

Non-invasive genetic sampling of brown bears and Asiatic black bears in the Russian Far East: A pilot study

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Abstract: Non-invasive genetic sampling (NGS) methods have been instrumental in providing robust population abundance and density estimates of bears. We conducted a small pilot study to (1) evaluate 2 NGS methods of hair traps and bear rubs in the Russian Far East (RFE) on sympatric populations of Asiatic black bears (*Ursus thibetanus*) and brown bears (*Ursus arctos*), and (2) to identify potential DNA marker sets for future study. Genetic analysis required 6 microsatellite markers to definitively identify individuals plus a gender marker, and closed population models estimated 142 Asiatic black bears and 18 brown bears. Spatially-explicit mark-recapture (SECR) density estimates for brown bears were 3 bears/100 km². Inflated Asiatic black bear estimates resulted from a lack of recaptures, although using combined detection data from the 2 NGS methods was found to improve precision for abundance estimates. Capture probabilities were higher for brown bears than for Asiatic black bears, but overall recapture probabilities were low for both species. The frequency of rubbing declined from June to August, possibly due to bears leaving the study area, and Asiatic black bears were detected less frequently on rubs than brown bears, suggesting that species-specific ecology must be incorporated into future study designs. We recommend that future applications of NGS in the RFE improve capture probabilities by sampling earlier in the season to mitigate geographic closure violation for abundance estimates and to increase the number of detections for robust spatially explicit capture-recapture analyses. Our results demonstrate that NGS methods have strong potential for monitoring of bear populations in the RFE.

Key words: Asiatic black bear, bear rubs, brown bear, DNA, hair trap, Huggins closed models, non-invasive genetic sampling, population estimates, Russian Far East, SECR, spatially-explicit capture-recapture, *Ursus arctos*, *Ursus thibetanus*

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The forests of the Russian Far East (RFE) are recognized as one of the 200 most significant ecoregions in the world (Olson and Dinerstein 1998) because of a unique assemblage of subtropical Asiatic and temperate and boreal species. For example, within the RFE brown bears (*Ursus arctos*) and Asiatic black bears (*U. thibetanus*) co-exist with other large-ranging carnivores such as Siberian tigers (*Panthera tigris altaica*) and Amur leopards (*P. pardus orientalis*). The co-occurrence of these 2 bear species is found elsewhere only in the forested areas of Pakistan (Nawaz 2007),

northeastern China (Servheen et al. 1999), and in the northwestern Himalayas (Sathyakumar 2001).

Asiatic black bears are listed as Vulnerable according to the IUCN (International Union for Conservation of Nature [IUCN] 2011), and they occur in Russia at the northern limits of their geographic range. The Russian population is a recognized subspecies ranging from the RFE to North and South Korea, and black bear cubs from the RFE have been translocated to restore a population in South Korea (Kim et al. 2011). Despite being a source for the subspecies and a species that was listed as endangered within Russia until 1997, the Asiatic black bear has received little attention from the conservation community due to

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an apparent priority of other species, such as the critically endangered Siberian tiger and Amur leopard. Brown bears are listed as Least Concern according to the IUCN (IUCN 2011) and are widespread across Russia. Both black bears and brown bears are managed as a huntable game species in Russia, though both bear species in the RFE may be currently threatened by poaching (Garshelis and Steinmetz 2008). They also are threatened loss of habitat quality due to intensive and largely illegal logging activities that are decimating key mast species such as Korean pine (*Pinus koraiensis*) and Mongolian oak (*Quercus mongolica*) (Seryodkin and Pikunov 2002, Pikunov and Seryodkin 2006). Unfortunately, reliable and consistent population abundance and density estimates that could be used to assess and monitor the status of both bear species are generally lacking (Pikunov and Seryodkin 2006). Survey methods to estimate distribution and abundance of bears in Russia have relied upon expert knowledge, snow track surveys, and observation counts (Chestin 1994). Despite the prevalence of these methods, they are viewed as less rigorous than more current mark-recapture and DNA-based methods established elsewhere (Garshelis 2006). The only bear telemetry study conducted in the region was also the largest undertaken in Russia and resulted in a total of 21 black bears and 23 brown bears collared between 1992–2002 (Seryodkin 2009). Due to the static nature of sampling within the RFE, little progress has been made in estimating abundance for these populations, and estimates cannot be relied upon to reflect true population processes (Nichols and Williams 2006).

