San Joaquin River Spring-run Chinook Technical Memorandum Group Meeting
Genetics Discussion
Thursday, July 24, 2014
10:00 am – 12:00 pm

Meeting Summary

Participants:

Philip Columbano, NMFS
Kim Webb, USFWS
Michael Banks, Oregon State University
Rob Whiter, BOR
Carl Mesick, USFWS
Kevin Reese, CDFW
Rob Whitler, BOR
Carlos Garza, NMFS Southwest Fisheries Science Center, Santa Cruz.
Anthony Clemento, NMFS Southwest Fisheries Science Center, Santa Cruz.
Chuck Hanson, representing Metropolitan Water District
Josh Israel, BOR
John Netto, USFWS
Carl Mesik, USFWS
John Rubin, Attorney with San Luis and Delta Water Authority
Elif Fehm-Sullivan, NMFS
Jonathan Schram, NMFS
Rhonda Reed, NMFS
Rob Nielsen, NMFS
Sheila Green, Westlands Water District
Pat Ferguson, CDFW
Erin Strange, NMFS
Jason Ushijima, Santa Clara Water Irrigation

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1. **Review of Meeting notes from June 26th:**

   Last month's notes on the use juvenile production estimates (JPEs) for Sacramento River winter-run Chinook salmon are still under review, and Erin will send them out for review as soon as they are available. For those participating in today's discussion that were also present for the JPE discussion, are there any outstanding questions? (None)

   We will have the opportunity to review of all our previous meetings and discussions during our meeting scheduled in September.

2. Meeting Purpose:

Dr. Banks from Oregon State University will first present to us his work on the use of Genetic Markers in tracking populations of Chinook salmon. Next, Dr. Garza will present us with his work on developing molecular markers for the San Joaquin River Broodstock and Feather River Hatchery spring run, then Kevin Reese from DWR will go over genetic sampling methods currently underway at the Delta facilities for winter-run.

3. Dr. Michael Banks, Oregon State University – Presentation (15 minutes)
"Using Genetic Markers in tracking Chinook salmon populations"

Presentation Summary:

Dr. Banks has been developing and practicing the use of genetic markers in tracking Chinook salmon populations for the past 20 years or so. Most of that time has been spent working with California Chinook salmon.

The advantage in using genetic markers for tracking purposes is that all individuals can be accounted for over several generations. There are two primary mechanisms/methods that have been used when implementing genetic markers: Frequency-based marking, and pedigree-based marking. Most of the work that Dr. Banks has done thus far in California has been using the frequency-based method. Recently a paper came out in a 2014 issue of *Animal Genetics* that focuses strictly on the use of microsatellites in tracking salmon, compares a number of other genetic baselines used over the years, and develops a blind test using genetic methods to match juvenile fish back to the adults previously identified by DWR scientists, in order to test the accuracy of using these genetic methods. The primary goal of the paper was to develop discriminatory techniques to identify winter and spring-runs of salmon from each other in the Central Valley. It's important to note that the spring-run fish from Deer, Mill, and Butte Creeks were discriminate whereas spring-run from the Feather River Hatchery were indiscriminate from fall-run.

In the 2000s Kathleen and Dr. Banks worked on discriminating early runs from late runs in the Feather River system. The results of this paper was that microsatellites do not discriminate early spring-run from later running spring-run, but that three of the clocked genes Kathleen worked on developing did.

Dr. Banks focused on frequency-based techniques instead of pedigree-based methods since only a single sample is needed for the prior, not a huge number of samples as would be needed when using pedigree-based methods.

Discussion:

Could we use the clocked genes technique as discussed by Dr. Banks to distinguish spring-run reintroduced into the San Joaquin River from winter-run, when both are entering the Delta facilities simultaneously.

For some background, as of April 15th and 16th around 54,000 juveniles were released into the San Joaquin River as part of the Reintroduction (starting from around 80,000 eggs), with an average return rate/survival rate being about 20 adult fish. Ultimately we would like to start reintroducing between 1 million to 1.5 million juveniles into the San Joaquin River at a time once the new hatchery facility is built (the current carrying capacity for the interim facility at this time is for 250,000 fish).

If you are interested in constraining costs when using genetic techniques, the more first generation fin-clipped parents you can catch from which you could get genetic samples, the more effective using genetic markers would be in this case. For the San Joaquin, since the system is already prone to hybridization between runs, pedigree methods would likely be more effective than using the clocked genes technique.

4. **Carlos Garza, NMFS Southwest Fisheries Science Center, Santa Cruz – Presentation (15 minutes)** "Developing molecular markers for the San Joaquin River Broodstoock and Feather River Hatchery spring run"

Presentation Summary:

Much of what Carlos is presenting today is work that Anthony Clemento has been working on for the past eight years on pedigree-based genetic tagging at the Feather River Hatchery.

The San Joaquin Chinook salmon populations were historically the Southern most natural populations of salmon in the world. Quite important, since these fish were more tolerant to warmer temperature regimes; a genetic trait which could become more beneficial with the onset of climate change.

