Study 49

Genetic Analysis for Spring- and Fall- Run San Joaquin River Chinook Salmon for the San Joaquin River Restoration Program

Final
2015 Monitoring and Analysis Plan

January 2015

Statement of Work for proposed Bureau of Reclamation/NOAA Fisheries Interagency Agreement to perform Genetic Analysis for Spring- and Fall-run San Joaquin River Chinook Salmon for the San Joaquin River Restoration Program
Project Principal Investigator: Dr. John Carlos Garza

1.0 Background

The proposed work will help to achieve the “Restoration Goal” of the San Joaquin River Restoration Program (SJRRP), as stipulated in the Settlement Agreement that brought an end to the lawsuit, *NRDC et al. v. Kirk Rodgers et al.* (Case No. CIV S-88-1658 LKK/GGH). The Restoration Goal is to restore and maintain fish populations in “good condition” in the mainstem San Joaquin River below Friant Dam to the confluence of the Merced River (the Restoration Area). The proposed work will contribute to this goal by providing genetic data and analyses to properly manage the captive breeding portion of this project at the new Salmon Conservation and Research Facility (SCARF) and through genetic monitoring of the in-river population in the Restoration Area. Spring-run Chinook salmon are scheduled to be reared and released into the Restoration Area during the project period and fall-run salmon are likely to volitionally enter the Restoration area as well.

Subgroups of the SJRRP Fisheries Management Workgroup, the SJRRP Technical Advisory Committee and the UC Davis Genomic Variation Laboratory all identified genetic analyses as a critical component of the BMPs for the SCARF, as well as the in-river monitoring of salmon populations in the Restoration Area. The use of genetic techniques to implement best management practices (BMPs) in captive propagation facilities for salmonid fishes, such as the SCARF, has a long history. In California, the use of genetic techniques in such programs began in 1998 with the identification to race (i.e. evolutionarily significant unit [ESU]) of potential spawners for the winter-run Chinook salmon conservation hatchery program in the upper Sacramento River basin. In 2001, genetic data and analyses began to be used to select minimally related individuals as broodstock, avoid inbred matings and identify the sex of coho salmon at conservation hatchery programs in the Russian River and Scott Creek. More recently, a genetic technique termed parentage-based tagging (PBT) has been developed and implemented by the proposing Principal Investigator and collaborators to provide comprehensive, individual-based monitoring and evaluation of anadromous salmonid populations in California. PBT uses multi-locus single nucleotide polymorphism (SNP) genotypes, in conjunction with large-scale parentage inference (i.e. pedigree reconstruction) to “tag” fish in such a way that they and their offspring can be unambiguously identified through analysis of a small non-lethally collected fin clip. Such PBT monitoring and evaluation has been underway with spring-run Chinook salmon stock at the Feather River Hatchery (FRH) since 2006. As this stock is currently the source of Chinook salmon for reintroduction into the Restoration area, the proposed work will leverage this previous investment for immediate biological inference to meet SJRRP goals.

2.0 Scope

The Southwest Fisheries Science Center (SWFSC), Santa Cruz, CA, will collect genotype data, perform genetic analyses, provide technical advice, and report consistent with the tasks detailed below in this Statement of Work (SOW).

3.0 Objectives

This SOW describes genetic analysis tasks for implementation of the SJRRP Restoration Goal. Genetic management of broodstock fish and of the in-river population are vital to the SJRRP's ability to establish self-sustaining salmon populations in good condition, minimize genetic impacts on donor stock populations and augment the long-term sustainability of the San Joaquin River salmon populations. The following will be delivered:

- Annual sex identification for all SCARF broodstock;
- Family reconstruction for all SCARF broodstock and creation of spawner candidate lists based on genetic relatedness for all spawner canidates;
- Establishment of Parentage Based Tags for San Joaquin River Chinook salmon populations;
- Parentage inference for San Joaquin River young of year juvenile and returning adult salmon;
- Population genetics analysis for the San Joaquin River population;
- Annual and summary reporting;
- Raw genotype data acquired through the contract
- Technical advising

4.0 Tasks

We will provide genetic broodstock management and monitoring of the interim SCARF hatchery Chinook salmon stock and the newly established in-river population. We will manage the scope, schedule, and technical quality of all administrative and final deliverables and will track the overall progress and quality of work, communicating with Reclamation's Project Manager and SJRRP program staff at regular intervals as is necessary.

