

Conservation Genetics in the USGS

Conservation genetics is the application of the tools and concepts of genetics to the conservation of biological resources. Once too sophisticated and expensive for routine use, the tools of conservation genetics are now widely used to address many complex management questions.

These novel methods of analysis can augment assessments made with traditional methods and can bring new information to light. The U.S. Geological Survey (USGS) is well suited to provide scientific information and expertise using these tools to support the management of biological resources.



©Michael Milford

A Hairy Undertaking

In northern Montana, a 400 lb. grizzly bear lumbers across the rugged landscape, pausing now and then to claw at the ground in search of roots, bulbs, and other food. Along the way, he encounters a liquid scent lure consisting of rotting fish and cattle blood sprinkled on a plot encircled with a single strand of barbed wire attached to trees. The bear leaves behind clumps of hair as he negotiates under and around the wire to wallow in the irresistible odors. Although no humans witnessed his passage, the hair collected two weeks later is analyzed by a scientist who identifies the bear and adds another point to a data set indicating detection locations for this particular animal. This work is part of a collaboration involving the USGS and many partners to estimate

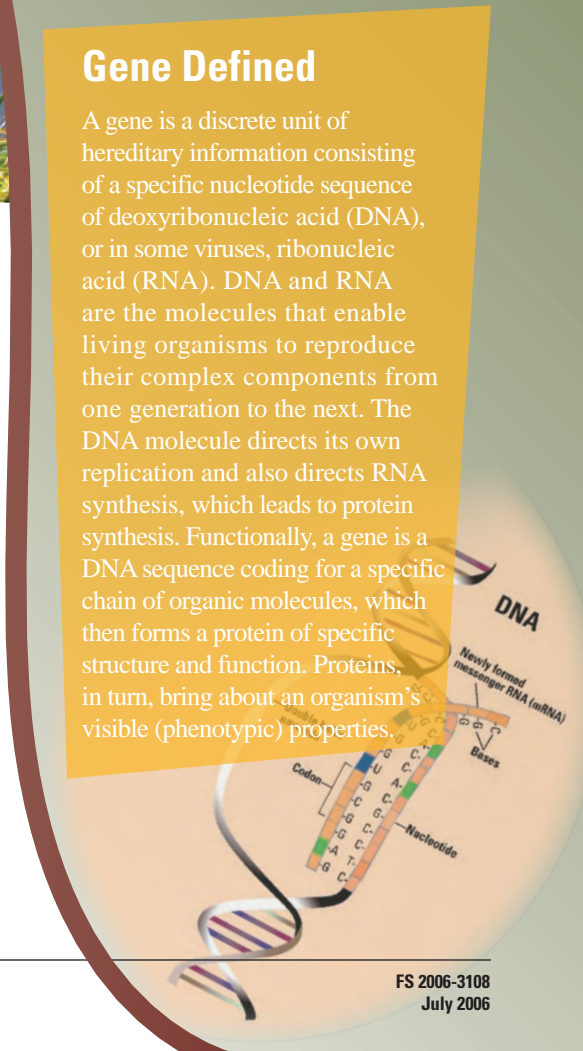
the size and distribution of the grizzly bear population within an area of 8 million acres. DNA analysis of hair samples makes this possible. Traditional mark and recapture methods are the basis of the study design; however, there is no need to see or capture bears because the DNA contained in their hair is sufficient for species, sex, and individual identification. In addition to gaining a good estimate of the size and distribution of the grizzly bear population, DNA profiles of the individual bears allow managers to address future conservation issues by providing them with information about genetic variation, the suitability of individual bears for augmenting small and isolated populations, the ratio of males to females, and connections with other populations.

Biological Diversity

Biological diversity, the variability among living organisms, includes diversity within species, between species, and across ecosystems. Each species is the repository of an immense amount of genetic information that determines its form, function, behavior, and reproductive success. A human, for example, has about 20,000 to 30,000 genes. Each species, human or otherwise, is made up of multiple individuals, and rarely are individuals genetically identical. At another level, many species consist of multiple breeding populations, with each population having its own pattern of genetic variation and ability to interact with other populations. Furthermore, populations of different species coexist in communities, which together with the physical environment and a host of interactions, constitute an ecosystem. Conservation of biological diversity, regardless of the level of organization considered, is important because of its significance in maintaining balanced, functioning systems.

