DELIMITING NUNAVUT CARIBOU POPULATIONS USING NUCLEAR DNA

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STATUS REPORT
TO THE NUNAVUT WILDLIFE MANAGEMENT BOARD

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Title: Delimiting Nunavut Caribou Populations Using Nuclear DNA.

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Summary:

The management of Nunavut caribou and muskox populations as distinct demographic units with associated harvesting recommendations requires research methodologies capable of delimiting these populations. Studies of caribou and muskox movement, population trends, and seasonal range will be used to direct the proposed study as well as compliment its results. Many methods have the potential of meeting these research goals however a genetic approach is proposed as a cost effective general first step towards defining demographic units to caribou and muskox populations across Nunavut.

Background:

Caribou (*Rangifer tarandus*) and Muskox (*Ovibos moschatus*) are valuable economic and cultural game species in Nunavut. Through traditional knowledge and scientific studies we know that these species, especially caribou, are not always a dependable resource due to the unpredictable nature of range shifts, population declines and resource availability. In the case of Peary caribou a changing environment has led to declines in many populations leading to their addition to the endangered species list. In addition to natural events many caribou and muskox populations have and many more will experience various levels of stress due to human impacts on their ranges. As caribou and muskox range conditions change with increased land use, the maintenance of existing genetic diversity could become more difficult ((Zittlau, 2004). Genetic diversity is considered a necessity if a population is to avoid the risk of inbreeding effects and adapt to changing environmental conditions (Zittlau, 2004; Proctor, 2003; Proctor and Paetkau, 2004).

It is therefore important to understand the genetic structure of caribou populations and to determine the current levels of diversity within these populations (Zittlau, 2004; Proctor, 2003; Proctor and Paetkau, 2004). The importance of this kind of study reaches into the very management regime and decision-making process where management decisions effecting one herd can have profound effects on related herds (Zittlau, 2004).

Objectives:

Much debate has surfaced over the years concerning the relatedness of caribou populations and muskox distributions across northern North America. Specific to this proposal is the need to delimit these populations and or groupings for many reasons:

1) To add depth to Nunavuts current understanding of caribou and muskox populations and management zones. *Biological rationale*:

2) To help wildlife managers understand the conservation issues involved when faced with local removals of caribou and/or muskox through either harvesting or natural events. *Biological rationale*:

3) To gain insight into the degree of mixing that may occur between populations. *Biological rationale*:.

4) To help define management units and associated harvesting recommendations such as total allowable harvest (TAH) etc to insure both conservation for and availability and accessibility to Nunavumiut. *Biological rationale*:.

Application of Results:

The proposed research is meant to provide a general knowledge base to both complement and help focus more specific population research including both future as well as ongoing telemetry studies, focused genetic studies, and demographic studies. The results of the study will be used to apply a more demographic approach to the management and conservation of Nunavut caribou and muskox populations. This research will also help to build the knowledge base necessary for a more predictive management approach. The results will also be used to direct future research as well as complement existing population and range studies pulling together both past and present research into a more demographic approach to the conservation of Nunavut wildlife.

Study Area:

The study area takes in the entire Nunavut territory and will include barren ground caribou (*Rangifer tarandus groenlandicus*), peary caribou (*Ranger tarandus peari*) and muskox (*Ovibos moschatus*) populations and/or evidenced aggregations. (Figure 1).

Project Design:

The intent is to provide sufficiently continuous coverage to allow detection and quantification of genetic subdivision. The strategy varies between species because of differences in population organization. For caribou we intend to sample 30 to 50 samples from each of 23 recognized herds of caribou. Muskoxen are distributed more continuously in space, and the option exists to obtain aim for continuous sample coverage or to collect clusters of samples at regular intervals. The latter approach will be employed because it fits with opportunistic collection exemplified through traditional harvesting methods. This approach also allows us to make 'point' estimates of within-population genetic variation.

