

Introduction

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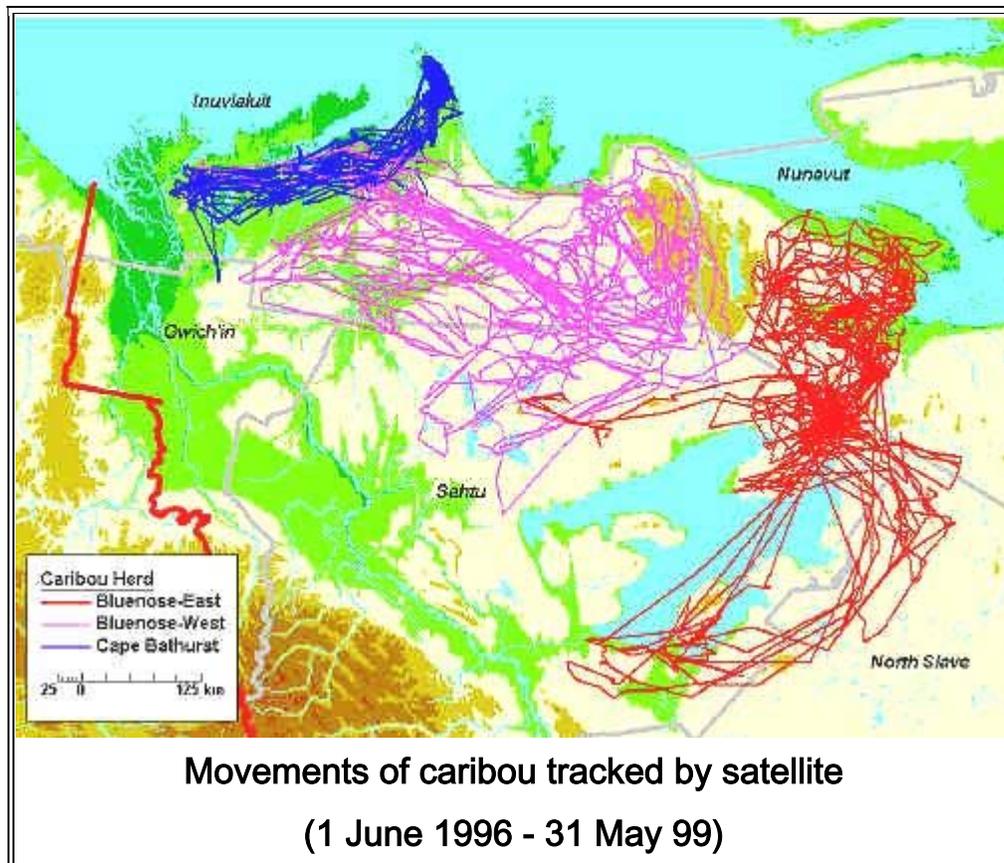
Barren-ground caribou (*Rangifer tarandus groenlandicus*) that occupy the northern portion of the Northwest Territories and western Nunavut, Canada, have been considered to be a part of the Bluenose herd (Thomas, 1969). Analyses of distribution information documented during surveys done between 1966 and 1993 using a computerized geographic information system (GIS) indicated that there were 3 calving and 2 rutting areas within that range. Caribou herds have been identified based on their use of traditional calving grounds (Thomas, 1969; Gunn & Miller, 1986). As a result, we hypothesized that there were 2 and possibly 3 herds within this range. In March 1996 satellite tracking and genetic studies similar to those done to define polar bear populations (Paetkau *et al.*, 1995, Bethke *et al.*, 1996) were initiated to determine if there were one or more herds in this area. Tissue samples were collected from Porcupine (*R. t. granti*) and Bathurst (*R. t. groenlandicus*) caribou, that occupy ranges to the west and east of the Bluenose range, respectively, for genetic comparisons.

