NWSF #244-14-02

Final Activities Report

Gjoa Haven Hunters and Trappers Association
Malcolm May, Kyle Aglukkaq
& Peter Van Coeverden de Groot

04/07/2022

Contribution agreement # 15-004-01 File # 150219

Table of Contents

I. Project Summary

Non-technical Summary:

This report describes an experimental method for non-invasive polar bear subpopulation management, involving the collection of hair-based genetic material that was carried out in May 2015. This study was conducted with financial aid from NWSF Contribution Agreement #15-004-01, as amended on March 2, 2015 [1]. The field work was completed by members of the Gjoa Haven Hunters' and Trappers' Association, and further genetic and economic analyses were completed by Queen's University and WGI international.

Highlights:

1. In 2015, 28 hair snaring stations were erected and dismantled 1 week as part of a sea-ice transect, off the coast of Cape Sydney, King William Island, Nunavut.
2. The study area covered ~ 2,100 km^2 of sea-ice.
3. 49 hairsnag samples were collected.
4. In the same area surveyed ~ 1 week prior via aerial biopsy [Government of Nunavut (GN)], 8 aerial biopsies tissue plugs were collected.
5. Sufficient genetic material was collected to positively identify and sex 14 polar bears (7F, 7M) with a 9-locus microsatellite genotype assay as used by the GN.
6. Suspected sex bias of the stations as suggested previously [6], was not supported by this study.
7. 3 of 14 identified polar bears were found to be resampled from previous aerial surveys conducted by the GN.
8. Maximum recapture rate of a single bear was 4 discrete captures
9. Complete genotype success rate was approximately 61% (30/49) across all hair samples. And the success rates of individual loci (9 loci) were similar: *min*. 61%, *max*. 63%, *sd =* 1%.
10. Only samples with roots genotyped with a success rate of 81% (30 of 37).
11. Management implications of these findings are discussed, and future work based on these findings is proposed.
12. Inuit diagnoses of footprints were not attempted in 2015
13. Biopsy darting on-the-land was not attempted in 2015.
14. Faecal sample collection was not attempted in 2015.

II. Project Objectives

There were 5 Original and 3 Supplementary Objectives – for a total of 8 Objectives

Original Objectives:

1. *Erect, Collect-hairsnags from contacted sampling stations, and Dismantle Polar Bear Sampling Stations.*   Accomplished in 2015, (see *Methods.)*

2. *Inuit diagnoses of footprints*   - not attempted in 2015

3. *Biopsy darting on-the-land*   - not attempted in 2015.

4. *Faecal sample collection*   - not attempted in 2015.

5. *Planning Reporting, and Communication*   - Accomplished and ongoing, (see *Discussion*.)

Supplemental Objectives:

6. *Compare microsatellite genotyping success for our polar bear hairsnags using similar loci and the identical genotyping process as currently used by the Government of Nunavut Wildlife Research (GN) for their aerial biopsy polar bear samples –* Accomplished and ongoing (see *Results).*

7. *Determine whether any of the bears sampled in this ground-based survey were previously sampled by the recently completed (one week prior) GN aerial biopsy survey of the same area –* Accomplished and ongoing (see *Results).*

8. *Compute preliminary economic analysis of field based hairsnag sample and genotyped collection. –* Accomplished and ongoing (see *Results).*

III. Materials & Methods

Sampling Methods

Study Area

This pilot study was conducted on the sea-ice north of Cape Sydney (69.8506, -97.6592), in the M'Clintock Channel Polar Bear Management Unit (MCMU). The study area covered an approximate 2100 square kilometres. Hair sampling stations were erected directly on the sea-ice, interspaced by approx. 10 km, and stations remained on the sea ice for between 2-4 days. This short study was conducted immediately following the Government of Nunavut's (GN) aerial biopsy survey, within a shared area in early May 2015 (see Figure 1).
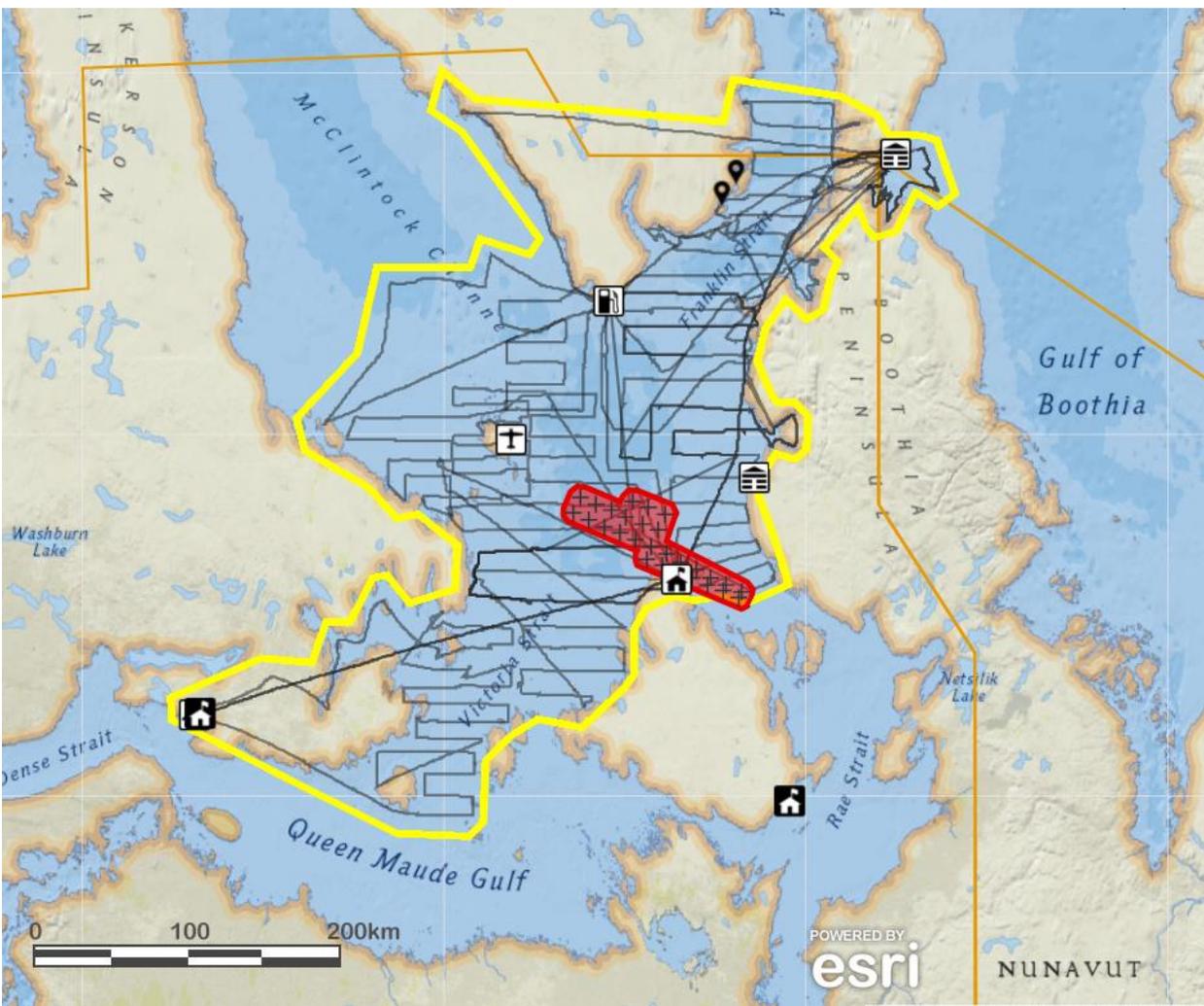
Figure 1: Location of the M'Clintock Channel polar bear surveys. The red polygon with **+** symbols represents the extent of the ground-based survey in 2015. The yellow polygon represents the GN's aerial biopsy survey of the M'Clintock Channel Management Unit (MCMU) in 2015. All helicopter tracks flown in MCMU in 2015 are shown in black. The last day of the GN aerial survey - covering our proposed study area - occurred 5 days before the first traps were erected near Cape Sydney (May 13, 2021). Track data provided by Markus Dyck.

