Continue Genetic Research on Winter-Run Chinook Salmon: Bodega Marine Lab

Scope

Continue on-going screening and development of nDNA markers (loci) to allow positive identification of individual salmon adults for use in the Service=s winter-run chinook salmon captive propagation and captive brood stock programs, and determine genetic impacts of the program on the wild population through genetic analysis and verification and refinement of an effective population size model.

Justification and benefits

Continue development of molecular markers and statistical tools to accomplish the following:

1) Identify winter-run chinook salmon among adult salmon captured in the mainstem Sacramento River or in Battle Creek for potential use in the artificial propagation program or for relocation.
2) Continue to assist in the design of pedigree mating systems for wild caught and captive brood stock winter-run chinook salmon to ensure the genetic integrity of progeny and avoid impacts on the wild/natural population.
3) Assist in the development of a winter-run chinook salmon genetic management plan which collates available genetic information and provide recommendations for the maintenance of genetic resources.
4) Assist in the refinement/verification of effective population size models (N_e) to monitor potential genetic impacts of the artificial propagation program on the natural population.

Monitoring and data evaluation

Tissue samples (i.e., fin clips) of the four runs of chinook salmon will be obtained from on-going research and monitoring activities and provided to the U.C. Davis= Bodega Marine Laboratory (BML). At BML, research will continue related to the genetic characterization and identification of winter-run chinook salmon. Genetic analyses are made possible by the development of highly variable, simply inherited, microsatellite DNA markers. These markers have core DNA sequences from 2-6 nucleotides in length that may be repeated from 10 to 100 times at a particular chromosomal site, and are transmitted from Aboth@ parents thus providing a more detailed record of past breeding activity than mtDNA. Microsatellite DNA markers can be amplified by the polymerase chain reaction (PCR) from small tissue samples (fin clips) and rapidly typed fluorescence imaging (Hedgecock et al. 1995; Banks et al. 1996). The genotype of individual fish may be determined for a series of polymorphic DNA markers.

Tissue samples from Central Valley chinook salmon stocks will be screened with new loci as a means of identifying additional informative molecular markers. For those loci selected, further characterization will be conducted to enable their application in the management of salmon populations. Further characterization will include investigation into details of transmission genetics, possible linkage and multiplexed PCR (a technique that facilitates rapid characterization of more than one locus at a time). Sections of the genome flanking more informative loci will also be characterized in hope of identifying other molecular markers for the identification of winter-run chinook salmon.

Budget: $200,000