NEXT PAGE: *Satellite Tracking Study*

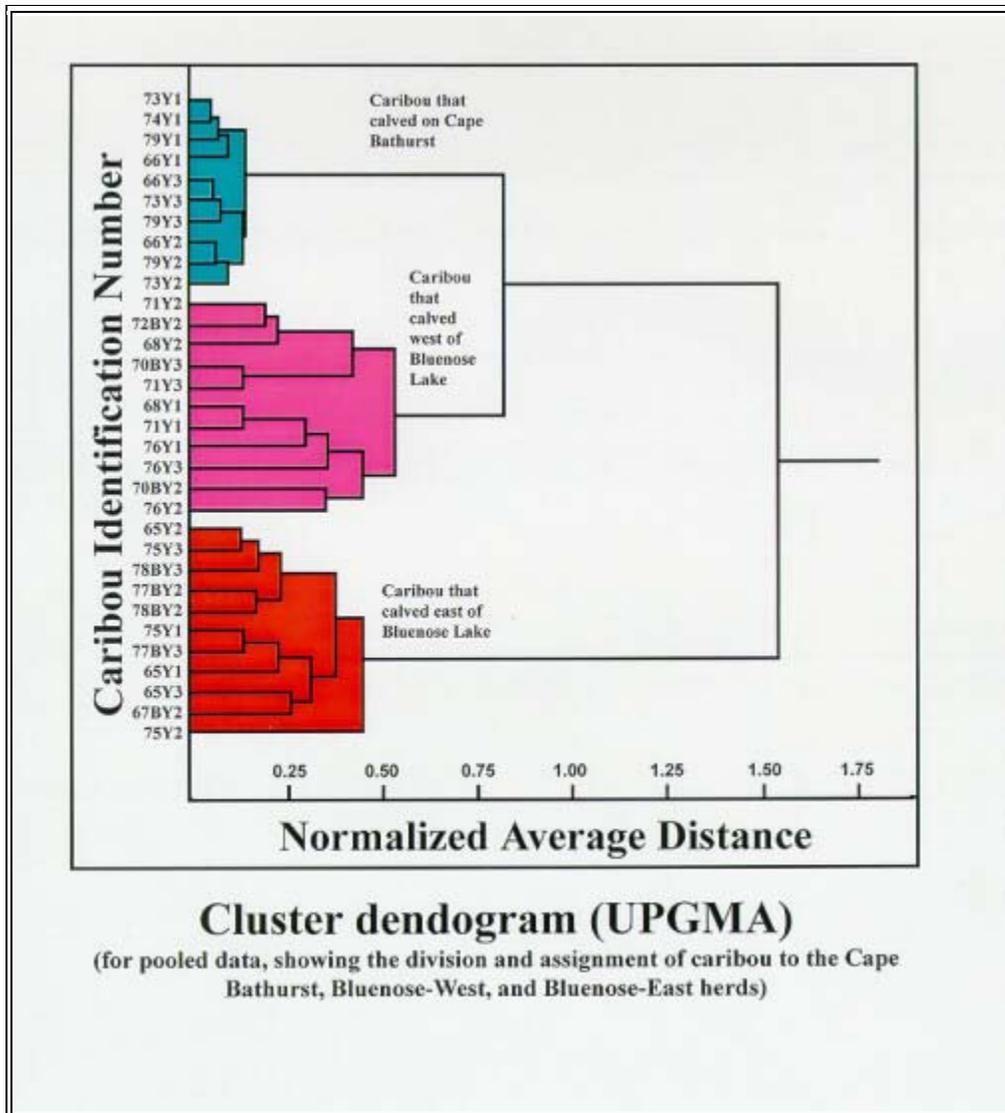
Satellite Tracking Study

Satellite Tracking: Satellite collars were deployed on female caribou in the eastern (n = 5), southern (n = 5), and western (n = 5) portion of the winter range. In 1996, 6 of the collared caribou died. The collars were recovered from those animals and were deployed on female caribou in the eastern and central portion of the winter range.

Movement data were obtained for 14 females in 1996-97 and 1997-98, and 13 in 1998-99. Maps showing the movements of these caribou were prepared using SPANS GIS (Tydac Research Inc., Nepean, Ontario, Canada). The lines showing the movements of each caribou were color coded based calving location. These maps strongly indicate that there were 3 herds in the area.

