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Appendix 2. Population genetic summary statistics for caribou genetic samples collected in the Sahtú region and Nahanni National Park Reserve of the Northwest Territories, Canada from 2012 to 2014.

Table A2.1. Summary of genetic diversity estimates for each microsatellite loci including allelic size range in base pairs, number of alleles (N_A), observed (H_O) and expected (H_E) heterozygosity, F_{IS} estimates and standard errors (SE) for caribou genetic data from the Northwest Territories, Canada. The original references for each loci are provided.

Microsatellite Locus	Allelic Range	N_A	H_O	SE	H_E	SE	F_{IS}	Source
BM848	356-386	16	0.819	0.0234	0.864	0.0150	0.053	Bishop et al. 1994
BM888	162-260	51	0.882	0.0041	0.865	0.0071	-0.019	Bishop et al. 1994
Map2C	89-115	16	0.824	0.0113	0.850	0.0232	0.030	Moore et al. 1992
RT5	88-116	15	0.768	0.0283	0.816	0.0373	0.058	McLoughlin et al. 2004 [†] , Wilson et al. 1997 [‡]
RT6	88-112	14	0.837	0.0122	0.833	0.0245	-0.005	Wilson et al. 1997
RT7	210-232	12	0.746	0.0242	0.772	0.0109	0.033	Wilson et al. 1997
RT9	100-128	15	0.840	0.0257	0.859	0.0077	0.022	Wilson et al. 1997
RT24	205-227	24	0.780	0.0497	0.786	0.0707	0.008	Wilson et al. 1997
RT30	183-211	19	0.829	0.0130	0.862	0.0242	0.039	Wilson et al. 1997

[†]Reverse primer

[‡]Forward primer

Table A2.2. Pairwise F_{ST} values based on microsatellites for the three major groups identified by structure analysis (below diagonal) and pairwise P values (above diagonal).

F_{ST}	Barren-ground	Boreal woodland	Mountain
Barren-ground	-	0.0000	0.0000
Boreal woodland	0.040	-	0.0000
Mountain	0.011	0.041	-

Table A2.3. Pairwise R_{ST} values based on microsatellites for the three major groups identified by structure analysis (below diagonal) and pairwise P values (above diagonal).

R_{ST}	Barren-ground	Boreal woodland	Mountain
Barren-ground	-	0.0303	0.0028
Boreal woodland	0.030	-	0.0269
Mountain	0.003	0.027	-

Table A2.4. Pairwise Φ_{ST} values based on mtDNA for the three major groups identified by structure analysis (below diagonal) and pairwise P values (above diagonal).

Φ_{ST}	Barren-ground	Boreal woodland	Mountain
Barren-ground	-	0.0000	0.0000
Boreal woodland	0.079	-	0.0000
Mountain	0.138	0.173	-

Table A2.5. Analysis of molecular variance (AMOVA) based on mtDNA haplotype data for the three groups identified by structure analysis. F_{ST} represents the variance within groups relative to the total variance.

Source of variation	d.f.	Variance components	% Variation	F	P
Among groups	2	0.63	13.9		
Within groups	334	3.91	86.1	$F_{ST} = 0.139$	0.0000

