

Appendix V4-9C

Doris North Gold Mine Project: Final Grizzly Bear DNA
Report, 2012



Hope Bay Mining Limited

DORIS NORTH GOLD MINE PROJECT Final Grizzly Bear DNA Report, 2012



Rescan™ Environmental Services Ltd.
Rescan Building, Sixth Floor - 1111 West Hastings Street
Vancouver, BC Canada V6E 2J3
Tel: (604) 689-9460 Fax: (604) 687-4277

August 2012

DORIS NORTH GOLD MINE PROJECT FINAL GRIZZLY BEAR DNA REPORT, 2012

August 2012
Project #1009-008-07

Citation:

Rescan. 2012. *Doris North Gold Mine Project: Final Grizzly Bear DNA Report, 2012*. Prepared for Hope Bay Mining Limited by Rescan Environmental Services Ltd.

Prepared for:



Hope Bay Mining Limited

Prepared by:



Rescan™ Environmental Services Ltd.
Vancouver, British Columbia

Executive Summary

Executive Summary

In 2010, Hope Bay Mining Ltd. (HBML) tasked Rescan Environmental Services Ltd. to conduct an estimate of the number of grizzly bears at the Doris North Project site. This was undertaken following a request by the Department of Environment, Government of Nunavut, and satisfies the Doris North Project Certificate obligations to monitor grizzly bear populations in this area.

The grizzly bear monitoring program was designed and implemented in 2010 and 2011 using baited hair capture stations arranged in a grid of 65 cells surrounding the Doris North Site; each grid being 10 x 10 km. On January 31, 2012, HBML placed the Doris North Project into Care and Maintenance. This document is a final report that describes the 2010-2011 fieldwork and sample analyses. The detailed genetic analysis data and a summary of the capture/recapture data for 2010-2011 are also presented and discussed.

In 2010, a total of 411 hair samples were collected. When analyzed, 163 of these samples could be assigned to individuals, yielding a total of 31 individual bears in the study area. During 2011, the study area was approximately doubled in size, from 3,700 km² to 6,500 km². A combination of increased study area, improved bait, improved location of stations and drier weather led to a four-fold increase in samples during 2011 to 1,623 samples. Stricter sub-selection rules resulted in a lower proportion of samples available for microsatellite genotyping. Of the samples submitted in 2011, 241 samples could be assigned to 39 individuals, 18 of which were recaptures from 2010. Overall, a total of 52 individual grizzly bears (27M:25F) were identified over the two-year program.

Changes to the study area configuration to accommodate potential future activities around the Boston deposit preclude inclusion of all 65 cells in the estimate of population size. As a result, a population estimate was derived only for the original northern portion of the Doris North study area (37 cells). The population estimate is only the number of animals estimated to be on the study area during the sampling period, and is not intended as a true population estimate or for the calculation of population density. A total of 41 individual grizzly bears were detected in the reduced study area over the two year program. Based on estimated capture and recapture probabilities, the population of grizzly bears on the northern portion of the Doris North study area was estimated at 45 (25M:20F) in 2010, and at 31 (13M:18F) in 2011. The marked reduction in males in 2011 is not a real decrease, but likely a function of small study area size relative to the large home ranges and movements of barren-ground grizzly bears that make them unlikely to be encountered repeatedly in a given year. The stability of females is consistent with the observation that 11 of the 14 female grizzly bears that were captured in 2010 were recaptured in 2011. Females also have much smaller home ranges and movements than males, and typically demonstrate high fidelity to those home ranges.

Despite some sampling limitations that are discussed further in this report, results from this study indicate that this northern coastal region of Nunavut is highly productive for grizzly bears, owing to extensive foraging and hunting opportunities (including seasonally available caribou, seal, and Arctic char), and access to productive fish bearing river corridors and riparian zones. Detection rates are on the order of 8-11 grizzly bears per 1,000 km², which is likely proportional to overall densities.