Gene Defined

A gene is a discrete unit of hereditary information consisting of a specific nucleotide sequence of deoxyribonucleic acid (DNA), or in some viruses, ribonucleic acid (RNA). DNA and RNA are the molecules that enable living organisms to reproduce their complex components from one generation to the next. The DNA molecule directs its own replication and also directs RNA synthesis, which leads to protein synthesis. Functionally, a gene is a DNA sequence coding for a specific chain of organic molecules, which then forms a protein of specific structure and function. Proteins, in turn, bring about an organism's visible (phenotypic) properties.



Documenting Genetic Variation

All organisms play roles that are essential to the persistence of ecosystems, and because we are part of those ecosystems, to the persistence of civilization. In most cases, numerous genetically diverse populations are necessary to ensure the survival and evolutionary potential of a species in the face of environmental change. This is true for domesticated and wild plants and animals, including those we view as benign, troublesome, or beneficial. The more we know about genetic diversity, the more we understand what can be managed and conserved. Information about genetic variation is used to select units for management, set priorities, test observations or presumptions, and meet management requirements.

Example: Spotting the Difference between Owls

Spotted owls are mostly non-migratory, long-lived birds whose populations have declined in mature forests of western North America. They are classified as three subspecies: California,

northern, and Mexican. Northern and Mexican spotted owls are listed as threatened under the U.S. Endangered Species Act, whereas California spotted owls are not. Using genetic information, we reaffirmed that the northern spotted owl is a separate subspecies from California and Mexican spotted owls. Genetic information also indicated a zone of mixing between northern and California spotted owls in a portion of southern Oregon. This suggests that the range of California spotted owls extends farther north than previously described. Management agencies used these findings to review the status of the northern spotted owl, and in combination with population estimates and habitat assessments, to consider management options for all three subspecies.



Recovering the Rare

Fragmentation, alteration, or complete conversion of a habitat can shift a population from a rare but viable status to a situation where existence is threatened.

Such populations often experience reductions in genetic variation; in fact, one of the biggest problems is loss of genetic diversity through a process called inbreeding depression. This occurs when only a few individuals interbreed in small groups and pass a limited array of genes, some harmful, to their offspring. Individuals gradually become genetic copies, lacking the built-in adaptability to environmental change that would occur in a diverse group through natural selection. This is particularly problematic for captive populations where artificial propagation occurs with a limited breeding stock. We routinely help managers working to recover rare populations by measuring genetic diversity in wild and captive-bred populations, suggesting mating assignments, and evaluating the origins of individuals that establish a new population.

Management Applications of Genetic Information

- Evaluate threats
- Identify and treat disease
- Meet policy requirements
- Evaluate relocation options
- Identify movement patterns
- Propagate wild or domesticated stocks
- Estimate relatedness and reconstruct lineages
- Evaluate settler (founder) stocks
- Uncover and monitor change
- Identify individuals for estimation of population characteristics
- Infer relationships to identify units of management and evaluate taxonomy

Example: Crown Jewel of Puerto Rico

The Puerto Rican parrot is considered one of the most endangered birds in the world. During Columbus' time, the parrot population may have exceeded one million but dropped to a low of 13 by 1975. For over 30 years, scientists and managers have studied and nurtured the few remaining wild and captive parrots. Success with reproduction of birds in captivity has given new hope for bolstering the wild population. USGS scientists have spent the past decade working with federal agencies and the Puerto Rican government to establish family trees for the captive and wild populations. We use molecular markers to identify individuals and verify their lineage to model potential strategies for moving birds to and from captive and wild populations and to set up pairings for breeding programs to maximize genetic diversity. Recovery of the parrot is far from realized, but some birds are being released into the wild — a major step in bringing the parrot back from the brink of extinction.

