



**OCCURRENCE OF GRIZZLY BEARS
IN THE PRAIRIE CREEK AREA**

GREATER NAHANNI ECOSYSTEM

Addendum to February 4, 2005, Letter

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INTRODUCTION

Nahanni National Park Reserve, a UNESCO World Heritage Site in the Northwest Territories of Canada, was created in 1972 to provide immediate protection to the spectacular waterfalls and canyons of the famed South Nahanni River. The Park Reserve, however, is only 5 km wide in some sections and encompasses only 14% of the larger watershed which has been called the 'Greater Nahanni Ecosystem' (Fig. 1). Such a small and narrow Park is vulnerable to impacts that may occur from industrial developments outside the protected area. This problem is particularly acute for wide-ranging carnivores that possess little resiliency to human impacts and thus require large, secure areas to sustain viable populations (Weaver et al. 1996).

In the early 1980s, Texas investors developed a mine site in Prairie Creek, just 14 km northeast of the boundary for Nahanni National Park Reserve. In addition, a 140 km-long winter road was constructed from the Liard Highway to the mine site. The investors abandoned the facility before actual operation began, however, when prices for silver plummeted. At present, Canadian Zinc Corporation holds the property and has proposed to reopen the mine site, explore further in the surrounding mountains, and construct an all-season road along the previous winter road that is now abandoned. Other companies have applied for permits to explore for minerals in the Prairie Creek area right to the Park boundary.

For the past three years, I have been conducting surveys to determine the distribution and relative abundance of grizzly bears (*Ursus arctos*) throughout the Greater Nahanni Ecosystem. The purpose of this brief report is to document the occurrence of grizzly bears in the Prairie Creek area.

METHODS

Field Surveys

In the late 1990s, Canadian bear researchers and geneticists pioneered a new technique for surveying bears using scented, barbwire corrals to collect hair for DNA analysis (Woods et al. 1999). I followed their basic protocols to survey bears in 1024-km² grids that were divided into 16 cells, each 8 km x 8 km in size (64 km²). In each cell, I chose the site that we judged to have the best likelihood of 'catching' a grizzly bear. Our field team piled up logs, brush, and moss and poured 3 liters of rotted cattle blood and 1 liter of rotted fish oil over the mound. We enclosed the site by running a single strand of barbed wire around several trees about 5 m out from the mound and uniformly about 50 cm above the ground (see Fig. 1 in Woods et al. 1999). In addition, we nailed 1 scented rubbing pad on a tree outside the enclosure.

Using a Bell 206B helicopter for access in this remote area, we established the 16 stations in the Prairie Creek grid June 5-6, 2003, and checked them approximately 20 days later. We also collected bear hair from natural rub trees at 15 sites along a 50-km stretch of Prairie Creek from the Park boundary to the headwaters June 27-28, 2004.

DNA Analysis

The Wildlife Genetics International (WGI) lab in Nelson, BC, under the direction of Dr. David Paetkau, conducted the DNA analyses. Dr. Paetkau has published extensively on genetics of North American bears and DNA analyses of bear hair (Paetkau and Strobeck 1994, Paetkau et al. 1998, Woods et al. 1999). To ensure rigorous and reliable identification of individual grizzly bears, the WGI lab selected a set of specific genetic markers that exceeded a high threshold of heterozygosity, culled marginal samples at an early stage in the process, scrutinized similar pairs of genotypes, and adhered to high laboratory standards for quality control (Paetkau 2003, Paetkau 2004).

Selection of Hair Samples and DNA Extraction. -- A WGI technician inspected hairs visually and excluded glossy black guard hairs because prior testing indicated that such hairs have a 98% likelihood of being from black bears (Woods et al. 1999). For samples that occurred in a consecutive series of adjacent barbs on the barbwire strand and appeared to be the same color (more likely to be from the same bear as it passed under the wire), the technician initially selected the best sample of every three in that series. Adjacent samples of different color as well as all non-adjacent hairs were extracted. All selected samples were extracted using QIAGEN's DNeasy kits.