Sampling Stations and Sampling

Hairsnag samples (Figure 2) were collected from 28 *sampling stations* (Figure 3) that were erected in a grid pattern on the sea-ice, extending from the M'Clintock Channel south-eastward into the James Ross Strait (Figure 4). Our proposed work was based around that of the late Markus Dyck (GN polar bear biologist) once he communicated he had finished his aerial survey, we commenced the erecting of our grid.

Functionality of our Sampling Stations was first demonstrated with the erection of a single station (#1) set-up over-night on the 13th of May. Hairsnags were collected the following day from station #1 and the remainder of the sampling grid was subsequently erected by two teams, each comprised of 2 snowmobiles and 3-4 personnel. Each team completed two trips on the sea-ice, the first trip being for the set-up of stations, and the second trip for the recovery of samples and the takedown of all stations. One team travelled north of Cape Sydney into the M'Clintock Channel, while a second team travelled south into the Clarence Islands and James Ross Strait.

Sampling stations comprised of 4 metal T-bars placed in a corral, with corners forming a 10ftx10ft square, that were wrapped with two strands of barbed wire. This station was used after our previous evaluations of alternate ursid hairsnagging methodologies in 2006 and 2007 [2]. The first and second layers of wire were ~1.5 ft and ~3 feet off the ground, respectively. A fifth T-bar was placed in the center of the square and baited with seal blood (Figure 3A). All stations were baited and checked between 1 and 3 days after being set and hair snags collected with tweezers from all sampling stations that were contacted (Figure 5). The stations were checked once and then dismantled.

Polar bear hairsnags were stored frozen in cryovials, and these vials were sent to Queen's University for subsequent microsatellite profiling at Wildlife Genetics International, Inc. (WGI; http://www.wildlifegenetics.ca/index.html). These samples were subjected to the same microsatellite profiling as the biopsy samples collected during the GN inventory surveys.

*Below we report:*

a) *The locations of our 28 sampling stations,*
b) *The total number of hairsnags collected,*
c) *The average number of hairsnags from each contacted sampling station.*

Footprint analyses by Inuit diagnoses and photographs, as outlined in the 2014 NWSF application, were not attempted in 2015. Live biopsy sampling was also not attempted in the 2015 fieldwork season.

Figure 2: Hairsnag - Hair sample recovered from a sampling station. Using similar genetic profiling as the GN, we determined the sex and identity of the bear. We also determined which bears sampled through the hairsnag method were also sampled through the recently completed GN aerial biopsy survey. Some hair roots are visible on the centre-left side of the hairsnag. Samples were collected from the wire using tweezers.

A **B**

Figure 3: Polar bear sampling stations used in past work. The metal T-Bars are driven into the sea-ice and wrapped with 2 barbed wires with the lower one about 1.5ft off ground and the top one 1.5 ft from the lower one (Fig 3A). A sampling station following a polar bear sampling event (Fig 3B.)
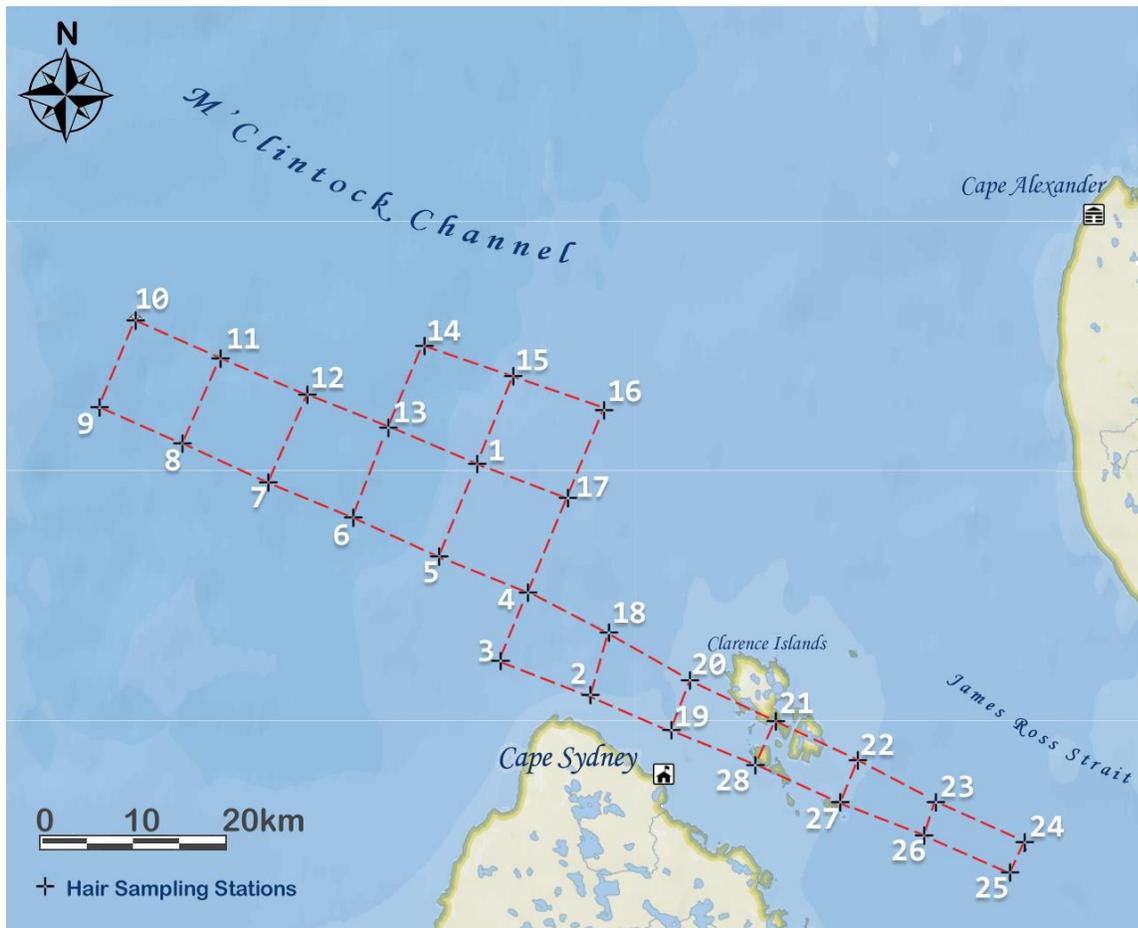
Figure 4: Hair sampling station locations north of King William Island, set during May 2015. We attempted to space 28 stations approximately 10 km apart. Sampling station '#1' was used to demonstrate station functionality overnight on the 13th of May. Between the 13th and 15th of May 2015 all stations were erected. Stations were checked for hairsnags between the 17th and 19th of May (see Figure 5). The location of the Gjoa Haven HTA camp at the tip of Kings William Island is shown with a house icon. A similar camp is indicated at Cape Alexander.

