III. Approach and Scope of Work

Fin tissue for DNA analysis will be collected from juvenile Chinook salmon captured in the trawl sampling conducted at Chipps Island per established protocols used for similar sampling at the SWP and CVP fish facilities (Appendix 1). Sample size is limited to3,000 fish per year by the capacity of Michael Banks' lab to analyze DNA samples, so a statistically rigorous sampling design will be developed to ensure that results can be expanded accurately to the total population. The priority in the sampling design will be given to estimating the fraction of winter- and spring- run among all Chinook smolts collected at any point in time.

Given that expansion of trawl catches are needed to estimate total abundance of winter and spring run, this project will also estimate trawl efficiency at Chipps Island. Coded wire tag (CWT) recoveries from several past releases (USFWS, 2001, Newman and Rice,2002, and Newman, 2003) will be reviewed, analyzed and modeled to identify trawl efficiency and apply it to known catches of winter- and spring-run (determined by DNA)to estimate total abundance of each race passing Chipps Island.

It would be possible to fund only the DNA sampling design or trawl efficiency aspects of this study, but it wouldn't be prudent to fund collection and analyses of DNA samples without designing an appropriate study plan. If only relative migration timing information of winter and spring-run at Chipps Island was selected for funding, the trawl efficiency aspect of the study could be deferred, but by doing so, it would limit our ability to estimate population abundances and compare results to population estimates earlier in the freshwater stage of the life-cycle.

The work plan that follows corresponds to the objectives above.

Objective 1: Design a sampling plan for collecting genetic samples

Task 1.1: Assemble data from previous DNA analyses

We will use data from past DNA sampling in the Delta and SWP and CVP Fish Facilities to guide the formulation of an appropriate sampling design (e.g., Figure 2, Figure 3 and Figure 5). These preliminary data identify the capture date and length of juveniles corresponding to genetic winter- and spring-run. Further review of these data will be used to summarize within-year and between-year variability in anticipated distributions of length, passage date, and relative abundance of spring- and winter-run Chinook salmon at Chipps Island.

Task 1.2: Design a sampling plan to allocate 3000 samples (one sample = 1 fish) per year

The genetic sampling program will target juvenile spring- and winter-run Chinook salmon, and will be designed to obtain both a representative sample as well as high levels of statistical confidence in estimating racial proportions during key passage periods. To accomplish this, we will collect 3000 samples per year - the maximum number of DNA samples that can be processed annually at the Marine Fisheries Genetics Laboratory based at the Hatfield Marine Science Center, Oregon State University. The collection of samples will be stratified by date and fish length, and sample sizes will be determined to just allocates a fish to their most likely population irrespective of how likely this fish may also be assigned to a second population. Thus, for example, 98.9% of spring from Deer and Mill are assigned appropriately, but 1.3% of fish from other runs are also assigned to spring at this stringency of O. Given that the other runs may exceed spring by 500 fold or more, this can result in a substantial assignment error. Selecting a stringency of 2 designates those fish with assignments that exceed the second most likely population, by 100 times or more. Borderline fish with genotypes that are marginally assigned to more than one population and comprise the bulk of miss-assignments would not be

assigned to any population with this higher stringency. Using a stringency of 2, accurate assignments for Deer and Mill Creek spring run chinook populations is 93%, but importantly, miss-assignment reduces to 0.14%. For further information on this topic, see page 612 in Banks (2005).

Objective 4: Estimate abundance of spring-and winter-run Chinook juveniles

Task 4.1: Estimate catch efficiency of trawl sampling

Estimates of catch efficiency of trawl samples at Chipps Island are required to expand observed catches into estimates of total abundance. Absolute abundance at Chipps Island, by race (using the size criteria) is presently estimated by using the survival of marked fish to Chipps Island to estimate trawl efficiency. Survival to Chipps Island is based on differential recoveries in the ocean fishery, of CWT groups released upstream and near Chipps Island. The trawl efficiency is the number recovered in the trawl divided by the number estimated to be available for capture for each release group. The number available for capture is the number released times the estimated survival rate to Chipps Island. Several estimates of trawl efficiency are averaged to obtain an annual trawl estimate which is then applied to catches through-out the year. These methods are explained in further detail in USFWS, 2003. A comprehensive list of all of the CWT groups used to estimate trawl efficiency is. available in USFWS, 2001.We propose to improve upon existing methods for estimating catch efficiencies by using statistical and modeling expertise to determine the best way to estimate trawl efficiency and associated confidence limits and apply them to catches of "true" juvenile winter- and spring-run Chinook salmon.

Task 4.2: Estimate abundance of spring- and winter-run Chinook juveniles at Chipps Island

Catch efficiency estimates will then be used to estimate total abundance of spring- and winter-run Chinook passing Chipps Island in each of the three project years. Abundance estimates and their standard errors will be computed at various times scales (e.g., annual, monthly, and where possible, weekly estimates).We will also determine if past DNA samples collected at Chipps Island can be used to estimate winter or spring run abundance in previous years.

Objective 5: Disseminate Findings

Task 5.1: Complete annual reports

We will submit semi-annual and annual progress reports to CALFED. Semi-annual reports will be submitted by March 1 of 2008, 2009 and 2010. Annual progress reports will be submitted by August 31 of 2008, 2009 and 2010. We will also submit a 1 page project summary for a public audience at the beginning and upon completion of the project.

Task 5.2: Present findings

We propose to present at least one oral presentation at the CALFED Science Conference. We will share data and results with other researchers conducting winter and spring run life-cycle modeling such as National Marine Fisheries Service's JPE, Lou Botsford, Steve Lindley, Wim Kimmerer and Steve Cramer. We will also share our sampling design process with the Winter Run Genetics Project Work Team for potential use at other sampling locations (e.g. Fish Facilities).

Task5.3: Submit findings to Peer-Refereed Journals(s).

We propose to submit at least one manuscript for publication in a peer-reviewed journal as we near completion of the three-year project.

Task 5.4: Evaluate using this technology to estimate abundance of winter- and spring-run juveniles at other monitoring locations such as Sacramento and Knights Landing.

This evaluation will be included in our final report on whether the methods we employ would be applicable to other salmon monitoring locations.