Table of Contents

DORIS NORTH GOLD MINE PROJECT

FINAL GRIZZLY BEAR DNA REPORT, 2012

Table of Contents

Executive Summary	i
Table of Contents	iii
List of Figures	iv
List of Tables	iv
List of Plates	iv
List of Appendices	iv
1. Introduction	1-1
2. Methods	2-1
2.1 2010	2-1
2.1.1 Study Area	2-1
2.1.2 Hair Collection	2-1
2.2 2011	2-2
2.3 Lab Analysis	2-2
2.3.1 Database Management and DNA Extraction	2-2
2.3.2 Microsatellite Genotyping	2-8
2.4 Population Analyses	2-8
3. Results	3-1
3.1 Lab Results	3-1
3.1.1 2010	3-1
3.1.2 2011	3-2
3.2 Population Analyses	3-3
4. Discussion	4-1
References	R-1

List of Figures

FIGURE	PAGE
Figure 1-1. Doris North Project Location	1-2
Figure 2.1-1. Grizzly Bear DNA Survey Grid, Doris North Project, 2010	2-3
Figure 2.2-1. Grizzly Bear DNA Survey Grid, Doris North Project, 2011	2-5
Figure 3.2-1. Grizzly Bear DNA Hair Capture Locations, Doris North Project, 2010	3-5
Figure 3.2-2. Grizzly Bear DNA Hair Capture Locations, Doris North Project, 2011	3-7

List of Tables

TABLE	PAGE
Table 3.2-1. Model Rankings for Grizzly Bear Population Estimation in the Doris North Study Area (Cells 1-37), 2010-2011	3-4
Table 3.2-2. Parameter Estimates Derived from the Top Model Describing Grizzly Bear Population Dynamics in the Doris North Study Area (Cells 1-37), 2010-2011	3-4

List of Plates

PLATE	PAGE
Plate 2.1-1. Tripod design used during 2010 grizzly bear DNA study.....	2-2
Plate 2.2-1. Fold-up tripod design used during the 2011 grizzly bear DNA study.	2-7
Plate 2.2-2. Fold-up hair snagging tripod anchored with wooden stakes.....	2-7

List of Appendices

Appendix 1. Detailed Field Hair Collection and Genetic Marker Data, 2010
Appendix 2. Summary of Individual Bear Genotypes and Capture/Recapture Rates, 2010
Appendix 3. Detailed Field Hair Collection and Genetic Marker Data, 2011
Appendix 4. Summary of Individual Bear Genotypes and Capture/Recapture Rates, 2011

1. Introduction

1. Introduction

The Doris North Gold Mine Project (the Project) is located approximately 125 km southwest of Cambridge Bay, Nunavut, on the south shore of Melville Sound (Figure 1-1). The nearest communities are Omingmaktok (75 km to the southwest of the property), Cambridge Bay, and Kingaok (Bathurst Inlet, 160 km to the southwest of the property).

The Project has received all necessary permits, licences, and authorizations for development. Hope Bay Mining Ltd. (HBML) began construction of the Project in 2010 and continued in 2011. On January 31, 2012, HBML announced that the Project would be transitioned into care and maintenance. The Wildlife Mitigation and Monitoring Program (WMMP), of which the grizzly bear DNA study is a component, is one of the requirements of the Doris North Gold Mine Project Certificate.

Prior to baseline data collection, a number of Valued Ecosystem Components (VECs) were identified in the 2005 Environmental Impact Statement (EIS) (Miramar 2005). The selection of these VECs was based on a three-day consultation and assessment workshop of Inuit Quajimajatuqangit (Inuit traditional knowledge [IQ]) held with elders in Cambridge Bay in September 2003. In addition, the Kitikmeot Inuit Association (KIA) highlighted a number of species for mitigation and monitoring (KIA 2004). Recommendations included monitoring and mitigation for the effects of roads on caribou and other wildlife, and concerns over the potential attraction and negative influence of the mine on caribou, wolverine, and grizzly bears. The KIA further recommended that data be collected in a manner that is consistent with understanding and managing regional cumulative effects. Similarly, the Government of Nunavut (GN DOE 2004), in discussions with HBML, identified that caribou, grizzly bears, and wolverines are key species that require monitoring. Other discussions involved developing mitigation measures for all wildlife, monitoring reactions of caribou to roads and facilities, and designing studies that will help participate in initiatives for understanding regional cumulative effects. Field programs then focused on collecting baseline information and assessing impacts on these VECs. Extending the VEC framework from the EIS to the WMMP facilitated the selection of ecological endpoints for indicators, which formed the basis for monitoring potential local and regional cumulative effects.

