Wildlife Services

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FY 2015

Genetic Methods to Manage Livestock-Wildlife Interactions

Contact Information

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Groups Affected By These Problems:

- Health officials
- Livestock producers and farmers
- U.S. citizens
- Veterinarians
- Wildlife and natural resource managers

Major Cooperators:

- Auburn University
- Christopher Newport University
- Colorado State University
- Savannah River Ecology Laboratory
- Tejon Ranch Conservancy
- Texas A&M University
- University of Colorado Boulder
- University of Florida
- University of Georgia
- University of Texas Medical Branch
- U.S. Fish and Wildlife Service
- U.S. Geological Survey

National Wildlife Research Center Scientists Develop Genetic Methods for Wildlife Damage Management

Wildlife Services' (WS) National Wildlife Research Center (NWRC) is the only Federal research organization devoted exclusively to resolving conflicts between people and wildlife through the development of effective, selective, and socially responsible methods, tools, and techniques.

Information about wildlife populations and diseases can be difficult to obtain with traditional sampling techniques. This is especially true for rare or elusive wildlife and emerging diseases. The field of wildlife genetics uses DNA samples collected from tissue, blood, hair, feces, saliva, water and soil to uncover valuable information about animals, their abundance, behavior, and evolution. Genetic analysis includes approaches such as DNA forensics, species abundance and monitoring, kinship/relatedness and gender determination, and species or individual animal identification.

Since 2000, NWRC scientists at the Center's wildlife genetics laboratory have applied genetic expertise to understand the intercontinental movement of pathogens, monitor endangered and invasive species, detect invasive species using environmental DNA found in water, and understand the movement of genes within and among animal populations.

Applying Science & Expertise to Wildlife Challenges

Detecting invasive species through Environmental DNA. — Understanding the distribution of an invasive species and having methods for detecting its spread are critical to wildlife management and control efforts. The Burmese python is a semiaquatic snake that has invaded Florida, where its elusive nature and cryptic coloration make it difficult to detect. A detection method that eliminates the need for direct observations or handling of snakes would make management activities more economical and efficient. Recent studies have shown that it is possible to detect environmental DNA from aquatic animals in bodies of water. Environmental DNA (eDNA) refers to DNA that is shed by an organism into the environment (i.e, water, soil or air). The genetic material could come from shed skin, hair or scales, mucous, urine, and feces.

To assist wildlife managers in Florida in their efforts to remove invasive Burmese pythons, NWRC researchers developed a diagnostic polymerase chain reaction (PCR) test that detects Burmese python DNA in water. Using captive Burmese pythons, researchers verified the PCR test and showed that python DNA can be detected in water for up to 96 hours. Then, in order to field test the method, researchers sampled water from six sites in south Florida. Samples from five sites where Burmese pythons have been observed tested positive for their eDNA. The final site, which had no prior evidence of Burmese pythons, tested negative. This promising new tool is now being used to monitor the distribution of Burmese pythons in Florida.

NWRC researchers are developing a similar method for detecting feral swine eDNA in water. The method will help experts monitor the current distribution of feral swine in the United States.

Sources of Island Rats. — Rodent control on islands to protect nesting seabirds and other threatened wildlife is an important conservation activity. When rats reappear after an eradication attempt, it is important to know whether eradication was incomplete or whether the island was recolonized. Using genetic analyses, NWRC researchers showed that in the case of Congo Cay in the U.S. Virgin Islands and Lehua Island in Hawaii the reemergence of rats likely was due to failed eradication attempts. This finding has led to reevaluations of rat eradication strategies and efforts.

U.S. Avian Influenza Genetics. In 2006 and 2007, approximately 75,000 bird fecal samples were collected from across the United States as part of an interagency avian influenza surveillance effort. NWRC researchers isolated and amplified 160 hemagglutinin (HA) DNA sequences from these samples. These sequences represented a broad diversity of HA subtypes with 13 of the possible 16 subtypes represented. NWRC used this and other data from around the world to generate information about relationships among and between HA subtypes of avian influenza virus (AIV). The researchers detected evidence of intercontinental exchange within some subtypes and a broad diversity of lineages unique to the United States. Through this extensive genetic surveillance effort some subtypes were detected in areas where they had not been

previously documented. Such information is useful because it identifies areas of high AIV diversity, which may be more likely to produce new outbreaks of high or low pathogenic AIV.