Laboratory Methods and Initial Genetic Analysis

To estimate the number and sex of bears contacted in the land-based survey, DNA extracted from hairsnags was genotyped and genetically sexed using the same microsatellites and genetic sex markers as used for DNA extracted from biopsies collected from GN polar bear aerial surveys. The 8 microsatellite loci were the same as used by the GN to genotype aerial biopsy samples: Ren 145P07, G10B, CXX20, MU50, G10H, UarMU59, G10P and G10X [3]. Also included was a ZFX/ZFY locus for sexing bears [3]. All laboratory work for this hairsnag and the accompanying GN aerial biopsy survey was completed by Wildlife Genetics International, Inc. (WGI; http://www.wildlifegenetics.ca/index.html).

DNA was extracted from hair samples and amplified and scored as per the 3-step protocol previously validated for bear aerial biopsy tissue [3]. The veracity of genotyping DNA from hairsnags at 6 variable microsatellite loci was demonstrated in 2013 using the following loci [2,4] G1D, G10B, G10L [5]; UarMU59, G10J [6]; and MSUT08 [7]. The 9 loci used by WGI only includes 2 of these previously optimized loci, but also include 2 additional microsatellites (8 vs 6) in this microsatellite genotype assay of polar bear hairsnags.

Below we report:

    a) *Genotyping success using the 9 study loci,*
    b) *The number and sex of bears contacted through our 28 sampling station method,*
    c) *The number of polar bears resampled in our study,*
    d) *The number of bears contacted in both the hairsnag and the GN aerial biopsy studies conducted in MCMU in 2015,*
    e) *The number of samplings stations visited by more than one bear - despite being set only once.*

Economic analysis

Along with calculation of hairsnagging efficiency and genotyping success, the calculation of direct field costs is needed to determine the relative cost-effectiveness of this non-invasive community-level polar bear 'monitoring' method when compared to the cost-effectiveness of current aerial biopsy polar bear surveys.

Our initial economic analysis used direct field costs of on- the-land field sampling derived from the NWSF #244-14-02 Financial Report [8] with additional estimated management wages based on the full-time effort (FTE) of a research scientist for a period of 2 months. Genotyping costs were not included as they are assumed to be equal across the 2015 hairsnagging and 2015 GN aerial biopsy surveys. All genotyping was carried out by WGI and per sample costs are reported as similar for these tissue types (D. Paetkau pers comm.)

We approximated the management costs of this survey at 2 months (0.1666) FTE for a Research Scientist @90K p.a. (including benefits).

Cost per unit of various outputs was calculated for:

- hairsnags,
- 8 microsatellite genotype & genetic sex - a *GN Genotype* - for a hairsnag,
- unique polar bears as per *GN Genotype* from their hairsnags and,
- erected sampling stations

These estimates were made by dividing total survey cost by the number of hairsnags, number of complete genotypes, number of individuals identified, and number of sampling stations erected

Below we report:

    i) *Total field project costs, including wages, camping supplies, field equipment, and management costs;*
    ii) *Costs per hairsnag, per successful GN Genotype, per individual ID, and per sampling station erected.*

IV. Results

Sampling Results

a)   *Sampling station locations*
  - Locations of the 28 sampling stations are shown in Figure 3.

