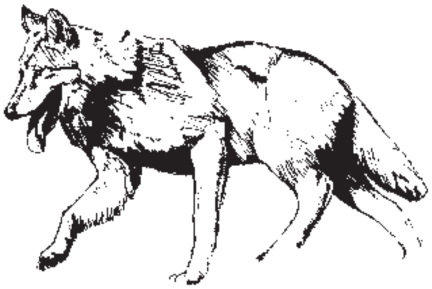
Resources, Wildlife and Economic Development

NORTHWEST TERRITORIES

WOLF NOTES



No. 6

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A Newsletter on Wolf Studies in the Central Arctic, NWT, Canada

Wolf Genetics

Barren-ground caribou are the main food for wolves in Canada's north. Therefore, many wolves follow migrating caribou when they move from summer ranges on the tundra to winter ranges in the trees and back again the following spring. Migratory caribou populations or "herds" are given names based on where their calving grounds are. They include the Bathurst, Beverly, and the Qamanirjuaq caribou herds. Wolves associated with a specific caribou herd have been classified with the same name, generally for convenience. For example, wolves that prey on caribou from the Bathurst caribou herd have been referred to as "Bathurst" wolves.

The usefulness of this classification for wolves was challenged during the winter of 1997/98 when hunters from northern Saskatchewan and the Northwest Territories harvested about 800 wolves. That winter an unusually high number of wolves and caribou, both from the Bathurst and Beverly caribou ranges, spent part of the winter together in the boreal forest region. Although range overlap is common with barren-ground caribou, this was the first documented overlap of Bathurst caribou within the Beverly range. The corresponding movement of wolves, which includes their mating season, forced us to re-consider the relationship between caribou and wolf populations.

It is possible that wolves associated with migratory caribou form distinct populations. However, tundra wolves could be part of a large, wide-ranging population characterized by extensive mixing of individuals and packs. In this case, wolves that hunt caribou from one caribou population in one year, may hunt caribou from another population the following year.

G. Calef

G. Calef

Do wolves follow the same caribou herd each year?

- Analyzing wolf DNA will help us find out.