Black and brown bears forage on rich succulents during the spring and summer and thrive on pine nuts and acorns available in the fall from Korean pine and Mongolian oak (Bromlei 1965, Seryodkin et al. 2003, Seryodkin 2006). To exploit these seasonal food resources, bears spend more time in low-elevation habitat during the summer and move to higher elevation habitat in the early fall (Seryodkin, unpublished data). Interspecific interactions of large predators are complex: brown bears are known to kill black bears, although predation by tigers on black bears appears more common (Seryodkin et al. 2005). Female and male brown bears have larger home ranges (145 km² and 968 km², respectively; Seryodkin et al. 2006) than female and male black bears (20 km² and 220 km², respectively; Kostyria et al. 2002).

The goal of our study was to assess the feasibility of applying noninvasive genetic sampling (NGS) in Russia as part of a capture-mark-recapture (CMR) study design to estimate bear abundance and density. The NGS framework has been used extensively to successfully obtain bear abundance and density estimates for large study areas (Mowat and Strobeck 2000, Boersen et al. 2003, Viteri 2007, Harris 2010). More recently, spatially explicit mark-recapture (SECR) modeling methods have been developed for studies with irregular sampling designs and smaller population sizes (<100 individuals; Efford 2004, Gardner et al. 2009, Obbard et al. 2010).

NGS methods may be compromised by heavy precipitation and DNA degradation (Foran et al. 1997) as well as the interference of other species with sampling sites, and sampling design issues such as geographic closure. Therefore, we conducted a pilot study to assess the reliability, affordability, and effectiveness of 2 NGS methods for estimating abundance and density of brown and black bears in the Russian Far East, and we focused on investigating capture probabilities by each sampling method. We also recommend study design improvements for future research and monitoring programs in the RFE.

Methods

Study area

The Sikhote-Alin Biosphere Zapovednik (SABZ) is a protected area situated in the central eastern portion of Primorski Province in the Russian Far East. The entire 4,000-km² reserve is closed to public access. We focused our study on the Zabolochnaya watershed, a tributary of the Serebryanka River that flows east into the Sea of Japan. The Zabolochnaya watershed, approximately 400 km², is bordered on its eastern side by the SABZ boundary and a main road (Fig. 1). The temperate climate of this region receives approximately 600–850 mm of rainfall/year with over half falling from June to August. Elevation ranges from 135 to 1200 m, and temperature ranges from –45°C to +30°C. The SABZ has been a protected area since 1935 with guard outposts at major entry points. The region is a mix of pine-broadleaf forest dominated by Korean pine, and at higher, more inland sites by spruce-fir forest dominated by Ajan spruce (*Picea ajanensis*) and white-bark fir (*Abies nephrolepis*). In the Zabolochnaya

