



Genetic Tools for Wildlife Management

A NEW TWS WORKING GROUP FOCUSES ON MOLECULAR ECOLOGY

By Emily Latch, Rachel Crowhurst, Sara Oyler-McCance and Stacie J. Robinson



Credit: Troye Fox/UWM

Emily Latch, Ph.D., is Associate Professor of Wildlife Genetics at the University of Wisconsin-Milwaukee and President-Elect of The Wildlife Society's Molecular Ecology Working Group.

Granted interim status in November, 2013, The Wildlife Society's (TWS) Molecular Ecology Working Group aims to promote scientific advancement by applying molecular techniques to wildlife ecology, management, and conservation. The working group—composed of scientists from diverse backgrounds—met for the first time in Pittsburgh at the TWS Annual Conference held in October. Our overarching goal is to enhance awareness of molecular ecology and genetic applications to wildlife biology and act as an informational and networking resource. During the group's interim status, which runs for three years, we intend to focus on a broad scope of molecular ecology that is applicable to wildlife including genetic and genomic methods, conservation genetics, non-invasive genetic population monitoring, landscape genetics, evolutionary genetics, and molecular forensics.

Molecular Technologies in Wildlife

Molecular methods have facilitated widespread advances in wildlife ecology and conservation, and rapid technological developments continue to expand possible applications to these disciplines. However, much work needs to be done to effectively

apply these innovative technologies to non-model wildlife species and to develop rigorous approaches for collecting, analyzing, and communicating data. Only with this knowledge, will our profession be able to take advantage of the diverse ways in which molecular ecology can support wildlife conservation and management.

One of the important advances that has opened the door for using these technologies in our field is known as the polymerase chain reaction (PCR)—a laboratory protocol that creates multiple copies of specific DNA sequences from small amounts of sample. Rather than using lethal sampling to obtain DNA from study populations, PCR-based approaches have made possible low-impact, non-invasive sampling methods that can be used to study elusive or protected species. For example, DNA extracted from feathers, scat, or hair left by the animal has facilitated important monitoring programs that help assess population recovery. This technology also has important forensic applications that aid efforts to combat poaching and the illegal wildlife trade.

In addition, advances in DNA sequencing technology and genomics allow biologists to examine a greater portion of a species' genome. Researchers already are using this genetic information to identify markers under natural selection, investigate the effects of management on fitness, or simply increase the number of markers available for poorly studied species. For example, DNA metabarcoding studies use genomic technologies to facilitate high-throughput collection of biodiversity data, often using DNA extracted from an environmental sample (eDNA) such as soil or water. These types of studies also have allowed multi-taxa biodiversity surveys from soil samples and gut contents, illuminated changes

Jennifer Fike, a geneticist at the U.S. Geological Survey's Molecular Ecology Laboratory in Fort Collins, loads samples on a DNA sequencer to quantify genetic variation within and among populations of sage grouse. Fike hopes to address questions related to the evolutionary history of the species and delineating appropriate units for conservation and management.



Credit: Dean Biggins



in microbial communities associated with environmental changes and revealed dietary preferences in various species using feces as a source of DNA. eDNA techniques also show great promise for monitoring rare species when observational detection is difficult and for tracking invasive species and diseases as soon as they begin to colonize new areas. With such innovative genetic approaches, molecular ecologists can enhance our ability to answer previously intractable ecological questions and address traditional research and management issues in an efficient and cost-effective way.

Despite the technological advances in molecular genetic analysis, the field of molecular ecology as applied to wildlife management faces numerous challenges. Molecular tools provide an exciting array of innovative technologies; however, there may be risks associated with employing these tools in the field before they are completely vetted by the wildlife community. Understanding the strengths and limitations of new genetic technologies is paramount to their use in wildlife management. Ensuring that data are of high quality and appropriate for the specific question is key, as is drawing from disparate fields in meaningful ways to maximize the value of genetic data in wildlife biology, landscape and community ecology, statistics, bioinformatics and functional genomics. Additionally, although clearly communicating genetic methods and results to managers and the public can be difficult, it is vital to effective science and policy implementation.

Without question, rapid advances in DNA sequencing technology as well as computational analysis have provided a dizzying array of new genomic tools that allow us to begin understanding how and why genetic variation is distributed across the landscape and the functional significance of that variation. This type of data provides more powerful ways to assess taxonomy, gene flow, hybridization, diets, demography, and even local adaptation of species. These advances in molecular technologies have been driven by research on the human genome; therefore, applying them to non-model wildlife species may seem rather daunting. Downstream data analysis pipelines and analytical approaches will need to be developed to make progress. But the promise of answering questions about genetic components of fitness and selection will likely provide the impetus for wildlife geneticists to develop

the necessary analytical and computational tools to overcome those obstacles.

Working Group Goals

The group is now actively recruiting members who want to promote scientific advancement by applying molecular techniques to wildlife ecology, management, and conservation. Coming together as a working group allows us to tap into our colleagues' expertise and address these challenges collectively. By creating inclusive networking and learning opportunities, we also aim to be an informational resource to the larger membership of TWS—from helping wildlife management agencies identify genetic tools for accomplishing management objectives to helping wildlife geneticists stay current in a rapidly advancing field. We will use venues like TWS conferences to share groundbreaking science through symposia, offer training in cutting-edge techniques through workshops, and provide networking and information-sharing opportunities through subunit meetings.

At our inaugural meeting, we discussed development of our charter and many exciting ways that we can contribute to the TWS membership at large. We are eager to act on these ideas and to continue building a network of people who are using and/or are interested in molecular methods in wildlife ecology. Our most immediate task is to secure members to transition from interim to official status. TWS members may add the working group through their [Member Portal](#). ■



To learn more about the Molecular Ecology Working Group, contact Stacie Robinson, President, at Stacie.Robinson@noaa.gov.

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