

Genetic Research for Wildlife and Fisheries Management—A Primer

Scientists at the U.S. Geological Survey (USGS) use a range of research approaches to investigate the genetics of native and non-native species that are being managed. This Fact Sheet outlines those approaches and explains the type of information they provide.

What's in a Gene?

Genetic research helps managers “peer under the hood” of a species’ biology by looking into the molecular units that are passed down from generation to generation to build and maintain an organism’s traits. Many traits are determined by deoxyribonucleic acid (DNA), sequences of coded molecules inside each living organism that provide blueprints for how that individual’s cells should develop and grow. DNA does this by producing ribonucleic acid (RNA), which in turn codes for proteins—the building blocks of an organism. This process is called gene expression.

Studying an organism’s genes allows scientists to identify individuals, and compare and contrast differences in populations and species. With sufficient data, scientists can also study the migration and breeding patterns that affect their long-term likelihood of survival. Studying gene expression opens up even more potential research avenues about how a species responds to its environmental conditions.

Many of these research questions would be impossible by surveying wild populations. Furthermore, new techniques offer managers alternative ways to ask research questions that once required large-scale field investigations.

The Importance of Markers

Genetic research examines the DNA and RNA sequences in an individual sample to decode and analyze variation in

their sequences. Researchers look for specific DNA sequences to create **molecular markers** that can be used to distinguish or differentiate cells, individuals, or species. Genetic studies often begin by compiling, comparing, and contrasting molecular markers in a large number of reference samples. Markers can then be used to develop more detailed analyses and address more complex research questions. Genetic markers can even be used to track the life histories of individual animals.

Species Identification

Genetic research can address logistical problems such as how to identify species that are very small, indistinguishable, cryptic, or otherwise hard to detect. Using samples of hair, skin, bone marrow, feathers, feces, or body fluids, geneticists can overcome limitations of traditional sampling methodologies. This is possible because tiny fragments can be used for identification, offering new techniques for monitoring or determining biological inventory.



Non-invasive swabs are used to collect DNA from hard-to-identify, imperiled mussel species.

Genetic Diversity

Genetic diversity is, in essence, the variation of DNA sequences within a species or population. Such variation increases the chances that some individuals may survive stressors that adversely affect a population. High genetic diversity improves a species’ ability to adapt to change, cope with disease, or rebound from environmental disturbances. Once genetic variation is lost from a population,

Genetic Expressions

You’ve probably heard of DNA (deoxyribonucleic acid), but have you heard of these other genetic terms?

Genome. An organism’s complete set of hereditary sequences.

Nuclear DNA. The genetic blueprint for a living organism, found in the nucleus of a cell.

Molecular (DNA) markers. Target sequences that researchers use for analysis. DNA markers can be microsatellites (found on nuclear DNA) or mitochondrial.

Mitochondrial DNA. Remember mitochondria, those powerhouses that help your cells convert oxygen to energy? These contain their own genome, which is passed on with the mitochondria from mother to child.

RNA. Copies of DNA used in actively expressed genes that code for proteins and can vary with different environmental and physiological conditions.

Functional (protein-coding) DNA. DNA that can be linked to a physical trait, such as eye color, by the RNA and proteins it codes for.

“Junk” (non-protein coding) DNA. This general term refers to any DNA sequence with no known gene function.

as is often the case with an imperiled species, it cannot be easily recovered. If diversity becomes too low, species can cross an inbreeding threshold and enter an extinction vortex—a period of

self-reinforcing population decline that makes it difficult for a species to recover. To help managers understand the diversity issues that threatened and endangered species face, geneticists can quantify the amount of diversity. These can focus on an entire species or be used to compare and contrast specific populations.

Staying Fit

A diverse gene pool helps a population adapt to its environment by offering a mix of potential traits for individuals. Traits that are well suited to the environment help organisms survive and pass genes down to future generations. In general, an organism's propensity for survival and reproduction is known as "fitness." Understanding how genes have been passed down through generations provides information that can be used to help manage a wild population. Managing for fitness involves understanding how gene flow influences diversity and affects locally adapted traits that may have developed in some populations. Therefore, it is useful to gain information about how different populations are interbreeding.



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Breeding Patterns

Depending on which type of DNA is sequenced, genetic studies can reveal deep evolutionary relationships using gene trees or more recent breeding patterns. Researchers use **mitochondrial markers** to study ancestry and **phylogenetics**. In contrast, nuclear DNA, which is inherited from both parents and used

to identify specific individuals, allows scientists to study contemporary gene flow. It can be used to look at pedigrees, population interbreeding, hybridization, and genetic differences found in different geographic groups.

Research Capabilities and their Management Applications

- **Functional genetics/transcriptomics.** The sequencing of expressed genes that influence health and adaptation, often produced in response to environmental challenges, such as disease outbreak or climate change.
- **Genetic diversity analysis.** Studies that use molecular markers to quantify diversity, estimate population sizes, learn how genetic material has been passed down, and infer how gene flow influences diversity and fitness.
- **Genetic population structure.** The study of a group of individuals over the landscape to determine related (interbreeding) and non-related groups. This type of analysis can be used to identify genetically-unique groups for conservation measures or to find migration pathways through which genetic material is exchanged.
- **Landscape genetics.** Research that examines how physical features such as oceans, waterfalls, dams, and culverts have influenced genetic variation across landscapes by interpreting movement patterns of individuals in terms of the biological processes that create and maintain them. This aids efforts to manage populations based on connectivity.
- **Molecular marker development.** Techniques used to create new, reliable markers for use in genetic investigations. New markers must be developed in situations where no existing marker offers the appropriate comparative detail needed for an analysis.
- **Microsatellite marker fragment analysis.** An analysis based on short, repeating base pairs (for example, ACTACTACT) of nuclear DNA sequence that are highly variable. These fragments are used to detect hybridization, evaluate pedigrees, identify individuals in order to predict survival rates, and characterize genetic population structure.
- **Mitochondrial DNA sequencing.** A study of sequences from the mitochondrial genome to determine the evolutionary history of a population (ancestral relatedness) through relationships in gene trees. Mitochondrial DNA is usually maternally inherited, meaning all offspring have gene copies matching their mothers.
- **Parentage assignment and pedigree analysis.** Reconstructions of genetic relationships of individuals and their families through time. This information allows researchers to estimate the heritability of traits in captive and wild populations, minimize inbreeding in captive populations, reveal patterns of sexual selection and dispersal, and determine rates of gene flow within and between populations.
- **Phylogenetics.** Studies of ancestry used to create relatedness trees on a geologic time scale and reveal evolutionary relationships between a species and its higher taxonomy (that is, Family, Order, and Class).
- **Phylogeography.** An analysis of breeding and genetic variation patterns in a geographic context that can reveal information about species boundaries and breeding not always detected by conventional taxonomic methodologies.
- **Species identification/DNA barcoding.** Identification of a species, by matching DNA in tissue from a specimen to a reference "barcode" sequence. This technique can also be used to identify prey species based on analysis of gut contents.