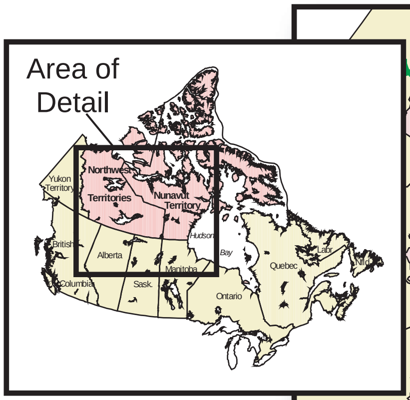
Wolf Populations

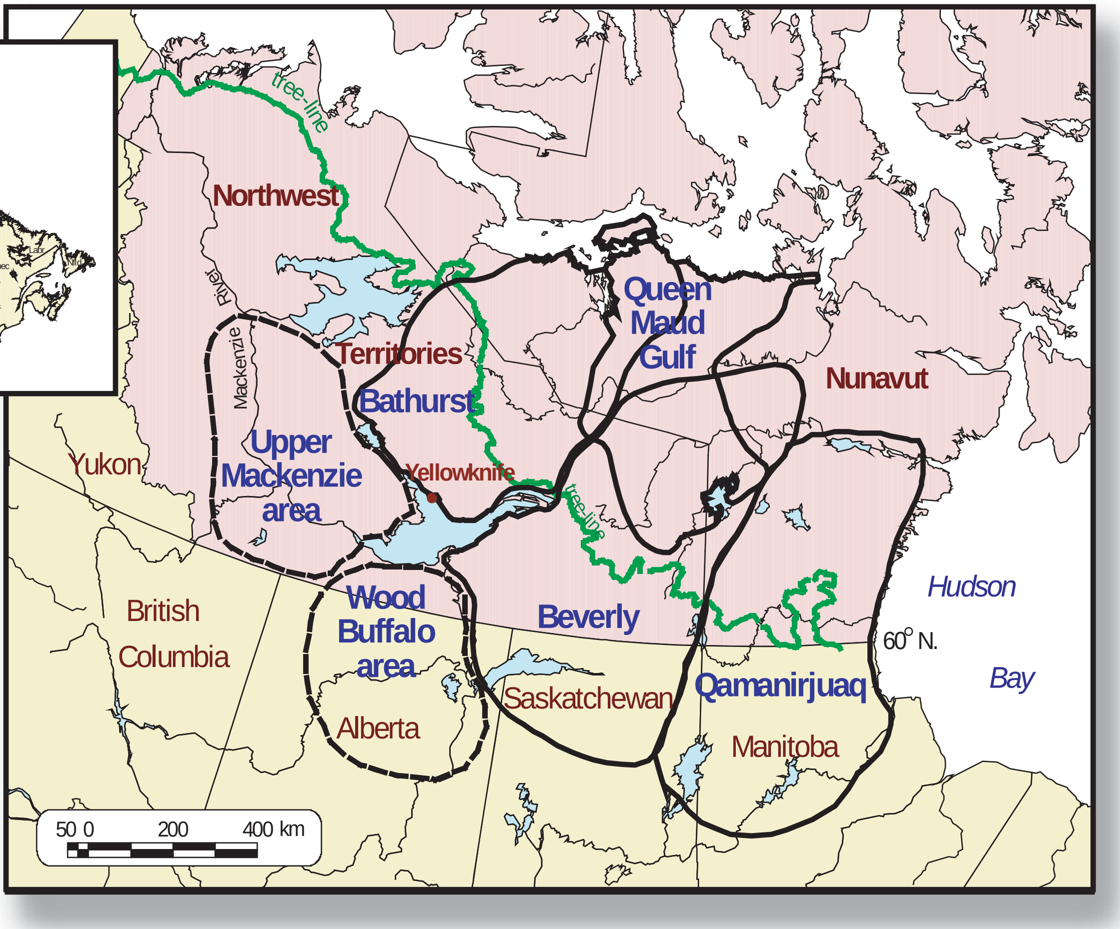
If tundra wolves do not form population units linked to specific caribou herds, wolf populations could be structured some other way, or not at all. Tundra wolves may also be genetically distinct from wolves that live year-round in the boreal forest because forest-dwelling wolves tend to establish territories that are maintained throughout the year and, therefore, they may not travel as far. Boreal forest wolves prey mostly on non-migratory caribou, moose, or bison.

Unlike southern Canada where wolves have been reduced or removed, wolf populations in the Northwest Territories and Nunavut remain widely distributed and abundant. However, people can still influence northern wolf populations. Local hunting of wolves can be substantial, and the effects of the harvest have not been fully explored.

Therefore, we need to evaluate human impacts on wolf populations. To do this, we are examining the genetic relationships and diversity within and among wolf populations characterized as migratory or resident, and lightly or heavily harvested. Radio-tracking and genetic techniques are then combined to look for overlap and interchange between wolf populations.

Our study area includes the mainland portion of the Northwest Territories and Nunavut from Hudson Bay in the east to the Mackenzie River in the west. Wolves are also sampled wolves from northern Alberta and Saskatchewan. These areas include wolves from the Bathurst, Beverly, Queen Maud Gulf (Ahiak), and Qamanirjuaq caribou herds, and from the Wood Buffalo National Park and Upper Mackenzie River regions.





Northern Wolf Genetics Study Area

Wolves that move with migratory caribou populations north and east of Great Slave Lake are considered migratory.

Wolves in the Wood Buffalo National Park and Upper Mackenzie River areas are not considered to be migratory.

Study Design

This study builds on previous work conducted during the Esker/Wolf Study but adds to the geographic scope and includes genetic information to help understand wolf movement patterns and their implications for management.

This study will:

1. Define genetic diffferences and gene flow between adjacent migratory and non-migratory wolf populations.
2. Examine the movement patterns, genetic diversity, and connectivity among wolf populations having different levels of harvest.
3. Identify sink and source populations within a possible inter-connected group of wolf populations.
4. Evaluate and predict the effect of hunting on genetic diversity of northern wolves.

