



INDICATOR: AMOUNT OF GENETIC VARIATION, GENETIC COMPOSITION AND SPATIAL STRUCTURE OF SELECTED SPECIES

STRATEGIC DIRECTION: Enhance Resilience

TARGET: N/A

THEME: State of Ecosystems and Species – Genetic Diversity

Background Information:

Changing land use and habitat loss increases fragmentation and isolation of populations on the landscape, which in turn reduces population size. Reductions in population size often lead to a loss of genetic diversity and an increase in inbreeding (Frankham et al. 2002). This may result in a reduction in survival and reproductive fitness.

The American Black Bear is an ecologically important species that is adapted to a range of environments across North America. Genetic studies of Black Bears have detected differentiation between populations on moderate geographic scales, despite the ability of bears to travel across considerable distances (e.g., Warrillow et al. 2001; Dixon et al. 2006; Onorato et al. 2007; Pelletier et al. 2011; Puckett et al. 2014). This has largely been attributed to population fragmentation resulting from human influences and activities such as transportation corridors, resource extraction, and urban and industrial development (Scheik and McCown 2014).

Ontario is home to a large number of Black Bears (95,000 individuals – Obbard, unpublished data) that occur within a region of primarily continuous boreal and mixed deciduous forest habitat. No obvious barriers to Black Bear movement exist in the province, except in the southern region, where human density and landscape fragmentation are high (Statistics Canada 2011). In light of increasing human populations, development and landscape fragmentation in the province, and particularly in southern Ontario, it is important to assess Black Bear genetic diversity throughout the province to understand how these growing human influences may affect the genetic diversity and viability of Ontario Black Bears.

This indicator assesses Black Bear genetic diversity and genetic differentiation at the provincial scale, providing an indication of the genetic health of the species in Ontario.

Data Analysis:

Information on the genetic differentiation and genetic diversity of Black Bears in Ontario is based on results detailed in Pelletier et al. (2011 and 2012). Genetic data were obtained from hair collected via baited barbed wire hair traps placed throughout Ontario between 1997 and 2012, as well as from samples obtained opportunistically (livetrapping, hunting, or road kills). A total of 2839 individual Black Bears were sampled from 61 sites throughout Ontario. This initiative was part of the Ontario's Enhanced Black Bear Management Program, whose goal is to monitor the number of Black Bears in the province over time to support Ontario's Enhanced Black Bear management Framework.

Following collection of hair samples, DNA was extracted, amplified and sequenced to obtain individual genotypes and sequences of maternal DNA. As such, individual genotypes provided information about



the current genetic diversity of Black Bears in the province. Diversity was assessed by i) looking at the differences between the paternal and maternal genetic information within each individual (“heterozygosity”), and ii) looking at the overall number of potential genetic types (or, “alleles”). Both of these measures were averaged across all individuals in the population, providing an indication of overall genetic diversity.

Sequences of maternal DNA (“haplotypes”) provided information on the historical genetic diversity of Black Bear populations in Ontario. Haplotypic diversity (number of haplotypes) was measured for each sampling site as an indication of historical genetic diversity. Analyses were conducted on a subset of individuals ($n = 660$).

Finally, genetic differentiation was examined using a measure called F_{ST} , where 1 indicates complete differentiation and 0 indicates no differentiation between two populations. F_{ST} was calculated among all possible pairs of identified genetic groups. These genetic groups were delineated based on the geographical distribution of similar haplotypes and similar alleles.

Results:

Trend: Baseline **Data Confidence:** Medium **Geographic Extent:** Provincial

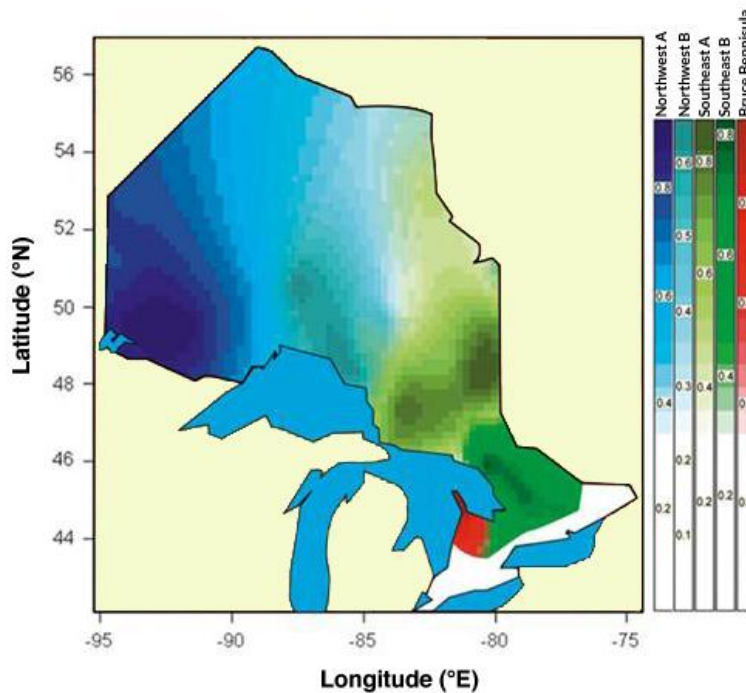


Figure 1. Map representing the 3 genetic groups of American Black Bears identified in Ontario. Blue: northwestern regional population; Green: southeastern regional population; Red: Bruce Peninsula population. The scale on the right indicates the probability that an individual would genetically correspond to the population it was sampled in. The two shades of blue and green respectively indicate the subgroups identified within the northwestern and southeastern populations (Source: Pelletier et al. 2012).

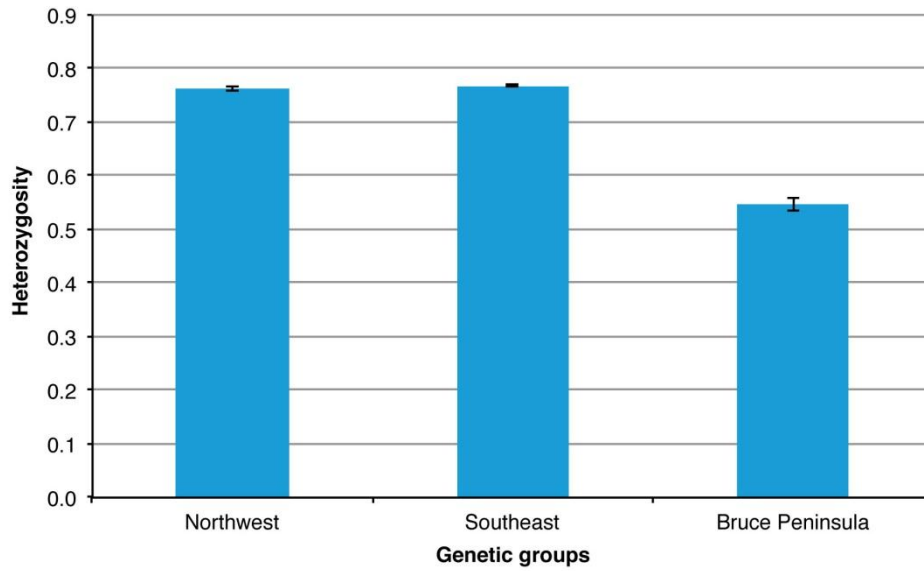


Figure 2. Heterozygosity level (scale 0 to 1) for each American Black Bear genetic group identified in Ontario ($n = 2839$ individuals; error bars represent Standard Deviation) (Source: Pelletier et al. 2012).