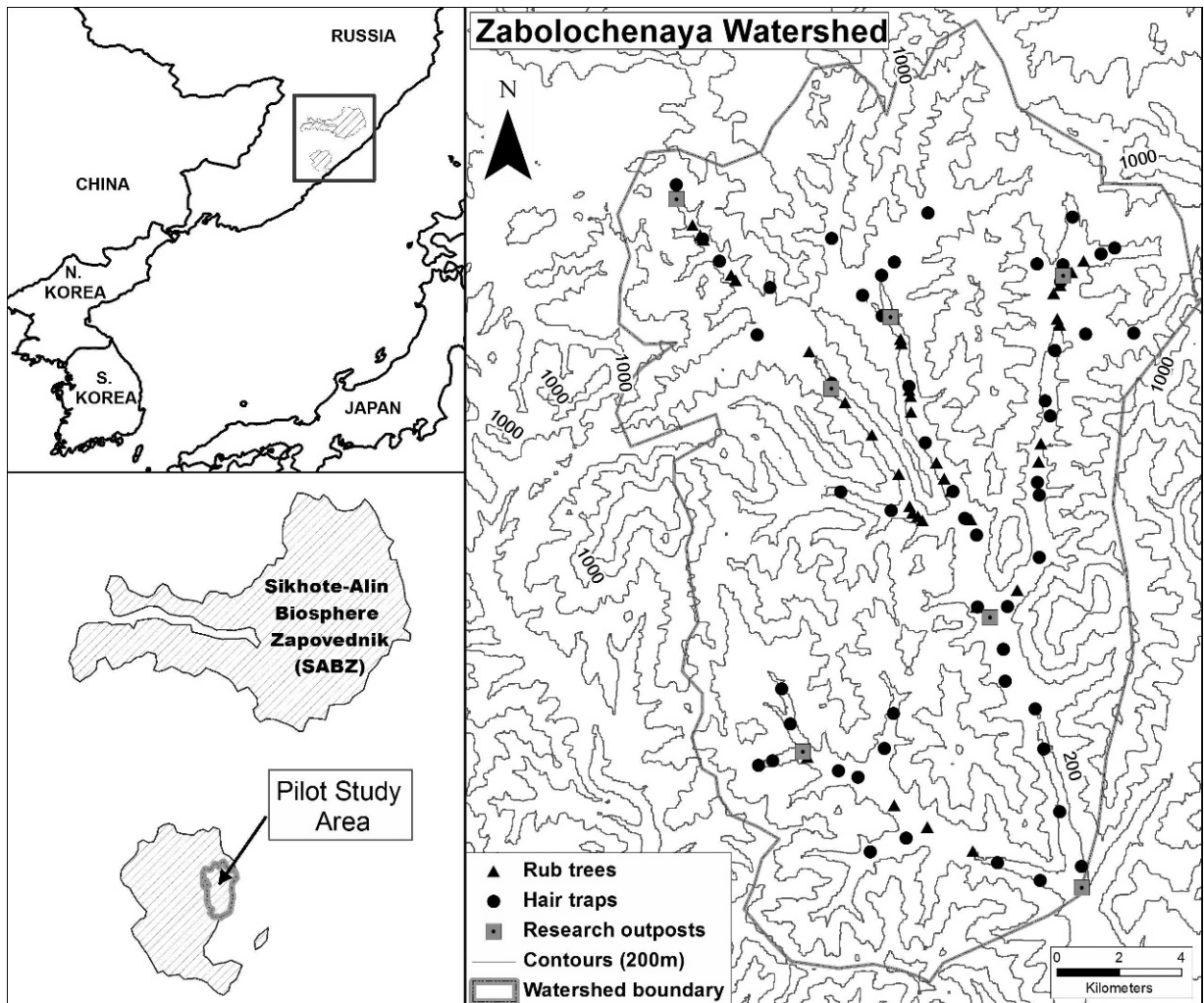


Fig. 1. Study area and location of sampling points in the Zabolochenaya watershed (~400 km²), part of the Sikhote-Alin Biosphere Zapovednik in the Russian Far East.

watershed, tigers, lynx (*Lynx lynx*), red deer (*Cervus elaphus*), sika deer (*C. nippon*), roe deer (*Capreolus capreolus*), musk deer (*Moschus moschiferus*), and wild boar (*Sus scrofa*) also occur. Wolves (*Canis lupus*) are rare in the SABZ, apparently due to competition with tigers (Miquelle et al. 2005). There are approximately 70 km of unmaintained trails along the 4 main tributaries of the Zabolochenaya watershed; these have persisted year to year due to human and wildlife use, and they provided access to the majority of our sampling points (Fig. 1).

Field sampling

We used hair samples obtained from bear rub trees and hair traps for 2 NGS methods in the RFE.