Task 1: Project Management

1.1 Project Management Plan:

A Project Management Plan will document the deliverable-specific quality metrics, roles, responsibilities, processes, and procedures outlined here. The plan will detail schedules indicating interim products and required inputs from other workgroup team members and agency decision makers. A calendar will be maintained that notes all project milestone dates, review periods and availability of project participants. Project participants will also present and interpret results to the Fisheries Management Workgroup and Project Management Team, and its subgroups, as necessary to inform future SJRRP actions related to the Restoration Goal.

Schedule:
- First Draft - within two (2) weeks from award
- Second Draft – 1 week after comments

Deliverables: Project Management Plan document in Microsoft Word.

1.2 Weekly Status Reports:

Regularly scheduled calls with the Reclamation Project Manager will be initiated to discuss upcoming coordination and milestones, accomplishments since previous update, planned actions to meet milestones and address any questions or problems requiring SJRRP input.

Schedule: Weekly 30-minute calls on Mondays, or others days through mutual agreement.

Deliverables: Email or Word document describing weekly details and any modifications to plan.

<u>Task 2: Genetic sex identification of the SCARF spring-run broodstock</u>

The SJRRP will segregate juvenile spring-run Chinook salmon by sex at the SCARF, in order to restrict male feeding rates and limit the incidence of precocious male maturation, as well as to maintain desirable sex ratios in the fish retained for captive spawning. Due to the difficulty of identifying the sex of Chinook salmon prior to maturity by morphological features, the OtY3 or equivalent Y-chromosome genetic marker (with Project Manager approval) will be used to identify the sex of spring-run salmon at the SCARF. Determination of and reporting on the genetic sex identification of up to 1000 spring-run broodstock samples for brood year 2013 and 2014 and up to 3000 samples for brood year 2015 will be completed by the dates below.

Schedule:
- BY2013 – completed by July 1, 2014
- BY2014 – completed by July 1, 2015
- BY2014 – completed by July 1, 2016

Deliverables: Annual report detailing genetic sex identification of all broodstock samples in 2014, 2015, 2016.

<u>Task 3: Family relationship determination and relatedness estimation for SCARF broodstock and for all potential pairs of spawners</u>

3.1 Family reconstruction analysis of spring-run broodstock samples:

When space within the SCARF is limited, relatedness will be used as a criterion to select brood stock individuals for release or culling in a manner that will reduce variance in family size in the remaining broodstock (which in turn, will minimize reductions to effective population size). A panel of at least 96 SNP markers will be used to genotype up to 1000 spring-run broodstock samples for brood years 2012, 2013 and 2014 and up to 3000 samples for brood year 2015. Familial relationships among annual broodstock individuals will be determined using parentage analysis and pedigree reconstruction techniques when possible or will be estimated using family/sibship reconstruction or pairwise relatedness coefficients otherwise. Annual reporting will be completed by the dates below.

Schedule:

- BY2012 – completed by April 1, 2014
- BY2013 – completed by February 1, 2015
- BY2014 – completed by February 1, 2016
- BY2015 – completed by August 1, 2016

Deliverables: Annual report detailing the estimation of familial relationships among spring-run broodstock individuals.

3.2 Pairwise relatedness mating matrix:

The SJRRP will implement genetic broodstock management to guide selection of breeding pairs on the basis of relatedness, so as to maximize genetic diversity/effective size of the experimental population and minimize inbreeding and consequent reductions in fitness. A pairwise relatedness mating matrix, supplemented and validated with direct determination of pedigree relationships when possible, will be developed each spawning season with the goal of directing matings to the least-related pairs of mature broodstock. This will include a list of all possible mates for each spawner arranged from least to most related. For spawning in Fall 2014, this matrix will be used to select up to 40 spawning pairs, and for Fall of 2015 and 2016 these matrices will be used to select up to 100 spawning pairs each year, although the provided matrices will accommodate larger or smaller numbers of crosses. The same SNP genotype data generated for Task 3.1 will be used for matrix construction. Spawning matrices will be submitted to SCARF hatchery personnel by the dates below.

Schedule:

- 2014 spawning season – completed by August 1, 2014
- 2015 spawning season – completed by August 1, 2015
- 2016 spawning season – completed by August 1, 2016

Deliverables: Annual spawning matrix based on genetic relatedness estimation and/or exact pedigree relationships between all broodstock candidates.