Effects of Pollutants

A special form of population monitoring considers effects of pollutants or other contaminants on plants and animals, even if those effects are not visible or lethal. Many pollutants are carcinogens or mutating agents that affect either the structure of DNA, its biological expression, or both. Genetic toxicologists study the interaction of DNA-damaging agents with the cell's genetic material in relation to subsequent effects on the health of the organism. The organism functions as an integrator of exposure. The magnitude of the change in DNA or change in its biological expression is used as an estimate of the severity of exposure. In another field called genetic ecotoxicology, we evaluate potential effects of pollution on the health of an ecosystem by assessing genetics of multiple individuals in populations or communities and correlate this information with exposure to contaminants. This field is still largely theoretical, but it is a fruitful area of research because it offers an opportunity to rapidly advance our knowledge and understanding of the effects of environmental pollutants.

Example: Duck Soup

Many lesser scaup winter in the Indiana Harbor Canal of southern Lake Michigan. This canal, now a "Superfund" site, was built to service a petroleum-based industrial corridor. The USGS studied wintering scaup to determine if they were exposed to contaminants from that site, and if so, were the contaminants associated with genetic damage. Some of the contaminants studied were a group of organic compounds called polycyclic aromatic hydrocarbons, which originate from fossil fuels and combustion residues. This was the first study of wild birds to demonstrate a correlation between concentrations of these hydrocarbons in tissues and genetic damage to red blood cells. The concern underlying this research was that contaminant exposure could compromise the welfare of lesser scaup, and the scaup served as an indicator for the well being of other species. Management agencies have used this information in clean-up, restoration, and mitigation actions.



Population Monitoring

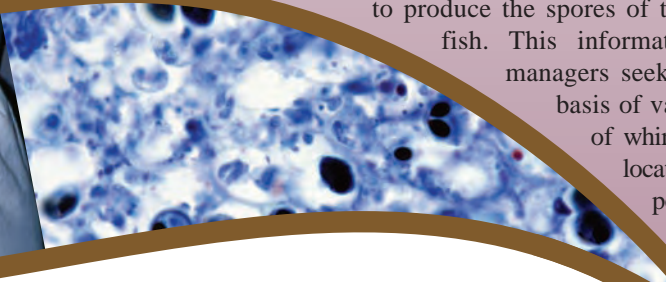
Information about abundance, population structure, reproduction, survival, and movement are important in management of plant and animal populations. Obtaining that information is often difficult or impossible for wide-ranging animals using traditional methods that involve capture, marking, and relocation. Genes already contain information coded in DNA that can be used as individual markers, and we use these "genetic tags" to accomplish population monitoring. There are many advantages to this approach. We are not restricted to monitoring the living population because genetic markers contain information that is inherited across generations. This means that information gathered in one year can be applied to both subsequent and previous generations, even over evolutionary time frames. Also, the same genetic information is obtainable at any life stage and frequently with little, if any, disruption to the organism of interest. An additional benefit is that we can monitor movements of individuals or populations throughout the course of a year or more, even if they travel to multiple, distant locations. We can even take DNA from museum specimens, assess the genetic variation of these specimens, and use this information to evaluate variation in current populations relative to variation in earlier populations.

Example: Monitoring the Wave

In springtime, colorful waves of adult Atlantic salmon begin returning to their rivers of birth in preparation for spawning. Most are finishing an ocean journey that began several years before and spanned hundreds, even thousands of miles of open water in the North Atlantic Ocean. While feeding on their wintering grounds off western Greenland, Atlantic salmon originating from locations in North America and Europe have ample opportunity to intermix. Nonetheless, when it is time to spawn, wild populations remain relatively faithful to their migration routes and rivers of origin based on thousands of generations of local adaptation. Wild Atlantic salmon populations in eastern Canada and the United States have dropped to historic low levels, with some populations going extinct. Research by the USGS uses segments of DNA to accurately assign Atlantic salmon caught off the coast of Greenland to their continent of origin, and reasonably well, to their country and province of origin. Genetic information also is used to assess trends in the number of salmon being harvested in the Greenland subsistence fishery, and to screen fish to ensure that aquaculture escapees are not incorporated into brood stocks used to maintain endangered wild populations.

Fish and Wildlife Health Research

Infectious disease is a natural component of all ecosystems, affecting the health and abundance of both plants and animals. Understanding the role of the microbes (pathogens) causing these diseases enables managers to adopt strategies to modify their influence when necessary. Disease control can be particularly urgent in situations where pathogens alter the population structure or function within an ecosystem. In general, we strive to understand disease processes, develop diagnostic methods, describe incidence and distribution of significant pathogens, and develop strategies for prevention and control. Genetic techniques are well suited to study disease agents, especially viruses, bacteria, and fungi, which are structurally simple organisms and for many of which the sequence of the entire genome is known.