We identified bear rubs along all trails in the study area based on presence of hair and other signs of use (Kendall et al. 2008). Rub tree species were predominantly white-bark fir and Ajan spruce as well as Korean pine, Cajander larch (*Larix cajanderi*), and Maximovich's poplar (*Populus maximowiczii*). We typically applied 3 barbed wire strands to cover the rub surface of each tree (approximately 50–200 cm from the ground) to facilitate hair collection. After setting 36 bear rubs along approximately 67 km of trail, we surveyed the bear rubs during 5 sampling occasions of 10 to 14 days' duration, 9 June–6 August 2008. We placed all hairs from each barb into numbered paper envelopes labeled with the location and date of collection.

Hair traps (Woods et al. 1999) consisted of a 40-foot strand of barbed wire affixed to standing trees at a height of 53 cm; they were spaced approximately 1–3 kilometers at low elevations along major travel routes and corridors throughout the watershed. We baited hair traps with 1 L of a non-rewarding liquid scent lure containing milk, eggs, canned fish, and food scraps aged for 1 month. We moved and baited hair traps ~1 km or more apart every 11–13 days during 3 July–6 August 2008, resulting in 3 sampling occasions. Hair traps were moved this short distance to reduce habituation to a certain site over the sampling season. Hair was collected as for bear rubs.

Genetic analyses

We stored hair samples on silica desiccating gel until analyzed by Wildlife Genetics International (Nelson, British Columbia, Canada), a laboratory that specializes in noninvasively obtained samples that often have low quantities of DNA. We did not attempt to extract DNA from hair samples that were clearly from wild boar or from samples with no guard hair follicles and <5 underfur hairs. As ours was the first study to use microsatellite markers in this region for either bear species, we initially used 12 markers to define individuals and to identify ≥ 1 marker to determine species. We then ran one sample from each individual at an additional 12 markers, for a total of 24. From these 24 markers, we used the following 10 markers to ensure conservative match probabilities for identifying individual bears for both species: REN145P07, CPH9, CXX110, CXX20, G10H, G10J, G10M, MU26, MU59, and G10P. Once individuals were identified, a gender test was performed on one sample from each bear using the amelogenin gender marker (Pilgrim et al. 2005).

To minimize genotyping errors in the final dataset, we followed the protocol of Paetkau (2003) where low quality and putatively mixed samples are excluded from further analyses. Genotyped samples that may have contained errors as indicated by the empirical mismatch distribution were selectively re-analyzed (Paetkau 2003). We used the examining bimodality and difference in capture history tests in program DROPOUT (McKelvey and Schwartz 2005) to detect any latent genotyping errors.

Data analysis

We based the boundaries of the Zabolochenaya study area on telemetry observations of bear movements from 1992–2002, which primarily followed

valley bottoms and ridgelines (Seryodkin 2009) and were delineated manually using the Hydrology Toolset of ArcGIS 9.3 (ESRI, Redlands, California, US). For the purposes of analysis, we assumed demographic and geographic closure of the study area. By using a high-density sampling network, we hoped to achieve high capture rates and subsequently employ modeling methods that would account for heterogeneity in capture probabilities (White et al. 2002, Boulanger et al. 2004). We developed a suite of Huggins (1991) closed population models in program MARK (White 2008, v. 6.1, accessed 12 May 2011) to test the NGS methods and to develop insights from the study design. We estimated capture probabilities for brown and black bears using detections from both hair collection methods in a single encounter history for each individual (Boulanger et al. 2008). We assumed that the capture probabilities of each hair capture method were independent and were thereby modeled separately to reduce bias in the closed-model estimates (Boulanger et al. 2008). Because sample size of detections was low, we combined the first 2 bear rub sessions and the last 2 bear rub sessions resulting in 3 sessions of 24, 13, and 22 days, respectively. Because of the sparse nature of the data, we treated species as groups within MARK models and did not attempt gender-specific estimates. We compared models that accounted for the effects of temporal changes in detection probabilities, and models that used the average distance of each animal to the edge of the sampled area (DTE; Boulanger and McLellan 2001; Kendall et al. 2008, 2009) plus an individual-level bear rub sampling effort covariate (BRE), to explain detection probability heterogeneity. We calculated BRE by summing the number of days that each bear rub was available to each individual within a given session within a buffer equal to the species-specific mean maximum distance moved (MMDM; based on ≥ 2 locations) and $\frac{1}{2}$ MMDM around the animal's average capture location using the DNA data. Model support was based on Akaike's Information Criterion adjusted for small sample size (AIC_c; Hurvich and Tsai 1989, Burnham and Anderson 2002).