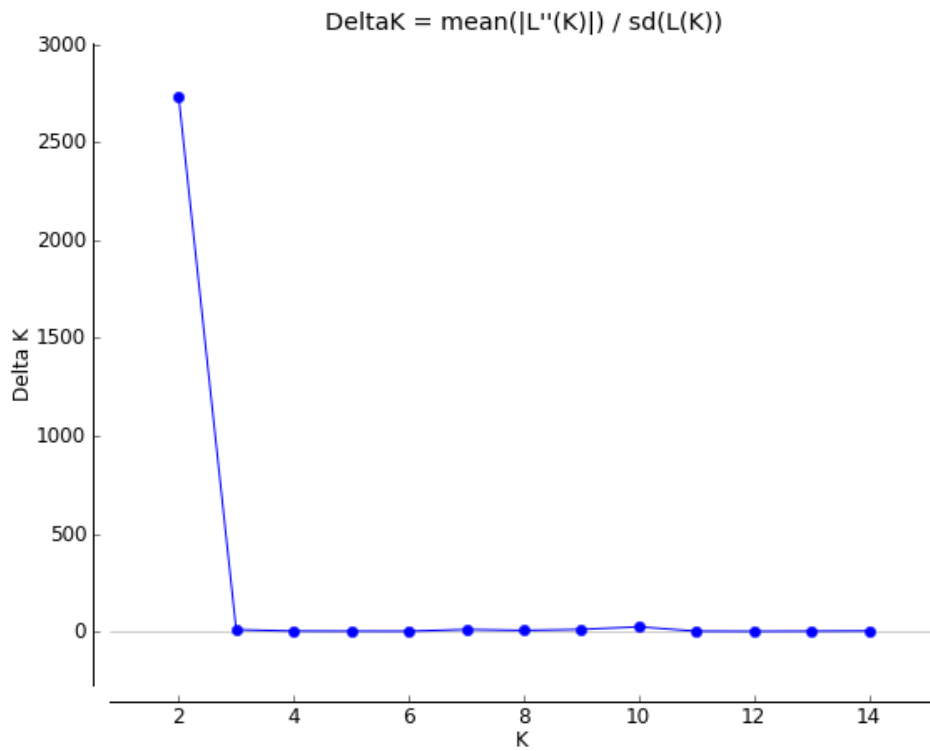


Figure A2.1. Most likely number of population clusters ($K = 2$) identified by the Evanno method (Evanno et al. 2005) using Structure Harvester v0.6.94 (Earl and vonHoldt 2012).

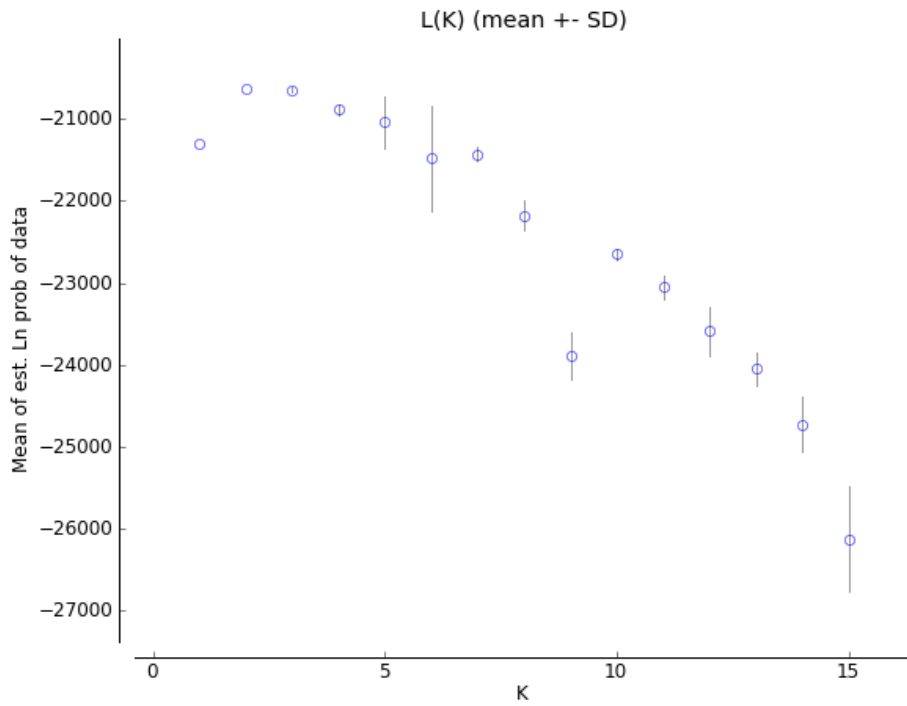


Figure A2.2. Mean likelihood for each K plus standard deviation as retrieved from Structure Harvester v0.6.94 (Earl and vonHoldt 2012).