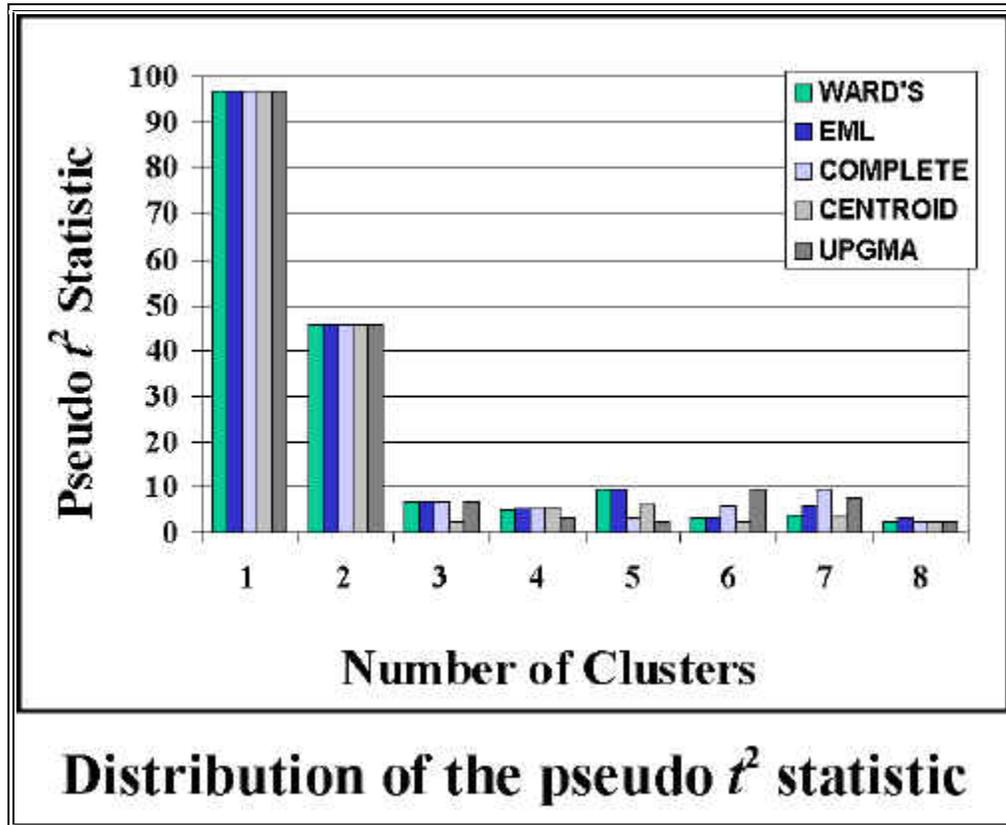


Cluster analysis: Locations for individual caribou were divided among 8 seasons: calving/post calving (1-25 June), early summer (26 June-15 July), mid summer (16 July-7 August), late summer (8 August-7 October), fall/rut (8-31 October), fall/post rut (1-30 November), winter (1 December-31 March), and spring/spring migration (1 April-31 May) (Porcupine Caribou Technical Committee, 1993). Cluster analyses were performed on the seasonal median locations for caribou for which we obtained movement data for a complete caribou year (1 June-31 May). The clustering methods used included: unweighted pair-group with arithmetic means (UPGMA); WARD'S minimum variance, CENTROID, COMPLETE linkage, and maximum-likelihood (EML) methods (Bethke et al., 1996; SAS Institute, 1989). Data were analyzed by year and pooled for all years.



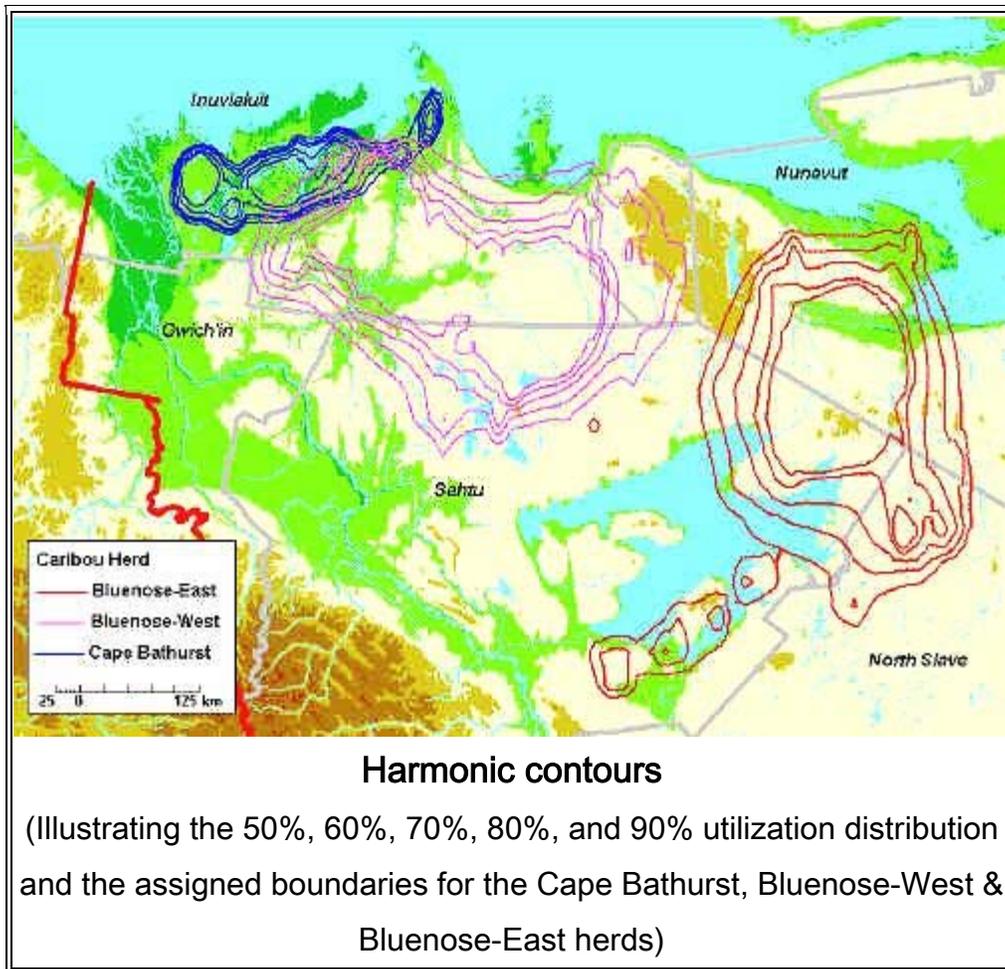
Nine collars provided records of movements for a complete caribou year in 1996/97, 13 in 1997/98, and 10 in 1998/99. In the cluster analysis of the data for those caribou, the pseudo t^2 statistics increased 9-fold between clusters 3 and 2 indicating that dissimilar groups of caribou were being grouped. At the cluster 3 level, all caribou that calved in the Cape Bathurst area formed one group, those that calved west and east of the Bluenose Lake formed the 2nd and 3rd groups respectively. The caribou were grouped in this way when the analysis was performed on the data by year or pooled among years. The results were independent of the cluster method used, indicating that separation of caribou into