Example: Whirling Disease

Whirling disease of salmon and trout is caused by the parasite, *Myxobolus cerebralis*. The disease, introduced in the United States in the 1950s, has spread to 23 states where it is sometimes associated with devastating declines in wild populations of rainbow trout. Using genetic tools, we evaluated the level of diversity among strains of the parasite from selected locations and found that genetic variation was relatively low, as might be expected for a recently introduced parasite. We also evaluated the diversity among strains of an oligochaete worm that is an essential alternate host during the parasite's life cycle. Oligochaetes from rivers in which trout showed different levels of disease severity were not as closely related as traditional taxonomy, based on morphology, would suggest. In fact, some strains of the worms could be considered separate species based on genetic differences, and the identified genetic lineages have been shown to have very different abilities to produce the spores of the parasite that infect fish. This information is beneficial to managers seeking to understand the basis of variation in the severity of whirling disease in different locations or in different fish populations and also in predicting future risks of whirling disease in new locations.

Rapidly Evolving Technologies

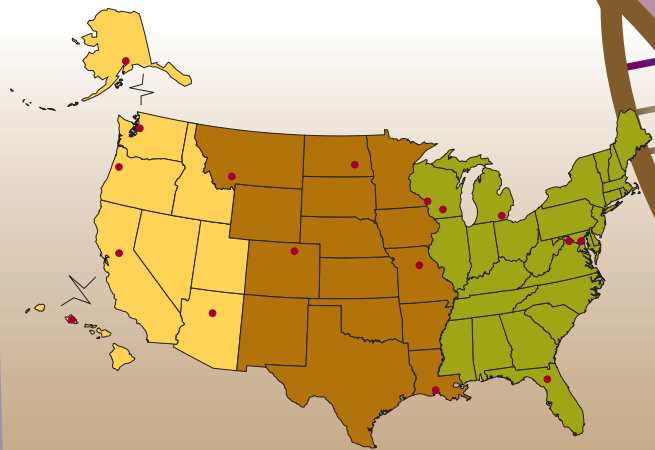
The USGS is using new technologies to study adaptations of individual species and communities and to identify potential effects of both human-related and natural changes.

Genomics involves the study of an organism's full genetic material, known as its genome. In the last decade, the number of sequenced genomes has grown to include mammals, birds, fishes, frogs, insects, marine organisms, plants, fungi, and bacteria. In addition to facilitating all molecular and genetics work, genomics has resulted in new technologies to study evolution, population structure, gene function, and effects of environmental change.

Success with genomics has led to proteomics, the study of the sets of proteins encoded by genes and their structure and function. This is an important step because the way that proteins interact with each other, with the environment, and with other molecules defines the organism. Furthermore, an organism will have radically different protein expression in different parts of its body, in different stages of its life cycle, and in different environmental conditions, whereas its genome is fairly constant.

A genetically modified organism, or GMO, is a plant or animal that has had its genetic material altered to exhibit new traits. These "transgenic" organisms can pass their new genes to close, wild relatives, and these cloned genes in wild organisms could tip balances within and between native populations, communities, and ecosystems. It is important to understand potential effects, positive or negative, of GMOs on native plants, animals, and their habitats.

USGS Biological Centers Conducting Genetics Research



Contact any of the USGS science centers at locations indicated on this map for additional information about conservation genetics research. Find contact information at www.usgs.gov.

Authors: Ruth Jacobs, Susan Haig, Sandy Talbot, James Winton, Tim King, Kate Kendall.

Graphic design: Sandie Arbogast.

Photo credits: grizzly bear, © Michael Melford; DNA, National Institute of Health; spotted owl, © Michael Sewell/Visualpursuit.com; Puerto Rican parrot, © Parrots International; Atlantic salmon, © Gilbert van Ryckevorsel; lesser scaup, © Richard Mittleman; whirling disease and lab sampling, USGS Western Fisheries Research Center.