Species Determination. -- WGI has established from thousands of known grizzly and black bear samples across North America that the microsatellite marker G10J is diagnostic of species: grizzly bears have even-numbered alleles while black bears and wolves have odd-numbered alleles. WGI determined the species of all extracted samples and eliminated black bear samples from further analysis.

Marker Selection and Power. -- From a set of 16 microsatellite markers that have been useful in DNA studies of bears, WGI examined data from study areas that bracketed Nahanni geographically: the Richardson Mountains to the north, Kluane National Park to the west, and the Prophet River area to the south (Paetkau et al. 1998, Poole et al. 2001). They tested 10 of the more promising markers for variability among individuals (= discriminating power) by analyzing 12 hair samples that likely represented different individuals in the Nahanni survey. The six-locus marker system selected for this project (G10J plus five others) displayed an exceptional level of genetic variability with an average of 8.2 alleles observed per locus and an average expected heterozygosity (H_e) of 80%. This surpassed WGI's threshold of 72% heterozygosity (roughly 1 in 1 million chance that two *unrelated* individuals exhibit the same genotype at these 6 loci).

Microsatellite Analyses and Error-checking of Individual Identification. -- WGI personnel genotyped the grizzly bear hair samples for individual identity using a step-down process of exclusion to ensure rigorous and conservative determination of identity. First, they excluded samples that produced strong signals at only 2 of 5 loci (other than G10J) because such samples are prone to genotyping errors. Next, they conducted a

second round of analysis in an attempt to produce more complete genotypes for samples that initially produced adequate signal at 3 or 4 loci. They eliminated all samples that still yielded only a 3-locus genotype. Next, they reviewed any samples that produced clear alleles at 4 loci; on a case-by-case basis, they decided whether to declare a unique individual. A second, highly experienced person confirmed scoring of all complete (5-locus) genotypes that comprised the final data set.

WGI conducted a thorough, computerized comparison of all pairs of identified individuals (unique genotypes) to check those that were suspiciously similar. All pairs of genotypes that differed at only two loci were scrutinized for possible error and re-analyzed if identification of an individual was based on only one available sample. All identified individuals that differed from another at just one locus were re-analyzed completely (including PCR, electrophoresis and scoring) -- regardless of how many samples had been observed with those particular genotypes. Finally, WGI selectively re-analyzed samples with unique genotypes when those genotypes were homozygous for more than half of the six loci (a possible sign of failure to amplify some alleles) even when those genotypes were not highly similar to other genotypes. All grizzly bear hair samples declared in this report as unique individuals differed at three or more of the six loci, thereby assuring that errors of identification were highly improbable.

Determination of Gender. -- For each individual grizzly bear thus identified, WGI selected 1 extraction of good quality to determine gender based on a size polymorphism in the amelogenin gene (Ennis and Gallagher 1994).

RESULTS

In the Prairie Creek grid in 2003, fifteen (94%) of the 16 stations had bear hair: 10 had grizzly bear hair and 8 had black bear hair (3 stations had hair from both species) (Fig. 2). During this single session, 10 different grizzly bears -- 6 males and 4 females -- visited stations. The mean number of grizzly bears per station was 1.19 (\pm 0.26 SE). One female grizzly (F32) visited 4 stations encompassing a minimum area of approximately 115 km². None of the bears at multi-bear stations appeared to be related and may have

represented breeding associations or independent visits. Most of the black bear visits occurred along the South Nahanni River whereas most of the grizzly visits were higher up in the mountains. A wolf visited one station.

In 2003, male grizzly bear #33 was detected at stations 7 and 8 in the Prairie Creek grid within 10 km of the mine site. Interestingly, the next year, this same grizzly bear was detected at another grid station some 65 km distant at the south end of the Tlogotsho Plateau near the Yukon border (Fig. 1- Meilleur Tlogotsho grid). It is highly likely that this grizzly traveled through Nahanni National Park Reserve with this movement.

