Work Task C48: Genetic Characterization of RASU Broodstock at Dexter NFH

FY10 Estimates	FY10 Actual	Cumulative Accomplishment Through FY10	FY11 Approved Estimate	FY12 Proposed Estimate	FY13 Proposed Estimate	FY14 Proposed Estimate
\$0	\$0	\$0.00	\$60,000	\$60,000	\$0	\$0

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Start Date: FY11

Expected Duration: FY12

Long-term Goal: To assess the effectiveness of the fish augmentation program.

Conservation Measures: RASU3, RASU4.

Location: Dexter NFH.

Purpose: To genetically assess RASU captive broodstock.

Connections with Other Work Tasks (past and future): Willow Beach National Fish Hatchery (B2), Dexter National Fish Hatchery (B4), Bubbling Ponds Fish Hatchery (B5), Uvalde National Fish Hatchery (B10), Razorback Sucker Rearing Studies (C10), and Razorback Sucker Genetic Diversity Assessment (C31).

Project Description: This two-year study will compare the genetic diversity of captive RASU broodstock and the source stock at Lake Mohave. Dexter NFH maintains three different stocks of RASU that originated from Lake Mohave. Concern has been expressed that captive fish stocks have lowered genetic diversity and thus less utility for conservation activities. To address this concern, razorback sucker broodstocks will be tested to ensure that they are genetically diverse and representative of wild populations. Levels of inbreeding, allelic diversity, and statistical measures used to identify genetic divergence will be calculated.

Previous Activities: This effort builds upon research from Dexter National Fish Hatchery (B4), Uvalde National Fish Hatchery (B10), Razorback Sucker Rearing Studies (C10), and Razorback Sucker Genetic Diversity Assessment (C31).

FY10 Accomplishments: New start in FY11.

FY11 Activities: A study design detailing how captive stocks of RASU will be genetically assessed was completed. The captive stocks held at Dexter NFH will be assessed for genetic similarity and compared to wild samples. Objectives to be

accomplished include assessment of the genetic variability within and between razorback sucker broodstocks, including the progeny of wild fish and F1 adults held at Dexter NFH, and analysis of broodstock tissues from Ouray NFH and Grand Valley FRO razorback sucker stocks for comparison to the Dexter stock. Microsatellite data will be used to generate an individual genotype (genetic profile) for each of the brood fish from the three stocks at Dexter NFH, in addition to captive stocks from the upper basin and from wild razorback sucker in Lake Mohave and in the Colorado River above Lake Mohave. Population genetics analysis will be performed using statistical programs to test for Hardy-Weinberg equilibrium (in which both alleles and genotype frequencies remain constant in a randomly breeding population), population subdivision, inbreeding, and levels of gene flow. Levels of polymorphism, population subdivision, and heterozygosity will also be assessed.

Proposed FY12 Activities: Research will continue based on findings from the first study year. Following individual genetic assessment, a pairwise relatedness analysis of all individuals potentially used for production at both Ouray NFH and Dexter NFH will be performed. Relatedness estimates will then be compared to the wild stock estimates to determine if the broodstocks are proportionally more related than the wild stocks. The results of this analysis will be used to ensure production of fish that are genetically diverse by allowing managers to avoid mating individuals that are related.

Pertinent Reports: The scope of work is available upon request. Annual reports will be posted to the LCR MSCP website upon completion.