Each sample from either species will be analyzed using 12 highly variable microsatellite markers. Markers will be selected to allow maximum overlap with published data, particularly for caribou where eight-locus microsatellite data have been collected for many herds (thesis chapters 3 & 4). The allele scoring done at WGI has been calibrated relative to the scoring used by Zittlau (2004), making it possible to merge any new data with existing results.

Once the microsatellite data have been generated, they can be analyzed — and re-analyzed at any time in the future with any number of programs that attempt to describe how genetic variation is partitioned within and between populations, and what that partitioning indicates about connectivity between populations. One of our core analyses would be to use the Bayesian clustering program Structure 2.1 (Pritchard, 2000). This program partitions samples into genetic clusters that are defined without reference to geographic location. Zittlau (2004) failed to identify distinct subgroups of Barren Ground caribou with this approach, and one of our goals would be to test whether increasing sample sizes, both in terms number of samples and number of locations in the genome (markers), would uncover population subdivisions that we didn't have the power to detect with existing data. Most other population genetics programs refer to user-defined population groups to quantify and illustrate genetic partitioning. A core program that we would use is Genepop, which provides basic estimates of intra- and inter-population genetic variation. These include heterozygosity estimates and estimates of F_{st}. The values produced by Genepop can be fed into a variety of downstream programs to test for such things as isolation-by-distance patterns, or population clustering.

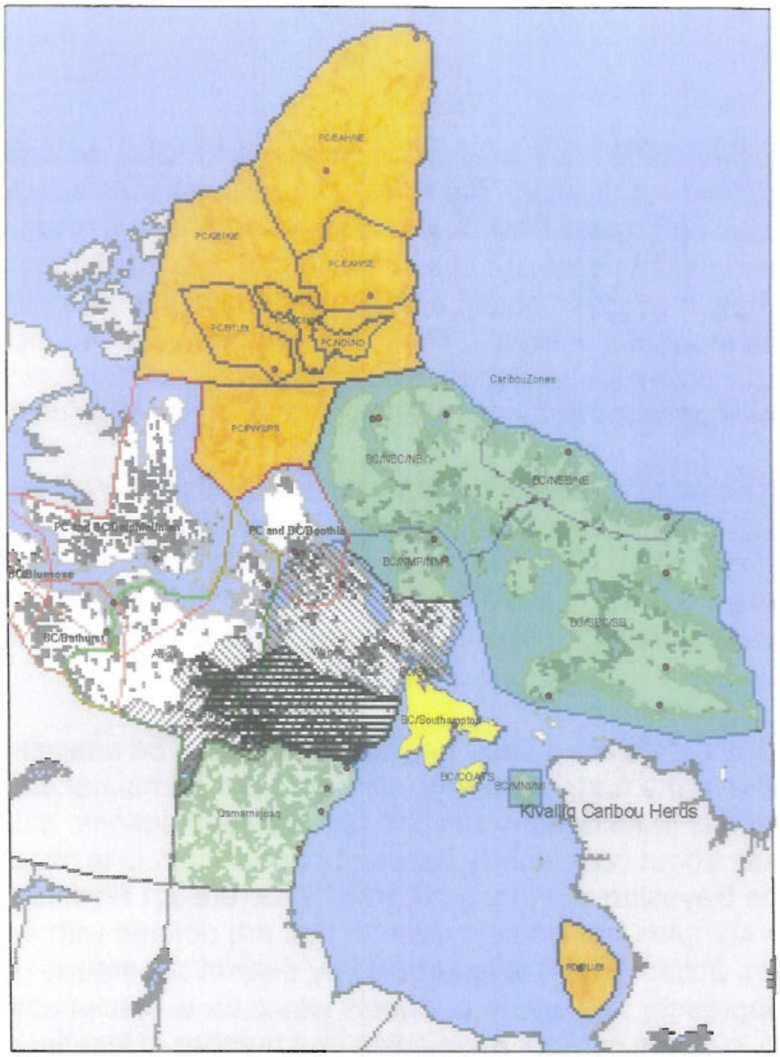

Figure 1 Nunavut Caribou populations and their probable range.