Genetic tools for predator management. — NWRC researchers use DNA forensics to identify predator species involved in depredation incidents of livestock, endangered and threatened species, and species of concern. For instance, DNA samples are collected from blood and saliva at bite wounds on livestock carcasses and analyzed to determine the species involved in predation incidents. By knowing which predator species was involved, managers can select the most appropriate methods for preventing future damage. Similar techniques are used for identifying predators of Greater sage grouse eggs. NWRC researchers analyze DNA collected from traces of saliva left on depredated eggshells. Understanding the impacts of predators on declining species, such as the Greater sage grouse, is critical to their successful management.

NWRC researchers have also developed a genetic method for identifying, monitoring, and estimating endangered Mexican wolf populations in Arizona. Instead of capturing, marking, and releasing animals, the method identifies individuals using genetic material from fecal samples. This allows the U.S. Fish and Wildlife Service, state management agencies, and Tribes to monitor recovery populations without having to see or handle animals. The method can distinguish between Mexican wolf, coyote and domestic dog feces, as well as identify individual Mexican wolves. In field tests, population estimates based on the new method closely matched counts of collared and tracked individuals indicating that the approach was an effective way of monitoring this endangered species.

Genetic tools for managing invasive feral swine. — Feral swine populations in the United States have increased dramatically during the past 30 years resulting in extensive damage to agriculture and native plants and animals. New methods are needed for measuring feral swine impacts to agricultural crops and native species such as alligators, sea turtles, turkey, and quail. NWRC geneticists are developing methods to detect and identify animal and plant DNA consumed by feral swine and found in their fecal samples. This will help managers better understand the impacts of feral swine on plant and animal species (particularly endangered and threatened species) and when those impacts occur. NWRC researchers are also using fecal samples to identify individual feral swine and estimate feral swine population sizes and distributions. This approach allows managers to develop effective management plans for this invasive species.

Selected Publications:

Herman, J.A., A.J. Piaggio, N.D. Halbert, J.C. Rhyan, M.D. Salman. 2014 Genetic analysis of a bison (Bison bison) herd derived from the Yellowstone National Park population. Wildlife Biology 20:335-343.

Pedersen, K., C.R. Quance, S. Robbe-Austerman, A.J. Piaggio, S.N. Bevins, S.M. Goldstein, W.D. Gaston, and T.J. DeLiberto. 2014. Identification of Brucella suis from feral swine in selected states in the USA. Journal of Wildlife Diseases 50(2):171-179. doi:10.7589/2013-09-235.

Piaggio, A.J., R.M. Engeman, M.W. Hopken, J.S. Humphrey, K.L. Keacher, W.E. Bruce, and M.L. Avery. 2014. Detecting an elusive invasive species: a diagnostic PCR to detect Burmese python in Florida waters and an assessment of persistence of environmental DNA. Molecular Ecology Resources, 14:374-380. doi:10.1111/1755-0998.12180.

Piaggio, A.J., B.A. Coghlan, A.E. Miscampbell, W.M. Arjo, D.B. Ransome, and C.E. Ritland. 2013. Molecular phylogeny of an ancient rodent family (Aplodontiidae). Journal of Mammalogy 94:529-543. doi: 10.1644/12-MAMM-A-016.1.

Root, J.J., M.W. Hopken, T. Gidlewski, A.J. Piaggio. 2013. Cottontail rabbit papillomavirus infection in a desert cottontail (Sylvilagus audubonii) from Colorado, USA. Journal of Wildlife Diseases 49(4):1060-1062. doi: 10.7589/2013-02-033.

Major Research Accomplishments:

- WS geneticists developed a method to detect invasive Burmese python DNA found in water.
- WS genetics research showed that the presence of rats on Congo Cay in the U.S. Virgin Islands and Lehua Island in Hawaii was likely due to failed eradication attempts.
- WS researchers analyzed DNA from 75,000 wild bird fecal samples to identify areas within the United States with high avian influenza virus diversity. These areas may be more likely to produce new outbreaks of high or low pathogenic avian influenza virus.
- WS researchers developed a method to identify predators of Greater sage grouse eggs by collecting DNA from traces of saliva left on depredated eggshells.
- WS geneticists developed methods for estimating population sizes of Mexican wolves and feral swine using DNA found in the species' fecal samples.
- WS geneticists are developing methods to detect and identify animal and plant DNA found in feral swine fecal samples.

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