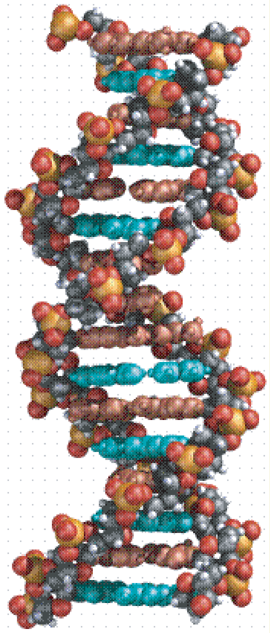
We are extracting DNA from wolf scats and from pelts harvested by hunters. Variations are detected in portions of the DNA for each wolf and we determine how common these variations are. Only part of the DNA string is sampled because the entire DNA is so large. However, this is not a problem because some parts of the DNA are highly variable. Therefore, differences can be detected even between individual wolves. Clusters within a wolf population (corresponding to packs), and separate populations, should also be detected.

Analyzing DNA

Deoxyribonucleic acid, more commonly known as DNA, is found in cells that make up tissues such as skin, hair, nails, muscle, blood, and even feces (scats). DNA is made up of a long string of molecules. A unique sequence of these molecules is called a gene. Genes are located on chromosomes and determine the hereditary characteristics of an individual. These include species, sex, eye color, and many other features.

Because each gene occupies a specific location on the DNA strand, it is possible to compare the same genes among different individuals. The key to making these comparisons is based on minor differences between individuals in their genes. These differences can arise from changes in a DNA sequence from generation to generation (mutations). These change rates can vary greatly depending the type of DNA examined or its relative location on the chromosome.

Some genes are so basic to the daily functioning of the animal that most changes will affect the individual's survival and therefore are not passed on to the next generation. Other genes determine more superficial traits and can accumulate mutations more quickly, while still other areas of DNA do not seem to control anything important and can show rapid change. Differences in these mutation rates can allow comparisons over a wide range in time, from changes millions of years ago to very recent divisions between parents and their young.



Part of a DNA molecule.

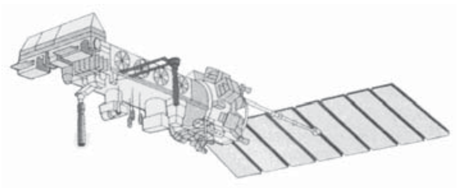
We will use these genetic techniques to link individuals that share similar characteristics, some of whom may be in separate areas. Migration patterns, geographic boundaries of populations, and connectivity between groups of wolves will also be determined. What may not be obvious in species with similar external characteristics may be revealed with genetic analysis.

Radio-Tracking

We used locations of radio-collared wolves as another method to examine wolf movement patterns. Wolves fitted with satellite radio-collars allow more frequent locations than what we can get from conventional VHF radio-collars. This is because conventional radio-collars requires someone to be close to the VHF transmitter to hear the signal. This requirement can make it difficult and expensive to locate wolves in this way because wolves can travel great distances between consecutive tracking sessions. Also, we cannot fly a plane at night, nor during bad weather.

***Right** - Small fixed-wing planes are used to track wolves with conventional (VHF) radio-collar transmitters*

Satellite radio-collars transmit their signal to an orbiting satellite and therefore a location is possible worldwide. Although satellite radio-collars are expensive they can provide cost-effective information for some study objectives. However, we still use conventional VHF radio-collars because they offer other advantages for monitoring wolves.