Local hunters will collect tissue samples at a time of year when the local herds and/or populations are most isolated from adjacent herds and/or populations. All sample collection will be coordinated through local HTO's and will involve the collection of a small dried sample of skin/hair. In populations where only historical samples exist other tissue samples can be used as deemed appropriate by the genetic lab chosen. Caution must be used to determine that sample duplication does not occur. Where possible whole ears or the tips of tails should be collected to insure the sampling of only one animal. Waypoint data, date, estimated age, sex, group size and the hunters name should accompany the sample in a sample bag provided. Up to 100 samples will be requested from HTOs in applicable communities at a cost of ten dollars per sample going to the hunter. Immediately following the sampling period samples will be shipped to the Arviat office for cataloging and final shipment to a DNA profiling facility for analysis. For seven Kivalliq communities the proposed research will continue over a four to five year period. For remaining Nunavut populations the sampling will be completed over the 2005/06 harvesting season.

Results:

Muskox tissue sampling and analysis 2005/2006

Sample collection was initiated April 1st, 2005 and is ongoing across Nunavut. To date the majority of the Nunavut wide muskox tissue samples have been collected from each of three locations; Kugluktok, Arviat, Baker Lake and Elsmere Island. Samples from the Western Kitikmeot are scheduled for collection this winter. The preparation of these samples for shipment and lab analysis is scheduled for completion by March 2006.

Caribou tissue sampling and analysis 2005/2006

Sample collection of caribou samples was initiated April 1st, 2005 and is ongoing across Nunavut. To date the ample samples from the Qamanirjuaq, Southampton Island, Ellsmere Island and the Northeast Mainland populations of caribou have been collected. Collections for the remaining herds are on going and expected to be complete by March 2006. Sample collections from the identified Peary caribou populations have been problematic due to the low densities and extremely low harvest rates. Efforts are currently being made to locate archived genetic material to meet study protocols.

Management Implications:

The goals and objectives of this study are to examine the demography of Nunavuts caribou populations through the examination of genetic relatedness. This information can then be used with other demographic studies in an attempt to define caribou populations as distinct populations for the purposes of harvest management and future conservation. An additional goal of the Nunavut Wildlife Research Group will be the development of population based management plans into which the results of this and other studies will be fed.

Community Consulting and Reporting:

Formal consultations regarding this project have been completed within seven Kivalliq communities and are proposed within communities Nunavut wide. Broad support for the project has been received within the Kivalliq. Proposed reporting of the results of this research will take place following the genetic analysis on or about March 2006.

Schedule:

Project: Delimiting Nunavut Caribou Populations Using Nuclear DNA.				
Output or Step	**Start Date**	**End Date**	**Person Days**	**Overtime Est. (hrs)**
Community meetings (Update)	August (2006)	August (2006)		
Sampling - All Kivalliq	April(2005)	April(2006)		
Sampling – Baffin	April(2005)	April(2006)		
Sampling - Kitikmeot	April(2005)	April(2006)		

Analysis	April (2005)	April (2005)		
Study Completion (All phases)	Feb. (2007)	Feb. (2007)		
Totals				

Anticipated Outputs:

1) Status reports to DOE, contributing agencies, community HTOs and co-managers.
2) Distribution of the Kivalliq Wildlife Research Update twice a year (Oct. and Mar.)
3) DOE file report following study completion.
4) Scientific papers in refereed journals following the completion of the project.
5) Community meetings and/or radio show describing methods and benefits of research and to obtain recommendations and/or address concerns.

Personnel:

Mitch Campbell, Regional Wildlife Biologist, DSD, Arviat, NU.
- project design and implementation, unsupervised classifications, supervising botanist.

Jonathon Pameolik, Regional Wildlife Technician, DSD, Arviat, NU.
- coordinator of project logistics, Botanical Technician.

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Partners:

The proposed study is partnered with the Arctic Net program 3.6 as apart of their Canada wide study of arctic ecosystems. Additional partnerships will be made with HTO's across Nunavut in the coordination and collection of tissue samples.