Task 4: Establishment of a parentage based tagging (PBT) program for the San Joaquin Chinook salmon population

Parentage based tagging (PBT) involves the annual sampling and genotyping of individuals comprising the parental generation of a population to create a database of their genotypes for future parentage assignment of their progeny. PBT requires neither the physical tagging of juveniles nor lethal take to differentiate the origin of fish (e.g. hatchery vs. natural). The SJRRP requires that all adult Chinook salmon (fall- and spring-run) released in the San Joaquin River be genotyped for the purpose of PBT. Two primary groups of adults are expected to contribute juvenile fish to San Joaquin Chinook salmon populations, and therefore need to be included in the parent database for PBT. Adult fall-run Chinook salmon in the San Joaquin River above the confluence with Merced River will be captured annually and relocated into the San Joaquin River below Friant Dam ('Trap and Haul') to circumvent physical barriers. These adult fish will be sampled and genotyped with the panel of 96 SNPs allowing for the identification of their juvenile offspring by genetic parentage analysis. For fall-run adults Trapped and Hauled in the Fall of 2013, 2014 and 2015, a maximum of 2000 individuals will be genotyped annually. Spring-run adults may also enter the Restoration Area during the project period and be Trapped and Hauled to Friant Dam. These fish must also be accounted for in the parent database for PBT, so that their progeny can be identified . A maximum of 100 spring-run adults each in the Spring of both 2014 and 2015 will genotyped with the same panel of 96 SNPs used for Task 3. Inclusion of the genotype data in the parent database and assignment of offspring via parentage analysis will be reported by the dates below.

Schedule:

- Fall 2013 collected fall-run – completed by October 1, 2014
- Fall 2014 collected fall-run; Spring collected 2014 spring-run – completed by August 1, 2015
- Fall 2015 collected fall-run; Spring collected 2015 spring-run – completed by August 1, 2016

Deliverables: A parent database containing SNP genotypes, updated annually, and annual reporting of the results of parentage analysis

Task 5: Parentage inference for returning adult and young of year juvenile Chinook salmon in the San Joaquin River:

All juvenile fish released in the Restoration Area from the SCARF, streamside spawning experiments, or other sources will be marked with an adipose fin clip; therefore, unmarked fish captured in the upper San Joaquin River Rotary Screw Trap (RST), should be of natural origin. Parentage inference of naturally origin juveniles found in the San Joaquin River will allow the SJRRP to identify offspring of specific 'Trap and Haul' adults and the minimum number of natural-origin crosses (in turn, number of redds) produced within the Restoration Area. Results from juvenile parentage inference analysis, which will include the identification of both parents for each individual, estimation of the total number of crosses that took place within the river, family line contribution, and identification of crosses not attributable to the SJRRP operations, will be provided by the dates below. In addition, parentage inference will be conducted annually for any adults returning to the Restoration Area that could potentially be progeny of fish previously genotyped and recorded in the SJRRP genetic database. A maximum of 100 unmarked young-of-the-year (YOY) captured at the RST in the Spring of 2013 will be genotyped and assigned to parents, while an annual maximum of 2000 samples of RST YOY captured in Spring 2014 and Spring 2015 will be genotyped. All returning adults, genotyped as part of Task 4, will also be subject to parentage inference, to determine if their parents were previously genotyped and the PI, in conjunction with the Project Manager, will determine if they are a product of the SJRRP. All genotyping will use the same panel of 96 SNPs as in Tasks 3 & 4.

Schedule:

- Spring 2013 collected unmarked RST YOY – completed by October 1, 2014
- Fall 2013 collected returning adults – completed by October 1, 2014
- Spring 2014 collected unmarked RST YOY – completed by October 1, 2014
- Spring 2014 collected returning adults – completed by August 1, 2015
- Fall 2014 collected returning adults – completed by August 1, 2015
- Spring 2015 collected unmarked RST YOY – completed by August 1, 2015
- Fall 2015 collected returning adults – completed by August 1, 2016
- Spring 2016 collected unmarked RST YOY – completed by August 1, 2016
- Spring 2016 collected returning adults – completed by August 1, 2016

Deliverables: Reporting summary of parentage inference for YOY and returning adults

Task 6: Data Management

All genetic information (i.e. genotypes, genomic data) acquired as part of the contract will be included in an SJRRP genetic database. The database will contain genetic (genotypes and summary statistics), logistical (sampling locations, dates) and other scientific (e.g. otolith signatures) information obtained or provided by SJRRP staff.

Schedule:

- For data collected in 2014 – completed by December 1, 2014
- For data collected in 2015 – completed by December 1, 2015
- For data collected in 2016 – completed by December 1, 2016

Deliverables: A database containing all genetic data and relevant information, updated annually, and provided to the Reclamation Project Manager.

