

# The Conservation Genetics Laboratory, Alaska Region

## *Applying Genetic Research to Fish and Wildlife Conservation*

The conservation of biodiversity through the use of modern genetic technology is the primary function of the Alaska Region's Conservation Genetics Laboratory (CGL). The sophisticated laboratory techniques and analytical methods used in conservation genetics are increasingly being applied to a variety of species in a variety of contexts. Some high profile examples include: evaluation of Pacific salmon populations for Endangered Species Act protection, forensic identification of illegally imported fish and wildlife products, examination of hybridization between wolves and coyotes, evaluation of migratory behavior of green sea turtles, and the identification and evaluation of exotics like the zebra mussel in the Northeast U.S.

In 1987 the CGL was established in Anchorage, Alaska as the first conservation genetics facility in the U.S. Fish and Wildlife Service. We work with biologists and managers to design and conduct genetic research and provide expertise to address conservation and management issues in Alaska, on its 16 National Wildlife Refuges, and in other Fish and Wildlife Service Regions. Collaboration with agencies and organizations outside the Fish and Wildlife Service is also critical to our success. Our partners include: Alaska Department of Fish & Game, National Marine Fisheries Service, U.S. Geological Survey, U.S. Forest Service, Alaska Sea Otter and Steller Sea Lion Commission, Canada Department of Fisheries and Oceans, Yukon River Drainage Fisheries Association, as well as Alaskan Native organizations and academic institutions in the U.S., Canada and Russia.



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*Male Dolly Varden from northwest Alaska, captured for non-lethal tissue sample.*

Our projects focus on species from salmon to sea otters, from Russia to California. We are equipped to perform multiple types of genetic research, from microsatellite analysis to direct DNA sequencing on our six DNA analyzers.



*Hook and line sampling for coho salmon.*

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Our work provides fish and wildlife professionals the support they need to integrate genetics into their management and conservation efforts. Two areas of emphasis are characterization of population structure and mixed-stock analysis:

## Population Structure Analysis

Sound management of any species necessitates knowing the scales at which its natural genetic diversity is structured. Identification of even basic biological parameters, such as population size, cannot be made without this information. Variations in life history traits and breeding strategies often lead to the formation of genetic population structuring that is unique to a given species and can even vary within a species across its range. While various types of traditional research methods (e.g., radio telemetry, mark-recapture, fish weirs, etc.) can yield valuable information about physical movements of organisms, they cannot determine the true geographic boundaries of populations or detect genetic exchange among them. Population structure analysis allows us to define populations (how they are structured spatially and temporally) and quantify genetic exchange between them; it is one of the most fundamental and useful techniques in conservation genetics.

We are currently characterizing population structure in many species, including: Dolly Varden and coho salmon throughout Alaska, steelhead and rainbow trout in Alaska and California, and coastal cutthroat trout and Dolly Varden in Southeast Alaska.

## Mixed-Stock Analysis

Many species form aggregations consisting of multiple populations at various stages in their life history. For example, multiple salmon populations often migrate together in both fresh and salt water. Estimating the populations contributing to these aggregations, and their proportions, is performed through mixed-stock analysis, which provides us with another powerful management tool.

Mixed-stock analysis provides managers with information on specific patterns of

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*Steelhead caught in a sport fishery prior to release.*

salmon migration and harvest allowing regulation of subsistence, commercial, and sport fisheries. Mixed-stock analysis is also useful for monitoring production and health of populations through, for example, determination of the origin of salmon smolt migrating to sea or juveniles in aggregate rearing areas.

We are currently performing mixed-stock analysis on multiple species, including chum and chinook salmon in the Yukon River, coho salmon in the Kenai and Kuskokwim rivers, and Dolly Varden from Southeast Alaska to Russia.

Our research not only allows us to evaluate patterns of natural genetic diversity for species in Alaska, it may often be extrapolated to other regions where anthropogenic factors may have obscured native patterns. Fish, wildlife, plants and their habitats remain in pristine and healthy condition throughout most of Alaska, allowing us to evaluate natural mechanisms that create and maintain genetic diversity. This information is often applicable to conservation efforts outside Alaska, such as the ones presently occurring for the multitude of Pacific salmon stocks that have been extirpated or are in decline along the West Coast of the U.S.

The need for genetic information to direct conservation efforts for North America's fish and wildlife species will continue to increase into the foreseeable future. In fact, due to the increasing awareness of the necessity for genetic information in fish and wildlife conservation throughout the Service, development of new genetic facilities has recently been initiated in several other Service Regions. Along with these facilities, the CGL will continue to provide the genetics expertise to ensure the continued health of ecosystems throughout North America.



*Front row left to right: Cara Lewis, Ora Stefanowski, Penny Crane, Steve Miller. Back row left to right: John Wenburg, Jeff Olsen, Steve Lillard, Bill Spearman, Eric Kretschmer, Blair Flannery. Not pictured: Lynsey Luiten, Victoria Sheffrey.*

The Conservation Genetics Laboratory was established in Anchorage, Alaska in 1987 as the first conservation genetics facility in the Fish & Wildlife Service. The large modern facility features six DNA sequencers and maintains a staff of 12 geneticists, biologists and technicians dedicated to working with others to conserve, protect and enhance, fish, wildlife, plants and their habitats for the continuing benefit of the American people.

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