b)   *Total number of hairsnags collected*
  - 14 of 28 sampling stations were contacted during the study – yielding a 50% success rate. (The location of the 14 sampling stations that were contacted by polar bears is shown in Figure 5)
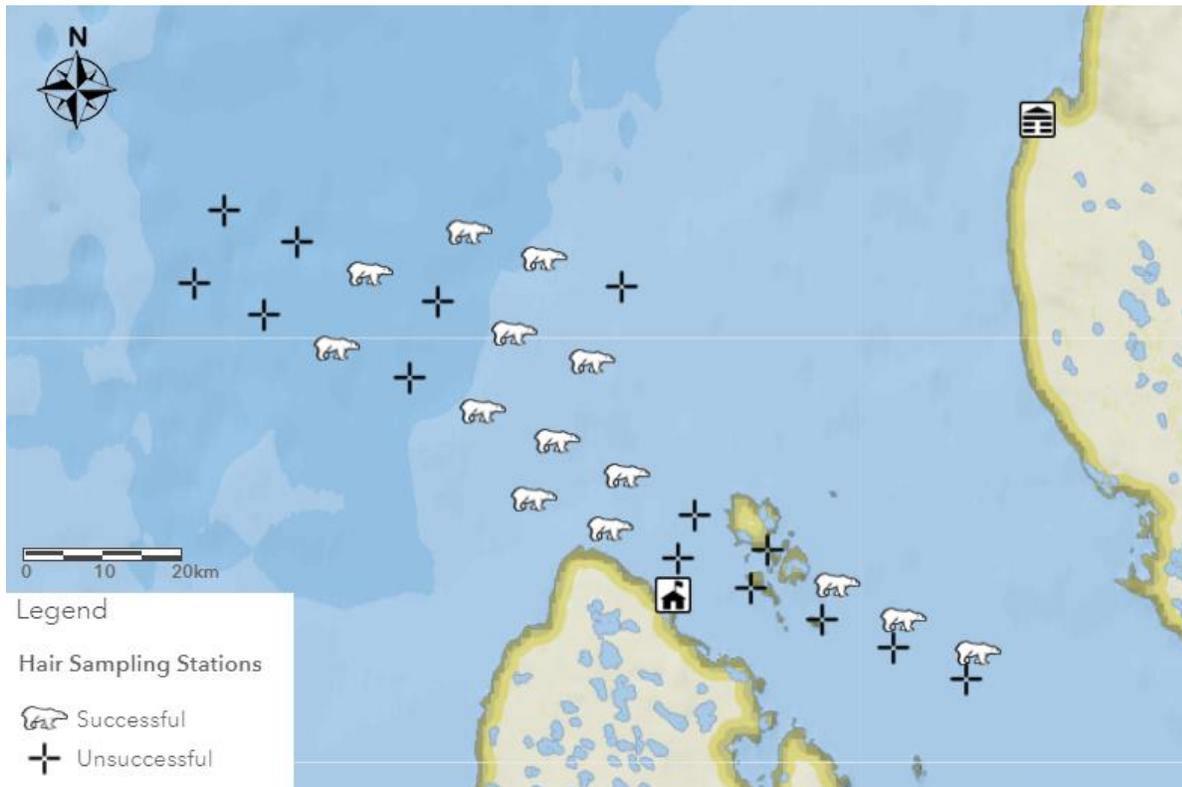
Figure 5. Successful and unsuccessful sampling stations in the ground based 2015 polar bear survey. 14 /28 (50%) of sampling stations were contacted by polar bears. An average 3.50 +/- 1.87 (σ) hair samples were collected from these 'successful stations' with a weighted average of 1.75 +/- 2.20 (σ) hair samples across all stations. Successful stations yielded hair samples, denoted by a polar bear, while unsuccessful stations did not yield any samples. The location of two field camps is shown by two house icons.

c)   *Average number of hairsnags from each contacted sampling station*

  - 49 hairsnags were collected from these 14 stations with the average number of hairsnags from each 'contacted' sampling station = 3.50 +/- 1.87 (σ), with a weighted average of 1.75 +/- 2.20 (σ) hair samples per station across all stations, (see Table 1 for more detail.)

Table 1: Hairsnag sampling success at 28 sampling stations erected in MCMU, May 2015.
49 hairsnags were recovered from 14 stations with an average of 3.50 +/- 1.87 (σ) hair samples
were collected from these 'successful stations' with a weighted average of 1.75 +/- 2.20 (σ) hair
samples across all stations. *Station* = station number as shown in Figure 3. *Contacted/Not
Contacted* = the contact success of the station. *Latitude* and *Longitude* are given in decimal-
degrees. *Samples* = the sample numbers (labelled on 1.5ml Eppendorf test tubes) collected at
each station. *Number of samples* = number of samples at each station.

Station	Contacted/not contacted	Latitude	Longitude	Samples	Number of Samples
1	Contacted	70.1462	-98.1766	**001, 002, 003**	3
2	Contacted	69.9242	-97.8596	**004, 005, 006, 007, 008, 009**	6
3	Contacted	69.9573	-98.1109	**010**	1
4	Contacted	70.0236	-98.0359	**011, 012, 013, 014, 015**	5
5	Contacted	70.0578	-98.2838	**016, 017, 018, 019, 020**	5
6	Not Contacted	70.0953	-98.5257	**None**	0
7	Contacted	70.1289	-98.7665	**021, 022, 023, 024, 025, 026**	6
8	Not Contacted	70.1663	-99.0064	**None**	0
9	Not Contacted	70.2007	-99.2406	**None**	0
10	Not Contacted	70.2837	-99.139	**None**	0
11	Not Contacted	70.2475	-98.8994	**None**	0
12	Contacted	70.2131	-98.6564	**027, 028, 029**	3
13	Not Contacted	70.1816	-98.4278	**None**	0
14	Contacted	70.2594	-98.3255	**030**	1
15	Contacted	70.23	-98.0763	**031, 032, 033, 034**	4
16	Not Contacted	70.1981	-97.8211	**None**	0
17	Contacted	70.1139	-97.9219	**035, 036, 037, 038**	4
18	Contacted	69.9842	-97.8067	**039**	1
19	Not Contacted	69.8906	-97.6321	**None**	0
20	Not Contacted	69.9387	-97.5778	**None**	0
21	Not Contacted	69.8989	-97.3387	**None**	0
22	Contacted	69.8607	-97.1063	**100, 200, 300, 400, 500**	5
23	Contacted	69.8202	-96.8861	**600, 700, 800, 110**	4
24	Contacted	69.7816	-96.6381	**900**	1
25	Not Contacted	69.7517	-96.6772	**None**	0
26	Not Contacted	69.7883	-96.9193	**None**	0
27	Not Contacted	69.8208	-97.1561	**None**	0
28	Not Contacted	69.8568	-97.3938	**None**	0

Note: A change in number format starting at station 19 reflects the collection by a different
snowmobile team for stations 19-28, versus stations 1-18.

Laboratory Results

a. *Genotyping success using the 9 study loci*

Hairsnag DNA amplified with three levels of success: 1. Complete 9-locus success, at all 9 GN loci assayed = a *GN genotype* (See Appendix A). 2. Amplification at some of the 9 loci = *partial genotypes* (See Appendix B). 3. Rootless samples failed to amplify at any loci = *failures* (See Appendix C).

Two estimates of genotyping success are presented:

Overall hairsnag success

- 30/49 hairsnag samples (61.1%) yielded a *GN genotype.*

Genotyping success of samples with roots

- 30/37 hairsnag samples with roots (81.1%) yielded a *GN genotype.*
- 7/49 (14.3%) hairsnag samples with roots yielded only *partial genotypes:*

  All *partial genotype*s had one or more alleles that were not found in the *GN Genotypes* and or had 3 alleles scored at some loci (should only have 2). Therefore these partials were not considered in amplification success estimates. Two samples amplified at 8 of 9 loci, one amplified at 7 of 9 loci, one amplified at 5 of 9 loci, and three amplified at 2 of 9 loci.