We used a maximum likelihood framework within the spatially-explicit mark-recapture program DENSITY (Borchers and Efford 2008) to generate gender-pooled density estimates for brown and black bears. We assumed a half-normal detection model, with home ranges following a Poisson distribution

Table 1. Bear rub survey results for brown bears and Asiatic black bears, 9 June to 6 August 2008, for 36 marked bear rubs in the Zabolochenaya watershed, Primorski Province, Russia.

Session	Dates	No. bear rub surveys ^a	Bear rub effort ^b	Species	% bear rub survey with hair	No. bear samples/rub (SD)	Total no. samples	No. new bears	No. unique bears
1	9 Jun–2 Jul	51	1094	black bear	3.9	7 (null)	7	4	4
2	4–15 Jul	38	523	black bear	5.3	4 (0)	8	1	2
3	17 Jul–6 Aug	74	879	black bear	2.7	3.5 (3.5)	7	0	0
Mean		54.3	832		4	4.8 (1.8)	7.3	1.7	2
Total		163	2496				22	5	6
1	9 Jun–2 Jul	51	1094	brown bear	31.4	3.5 (2.7)	49	5	5
2	4–15 Jul	38	523	brown bear	18.4	3.2 (1.2)	19	3	5
3	17 Jul–6 Aug	74	879	brown bear	6.8	3.2 (1.9)	16	2	6
Mean		54.3	832		18.9	3.3 (1.9)	28	3.3	5.3
Total		163	2496				84	10	16

^aRub survey is the cumulative number of times the bear rubs were sampled.^bBear rub effort is the number of days between hair collections for each bear rub surveyed.

(Obbard et al. 2010). We modeled both hair traps and bear rubs as proximity detectors, with hair traps coded as available on a session-specific basis (i.e., an ‘incomplete trap layout’), whereas bear rubs were modeled as continuously available. We compared models that included effects of time, individual heterogeneity, and DTE on detection magnitude (g), along with time and individual heterogeneity on the detection scale (σ). All models used a likelihood, conditional on the number of animals captured, with a buffer of 20 km. As with program MARK models, we used AIC_c to rank support for models given the data. Although it was not our goal to quantitatively evaluate the density estimators, we provide density estimates for comparison by dividing MARK abundance estimates by the estimated effective sampling area of the watershed. The sampling areas were calculated by adding distance buffers of

MMDM and $\frac{1}{2}$ MMDM for both species to the delineated watershed.

Results

Sampling effort

We collected 164 samples from 163 visits to 36 bear rubs (Table 1), and 108 samples from 53 hair traps over 3 sampling occasions, 3 July–6 August 2008 (Table 2). The first and second trap occasion resulted in 22 and 21 traps set, respectively, but the third hair trap occasion could not be completed due to logistical constraints and resulted in a total of 10 hair traps. Brown bear hair was obtained mainly at bear rubs (10 of 13 individuals), and conversely, black bear hairs were obtained mainly by hair traps (12 of 17 individuals). Three brown bears visited both hair traps and bear rubs.

Table 2. Results from 53 hair traps for brown bears and Asiatic black bears collected 3 July to 6 August 2008, in the Zabolochenaya watershed, Primorski Krai, Russia.

Session	Dates	No. sites	Species	% traps with >1 hair sample	No. bear samples/trap (SD)	Total samples	No. new bears	No. unique bears
1	3–15 Jul	21	black bear	38.1	4 (1.5)	32	8	8
2	17–26 Jul	22	black bear	9.1	5 (5.7)	10	2	2
3 ^a	27 Jul–6 Aug	10	black bear	20	2 (0)	4	2	2
Mean		17.7		22.4	3.7 (2.4)	15.3	4	4
Total		53				46	12	12
1	3–15 Jul	21	brown bear	14.3	7 (7.8)	21	6	6
2	17–26 Jul	22	brown bear	0	0 (0)	0	0	0
3 ^a	27 Jul–6 Aug	10	brown bear	0	0 (0)	0	0	0
Mean		17.7		4.8	2.3 (2.6)	7	2	2
Total		53				21	6	6

^aThis session could not be fully completed due to logistical constraints.

