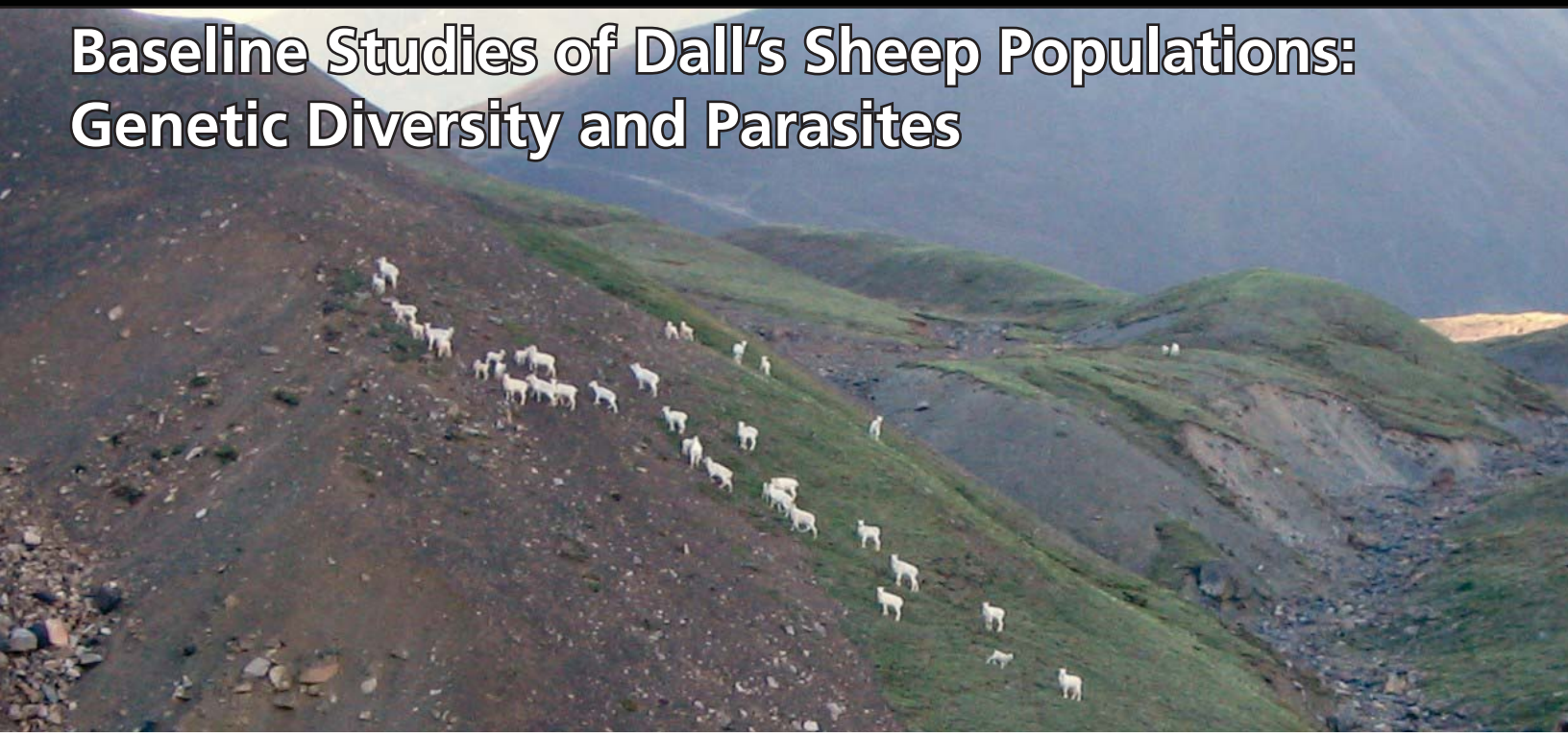
National Park Service
U.S. Department of the Interior

Wrangell - St. Elias National Park and Preserve

Baseline Studies of Dall's Sheep Populations: Genetic Diversity and Parasites



In Wrangell - St. Elias, Dall's sheep populations are found in the alpine zone (see photo) of the mountain ranges. The populations may be different genetically because the mountainous terrain is separated by major glaciers and rivers.