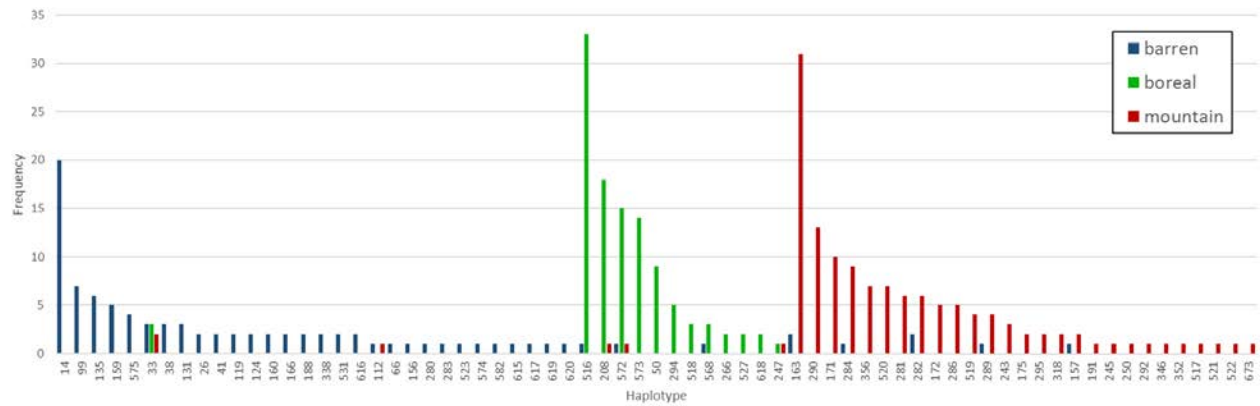


Figure A2.3. Frequency of mtDNA haplotypes for the three major groups identified by structure analysis: 1) barren-ground (blue), 2) boreal woodland (green), and 3) mountain (red). Three haplotypes belong to the North American haplogroup lineage (NAL): 50, 522 and 523, all other haplotypes belong to the Beringian-Eurasian haplogroup lineage (BEL).