Based on the comments and recommendations of stakeholders, the barren-ground grizzly bear (*Ursus arctos*) was selected as a VEC to be incorporated into the WMMP. The northwestern (BC, YT, AB, NT, NU) population of grizzly bears is considered to be of “special concern” by the Committee on the Status of Endangered Wildlife in Canada (COSEWIC 2002). Incidental observations of grizzly bears have been recorded during each year of exploration and baseline studies in the Hope Bay area. The combination of direct (i.e., changes in habitat availability) and indirect effects from infrastructure related activities may negatively influence the survival and reproduction of grizzly bears with home ranges that overlap the study area. The EIS predicted that the Project would have a minor impact on the movement and distribution of carnivores (Miramar 2005).

The original objective of the WMMP for grizzly bears was to:

- determine the abundance and distribution of grizzly bears within the study area.

During 2005 to 2008, this objective was addressed by quantifying habitat use by grizzly bears at various distances from the Project footprint. Habitat use was quantified as the proportion of riparian vegetation plots which had been used by grizzly bears during each year. These studies were discontinued in 2009 due to safety concerns over staff working in prime grizzly bear habitat and because it was deemed that



Figure 1-1

sufficient baseline data of this type had been recorded. HBML was also interested in evaluating alternatives that would more directly measure grizzly bear abundance and habitat use.

Researchers have used live capture to mark bears and then recaptured bears using camera stations (Mace et al. 1994), aerial survey (Larsen and Markel 1989), and hair removal and DNA fingerprinting analysis (Proctor et al. 2005). Most recently, hair removal and DNA fingerprinting have been used to mark and recapture bears (Woods et al. 1999; Poole et al. 2001, Mowat and Strobeck 2000, Boulanger et al. 2002, Proctor et al. 2005, Apps et al. 2006, Rescan 2011). This latter method has several benefits because live capture of bears is unnecessary, individuals can be identified with a small risk of error, and hair removal sites are faster to set up and are checked less often than live-capture sites (Mowat and Strobeck 2000). Roots of mammalian hair contain sufficient DNA for analysis (Higuchi et al. 1988). For free-ranging bears, hair is an attractive DNA source because bears frequently leave hair on rub trees, in beds, and at foraging sites (Taberlet et al. 1993). Because bears are readily attracted by scent lures, methods to obtain hair samples from free-ranging bears permits systematic sampling regimes necessary for many ecological studies, such as animal censuses (Woods et al. 1999). In mark-recapture studies, an initial population sample is captured, marked, and released. The population is then resampled during ≥ 1 additional sessions (Woods et al. 1999). The ratio of newly captured animals to recaptures is then used to compute a population estimate (White et al. 1982).

Bears traverse in and out of grid areas during sampling, which violates the assumption of geographic closure in most studies that use mark-recapture or related methods (Miller et al. 1997). Abundance estimates derived from mark-recapture correspond to the “superpopulation” if movement is random across grid boundaries (Kendall 1999). In the context of mark-recapture DNA studies, the superpopulation is defined as the number of animals that inhabit the sampling grid and surrounding area (as opposed to the grid alone) (Boulanger et al. 2004). While the superpopulation estimate represents the number of animals that traverse an area, the estimate is compromised by the undefined sampling area and therefore cannot be used to estimate density (Boulanger et al. 2004). Under a trend monitoring objective, however, an absolute abundance or density estimate is not necessary, and the assumptions of population closure can be relaxed (Apps 2010). In this case, the initial superpopulation estimate can be used as the basis for monitoring relative changes over the long term.

HBML has conducted a two year assessment of grizzly bear abundance and distribution using a DNA hair-capture study (2010-2011). This report provides final results from 2010 and 2011.

The objectives for the overall grizzly bear DNA program were to:

- generate a superpopulation estimate for the Doris North study area as a potential baseline for trend monitoring; and
- describe the spatial and temporal distribution grizzly bears on site.

