

Nova Scotia Habitat Conservation Fund

Black bear population structure and distribution in relation to habitat in Nova Scotia.

May 1, 2017 to 30 April 2018

Submitted by Don Stewart and S. Bondrup-Nielsen

This study of Black Bears (*Ursus americanus*) in Nova Scotia builds on previous research which accomplished the following: 1. A thorough collection of the most relevant publications on black bears in northeastern North America, 2. A summarization of all the data collected by DNR on black bears, and 3. Optimization of the molecular genetic techniques to identify individuals and determine genetic relationships among individuals using microsatellite markers. 4. Collected bi-monthly hair samples from the study site of 67 scent stations. 5. Obtained hair/teeth samples of bears harvested across the province for microsatellite analysis.

Here we report on the data collected during the summer of 2017.

Project Goals:

Goals:

- provide information on bear movement patterns, habitat requirements, as well as population sub-structuring in Nova Scotia. Ultimately, this will help in management strategy development and human-bear conflict resolution.
- Analyze molecular genetics of black bears using teeth (extracting genetic material from the tissue attached to the teeth) from all regions in Nova Scotia through collaboration with NSDNR, NS Federation of Anglers and Hunters, and the Trappers Association
- Establish up to 3 sampling sites with approximately 50 scented hair snag stations each to collect and analyze molecular genetics of black bears based on hair from black bears in these different regions of NS.

Results

A research assistant was hired to develop DNA extraction protocols for black bear hair follicles in Don Stewart's lab at Acadia University. Once successful protocols were made, DNA was extracted from bear hair samples collected in 2015 from the Kings county study site. The research assistant then worked to optimize PCRs for eight microsatellite regions known to be useful in black bear population studies (G1A, G1D, G10B, G10C, G10L, G10M, G10P, and G10X; Robinson et al. 2009), and PCR products were sent to McGill University and Genome Quebec Innovation Centre to be scored.

A master's student was hired in May 2017 to conduct field and laboratory work for this project. She took the Molecular Markers course at Acadia University in June 2017 to learn necessary laboratory skills. With these skills, she helped process samples from 2015, and also

learned how to apply PCR to these DNA samples to determine the sex of the individual. Upon analysis of results from the 2015 samples, it was found that there was very little reappearance of the same individual bears at the study site. Because of this, it was concluded that a study site with a higher density of hair snags would be beneficial to help aid in recapture events. Where the original study site had hair snags roughly every 1km, it was decided that a portion of the study site would be used to increase the hair snag density to be roughly one every 0.5km. In the summer of 2017, the selected section went from having 20 hair snags to 58 (Figure 1). These hair snags were checked for hair and rebaited every two weeks from June to September 2017. A total of 94 hair samples were collected in this time frame. DNA extraction was performed on the hair follicles of these samples (>10 follicles when possible). These DNA samples were sent to the Natural Resources DNA Profiling and Forensic Centre at Trent University to undergo PCRs. There, 16 microsatellite regions were amplified per sample, increasing our ability to identify individuals and detect genetic patterns.

Robinson, S. J., Waits, L. P. & Martin, I. D. Estimating abundance of American black bears using DNA-based capture-mark-recapture models. *Ursus* **20**, 1–11 (2009).

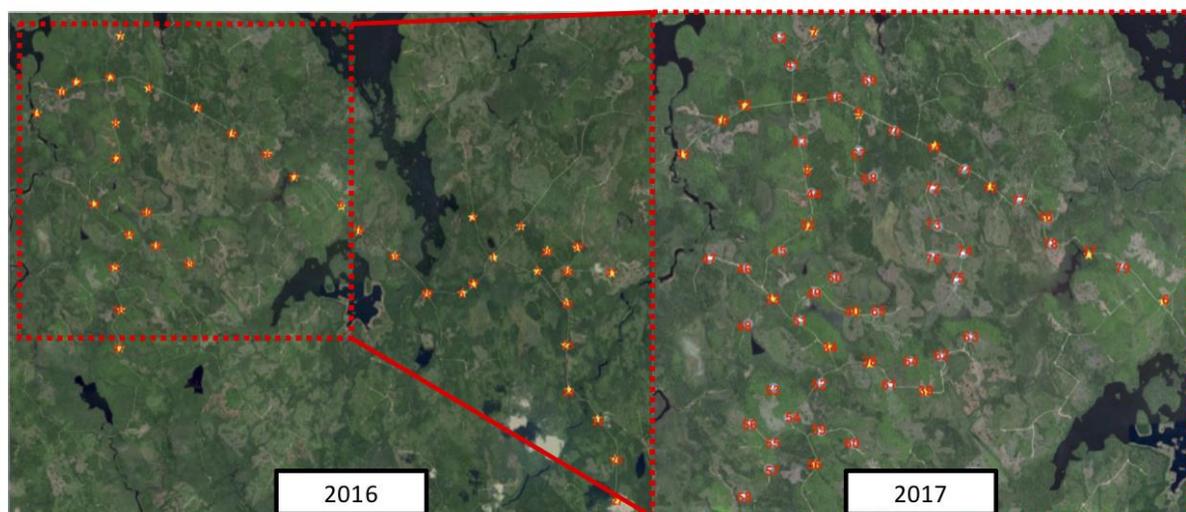


Figure 1: Map showing the Kings county study site from summer 2016 compared to summer 2017. Hair snag density was increased from one every ~1km to one every 0.5km