3 herds was relatively robust. For convenience we refer to these as the Cape Bathurst, Bluenose-West, and Bluenose-East herds.



Harmonic contouring of location data: The time interval between satellite locations varied during the year. As a result, the data set for each caribou was sub-sampled to provide locations on an 8-10 day interval to remove bias caused by sampling intensity. The resulting data were analyzed with the harmonic mean range estimator (Dixon and Chapman, 1980) using Range Manager, MapInfo.

The 50%, 60%, 70%, 80%, and 90% harmonic contours showed a clear separation between the Bluenose-East and Bluenose-West herds. There was overlap between the Cape Bathurst and Bluenose-West herds.



NEXT PAGE: Genetic Analysis

Genetic Analysis

Analysis of samples: DNA was isolated from tissue samples collected on the 3 calving grounds in the study area and from Porcupine and Bathurst caribou harvested by local residences. Using the polymerase chain reaction (PCR) the DNA was amplified at 8 microsatellite regions (highly variable regions of DNA).

Alleles (different sized DNA fragments) were resolved by polyacrylamide gel electrophoresis on automated sequencers.

Genetic Variation: The genetic variation present in each population was estimated by the means of alleles per locus, unbiased expected heterozygosity (H_e), and unbiased probability of identity (P_{id}). H_e is the proportion of individuals in a population that is expected to have two different sized alleles at a given locus. P_{id} is the chance that two randomly chosen, unrelated individuals from a population will have the same genotype at all 8 loci.

The number of alleles per locus, H_e , and P_{id} indicate that the 5 herds exhibit a high degree of genetic variation.