The Feather River spring-run Chinook salmon have been introgressing with fall-run Chinook probably due to a few factors: not only because of hatchery practices, but also because the natural spawning habitat in the Feather River has been dramatically compressed from what was historically. Carlos Garza and Anthony Celmento conducted a meta-analysis of spring-run Chinook salmon genetic data available, and found that in spite of the larger census size of fish in Butte Creek to be used for the reintroduction, Butte Creek fish actually had the lowest genetic diversity when compared with Mill Creek, Deer Creek, and Feather River fish. It is likely that this pattern has occurred because during the 1980's, the total number of Chinook salmon for the Butte Creek stock was almost 3 times lower than stocks found in any other system in the Central Valley, creating a bottleneck in the genetic profile of Butte Creek Chinook during this window of time.

A number of spring-running fish have been observed over the years in Clear Creek, Battle Creek, and the Yuba River. Some analyses were conducted on these different populations in collaboration with Abernathy and CDFW, and what Anthony Clemento and Carlos Garza found out is that fish in Battle and Clear Creek are primarily from the natural spawning populations of Mill Creek, Deer Creek, and Butte Creek. Spring-running fish observed in the Yuba River are almost entirely attributable to the Feather River stock.

Presently, Anthony and Carlos are identifying siblings of other close relatives to minimize inbreeding when selecting the donor stock for the SJRRP. When using the long-term category reconstruction efforts Anthony started in Feather River, we have been using the pedigree results to identify when fish taken for the donor stock are closely related. As the SJRRP population matures, Anthony and Carlos will be providing on an annual and even real-time basis the pedigree results identifying closely related individuals to avoid the risk of mating them together at the SCARF. This will provide unambiguous identification of fish at an individual level.

Anthony has demonstrated in his dissertation work that about 40% of the spawners in the Feather River Hatchery have siblings that are in fact also spawners in the Feather River Hatchery, and that these siblings are all spawning in the same year. This means that the likelihood that inbreeding is taking place at the Feather River Hatchery is quite high, thereby greatly reducing the survivability of any inbred progeny. In 2012, of 128 parents for which their parentage could be confidently assigned, 28% had at least one full sibling amongst the broodstock at the Feather River Hatchery. Working through the technical work teams, we have secured a larger broodstock to be taken to the Interim facility for future use. As early as September, the identification of siblings and other close relatives to avoid inbreeding should be possible at SCARF. To do this, spawning matrices are created, which are genetic marker based estimates of individual relatedness and inbreeding coefficients present between all spawning pairs in a hatchery setting. This model has been used for years, particularly in the Russian River with Coho salmon.

Moving forward, there is a program goal of reintroducing multiple stocks from more than one spring-running population available, but there are a lot of questions that need to be answered from a genetics standpoint, in order to make sure reproductive success and survivability of progeny is maximized using pedigree-based genetic marking techniques.

Right now, Anthony and Carlos are also testing whether or not inbreeding is occurring between Mill Creek, Deer Creek, and Clear Creek fish.

Discussion:

It will be important to take an adaptive management approach when dealing with these issues being discussed for the SJRRP.

If a fish shows up at a Delta facility today, are there protocols currently in place that would identify that fish as a spring-run fish originating from the San Joaquin River? If it's an SJRRP fish of which we have their genetic information on hand, then yes. Unless there is a process of selection and documentation of fish from separate translocations, then the translocated fish will not be distinguishable from fish originating from the Feather River Hatchery.

For the purposes of salvage, would there be a higher level of certainty indirectly identifying fish used in the restoration by targeting identification of winter-run at the facilities? Not necessarily, since fish that are winter-run can be very easily identified following the Pedigree procedures described earlier.

5. **Kevin Reese, DWR – Presentation (15 minutes)** *"Genetic sampling methods currently underway at the Delta facilities for winter-run".*

Presentation Summary:

Since 1995, the Delta facilities have been taking genetic samples from entrained winter-run Chinook salmon. From about 2006 on, 100% of these genetic samples have been processed. Now for the past few years, it is required that all DNA taken and processed from these samples is destroyed afterward. Kevin is currently trying to work with CDFW and NMFS in changing the conditions of the associated permit. Kevin is holding the samples he is currently in possession of while he works on revising the permit, which isn't a problem for now. Kevin will also create a DNA repository at his office should be allowed to keep DNA samples from captured fish in the future, rather than destroy them once they've been processed. Getting the Central Valley Tissue Archive Lab to take the samples would be the preferred alternative rather than relying solely on an in-office DNA repository, especially if we are talking about taking thousands of DNA samples for processing as part of the SJRRP reintroduction effort. As of now, there is no state wide system to manage such a proposed volume of samples in place.

Genetic baselines used to identify Chinook salmon at the facilities come from NMFS, UC Davis, and Dr. Michael Banks' work. Currently, frequency-based methods are used at the facilities.

Identifying SJRRP spring-run fish from other runs at the Delta facilities is only part of what needs to be done so that operations at the Delta facilities aren't affected by the reintroduction effort. We should also revamp timing of operations, what we define as "take", etc.

Discussion:

Could the proliferation of work groups for the SJRRP actually be detrimental to the goals of the overall program? Need to make sure that the sharing of technical knowledge doesn't

get too dispersed. Should better streamline and centralize information sharing for this program.

Action Items:

- Should have a genetics process written into the tech memo in time for the next water year. Josh and Kevin can coordinate with Erin Strange on this.