What geographic features have presented historical barriers to sheep movement, and therefore gene flow?

Dall's sheep (*Ovis dalli dalli*) in Wrangell - St. Elias National Park and Preserve are estimated at 15,000 -25,000 individuals, constituting 25-30 percent of Alaska's total sheep population. Dall's sheep are well distributed throughout the extensive montane landscape of the park and occur at ancestral population levels, unlike the fragmented bighorn sheep (*Ovis canadensis*) populations scattered throughout their North American ranges.

Little is known of the genetic structure of Dall's sheep populations within contiguous mountain ranges, such as the Wrangell, Chugach, and St. Elias Mountains of southcentral Alaska. An understanding of the genetic composition of wild sheep populations over broad landscapes may be useful to assess natural patterns of genetic variability and gene flow. Knowledge of genetic structure can provide resource managers necessary information about the appropriate geographic scales for population monitoring and harvest management. Additionally, evidence suggests a linkage between Dall's sheep genetic diversity and the sheep populations' resistance to internal parasites.

Until recently, broad-scale evaluations of Dall's sheep genetics have been limited by the expense of collecting tissue from live sheep or by the limited availability of archived samples. Researchers have initiated a new effort to describe the genetic structure and gene flow among Dall's sheep populations in southcentral Alaska. This new research uses a non-invasive technique of extracting DNA and parasite samples from Dall's sheep feces.

Using sheep feces for genetic studies

DNA extracted from feces of other species of wild sheep has proven to be as effective and accurate as methods involving blood and tissue. Population studies can be improved because fecal pellets are relatively easy to collect from a large sample of individuals over a wide geographical area and the technique is less expensive than collecting tissue samples from live sheep. Importantly, collection of fecal pellets is non-invasive because it does not require the physical capture of animals.

Beginning in 2007, Gretchen Roffler, a researcher at the U.S. Geological Survey-Alaska Science Center, collaborated with colleagues at the Alaska Science Center, the University of Montana, the U.S. Forest Service Rocky Mountain Research Station, and the Alaska Department of Fish and Game to develop and validate the non-invasive fecal DNA techniques in free-ranging Dall's sheep in Wrangell - St. Elias.

Using these techniques, they assessed genetic diversity and gene flow of sheep within the Chitina River drainage using two types of genetic markers: mitochondrial DNA inherited from the mother, and nuclear DNA inherited from both parents. In addition to the genetic investigation, the researchers collected information on parasite loads (what types of parasites and how many) and compared this to genetic variation.

Collecting Dall's sheep fecal pellets and tissue

Roffler conducted her work in the Chitina River drainage of the park during late summer of 2007 and 2008. Approximately 2,500 to 3,600 Dall's sheep live in this 13,000-mile^2 (20,000-km^2) area,

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The field team lands by helicopter (top photo).

Researcher samples Dall's sheep fecal pellets.

Analyses of Dall's sheep fecal pellets (bottom photo) provide a non-invasive way to study Dall's sheep across large spatial scales.

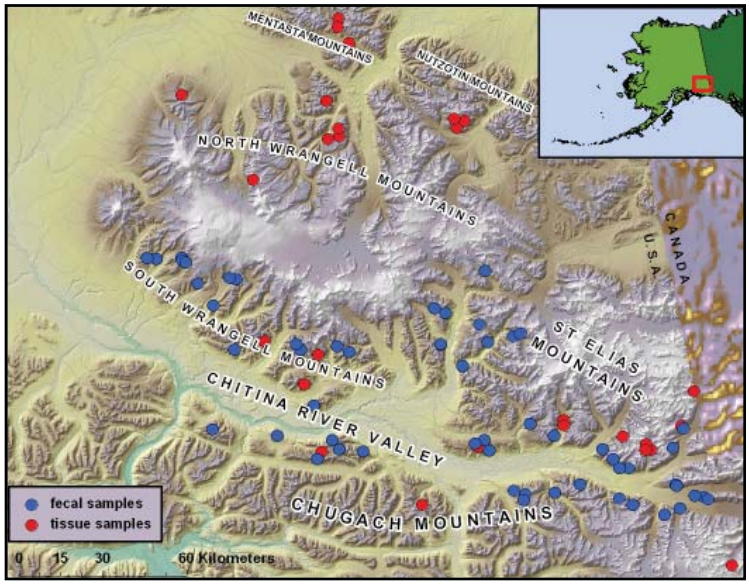
which contains the Wrangells, the St. Elias, and the Chugach mountain ranges. Large glaciers and major rivers subdivide the terrain and could present barriers to sheep movement, thereby contributing to genetic sub-structuring of the population over time (see map below). Sheep are typically located at an elevation between 3000 to 5000 feet (900 to 1500 m).