2. Methods

2. Methods

2.1 2010

2.1.1 Study Area

A study area of approximately 3,700 km² (37 cells, each measuring 10 × 10 km; Figure 2.1-1) was initially selected to begin the program (GB1 to GB37) in 2010. During the last two sampling periods, cells GB38 to GB49 were added to incorporate the Boston deposit area, increasing the study area to approximately 5,000 km². The choice of cell size was dependent on several factors, including the need to maximize capture probabilities (i.e., the likelihood of obtaining a hair sample), minimizing capture heterogeneity (i.e., variation in capture rates by sex and age class), and logistics. The cell size was chosen so that it was not larger than the expected area used by an individual bear over a sampling period, and it was assumed that a bear traveling through a cell had an equal probability of encountering a sampling post as any other bear (Apps 2010).

2.1.2 Hair Collection

One wooden tripod wrapped in barbed wire was used to collect grizzly bear hair (Plate 2.1-1) in a given cell, and the tripod remained at that location for the duration of the sampling season. Within each cell, the tripod was located in an area of high quality grizzly bear habitat (e.g., esker, riparian area, upland meadow, wetland meadow) to increase the likelihood of “capturing” a bear. A short-distance, non-reward synthetic lure (e.g., fish oil, castor oil, commercial bear bait, and sweeter scents like anise oil and cherry oil) was used to attract bears to the tripods. The lures were poured on the top of the posts, down the legs, and in the centre on the ground to encourage a bear to squeeze between the legs. The posts were not relocated between each sampling period; therefore, a novel scent combination was used each session to prevent habituation.

There were six sampling periods between June 12 and August 30, at approximately two week intervals. Most studies in British Columbia opt for three to four sessions (Apps 2010); however, given the relatively low densities of grizzly bears in the Arctic, and their large home ranges (~2,000 km² for females) and movement patterns, it was decided that more sessions were required to ensure sufficient captures and recaptures of individuals for population analyses.

Hairs were collected from each individual barb and placed in a separate coin envelope. Once collected, hair samples were air dried for 48 hours and stored in paper bags. For each tripod, the three posts were arbitrarily selected as post 1, 2, or 3. Hair samples were labelled according to which post they were found on. For subsampling purposes, hair samples along a post were grouped into clusters. A cluster is defined as a series of hair samples from consecutive barbs. A new cluster is identified following an empty barb. Samples within a cluster were assumed to be from the same individual. All hair samples were sent to Wildlife Genetics International (WGI), Nelson, British Columbia for DNA analyses. Sub-selection rules were also provided that attempted to balance budgetary considerations with sample size and hair sample quality. Based on these sub-selection rules, WGI selected hair samples within a cluster they deemed most suitable for DNA extraction. All clusters were sampled. Leftover hairs have been archived at WGI.



Plate 2.1-1. Tripod design used during 2010 grizzly bear DNA study.

2.2 2011

In 2011, the study area was expanded to approximately 6,500 km² (Figure 2.2-1) to include the full Doris North Regional Study Area (RSA), which covers the area of potential future Phase 2 development. To simplify deployment, a fold-up tripod design was used (Plate 2.2-1), where the legs were anchored with twine tied to a stake (Plate 2.2-2). As in 2010, non-reward lures were used during each session, consisting of cured cows blood (500 mL per station), fish oil, castor oil, commercial bear bait, or sweeter oils (later in the season to mimic berries). Samples were collected at approximately two week intervals between June 14 and August 30. Hair samples were collected, labelled, stored, and shipped using the same procedures as 2010.

2.3 LAB ANALYSIS

2.3.1 Database Management and DNA Extraction

As per the sub-selection rules, WGI selected samples by setting aside up to half of the samples in each cluster. WGI attempted to bias towards high quality samples while also picking samples least likely to come from the same bear (i.e., samples that were not collected from adjacent barbs).

DNA was extracted using QIAGEN's DNeasy Tissue kits, and following the manufacturer's instructions (for details search <http://www.qiagen.com>). WGI aimed to use 10-20 guard hair roots where available. When underfurs were used, the number of roots used in the analysis was an estimate because entire clumps of whole underfur were extracted rather than clipping individual roots.