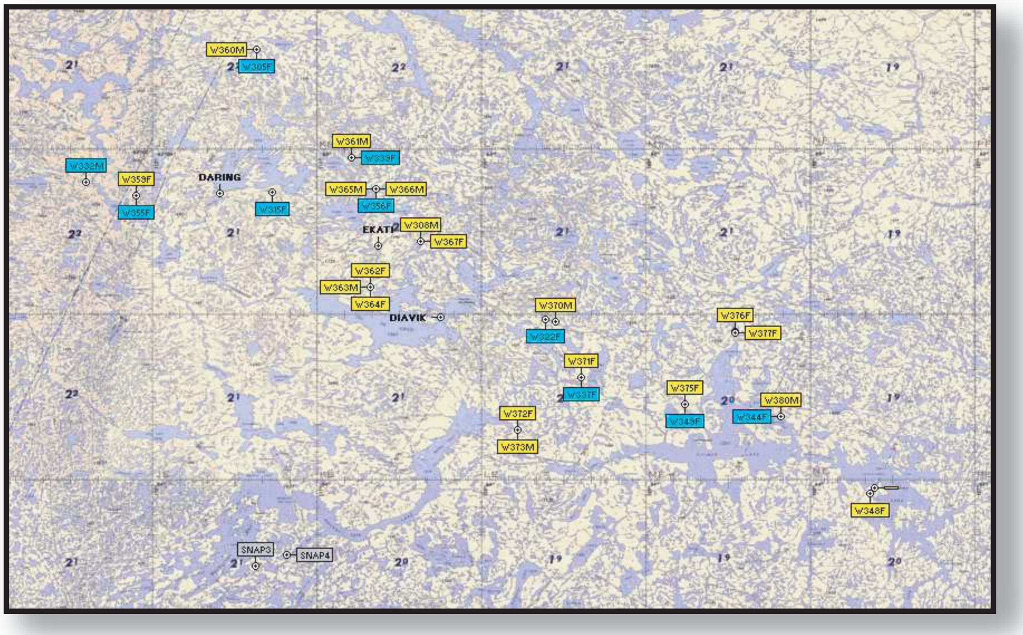


***Above** - Service Argos uses several polar orbiting NOAA satellites to locate wide-ranging widlife such as wolves. A signal received from the collar is used to calculate the animal's position anywhere on the earth.*

Between June 1997 to September 1999, 58 individual wolves from 21 unique packs were captured, marked, and released in the Bathurst tundra range. Satellite collars and conventional VHF radio-collars were deployed in various combinations. The objective was to maintain a VHF and satellite radio-collar in each pack.

We have since removed the satellite collars because their battery power supply was expected to expire. Satellite collars were replaced with VHF radio-collars to extend the monitoring of these wolves. We recently captured another 24 wolves in June 2001 and deployed VHF radio-collars on 19 of them.

This effort is primarily intended to study wolf den ecology and the genetic diversity and movements of these wolves. Position data and related observations will be used to determine wolf movements, home ranges, social units, and pack composition.



***Left** - The distribution of new VHF radio-collars (yellow labels) deployed in June 2001 and those from previously captured wolves (blue labels).*

Marked wolves killed by hunters within and outside of the Bathurst range will assist in estimating movement distances and exchange with other wolf packs and populations.