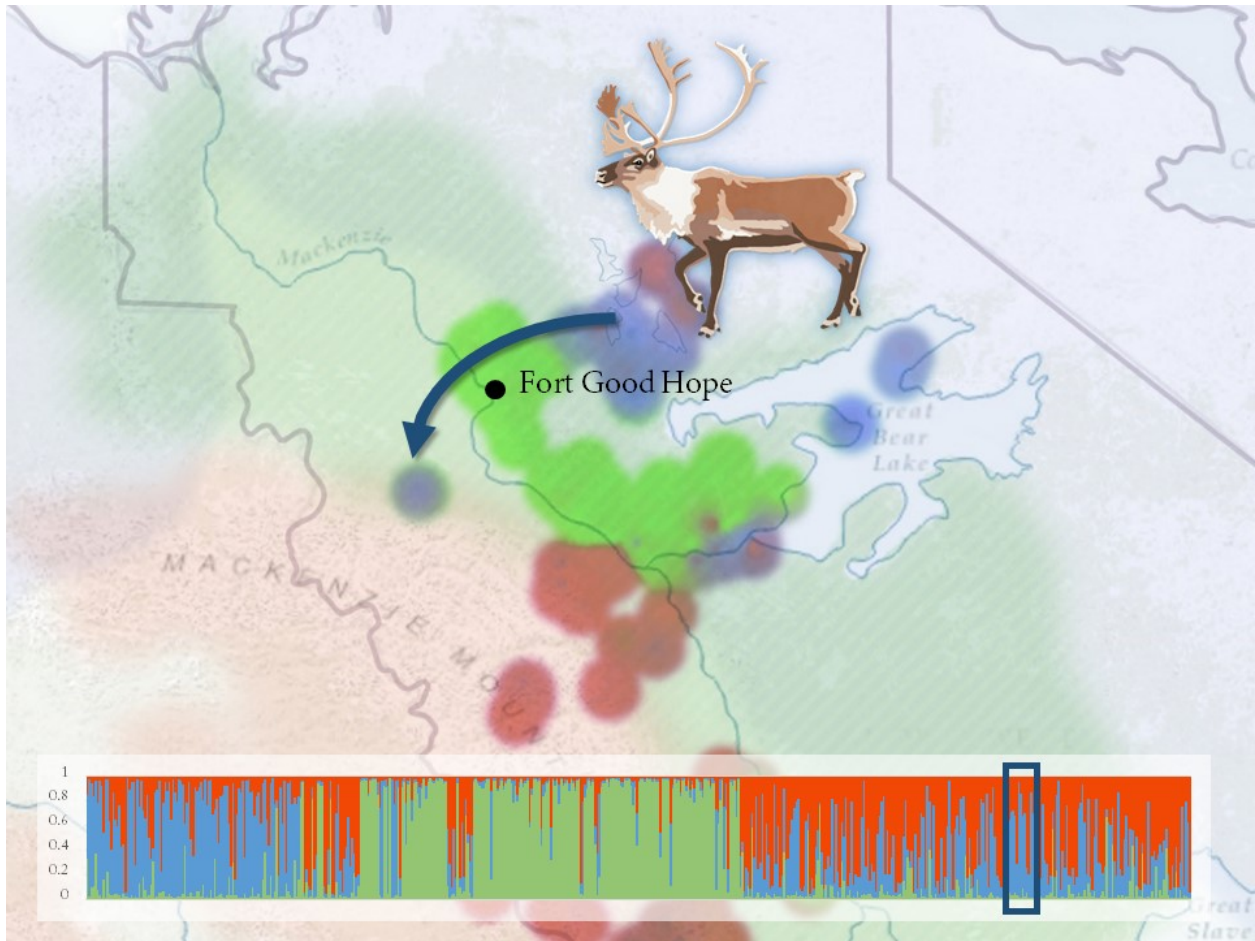


Figure A2.4. During a focus group meeting, Gabe Kochon of Fort Good Hope, Northwest Territories, Canada, described a historic event where a large herd of caribou crossed the Dehcho (Mackenzie River) and headed into the foothills of the mountains many years ago. We collected samples from the area identified by the arrow during our 2 April 2014 helicopter survey and identified 9 individual caribou from the site in subsequent genetic analysis. Structure analysis of these samples found a high probability of assignment (average 0.73) to the barren-ground caribou cluster (shown as blue in bottom bar and represented as blue on the map). Genetic structure analysis identified $k=3$ clusters of 1) barren-ground (blue) 2) boreal woodland (green) and 3) mountain (red).

LITERATURE CITED

- Bishop, M. D., S. M. Kappes, J. W. Keele, R. T. Stone, S. Sunden, G. A. Hawkins, S. S. Toldo, R. Fries, M. D. Grosz, and J. Yoo. 1994. A genetic linkage map for cattle. *Genetics* 136:619-639.
- Earl, D. A., and B. M. vonHoldt. 2012. STRUCTURE HARVESTER: a website and program for visualizing STRUCTURE output and implementing the Evanno method. *Conservation Genetics Resources* 4:359-361.
- Evanno, G., S. Regnaut, and J. Goudet. 2005. Detecting the number of clusters of individuals using the software STRUCTURE: a simulation study. *Molecular Ecology* 14:2611-2620.
- McLoughlin, P. D., D. Paetkau, M. Duda, and S. Boutin. 2004. Genetic diversity and relatedness of boreal caribou populations in western Canada. *Biological Conservation* 118:593-598.
- Moore, S., W. Barendse, K. Berger, S. Armitage, and D. Hetzel. 1992. Bovine and ovine DNA microsatellites from the EMBL and GENBANK databases. *Animal Genetics* 23:463-467.
- Wilson, G., C. Strobeck, L. Wu, and J. Coffin. 1997. Characterization of microsatellite loci in caribou *Rangifer tarandus*, and their use in other artiodactyls. *Molecular Ecology* 6:697-699.