We collected hair samples from 36 rub trees at 15 sites along Prairie Creek. Unfortunately, most (83%) of these samples were too deteriorated already to produce reliable DNA for identification. Grizzly bear hair occurred on trees at 2 sites along Prairie Creek about 3 km and 11 km upstream of the mine site.

DISCUSSION

The Prairie Creek area ranks moderately high in grizzly bear occurrence compared to other areas in the Greater Nahanni Ecosystem. The Prairie Creek grid tied for 2nd highest in the average number of grizzly bears per station (1.19 ± 0.26 SE) and 3rd highest in the minimum number of grizzlies detected (10).

We have developed a provisional model and map of grizzly bear distribution and relative abundance across the Greater Nahanni Ecosystem following the modeling approach of Apps et al. (2004). This preliminary model also indicates that much of the Prairie Creek area, particularly in the valleys and mountains above the mine site, ranks moderately high in the likelihood of grizzly bear occurrence. Ground reconnaissance in 2004 revealed that sweet-vetch (*Hedysarum* spp.), a common plant food for grizzly bears in the Mackenzie Mountains (Miller et al. 1982), occurs consistently along the edges of the floodplain.

The mine site, airstrip, and winter access road are located near the center of the Prairie Creek survey grid (Fig. 2). Four grizzly bears (2M:2F) visited 5 sites within 10 km of the mine; all 10 sites visited by grizzlies lay within 20 km of the mine. A total of 6 different grizzly bears (4M:2F) visited the 3 sites that occurred along the section of the access road within the grid.

If additional mining activity is proposed in the Prairie Creek area, the notable concentration of grizzly bear activity documented herein warrants a detailed environmental assessment. Improved and/or unregulated road access would be an issue of special concern.

LITERATURE CITED

- Apps, C. D., B. N. McLellan, J. G. Woods, and M. F. Proctor. 2004. Estimating grizzly bear distribution and abundance relative to habitat and human influence. *The Journal of Wildlife Management* 68:138-152.
- Ennis, S., and T. F. Gallagher. 1994. PCR-based sex determination assay in cattle based on the bovine Amelogenin locus. *Animal Genetics* 25:425-427.
- Miller, S. J., N. Barichello, and D. Tait. 1982. The grizzly bears of the Mackenzie Mountains, Northwest Territories. NWT Wildlife Service Completion Report No. 3, Yellowknife. 118 pp.
- Paetkau, D. 2003. An empirical exploration of data quality in DNA-based population inventories. *Molecular Ecology* 12:1375-1387.
- Paetkau, D. 2004. The optimal number of markers in genetic capture-mark-recapture studies. *The Journal of Wildlife Management* 68:449-452.
- Paetkau, D., and C. Strobeck. 1994. Microsatellite analysis of genetic variation in black bear populations. *Molecular Ecology* 4:347-354.
- Paetkau, D., L. Waits, P. Clarkson, L. Craighead, E. Vyse, R. Ward, and C. Strobeck. 1998. Variation in genetic diversity across the range of North American brown bears. *Conservation Biology* 12:418-429.
- Poole, K. G., G. Mowat, and D. A. Fear. 2001. DNA-based population estimate for grizzly bears *Ursus arctos* in northeastern British Columbia, Canada. *Wildlife Biology* 7:105-115.

Weaver, J. L., P. C. Paquet, and L. F. Ruggiero. 1996. Resilience and conservation of large carnivores in the Rocky Mountains. *Conservation Biology* 10:964-976.

Woods, J. G., D. Paetkau, D. Lewis, B. N. McLellan, M. Proctor, and C. Strobeck. 1999. Genetic tagging free ranging black and brown bears. *Wildlife Society Bulletin* 27:616-627.

Fig. 1 Grizzly Bear Survey Areas in the Greater Nahanni Ecosystem