Table 3. Variability of microsatellite markers used in assigning individuals identities of brown bears in the Zabolochenaya watershed of Primorski Krai, Russia from samples collected in 2008.

Marker	H_E^a	H_O^b	A^c	P_{ID}^d	P_{SIB}^e	P_{P-SIB}^f
REN145P07	0.527	0.692	5	0.264	0.553	0.553
CPH9	0.698	0.769	6	0.141	0.436	0.241
CXX110	0.749	0.846	6	0.093	0.399	0.096
CXX20	0.68	0.538	5	0.158	0.449	0.043
G10H	0.796	0.769	6	0.071	0.37	0.016
G10J	0.852	0.846	9	0.039	0.334	0.005
G10M	0.76	0.846	7	0.091	0.393	0.002
MU26	0.84	0.923	9	0.045	0.341	0.001
G10P	0.743	0.846	6	0.099	0.403	0
MU59	0.574	0.462	6	0.218	0.518	0
x	0.722	0.754	6.5			
Overall probability of identity				1.32×10^{-10}	1.49×10^{-5}	

^a H_E : expected heterozygosity.^b H_O : observed heterozygosity.^cA: number of alleles per locus.^d P_{ID} : probability of identity.^e P_{SIB} : probability of identity given siblings.^f P_{P-SIB} : probability of identity given siblings by increasing marker selection.

Genetics

Both brown and black bears had black fur and were indistinguishable upon visual inspection. Therefore, all putative bear hair samples were sent to the laboratory for analysis. Sample quality was likely affected by under-fur samples that lacked sufficient DNA rather than by DNA degradation resulting from >2 years of storage (D. Paetkau, Wildlife Genetics International, Nelson, British Columbia, Canada, personal communication, 2011). Of the 272 samples sent to the laboratory, 32 (11.8%) were excluded from the analysis due to insufficient

genetic material. Of the 240 samples that we attempted to analyze, 4 (1.7%) appeared to contain DNA from >1 individual, and 63 samples (26.3%) failed the DNA extraction process. The remaining 173 samples (63.6% of total collected) produced complete 10-locus genotypes plus gender assignment. We identified 30 individuals from these 173 samples: 13 brown bears (3F, 10M) and 17 black bears (2F, 15M).

Mean observed heterozygosity for the 10 loci used to define individual identity was 0.75 for both brown (Table 3) and black bears (Table 4), with just over 6

Table 4. Variability of microsatellite markers used in assigning individuals identities of Asiatic black bears in the Zabolochenaya watershed of Primorski Krai, Russia from samples collected in 2008.

Marker	H_E^a	H_O^b	A^c	P_{ID}^d	P_{SIB}^e	P_{P-SIB}^f
REN145P07	0.817	0.824	9	0.055	0.355	0.355
CPH9	0.699	0.647	5	0.144	0.437	0.155
CXX110	0.81	0.765	8	0.064	0.361	0.056
CXX20	0.772	0.824	6	0.09	0.387	0.022
G10H	0.787	0.765	6	0.077	0.376	0.008
G10J	0.676	0.765	4	0.163	0.453	0.004
MU26	0.744	0.706	5	0.11	0.406	0.001
G10M	0.753	0.529	5	0.098	0.398	0.001
MU59	0.754	0.765	7	0.09	0.395	0
G10P	0.841	0.941	8	0.045	0.341	0
x	0.765	0.753	6.3			
Overall probability of identity				2.48×10^{-11}	8.01×10^{-5}	

^a H_E : expected heterozygosity.^b H_O : observed heterozygosity.^cA: number of alleles per locus.^d P_{ID} : probability of identity.^e P_{SIB} : probability of identity given siblings.^f P_{P-SIB} : probability of identity given siblings by increasing marker selection.