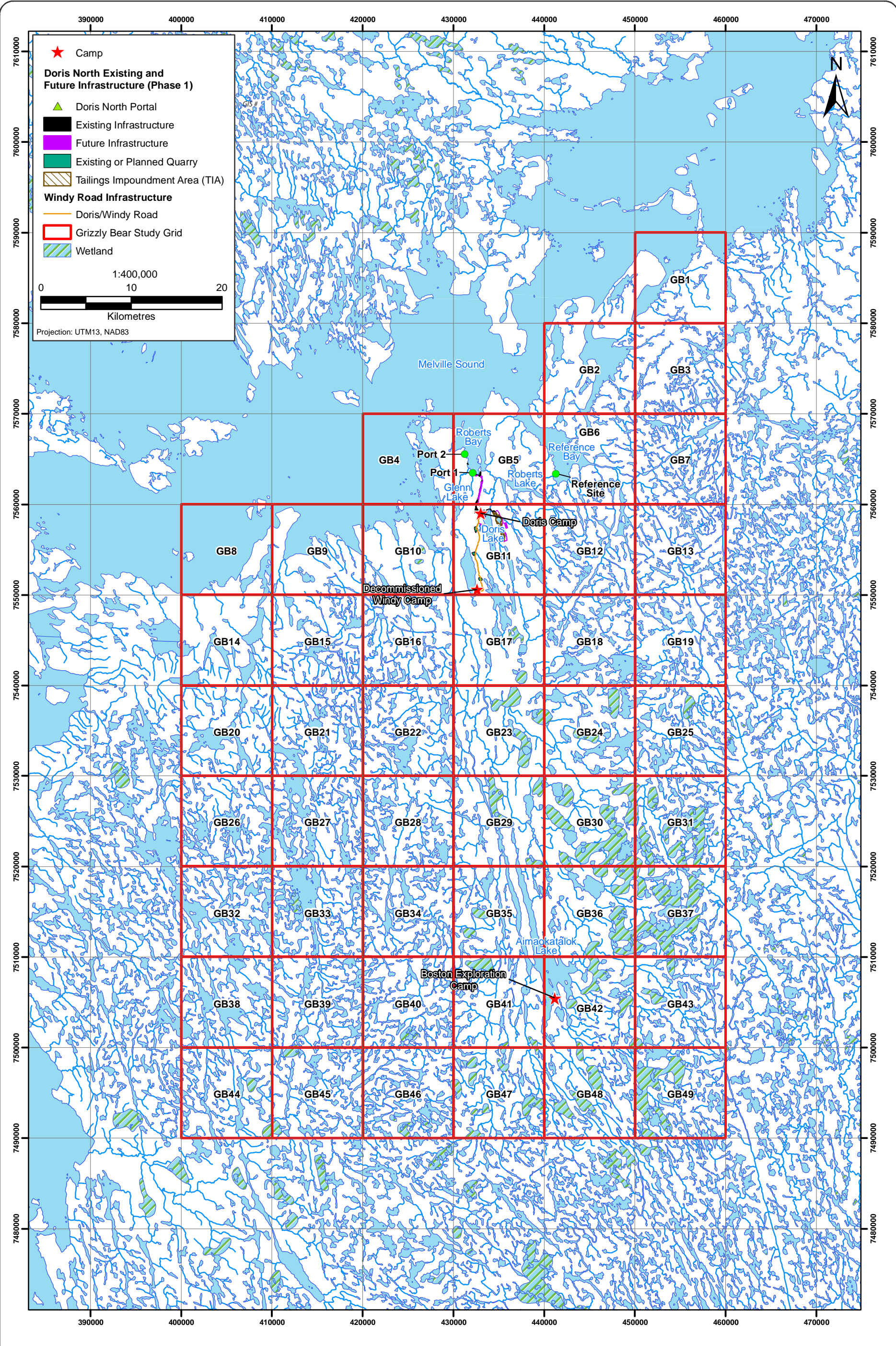


Figure 2.1-1

Figure 2.1-1