Hairsnags without roots did not amplify

- 12 /49 (24.5%) hairsnag samples lacked hair roots, and failed to amplify at any loci = *failures.*

b. *Number and sex of polar bears*

- 14 individual polar bears (7M/7F) were successfully identified and sexed, from 30 successful genotypes of 49 total samples *(See Table 2)*

c. *Resampled polar bears within this study*

- 2 bears were resampled three times. Hair samples of polar bear ID "17" (male) were found at stations 5, 22, and 23, and hair samples of polar bear ID "30" (female) were found at stations 14, 15, and 17. (See Table 3)

d. *Resampled polar bears from the near-simultaneous 2015 aerial biopsy survey*

- 3 individuals were resampled from the Nunavut harvest and aerial biopsies (See Table 2):
  - MC-2014-29;
  - MC-2014-39;
  - MC-2015-60.

e. *The number of samplings stations visited by more than one bear - despite being set only once.*

- 2 sampling stations (#2 & #7) were each visited by 3 individuals.
  - Sampling station #2 by bears 8 (M), 9 (F), and MC-2015-60 (M).
  - Sampling station #7 by 21 (F), 23 (F), and 26 (F).

Table 3: Characteristic of Polar bear Individuals and their corresponding samples. 14 (7M/7F) polar bears were identified using 8 microsatellite loci and genetically sexed. These data were derived from 30 complete 9 locus genotypes from 49 hairsnag samples. 7 hairsnags yielded incomplete genotypes and 12 hairsnags yielded no amplifiable DNA. 2 Polar bears - ID 17 and 30 - each visited 3 different sampling stations. 3 Polar bears - MC-2014-29, 2014-39 and 2015-60 - were resampled from 2014 and 2015 Nunavut aerial biopsy surveys. Also, 2 sampling stations - #2 and #7 - were visited by 3 different bears. (See Appendix A, B, and C for more details). *Genotype ID* = individual bear named for its first unique sample, unless previously tagged in the GN aerial biopsy surveys. *Sex* = sex as per ZFX/ZFY locus [5]. *Hair Samples* = successfully genotyped hairsnag samples that can be attributed to an individual via their genotype. *Sampling Stations* = stations where this individual was sampled.

Genotype ID	Sex	Hair Samples	Sampling Stations
MC-2014-29	M	011; 015;	4
MC-2014-39	M	900;	24
MC-2015-60	M	004; 005;	2
8	M	008;	2
9	F	009;	2
10	F	010;	3
14	M	014;	4
16	M	016;	5
17	M	017; 100; 200; 600; 700; 800; 110;	5, 22, 23
21	F	021; 024;	7
23	F	023;	7
26	F	026;	7
27	F	027; 028; 029;	12
30	F	030; 032; 034; 035; 036; 038;	14, 15, 17

Economic Results

i) Wages, camping supplies, and field equipment costs.

• Wages, camping supplies, field equipment and Management costs are reported in Table 4.

Table 5: Total project costs of the 2015 hairsnag project, including direct and management costs. Direct project costs were reported in the accompanying Financial Report for NWSF #244-11-02 [8]. Wages and camping supplies were over budget due to weather delays. Conversely, field equipment was less costly than anticipated in 2015. Management cost was estimated from 2/12 months FTE @ 90k p.a., benefits included. *Budget Item* = Nature of costs. *Budgeted* = Proposed item cost. *Variance* = Budgeted ÷ Disbursed. *Disbursed* = Final costs of budget items.

Budget Item	Budgeted	Variance	Disbursed
Wages	*21,600*	*+6.00%*	*22,829*
Camping supplies	*5,850*	*+3.00%*	*6,009*
*Field equipment**	*2,550*	*-54.00%*	*1,162*
Subtotal Field Costs	*30,000*	*=0.00%*	*30,000*
Management Cost			*15,000.00*
Total			*45,000.00*

** Field equipment is underreported, as T bars and barbed wire were purchased in previous fiscal years. An additional $10,000 was added subsequently to estimate the total cost of purchasing new field equipment (see Table 6)

ii) Total costs per hairsnag, per 9-locus microsatellite & genetic sex genotype, per individual ID, and per sampling station erected are reported in Tables 5.

Table 6. Cost of Field Work Outputs in 2015 - Hairsnags, *GN Genotype*, individual bears, and sampling stations - modelled for $45,000.00 and $55,000.00 total direct project cost. The total project cost of $45,000.00 was divided by the counts for each output of interest. In a second set of calculation, $10,000.00 was added to account for previously obtained field equipment, bringing the total cost to $55,000.00. *Measures of Output* = Different project outcomes. *2015 f.y.* = per unit costs of outputs, assuming a total project cost of $45,000.00 for the *fiscal year* of 2015. *2015 f.y. + 10k* = per-unit costs, assuming a total project cost of $55,000.00.

Measures of Output	2015 f.y.	2015 f.y. + 10k
Cost per Hair Sample (n=49)	$918.40	$1,122.45
Cost per 9 Locus genotype (n=30)	$1,500.00	$1,833.33
Cost per unique bear (n=14)	$3,214.30	$3,928.60
Cost per Sampling station (N=28)	$1,607.20	$1,964.30
Total Survey Cost	*$45,000.00*	*$55,000.00*

V. Discussion & Implications for Management

By demonstrating the minimum condition that the *same genetic data* can be collected from polar bear hairsnags as that collected from polar bear biopsy tissue plugs (collected via aerial survey), we believe that further an evaluation of the management utility of hairsnags is warranted. To further this evaluation, we i) contextualize our findings within general polar bear management potential, ii) describe recent genetic progress that amplifies the value of continued evaluation of land-based non-invasive polar bear genotype data as management inputs, iii) describe next steps to determine sampling strategies for non-invasive tissue needed to best inform management decisions with reference to the role of local Polar Bear Traditional Ecological Knowledge (TEK) may play in specific case of MCMU and iv) highlight the need for expanded economic characterization and comparison of polar bear alternate polar bear genotype ' supply chains'.

Polar Bear Hairsnags – an assessment of current polar bear management utility

Our results indicate that when a polar bear contacts the sampling station, this contact has 90% likelihood yielding a 9 locus polar bear *GN Genotype.* The composite success rate of 90% reflects the fact that not all contacts leave the same number of hairsnags (Table 1), not all hairsnags have roots, and not all hairsnags with roots yield a *GN Genotype.* The breakdown of hairsnag deposition and genotyping success is summarized below:

- on average 3.5 hairsnags are collected when a polar bear contacted our sampling stations;
- of these hairsnags, 76 % had hair with a root (37/49);
- of hairsnags with roots, 81% yielded a *GN Genotype* (30/37*)*
- on average each polar bear contact will yield on average 2.0 hairsnags that will each generate a *GN Genotype*.

