (mutation) and high resolving power. The detailed resolution of SNPs is particularly well suited for studies of anadromous fishes such as Chinook salmon (*Oncorhynchus tshawytscha*), as their fidelity to their natal rivers leads to a hierarchical population structure. This project demonstrates applications and advantages of SNP markers for California’s most commercially important salmon species.

PROJECT

Prior to this project, only 30 SNPs had been identified for Chinook. These were used to analyze the stock composition of bycatch in Oregon’s hake fishery. The research mentors for this project estimated that another 70 SNPs would be needed to discern parentage.

The first half of this project involved sequencing more than 3 million base pairs, and from this surveying the variation at more than 650 sites in 225 genes, to locate 117 new SNPs. These were tested to verify their ability to resolve population structure among the major stocks from the Sacramento, Klamath and Columbia river systems, as well as federally protected Evolutionarily Significant Units from the Central Coast. This level of resolution was deemed sufficient for both genetic stock identification (GSI) and parentage-based tagging (PBT).

Because the genotyping platform used for this project had a maximum capacity of 96 loci, scientists selected a subset of SNPs that would preserve the resolving power of the larger ensemble while allowing for the genotyping of about 500 fish per day.

As of this writing, about 7,500 Chinook specimens from 75 known populations (i.e., natal streams) from California to Alaska have been genotyped at the 96 loci and added to an existing GSI baseline,



A leaping Chinook salmon. Credit: D. Killam/CA DFG

against which ocean-caught specimens can be later compared. The resolution of the GSI hinges on the number of fish from different populations in the baseline, and the degree of genetic differentiation among populations.

To date, scientists estimate that the baseline should allow for the accurate assignment of a salmon’s management unit for more than 99% of Chinook off California and Oregon. In addition, more than 10,000 Chinook samples collected at California’s ports during the last decade have been genotyped to provide managers with insights into trends in the stock composition of landings.

The second application of the SNP analysis was to identify the parentage of Chinook born at the Feather River Hatchery in the Central Valley. To do this, all individuals in the spring-run broodstock were genotyped, and a reference database was created for all possible parent pairings and their associated SNP signatures. Offspring are automatically tagged: The recovery of the tag merely requires genotyping the 96 loci (from a nonlethal fin clipping). The parent database is then queried for a match. In this project, researchers verified the method with multiple cohorts of offspring from known matings.

MANAGEMENT APPLICATIONS

Different runs of Chinook, some of which are threatened by extinction, intermingle in the ocean. To set harvesting guidelines, managers must know the composition of these intermingled stocks. GSI allows managers to determine the origins of salmon caught in mixed-stock fisheries as either target species or bycatch.

In this project, for example, GSI was applied to samples of sport and commercial Chinook caught off California in 2010. Central Valley fall-run Chinook (all hatchery born) were found to represent about 83% of the sport and 76% of the commercial catch, while federally protected Central Coast stocks comprised 2.7% of the sport and less than 1% of the commercial fishery. This type of information can help managers prevent overharvesting of protected stocks and potentially help reduce bycatch in otherwise healthy fisheries.

Since 1943, about 1.7 billion juvenile Chinook have been released into California streams. Managers, since the 1960s, have been surgically implanting tiny coded-wire ID tags into the snouts of juveniles, extrapolating rates of returning spawners from the minute fraction (much less than 1%) of recovered tags. The tagging data is used to

estimate ocean abundances of different stocks, from which harvesting guidelines are, in part, set.

Genetic tags will likely replace coded-wire tagging over time because PBT provides the same information on origin and cohort with 100% coverage and none of the issues associated with physical tags (i.e., lost tags, stress from handling, low rates of recovery, etc.)

In addition, PBT allows managers to investigate the genetic component of survivorship (i.e., whether certain families are more likely to return to spawn) and the heritability of body size and age of sexual maturity. Genetic analyses can also be used to prevent inbreeding and document a hatchery's selective pressure on fish. Yet another advantage, the markers permit stock identification of wild fish co-mingled with spawning hatchery ones. Coded-wire tagging never accounts for these untagged wild stocks.

As genetic sequencing becomes even more affordable, genetic tagging will likely be implemented at all 13 of California's Chinook hatcheries; the tissue samples for this are already being collected.

OUTREACH

The SNP markers identified in this project represent more than half of the assays currently available for Chinook. These markers have been shared with the Genetic Analysis of Pacific Salmonids (GAPS) group funded by the U.S. Section of the Chinook Technical Committee of the Pacific Salmon Commission and are being used by GAPS' consortium partner labs in Oregon, Washington, Idaho and Alaska.

These labs are also using a software program for rapid SNP-based parentage assessments, known as SNPPIT, developed by a research mentor on the project. The DNA sequences have been made publicly available through the National Institutes of Health's GenBank, while the SNPs were added to a related public database known as dbSNP.

PUBLICATION

Clemento AJ, A Abadia-Cardoso, HA Starks, JC Garza. 2011. Discovery and characterization of single-nucleotide polymorphisms in Chinook salmon. *Molecular Ecology Resources* 11(supp.1):50-66

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Former Delta Science Fellow Anthony Clemento. Credit: UCSC