To collect a representative sample, Roffler divided the study area into smaller grid cells of 30 miles^2 (50 km^2), and randomly selected cells from which to gather feces. The field team located sheep groups from a fixed-wing aircraft, and landed near the sheep by helicopter. They collected feces from 1-3 adults from 1 sheep group for each selected grid cell, for a total of 47 sheep sampled in 2007 and 69 sheep in 2008. This included feces from both females (ewes) and males (rams). For separate parasite analyses, 10-20 more fecal pellets were gathered from each individual sheep and analyzed for types and quantities of parasites.

To compare the genetic analyses from feces to those from tissue samples, the researchers arranged to obtain tissue samples from male sheep taken during the hunting season in 2007 (30 rams) and 2008 (16 rams). The tissue samples came from a larger geographical area (some beyond the Chitina drainage) than the fecal samples and thus provide a basis for comparison of genetic differentiation at a larger scale.

Genetic analyses

Roffler arranged for DNA to be extracted from the tissue samples to test a set of 15 microsatellite *loci* (nuclear genetic markers) previously used in bighorn sheep. These loci were then used to screen and develop other markers for evaluating DNA extracted from the fecal samples. A variety of statistical tests were performed to determine if individual sheep could be identified by population of origin, and to identify the degree to which the populations were genetically different. The four populations were defined by the mountain range from which the samples were collected (North Wrangell, South Wrangell, St. Elias, and Chugach).



Genetic diversity in Dall's sheep is being analyzed from fecal pellets (blue) from the Chitina drainage, and from muscle tissue (red) sampled more broadly.

Preliminary results—genetics

Complete *genotypes* (a combination of genes that an organism possesses) from the four sheep groups were obtained using the nuclear markers from fecal and tissue samples. Levels of genetic diversity were high and similar among all groups. From the mitochondrial DNA, *haplotype* (half a genotype) diversity (in this case from the mother) was highly variable between groups, the lowest in the Chugach sheep and the highest in the North Wrangell sheep.

Genetic analyses based on the percentage of DNA inherited from both parents revealed substantial population differentiation among the four sampling areas (see map) and suggested that the South and North Wrangell sheep are closely related, as are the St. Elias and Chugach sheep. Comparing the maternally-inherited DNA from the sheep populations, the Chugach population was similar to both the St. Elias and South Wrangell sheep. This could indicate an ancestral common origin or historical gene flow between the groups. Like other sheep, Dall's sheep ewes tend to remain in the same geographical area as their mothers, while males move to new groups as they approach breeding age; thus rams appear to mediate the gene flow between populations structured by maternally-inherited DNA.

Preliminary results—parasites

Internal parasite loads (estimated as the number of larvae or eggs per gram of feces) indicated that 97 percent of sheep sampled were infected with one species of dorsal spine larvae (*Parelaphostrongylus odocoilei*), a type of common lungworm nematode associated with pneumonia in wild sheep. This finding was consistent with previous collections in the area. The high levels of infection are noteworthy, although there have been no reports thus far of respiratory diseases in the park's sheep. Prevalence of other parasites ranged from 11 - 84 percent across all populations, but infection levels were not considered to be debilitating to the population.

Future research

In 2009, Roffler plans to collect more fecal and tissue samples, and to continue processing and analyzing previously collected samples. The next step is to use the genetic markers to further assess the spatial scale of population differentiation in relation to geographic features that have been barriers to sheep movement, and therefore to gene flow. Once genetic and parasite collections and analyses are completed, researchers can explore the relationship between genetic diversity in the sheep populations and individual parasite loads.

Acknowledgements

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For more information

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