The rate of successfully genotyping microsatellites across all hairsnags has improved. Here we report 61% success at determining a *GN Genotyp*e for 9 loci (n=49 samples), whereas our previous hairsnag microsatellite genotyping success rate was 53.6% using only 6 loci (n=595 hairsnags from 145 stations from 2006-2009) [2]. The increased genotyping success with 50% more loci speaks to the proficiency of later WGI genotyping versus that of our earlier work.

Based on our genetic profiling we can confirm that sampling stations appear not to be sex biased with 7M and 7F contacting the sampling stations and a polar bear's contact with sampling stations does not lead to subsequent trap avoidance as a number of bears contacted more than one sampling station. At this time we are unable to speak to any age and size bias these sampling stations may have, but earlier work would suggest Inuit hunters may provide these diagnoses for polar bears contacting sampling stations [9].

Genetic Advances that increase the types of tissue to be included in non-invasive polar bear monitoring

One can now collect polar bear DNA from their hairsnags [2] as well as their scat (Figure 6) [10] and we have shown promising results in optimizing genetic profiling of polar bears from the eDNA of their tracks (Figure 7). 321 polar bear SNPs (Single Nucleotide Polymorphism) which can uniquely genetically profile both polar bear epithelial cells shed in their faeces have been optimized [10] and appear to be able to do the same with polar bear eDNA to be found in their footprints and dens. These SNPs also work on polar bear biopsy and harvest tissues [10,11]

The advances in the genetic profiling of different non-invasively collected polar bear samples, suggests the evaluation of *management inference potential* from alternative sampling methods for these non-invasive tissues - coupled with the associated costs of collection, genetic profiling, and the analysis of the samples - would be timely and fruitful.

Figure 7: Polar bear faeces near a seal kill. Using 321 SNP loci polar bear epithelia in their faeces can be uniquely genotyped [10].　The inclusion of these samples can be increase the number of polar bears sampled in a future multimethod land based polar bear sample collection for polar bear management.

Figure 8: Polar bear footprints - potentially a source polar bear genotypes for a larger amount of easily sampled polar bears. Preliminary results suggest polar bear eDNA studies can be profiled from the snow found in their footprints and previous work suggest hunters can diagnose sex, age, size, and age of track [9].

Non-invasive Sampling and the challenge of Scale

While we have shown the high likelihood of obtaining the same 9 locus *GN Genotype* from polar bear hairsnags as that obtained through biopsy sampling, the sampling strategy needed to maximize management inference from MU wide sampling station deployment awaits further research. The most obvious hurdle facing the MU-wide deployment of hair sampling stations for optimum management inference is scale. The area covered by the helicopter as part of the biopsy survey was ~ 92,000 km^2. The covering of such an area with sampling stations at the same grid density used here is a substantial task.
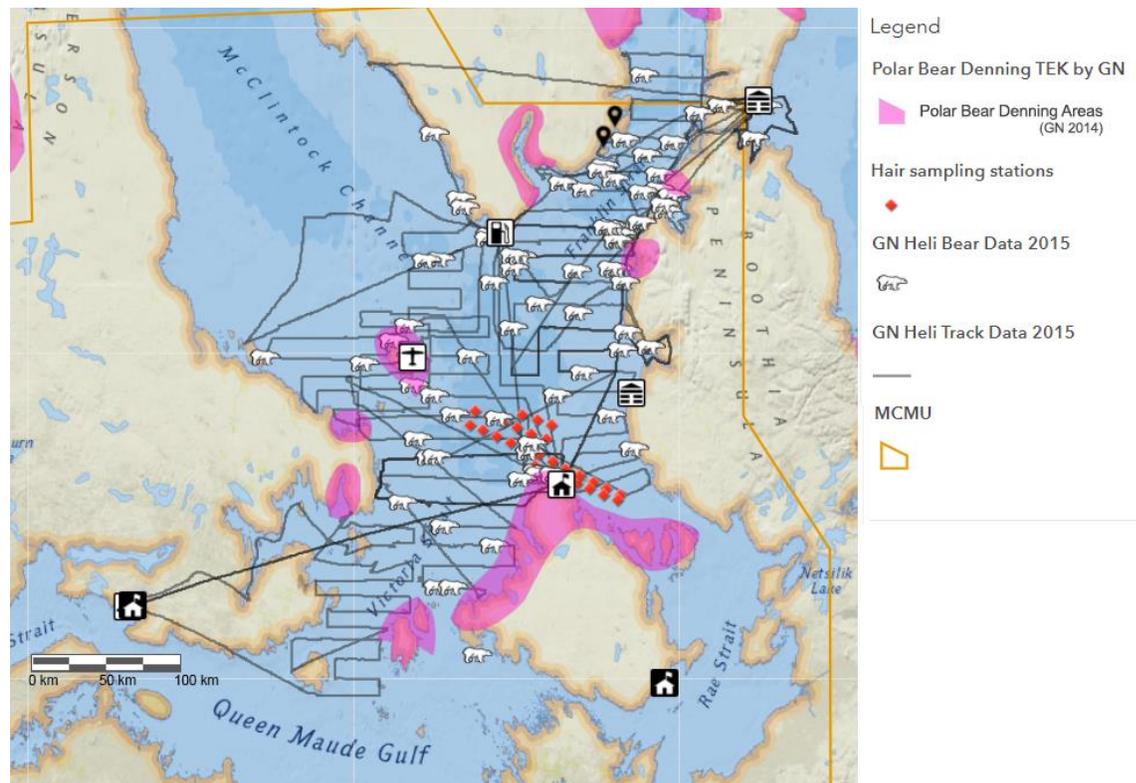
Figure 8: Polar bears biopsied in M'Clintock Channel in 2015 with distribution of Sampling Stations and preferred polar bear denning areas as identified through Inuit polar bear TEK. 2015 biopsy sampled bears [5] are indicated with white polar bears and tracks flown by the helicopter are depicted by black lines. The locations of the 28 sampling stations in this study are identified by red diamonds. Also shown here are polar bear denning areas as identified by local Inuit polar bear TEK [12] (pink polygons) which comprise a much smaller area that covered by helicopter in MCMU in 2015.

An obvious starting point for more practicable sampling station usage would be to restrict placement to areas identified by Inuit polar bear TEK as preferred polar bear habitat within *Management Units*. These areas would be preferentially sampled using non-invasive methods. As example, the preferred MCMU denning areas as per the Draft Nunavut Land Use Plan [12] are

shown in Figure 8. Restricting non-invasive sampling to these areas would be far less resource intensive than sampling an MU to the same degree achievable with a helicopter.