Genetic Analysis

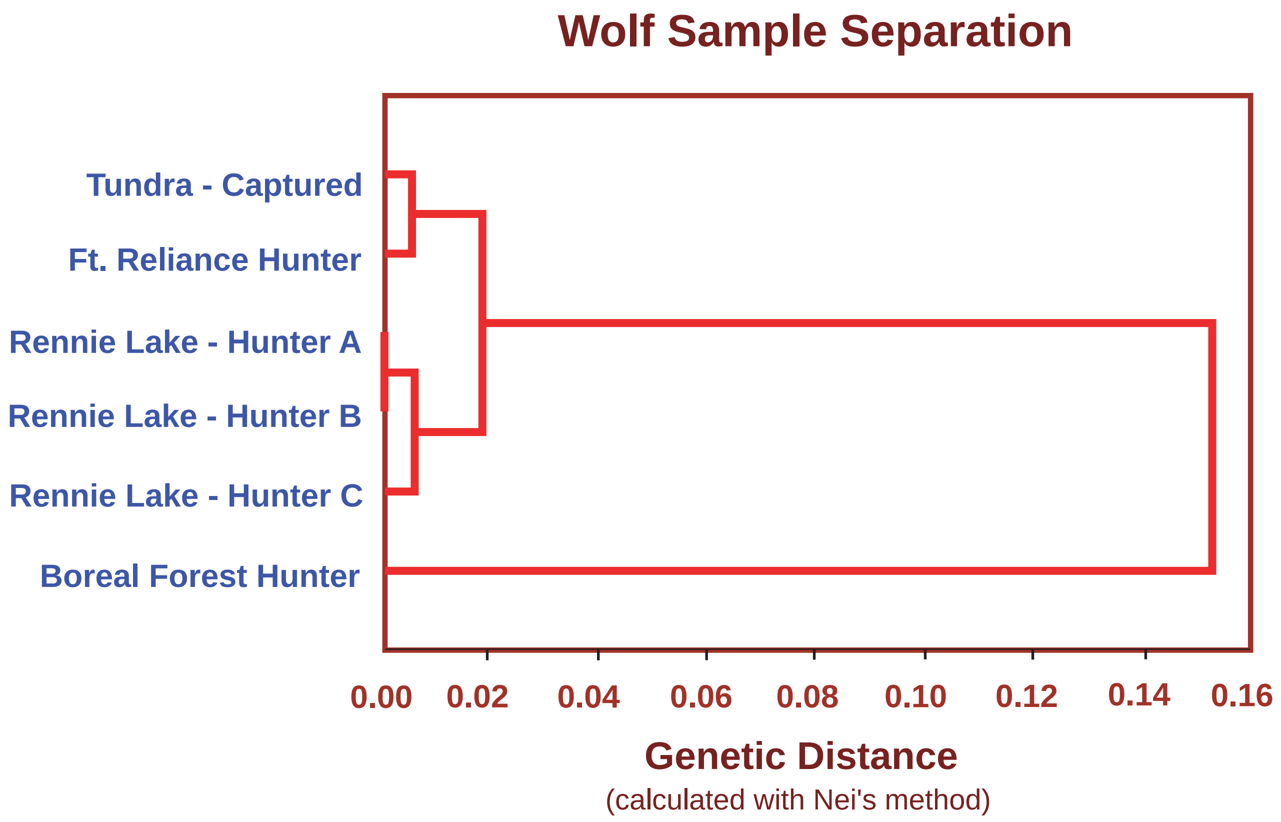
Grouping Wolf Samples

Groups of wolves were defined by geographic location and by hunters who supplied samples. Samples included wolf blood or hair that we collected from captured wolves and slivers of hide from wolf pelts that hunters brought in from the winter harvest. The following groups were defined:

- Wolves captured in the tundra around the mining areas in the Lac de Gras region.
- Wolves killed in the treeline areas east of Great Slave Lake
- Wolves killed in the Rennie Lake tree-line area by three hunters (A, B, C)
- Wolves killed by a hunter in the boreal forest west of Yellowknife.

Genetic Relationships Tree

We constructed a tree of genetic relationships of wolves sampled in the above areas. The genetic tree was calculated using a method developed by Dr. Masatoshi Nei at Pennsylvania State University. This diagram is called a genetic tree because the groups on the left are similar to branches of a tree. All branches are ultimately connected. The further the connection is to the right, the less related (or more separate) are the groups of wolves.



The genetic tree shows that tundra wolves are closely related to those hunted in the tree-line in the Fort Reliance and Rennie Lake areas. However, wolves from the boreal forest are separated from tundra and tree-line wolves. The graph also suggests that wolves killed by hunters A and B in the Rennie Lake area are genetically identical, but are slightly different from wolves killed by Hunter C. The number of samples from the boreal forest is low (3), but more samples will be analyzed this winter.

