**Science- Genetics Sub-group pilot project 2**

**Paired Spawning**

I. Initiate paired spawning pilot studies at each facility as initial step for evaluating equipment requirements and logistics.

* 1. Objectives
     1. Establish equipment requirements for concurrent paired spawning
     2. Evaluate paired spawning duration to evaluate consecutive paired spawning
     3. Evaluate facility needs for holding individual lots of offspring for durations of 2 weeks to 5 months
  2. This project would address comments 2.2, 2.4. 2.5, 2.13, 2.14. It would reduce the need and costs required for genetic analysis of the progeny prior to release into the river.
     1. 2.2 Conduct genetic sample collection and analysis of hatchery stocks well in advance of RGSM release so that decisions can be made regarding which family lots are to be released, and the number of progeny to release per family, to avoid a reduction in the effective population size of the overall population.

As currently practiced, the timing of genetic sampling of released offspring does not permit the development of recommendations for stocking in that year.

* + 1. 2.4 Conduct annual genotyping of brood stock adults to accomplish the following objectives:
* To accurately estimate the effective number of breeders and to assess their respective contributions to the resulting offspring.
* To thoroughly assess potential domestication selection for all propagation activities and set up procedures to minimize such selection.
* To improve the genetic characterizations by (i) using large numbers of breeders that contribute equally to the augmentation population, and (ii) minimizing domestication selection during propagation. (Equalizing the family size solves many of these identified problems. Paired spawning accomplishes this without having to know anything else.)
* To genotype all brood stock and a sufficient subset of all pre-release juveniles, with the contribution of each brood stock individual determined. (First, will require developing high-throughput markers.)
* To calculate relatedness of brood stock prior to artificially spawning to choose specific crosses that avoid inbreeding. Alternatively, if group spawning continues, use relatedness estimates to ensure that potential spawners in a group have low kinship. See Project 5.
* To assess whether mortality causes a non-random shift in genotypic frequencies in the actual brood stock used in the hatcheries or in their progeny from hatching to release.
* To assess whether the composition of the gene pool shifts from generation to generation and to help establish whether there is “drift" in the gene pool due to sampling effects and population bottlenecks. (This is related to development of better markers and sampling effort. For future genetic monitoring it is important to ensure adequate sample sizes to detect change, and to have a “Plan B” for years with few wild samples.)
  + 1. 2.5 All hatcheries must use the same breeding protocols, and all hatchery personnel should be extensively trained in the important costs of deviating from the protocols.
    2. 2.13 Artificially spawn brood stock using a one female by one male RGSM mating scheme, while not reducing the total number of brood stock adults spawned.
    3. 2.14 Equalize family sizes, Equalize contributions of different adults in the captive brood stock to new broods/lots as much as possible

II. Conduct a study to compare paired crosses of fish that have been genetically selected to maximize diversity, randomly paired fish, communal spawn with selected fish, communal spawn with randomly selected fish.