Task 7: Annual Report

An annual report will be provided summarizing the genetic status of the San Joaquin River salmon populations. The following genetic parameters for outmigrating smolts and/or returning adults in the San Joaquin River will be included:

a. Effective number of breeders (N_b) and/or effective population size (N_e)
b. Genetic diversity indices (e.g. heterozygosity, allelic richness)
c. Temporal changes in allele frequency/comparison among brood years if available

A summary report will be provided, as well as copies of all published and unpublished genetic work completed as part of this contract. The report will include documentation of all work done under the contract during that period and recommendations on future studies for the SJRRP.

Schedule:

- Draft Report 2014 – October 1, 2014
- Final Report 2014 – December 1, 2014
- Draft Report 2015 – October 1, 2015
- Final Report 2015 – December 1, 2015
- Draft Report 2016 – October 1, 2016
- Final Report 2016 – December 1, 2016

Deliverables: Annual report

5.0 Delivery

Task-ID	**Sub-ID**	**FY**	**DELIVERABLE/ACTIVITY**	**COMPLETION DATE**
1			**Task 1:Project Management**	
1	1	2014	Project Management Plan	
1	1	2014	Initial Development	
1	1	2014	Draft 1	2 weeks from award
1	1	2014	Draft 2	3 weeks from award
1	2	2014	Weekly Status Reports	Weekly
1	2	2015	Project Management- Option Year 1	Weekly
1	2	2016	Project Management- Option Year 2	Weekly
2			**Task 2: Sex Identification Report**	
2		2014	2013 SCARF Broodstock	July 1, 2014
2		2015	2014 SCARF Broodstock	July 1, 2015
2		2016	2015 SCARF Broodstock	July 1, 2016
3			**Task 3: Broodstock Family Reconstruction**	
3	1		**Family Reconstruction/Relatedness Report**	
3	1	2014	2012 SCARF Broodstock	April 1, 2014
3	1	2014	2013 SCARF Broodstock	February 1, 2015
3	1	2015	2014 SCARF Broodstock	February 1, 2016
3	1	2016	2015 SCARF Broodstock	August 1, 2016
3	2		**Mating Matrix Report**	
3	2	2014	2014 Spawning Season	August 1, 2014
3	2	2015	2015 Spawning Season	August 1, 2015
3	2	2016	2016 Spawning Season	August 1, 2016
4			**Task 4: Genotype Data for PBT**	
4		2014	2013 Spawning Season (Trap and Haul Adults)	October 1, 2014
4		2015	2014 Spawning Season (Trap and Haul Adults)	August 1, 2015
4		2016	2015 Spawning Season (Trap and Haul Adults)	August 1, 2016
5			**Task 5: Parentage Assignment Report**	
5		2014	Spring 2013 – Spring 2014 Season	October 1, 2014
5		2015	Fall 2014 – Spring 2015 Season	August 1, 2015
5		2016	Fall 2015 – Spring 2016 Season	August 1, 2016
6			**Task 6: Data Management**	
6		2014	Update SJRRP Genetic Database with Base Year Data	December 1, 2014
6		2015	Update SJRRP Genetic Database with Option Year 1 Data	December 1, 2015
6		2016	Update SJRRP Genetic Database with Option Year 2 Data	December 1, 2016
7			**Task 7: Annual Report**	
7		2014	Draft Annual Report- Base Year 1	October 1, 2014
7		2014	Annual Report- Base Year 1	December 1, 2014
7		2015	Draft Annual Report- Option Year1	October 1, 2015

Task-ID	**Sub-ID**	**FY**	**DELIVERABLE/ACTIVITY**	**COMPLETION DATE**
7		2015	Annual Report- Option Year 1	December 1, 2015
7		2016	Draft Annual Report- Option Year 2	October 1, 2016
7		2016	Annual Report- Option Year 2	December 1, 2016

6.0 Government-Furnished Property

Reclamation is not required to furnish government property as part of the proposed work. All equipment necessary for completion of the deliverables described in this SOW are available to the PI and no equipment purchases are requested.

7.0 Security

There are no special security requirements.

8.0 Place of Performance

All work will be performed at the Southwest Fisheries Science Center laboratory located on the Marine Sciences Campus of the University of California, Santa Cruz at 110 Shaffer Rd. Santa Cruz, CA 95060.

9.0 Period of Performance

Date of award through December 2016.