

2001

McDonald: F-113-R-1

3829

Statewide

# 72174

## PERFORMANCE REPORT

**STATE:** MONTANA  
**GRANT TITLE:** SALMONID GENETIC ANALYSIS  
**GRANT NUMBER:** F-113 R-1  
**PROJECT NUMBER:** 3829  
**LOCATION:** MONTANA – Statewide  
**PERIOD COVERED:** July 1, 2000 through June 30, 2001  
**PROJECT PERSONNEL:** Ken McDonald, Special Projects Bureau Chief, Helena

### OBJECTIVE:

The primary objective for work funded under this project was to identify and prioritize streams where native trout genetics data is needed for developing and implementing conservation recommendations, and to monitor the genetic status of wild and hatchery brood stocks of native trout to ensure the genetic integrity and diversity of Montana's native fish species are maintained.

Specific tasks to be accomplished included:

- Prioritize locations where genetics tissue samples are needed or larger sample size is required
- Develop a standardized data sheet to be filled out and submitted with all samples submitted for analysis
- Develop a data tracking and data entry program for logging in samples and entering analysis results
- Contract with the University of Montana's Wild Trout and Salmon Genetics Lab for analysis of fish tissue samples provided by the Department to determine introgression/hybridization of wild fish, genetic diversity of wild and hatchery stocks of fish, to determine "relatedness" of populations, and to address other specific questions, and
- Develop and implement management recommendations and corrective measures based on genetics analysis results, if required

**COSTS:** \$50,000

**RESULTS:** Regional staff collected tissue samples from wild salmonids as part of their management programs. They were requested to provide a prioritized list of samples from their region for analysis over the fiscal year. Samples were then analyzed based on priority and available funding.

Tissue samples from wild westslope cutthroat trout, Yellowstone cutthroat trout, bull trout, and red band trout were submitted for analysis to determine genetic purity or percent introgression. Some bull trout analysis was also done to determine relatedness with bull trout from other waters in the upper Columbia River system. Hatchery brood fish were submitted and analyzed as part of an ongoing effort to monitor and maintain genetic diversity of hatchery stock.

A total of 660 tissue samples from wild salmonids were analyzed using the PINES technique. An additional 418 samples were analyzed using protein electrophoresis, including 175 hatchery samples.

A data entry program was developed and provided to the University of Montana genetics lab so that each sample could be provided with a unique identifier number and logged in. Results were entered into the database as they were determined, which was then regularly uploaded into the Montana Rivers Information System (MRIS).

An additional 1,321 samples were analyzed with funding provided by a variety of other sources. These additional samples were analyzed for the same purposes as those analyzed as part of this project, and they complemented the work done under this project.

Genetics analysis results were used by managers to help guide restoration, protection, and management efforts for native salmonids in Montana, and by the hatchery system to ensure brood stock was being maintained with adequate genetic diversity.