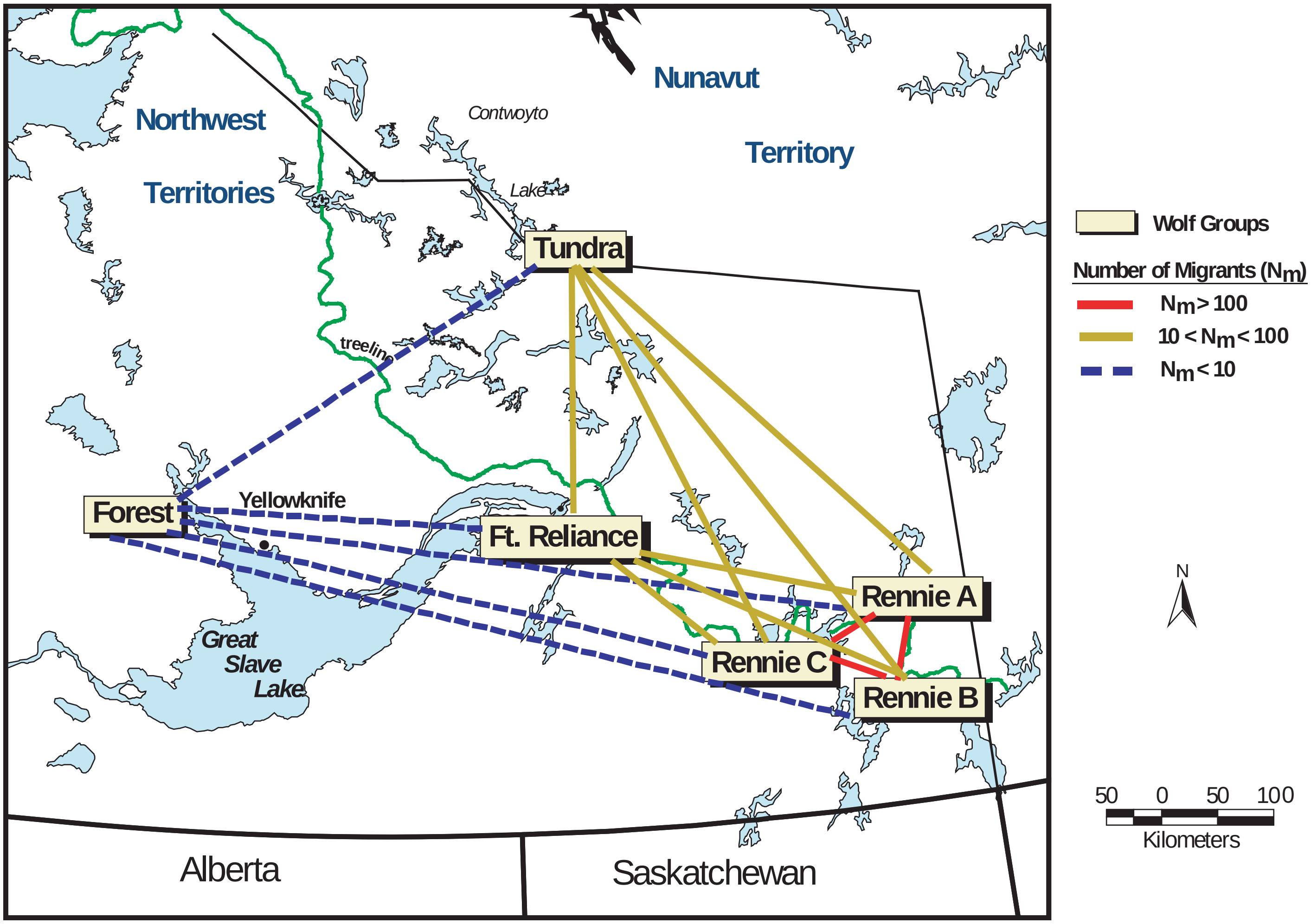
Migration Between Groups

Genetic Information

Marco Musiani prepares a wolf hide sample for genetic analysis.

Tundra, Fort Reliance and Rennie Lake area wolves are closely related. Fort Reliance area wolves are genetically similar to those sampled from the tundra and could be of tundra origin. Also, some of the Rennie Lake area wolves might be migrants from the tundra, although there is some differentiation between Rennie Lake and tundra/Fort Reliance wolves. Boreal forest wolves, however, are significantly distinct genetically from the tundra and tree-line groups.