The progress towards SNP profiling of polar bear faeces [10] and snow from polar bear footprints, anticipates a new feasibility for the inclusion of non-invasive polar bear tissue collected by Nunavummiut to inform polar bear management. Against a backdrop of increasing ease of collection of polar bear hairsnags, through faeces to snow from footprints, the feasibility of multimethod land based polar bear sample collection for polar bear management inference requires:

- the modelling of management inference from individual polar bear genotypes and genetic sex determination derived from alternate hairsnag samplings, alternate faecal samplings and alternate snow from footprints samplings of a targeted MU,
- the modelling of management inference from individual polar bear genotypes and genetic sex determinations derived from multimethod sampling involving all 3 sample types for a targeted MU,
- the modelling of management inference from individual polar bear genotypes and genetic sex determinations derived from multimethod sampling involving all 3 sample types from restricted samplings of large MU's as guided by local Inuit polar bear TEK.

Critical Economic Analyses of polar bear genotype 'supply chain'

In addition to the modelling of management inferences from alternate non-invasive tissue samples, the comprehensive evaluation of multi-method land-based sample collection for polar bear management requires the calculation of the costs of collection of non-invasive polar bear tissues. Initially, the cost of genotyping can be assumed to be constant as the cost of genotyping these *nanuq miqqu* and the 2014-2016 GN aerial biopsies tissue plugs was the same (D. Patkeau, pers. comm.). These costs will change as new genotyping methods, such as SNP genotyping [10,11, 13, 14] become more common, and costs may also vary by tissue type.

Our rudimentary economic analysis represents the first of its kind for the major expenses of collection of for 9 locus *GN Genotypes* from non-invasively collected polar bear tissue. While this *GN genotype 'supply chain'* needs rigorous characterization, it is a critical component to the evaluation of land-based non-invasive alternatives. In the event that methodological and economical valuations support multi-method land-based sample collection for polar bear management, much of the cost of non-invasive sampling will be to the direct compensation for Nunavummiut labour, versus fees paid to helicopter companies.

Coupled with the modelling analyses needed for the collection of genotype information from polar bear harisnags, to polar bear faeces, to the snow from their footprints, the feasibility of multi-method land-based sample collection for polar bear management inference requires the following:
- The fulsome cost analysis of the collection of individual genotypes, and genetic sex, for management inference from alternate hairsnag samplings, alternate faecal samplings and alternate snow from footprint samplings of a targeted MU,
- The fulsome cost analysis of the collection of individual genotypes, and genetic sex, for management inference from a multi-method sampling involving all 3 sample types for a targeted MU alternative,

- The fulsome cost analysis of the collection of individual genotypes, and genetic sex, for management inference from a multi-method sampling involving all 3 sample types from restricted samplings of large MU's as guided by local Inuit polar bear TEK.

VI. Reporting to the Communities & Resource Users

Sampling results were communicated to our (Gjoa Haven Hunters' and Trappers' Association - HTA) - board, following the completion of field work, as well as subsequent to the (later) completion of the genetics work.

This report is being disseminated among others to the Department of Wildlife GN, Wildlife at NTI, ENR @ Government of NWT and Environment Canada.

These results are also being compiled into a journal publication, to be submitted for peer review.

VII. Acknowledgements

VIII. References

1. Contribution Agreement # 15-004-01. NWMB Studies Fund Awarded to the Gjoa Haven Hunters' and Trappers' Association (GH HTA)
2. Van Coeverden De Groot, P., PBY Wong, C. Harris, M. Dyck, L. Kamookak, M. Pagès, J. Michaux and P. Boag. (2013) Toward a Non-Invasive Inuit Polar Bear Survey: Genetic Data From Polar Bear Hair Snags. *Wildlife Society Bulletin*. 37:394–401.
3. M. Dyck, Lukacs, P.M., and Ware. J.V. (2020) Re-estimating the abundance of a recovering polar bear subpopulation by genetic mark-recapture in M'Clintock Channel, Nunavut, Canada. Final report to the Nunavut Department of Environment.
4. Van Coeverden de Groot, P.J, C. Chris, P.B.Y. Wong, M. Dyck, and P. T. Boag. (2011) Report to the Gjoa Haven HTO on polar bear field work 2006 – 2010.
5. Paetkau, D., W. Calvert, I. Stirling, and C. Strobeck. (1995) Microsatellite analysis of population structure in Canadian polar bears. Molecular Ecology 4:347–354.
6. Taberlet, P., J. J. Camarra, S. Griffin, E. Uhrès,O. Hanotte, L. P. Waits, C.Dubois-Paganon, T. Burke, and J. Bouvet. (1997) Noninvasive genetic tracking of the endangered Pyrenean brown bear population. Molecular Ecology 6:869–876.
7. Kitahara, E., Y. Isagi, Y. Ishibashi, and T. Saitoh. (2000) Polymorphic microsatellite DNA markers in the Asiatic black bear (Ursus thibetanus). Molecular Ecology 9:1661–1686.

8. NWSF Financial Report #244-11-02. Gjoa Haven Non-Invasive Polar Bear Survey. Financial Report FY 2015-2016.
9. Wong, P.B.Y., P. Van Coeverden de Groot, C. Fekken, H. Smith, M. Pagès and P. T. Boag. 2011. Interpretations of polar bear (*Ursus maritimus*) tracks by Inuit hunters: inter-rater reliability and inferences concerning accuracy. Canadian Field-Naturalist 125: 140–153.
10. Hayward, K.M., R. B.G. Clemente-Carvalho, E.L. Jensen, P. V.C. de Groot, M. Branigan, M. Dyck, C. Tschritter, Z. Sun & S.C. Lougheed. 2022. Genotyping-in-thousands by sequencing (GT-seq) of noninvasive faecal and degraded samples: A new panel to enable ongoing monitoring of Canadian polar bear populations. Molecular Ecology. https://doi.org/10.1111/1755-0998.13583
11. Jensen, E. L., Tschritter, C., de Groot, P. V. C., Hayward, K. M., Branigan, M., Dyck, M., Clemente-Carvalho, R. B. G., and Lougheed, S. C. (2020) Canadian polar bear population structure using genome-wide markers. Ecology and Evolution. 10, 3706–3714
12. Draft Nunavut Landuse Plans 2021 (https://www.nunavut.ca/land-use-plans/draft-nunavut-land-use-plan) Accessed 04_07_2022.
13. Viengkone, M., Derocher, A. E., Richardson, E. S., Malenfant, R. M., Miller, J. M., Obbard, M. E., Dyck, M. G., Lunn, N. J., Sahanatien, V., and Davis, C. S. (2016) Assessing polar bear (Ursus maritimus) population structure in the Hudson Bay region using SNPs. *Ecol Evol*. **6**, 8474–8484
14. Malenfant, R.M., Coltman, D.W., and Davis, C.S. 2015. Design of a 9K Illumina BeadChip for polar bears (*Ursus maritimus*) from transcriptomic and RAD sequencing. *Molecular Ecology Resources* 15(3): 587–600.