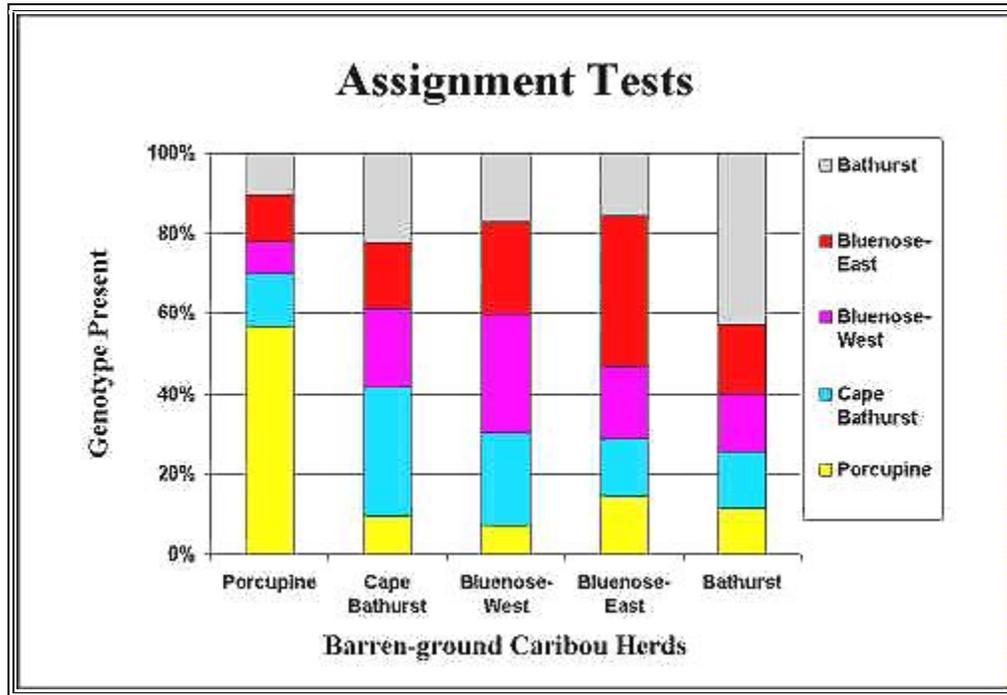
MEASURE OF GENETIC VARIATION

Herd	Sample Size	Mean No. of Alleles/ Locus	Heterozygosity (H_e)	Probability of Identity (P_{id})
Porcupine	76	14.25	0.878	5.43×10^{-12}
Cape Bathurst	31	11.25	0.867	2.31×10^{-12}
Bluenose-West	82	14.13	0.869	3.23×10^{-12}
Bluenose-East	83	13.00	0.861	1.32×10^{-12}
Bathurst	35	12.00	0.860	1.47×10^{-12}

Assignment Test: Using the allele frequencies in the populations, individuals' genotypes were assigned to the herd from which they most likely originated (Paetkau *et al.*, 1995). A G-test for heterogeneity was used to determine if there were significant genetic differences between pairs of populations.

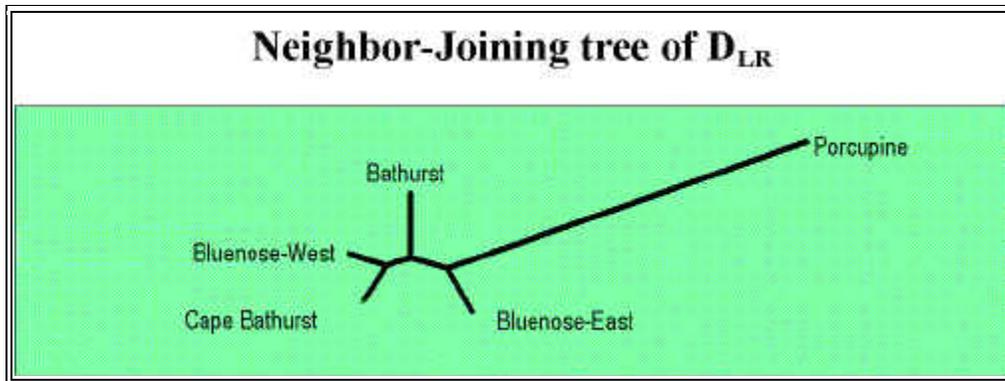
The assignment test indicated that there is genetic differentiation among all populations. The Porcupine herd is the most genetically distinct, although the genetic difference between this herd and the other 4 herds is not as large as

expected given the subspecific status of this herd. The G-test for heterogeneity revealed that the herds were genetically different ($p < .001$).



Genetic Distances: The likelihood ratio distance (D/r) was used to compare each individuals' genotype to the allele frequencies of each herd to establish a genetic distance between populations (Paetkau *et al.*, 1997). A neighbor-joining tree was prepared to illustrate the genetic distances among populations.

The D/r between the Cape Bathurst, Bluenose-West, and Bluenose-East herds (0.21-0.33) are similar to D/r between these herds and the Bathurst herd (0.29-0.34). This indicates that the Cape Bathurst, Bluenose-West, and Bluenose-East herds are as genetically distant from each other as they are from the Bathurst herd. The D/r between these 4 herds and the Porcupine herd ranged from 0.78-1.05, indicating that the Porcupine herd is more distantly, but still closely related to those herds.



NEXT PAGE: Conclusions

Conclusions

The results of our satellite tracking and DNA analyses strongly support the hypothesis that there are 3 herds of barren-ground caribou within the range previously ascribed to the “Bluenose” caribou herd. The data shows that these herds use different seasonal ranges (calving and especially rutting) and are genetically significantly different. The results of this study will have significant implications for future research and co-management of caribou in the northern NWT and western Nunavut.

The current subspecific designation of Porcupine caribou should be reconsidered.

References

Acknowledgements/References

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