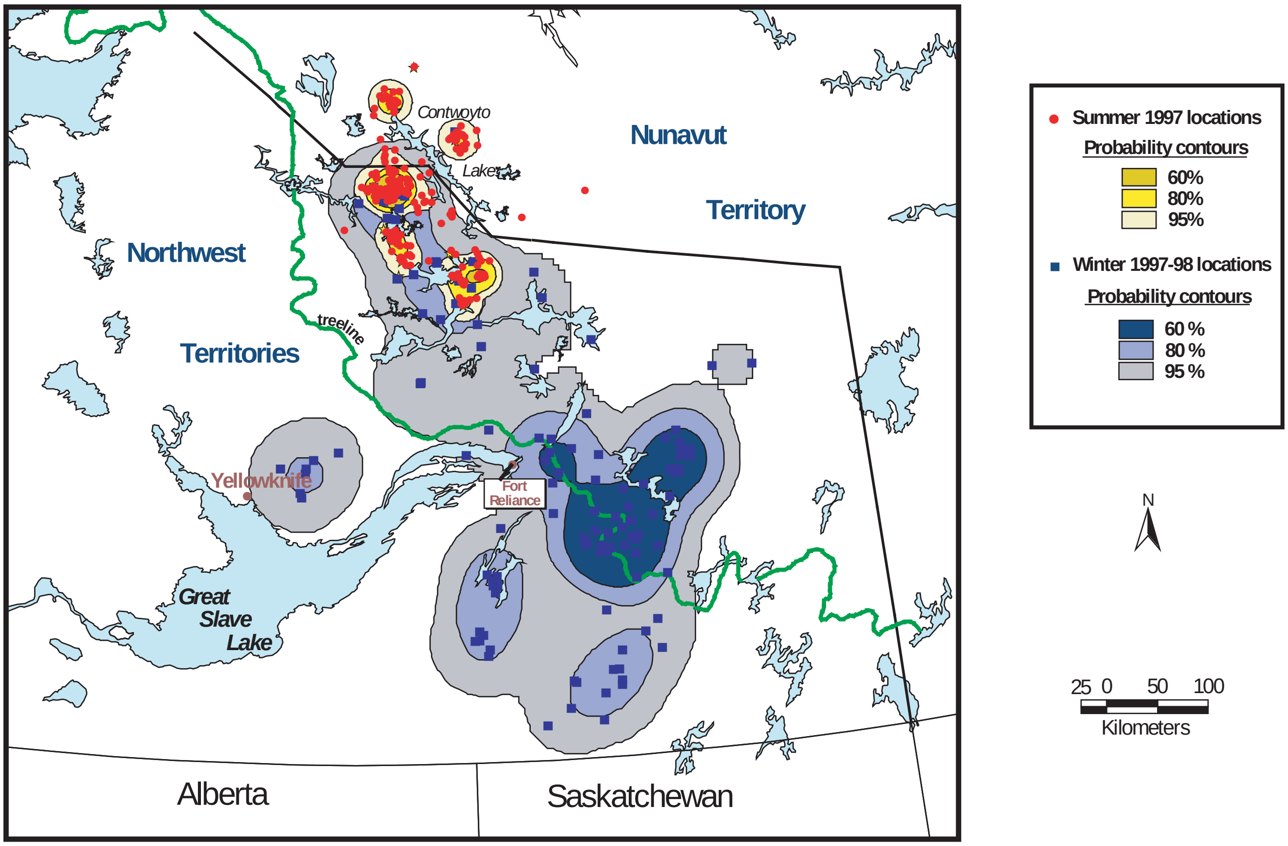
Based on this information, we calculated the theoretical number of wolf migrants per generation between the groups of wolves identified. We used the symbol N_m to represent the number of wolf migrants. N_m is higher for more genetically connected populations.



Groups of wolves are connected by different types of lines according to the number of migrants (N_m) between them. Red lines indicate more than 100 migrants per generation between two given populations, yellow lines between 10 and 100 migrants, and blue-dashed lines for less than 10 migrants.

Radio-Tracking Information

Our results on genetic connectivity among wolves are supported by wolf movements documented by radio-tracking. Radio-tracked wolves have migrated between tundra and tree-line locations such as Rennie Lake. Many wolves hunted along the tree-line area are likely winter migrants from the tundra. This was also confirmed by genetic analysis.



In the map above, we plotted the locations and areas used by radio-collared tundra wolves tracked by satellite during summer 1997 and winter 1997/1998. That winter, the Rennie Lake wolf hunt received widespread public attention. The areas of use indicated are kernel-based seasonal home ranges. The technique uses radio-collared wolf locations and calculates areas of probability where wolves would occur. Lower percent probabilities indicate smaller areas but with more frequent use. Shown are the 60%, 80%, and 95% probability areas that these wolves could have used during the season, based on the location data.

Implications

Our preliminary analysis of genetic and movement data of northern wolves indicate that tundra wolves serve as a source population for wolves hunted in tree-line areas such as Rennie Lake. The data suggest that existing links between tundra and tree-line wolves could play an important role in maintaining wolf genetic diversity on a regional basis. The area east of Great Slave Lake is likely an important movement corridor for wolf migration, and for caribou as well.

Preliminary results also suggest that tundra and tree-line wolves might be genetically different from boreal forest wolves. We still cannot distinguish between wolves based on the different migratory caribou herds, but we have detected different sub-populations among tundra and tree-line wolves killed by the different hunters there. Further sampling this year and next should clarify these results.

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