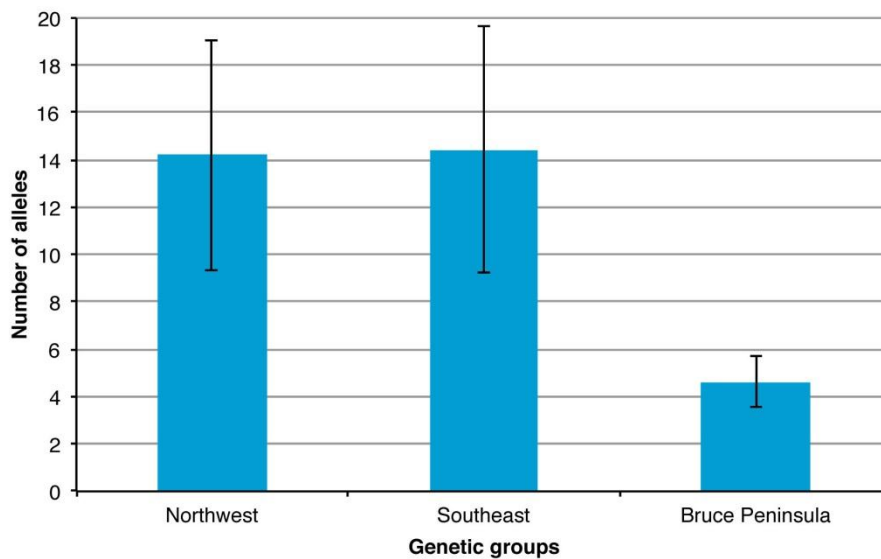


Figure 3. Number of different alleles for each American Black Bear genetic group identified in Ontario ($n = 2839$ individuals; error bars represent Standard Deviation) (Source: Pelletier et al. 2012).

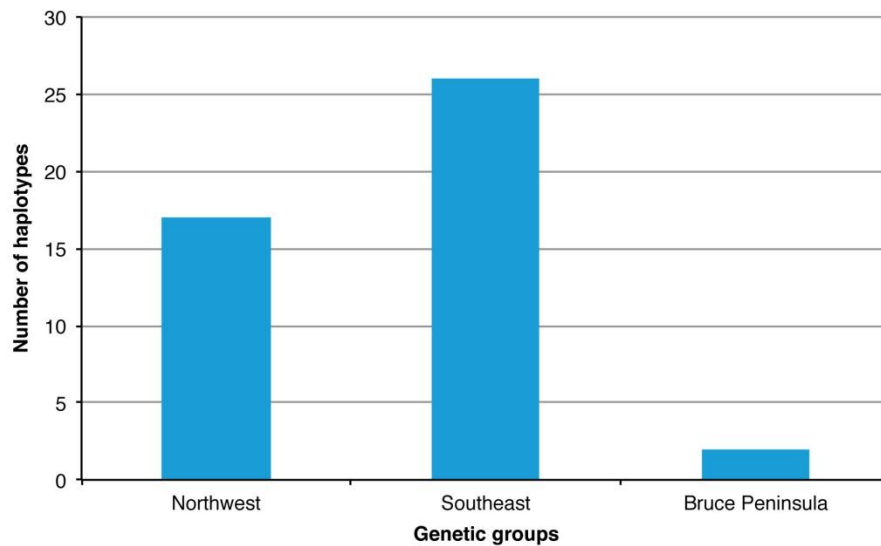


Figure 4. Number of haplotypes present within each American Black Bear genetic group in Ontario. Note: Analyses were conducted on a subset of individuals: $n = 230, 392,$ and 38 for the northwestern, southeastern, and Bruce Peninsula populations, respectively (Source: Pelletier et al. 2011).

Status:

- Three distinct genetic groups of Black Bears were identified in Ontario: the northwestern regional population, the southeastern regional population, and the Bruce Peninsula population.
- While overall genetic differentiation among the three groups was generally low, the Bruce Peninsula population showed a level of differentiation with the larger northwestern and southeastern populations ($F_{ST} = 0.13$ and 0.12 , respectively) more than 10 times as high as the level detected between the northwestern and southeastern populations ($F_{ST} = 0.01$). This indicates a lack of Black Bear movement between the Bruce Peninsula and the other regions of Ontario.
- The northwestern and southeastern Ontario Black Bear populations show high levels of historical (# of haplotypes = 17 and 26, respectively) and contemporary genetic diversity (heterozygosity = 0.76 and 0.77, respectively; # of alleles = 14.2 and 14.4, respectively).
- In contrast, the Bruce Peninsula population shows reduced historical (# of haplotypes = 2) and contemporary genetic diversity (heterozygosity = 0.55 and # of alleles = 4.6), likely related to geographic isolation resulting from habitat fragmentation. This population may be at risk of inbreeding depression and reduced population viability.

Links:

Related Targets: N/A

Related Themes: N/A

Web Links:

Ontario Black Bear Density Map <https://www.ontario.ca/document/bear-density-map>



References:

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Citation

Ontario Biodiversity Council. 2015. *State of Ontario's Biodiversity* [web application]. Ontario Biodiversity Council, Peterborough, Ontario. [Available at: <http://ontariobiodiversitycouncil.ca/sobr> (Date Accessed: May 19, 2015)].