

**Department of Natural Resources  
SCI-MIC Supported Research Projects  
2020 Progress Reports**

---

**ADVANCING GENETIC ANALYSIS CAPACITY OF MICHIGAN DNR TO SUPPORT WILDLIFE DISEASE AND POPULATION MANAGEMENT**

**BACKGROUND:** The Michigan Department of Natural Resources Wildlife Division proposes to purchase an Illumina MiniSeq Sequencing System (MiniSeq) 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. For example, this machine will allow us to address needs for large-scale surveys and will facilitate genomic sequencing approaches to better address host-pathogen interactions. This machine 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 (\$233,697) and the Fish and Wildlife Multi-state Conservation Grants Program (\$143,000) for the development of a standardized, high-throughput genetic resource to inform white-tailed deer population and disease management. The end-product of this work will include 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 for spread in 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 is proposing a project that could benefit from the MiniSeq for estimation of black bear populations in the Upper Peninsula (UP). Most Michigan black bears are found in the UP, and they have important biological, social, and economic impacts. Hunting is the primary tool for management of bear populations in Michigan. 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. A sound population estimate helps ensure bear populations remain at levels that provide sustainable harvest, minimize nuisance issues, and maintain a positive public perception of bears.

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 about 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 recent changes in federal regulatory guidelines, the DNR can no longer conduct the tetracycline survey and is researching a replacement technique. The newly developed technique called close-kin mark-recapture (CKMR) shows promise, but the proposed methodology is dependent on a MiniSeq platform. The CKMR technique would allow the DNR to estimate the bear population in the UP based on genetic identification of parent-offspring pairs in the bear harvest. Using the CKMR technique could save the DNR at least 2,000 hours of staff time per survey year over the tetracycline survey and would 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 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 proposed for bear to assist the Department with high quality genetic data to inform management decisions.

*Progress 2020* - Because of the substantial cost of the MiniSeq (see Timeline and Budget below), in 2020 SCI-MIC (Joseph Konwinski) prepared an application for additional funding through the Glassen Foundation. Glassen Foundation declined to fund the MiniSeq due to the uncertainties involved with the ongoing pandemic and the conclusion that their limited resources are best aligned with other initiatives.

*Partners:* DNR and SCI-MIC.

*Timeline and Budget:* Targeted funding request from SCI-MIC to cover the purchase of the MiniSeq is \$49,500. The genomic panel necessary to use the MiniSeq for the deer CWD project and funds to initiate the bear CKRM project will not be available until at least FY2022. Initial results from the deer CWD project would be available beginning no later than FY2023 and follow-up results on new requests would be available thereafter on a much shorter, as-needed timeline. The exact timeline of the bear CKMR project has not been determined, however; if the MiniSeq was purchased in FY2023, final results would likely be available by FY2025.

---