

Department of Natural Resources SCI-MIC Supported Research Projects 2021 Progress Reports

Project Title - Advancing Genetic Analysis Capacity to Support Wildlife Disease and Population Management

Project Background - The DNR - Wildlife Division proposes to purchase an Illumina MiniSeq Sequencing System to facilitate high-throughput genetic analyses for wildlife population health and management. This machine implements recent technological advances in genomic science and will allow for the expansion of capabilities currently available through the Wildlife Health Section's Genetic Program. For example, this machine will allow us to address needs for large-scale population surveys and facilitate genomic sequencing approaches to better address host-pathogen interactions. The MiniSeq harnesses cutting-edge technology to allow for many animals to be analyzed at a single time, both driving down costs for personnel time and consumables while producing high-quality digitized data readily available for analysis.

Management Need and Application:

Wildlife Disease Assessment

The DNR has received funding through the Michigan State University and Michigan DNR joint Wildlife Disease Initiative (\$311,697) and the Fish and Wildlife Multi-state Conservation Grants Program (\$337,757) to develop standardized, high-throughput genetic resources to inform white-tailed deer population and disease management. One product of this work will be a genomic panel designed specifically for wildlife managers to identify genetic variation in white-tailed deer relative to disease status. The panel will be faster, more universal, provide more information, and be less expensive than current methods being employed.

Once the panel is available, the DNR will be able to use the MiniSeq to gather genetic data to assess the susceptibility of deer to Chronic Wasting Disease (CWD), determine whether CWD or tuberculosis (Tb) positive deer are of local origin, resolve relationships among diseased animals, and determine how landscape features impact population connectivity and disease spread. These data could help inform decisions on several important management issues including: 1) delineation of deer management units to better align with disease presence and potential spread over the local landscape; 2) identifying harvest regulations that could impact spread or prevalence of disease; 3) planning for long-term disease surveillance to align with the genetic potential for deer to harbor the disease without apparent symptoms; and 4) allocation of local population control augmentation efforts to maximize the potential to limit spread of disease.

Black Bear Population Monitoring

The Wildlife Division's black bear program has begun a project that would benefit from the MiniSeq for estimation of black bear populations in the Upper Peninsula (UP). Hunting is the primary tool for management of bear populations in Michigan and a black bear population estimate is critical to ensure the DNR can make appropriate harvest quota recommendations and evaluate the effects of previous harvests on the UP-bear population.

The DNR's current bear population estimation technique relies on a statistical modeling framework called statistical catch-at-age analysis (SCAA), which provides detailed, annual estimates of the bear population in the UP and northern Lower Peninsula (NLP). The SCAA models combine harvest composition and effort data provided by hunters to model changes in the bear population over time, scaling the population abundance estimate with information from periodic independent population estimates. Past research has indicated that without an independent population estimate every 5 years, the UP SCAA model would overestimate the bear population, which could affect the quota-setting process and potentially the bear population. Since 1990, the DNR has used a mark-recapture technique, using the antibiotic tetracycline, to estimate the UP-bear population. Due to changes in federal regulatory guidelines, the DNR can no longer conduct the tetracycline survey and has begun testing a replacement technique called close-kin mark-recapture (CKMR). The CKMR technique will allow the DNR to estimate the bear population in the UP based on genetic identification of related individuals in the bear harvest. CKMR shows promise but continued use of CKMR will be dependent on a MiniSeq platform. Using the CKMR technique is estimated to save the DNR at least 2,000 hours of staff time in survey years and provide estimates 1.5 years earlier than with the tetracycline survey. If successful, the DNR could also use the CKMR technique in the northern Lower Peninsula, replacing the current hair snare genetic mark-recapture survey and saving an additional 3,000 hours of staff time per survey year. In both cases, the DNR would use the CKMR-based population estimate as input for the SCAA models.

The MiniSeq platform would allow for the development of similar panels for other managed wildlife species as being done for deer and bear to assist the Department with high quality genetic data to inform management decisions.

Progress 2021 – Genomic data was obtained from white-tailed deer across 17 partnering states. This data is being provided to a postdoctoral fellow, hired to begin in 2022, to design and test the genomic panel for wildlife managers.

Objectives, funding, and external university researcher contracts were put into place in 2021 for the black bear genomic panel. Genetic specialists at Michigan Technological University have been selected to create the CKMR genetic panel which is estimated to be completed in late 2022. Sampling was also done through hunter harvest which will be used for the first survey.

Partners - DNR and SCI-MIC.

Timeline and Budget - Targeted funding request from SCI-MIC to cover the purchase of the MiniSeq is approximately \$49,500. The deer and black bear genomic panels necessitating a MiniSeq are estimated to be completed by early FY2023.