Appendix A

Laboratory data: Samples yielding complete genotypes. 49 hair samples underwent a 3-phase protocol genotype assay at 9 study loci for the sexing and identification of polar bears, using hair samples collected in this study. 30 of 49 hair samples were completely genotyped, shown in the table below, with the observed diploid allele lengths "one.two" at each of the 9 loci assayed. Samples attributed to three bears that were resampled from the GN aerial biopsy survey are shown in the first five rows. *Sample # =* Identification number of all hairsnags. *Individual ID =* discrete bears identified through genotype. 9 loci assayed: *REN 145P07, G10B, CXX20, MU50, G10H, MU59, G10P, G10X,* and *Sex* (ZFY/ZFX).

Sample #	Individual ID	REN 145P07	G10B	CXX20	MU50	G10H	MU59	G10P	G10X	Sex
004	MC-2015-60	167.169	142.152	135.135	124.126	237.243	241.241	145.145	143.149	204.250
005	MC-2015-60	167.169	142.152	135.135	124.126	237.243	241.241	145.145	143.149	204.250
011	MC-2014-29	163.173	142.156	135.137	122.126	227.237	231.243	149.155	143.149	204.250
015	MC-2014-29	163.173	142.156	135.137	122.126	227.237	231.243	149.155	143.149	204.250
900	MC-2014-39	163.173	158.158	135.137	126.130	239.239	243.245	145.149	133.133	204.250
008	008	165.173	142.158	135.137	126.126	237.239	231.245	145.149	133.133	204.250
009	009	163.169	150.156	137.143	130.130	237.247	231.235	145.153	137.137	250.250
010	010	171.171	150.154	135.137	124.126	237.247	231.243	149.151	133.143	250.250
014	014	165.169	142.150	135.139	122.126	235.249	241.245	145.153	133.137	204.250
016	016	167.171	142.152	139.141	122.130	237.243	243.245	145.145	135.143	204.250
017	017	167.169	142.152	135.137	124.126	237.243	239.243	145.145	143.147	204.250
021	021	163.169	152.154	135.135	126.130	227.237	241.245	145.151	137.147	250.250
023	023	167.171	154.156	135.137	126.130	243.249	241.241	149.157	133.137	250.250
024	021	163.169	152.154	135.135	126.130	227.237	241.245	145.151	137.147	250.250
026	026	167.171	142.142	135.137	126.126	231.237	231.239	145.145	133.143	250.250
027	027	163.171	154.154	135.137	126.130	243.243	237.245	145.149	133.137	250.250
028	027	163.171	154.154	135.137	126.130	243.243	237.245	145.149	133.137	250.250
029	027	163.171	154.154	135.137	126.130	243.243	237.245	145.149	133.137	250.250
030	030	169.169	142.158	135.137	124.126	239.243	241.245	145.151	143.147	250.250

Appendix A - Continued.

Sample #	Individual ID	REN 145P07	G10B	CXX20	MU50	G10H	MU59	G10P	G10X	Sex
032	030	169.169	142.158	135.137	124.126	239.243	241.245	145.151	143.147	250.250
034	030	169.169	142.158	135.137	124.126	239.243	241.245	145.151	143.147	250.250
035	030	169.169	142.158	135.137	124.126	239.243	241.245	145.151	143.147	250.250
036	030	169.169	142.158	135.137	124.126	239.243	241.245	145.151	143.147	250.250
038	030	169.169	142.158	135.137	124.126	239.243	241.245	145.151	143.147	250.250
100	017	167.169	142.152	135.137	124.126	237.243	239.243	145.145	143.147	204.250
110	017	167.169	142.152	135.137	124.126	237.243	239.243	145.145	143.147	204.250
200	017	167.169	142.152	135.137	124.126	237.243	239.243	145.145	143.147	204.250
600	017	167.169	142.152	135.137	124.126	237.243	239.243	145.145	143.147	204.250
700	017	167.169	142.152	135.137	124.126	237.243	239.243	145.145	143.147	204.250
800	017	167.169	142.152	135.137	124.126	237.243	239.243	145.145	143.147	204.250

Appendix B

Laboratory data: Samples that failed to amplify above threshold. 7 of 49 samples fell below strength criteria for the assay protocol, but contained amplifiable DNA. Triploid data (**bold**) represent ambiguous allele length results. Allele lengths with only 2 digits (*italicised*) are representative of incomplete results. Empty cells reflect missing data. *Sample # =* Identification number of all hairsnags. *Individual ID =* discrete bears identified through genotype. 9 loci assayed: *REN 145P07, G10B, CXX20, MU50, G10H, MU59, G10P, G10X,* and *Sex* (ZFY/ZFX).

Sample #	Individual ID	REN 145P07	G10B	CXX20	MU50	G10H	MU59	G10P	G10X	Sex
001	X	*63.171*	*156.58*		*28.134*	*43.243*	*37.243*	*45.45*	*43.43*	
012	X	**165.67.69**	142.150	*135.39*	122.126	*35.249*	**241.43.45**	*45.153*	133.137	
022	X		*56.156*		*30.132*					
025	X			*35.135*	*26.126*	*27.33*	*45.245*		*37.37*	
031	X						*41.41*		*47.47*	
037	X				*26.126*				*43.43*	
039	X	**63.167.169**	**142.52.56**	*135.37*	**22.124.126**	**31.237.243**	*241.43*	*145.49*	**33.43.149**	

Appendix C

Laboratory data: Samples with inadequate DNA for amplification. 12 of 49 samples contained inadequate DNA for amplification, due to a lack in quantity or accessibility of the genetic material. 2 of 12 were marked "empty" by the lab. These samples all lacked a hair root. No data could be collected via the assay protocol. *Sample #* = Identification number of all hairsnags. *Individual ID* = discrete bears identified through genotype. 9 loci assayed: *REN 145P07, G10B, CXX20, MU50, G10H, MU59, G10P, G10X,* and *Sex* (ZFY/ZFX).

Sample ID	Individual	REN 145P07	G10B	CXX20	MU50	G10H	MU59	G10P	G10X	Sex
002	X									
003	X									
006	X									
007	X									
013	X									
018	X									
019	X									
020	X									
033	X									
300	X									
400	X									
500	X									