Table 5. Huggins (1991) closed models for brown bears and Asiatic black bears based on hair samples collected in 2008 from bear rubs and hair traps in the Zabolochenaya watershed of Primorski Krai, Russia.

Model	Parameters ^a	AIC _c ^b	No. parameters	ΔAIC _c	w _i ^c
1	HT(species+time+ DTE) BR(species+time+ DTE)	138.49	10	0.00	0.748
2	HT(species+time+ DTE) BR(species+time+BRE+ DTE)	140.76	11	2.27	0.240
3	HT(species+time) BR(species+time)	147.34	8	8.85	0.009
4	HT(species+ DTE) BR(species+ DTE)	149.56	6	11.07	0.003
5	HT(species) BR(species+BRE)	160.37	5	21.88	0.000
6	HT(.) BR (.)	171.56	2	33.07	0.000

^aHT: hair trap, BR: bear rub, DTE: distance to edge, BRE: rub tree effort.^bAIC_c: Akaike's Information Criterion adjusted for small sample size.^cw_i: Akaike weight.

alleles per locus on average for both species. We calculated the probability that 2 randomly drawn, unrelated individuals would have matching genotypes at all 10 loci (P_{ID}) to be 2.5×10^{-11} and the probability that full siblings would have identical genotypes (P_{SIB}) to be 8×10^{-8} for black bears, with brown bears having P_{ID} and P_{SIB} of 1.3×10^{-10} and 1.5×10^{-5} , respectively.

Error checking efforts followed the selective reanalysis protocol of Paetkau (2003), where samples with weak or inconsistent results were reanalyzed, as were any genotypes that differed at a single locus (1 mismatch) or <3 loci if those results were consistent with allelic dropout. After correcting errors, no individual assignments differed by fewer than 6 loci, far exceeding mismatch distributions typical of noninvasive studies (Paetkau 2003). Further, the tests in program DROPOUT did not detect any problematic loci.

We used 3 approaches to confirm species for each genotyped individual. First, we observed that the G10H locus produced non-overlapping ranges of allele sizes, with each sample either having alleles of <240 or >274 base-pairs. We next used factorial correspondence analysis in program Genetix (Belkhir et al. 1996–2004), where we observed clustering that matched the assignment based on G10H results. Finally, we analyzed 3 samples from each putative species at the 16S rRNA mtDNA gene. The

presumed brown bear profiles were identical to those of North American brown bears, whereas presumed Asiatic black bear profiles did not match any North American mammal, but were similar to those of American black bears (*Ursus americanus*).

Abundance and density estimates

The top-ranked model from Program MARK included species and time effects, with the DTE covariate supported for both sampling methods (Table 5). Our Huggins closed-model abundance estimates for brown bears and black bears were 18 (95% CI = 14.2–36.5) and 142 (95% CI = 35.7–852.0), respectively. Our brown bear estimate had a coefficient of variation (CV) of 26%, whereas precision was very poor for the estimate for black bears (Table 6).

Capture probabilities declined for both species and methods over the sampling season (Fig. 2). Brown bear hair-trap capture probabilities declined from 24.9% to 4.0%, and despite an increase in bear rub sampling effort during the second recapture session, bear rub capture probabilities also declined from 36.3% to 12.8%. Black bear capture probabilities after the initial session were very low (<7%) and were lower for both hair traps and bear rubs than brown bears.

The top ranked SECR model for brown bears was the null model (Table 7). The second ranked model

Table 6. Huggins (1991) abundance closed-population estimates from most supported model (HT [species + time + DTE] + BR [species + time + DTE]; Table 5) for brown bears and Asiatic black bears based on hair samples collected in 2008 from bear rubs and hair traps in the Zabolochenaya watershed of Primorski Krai, Russia.

Parameter	Minimum count	Estimate (SE)	CV (%)	95%-log based CI	
				Lower	Upper
Brown bears	13	18.23 (4.68)	25.68	14.16	36.52
Black bears	17	141.88 (155.94)	109.92	35.68	851.99

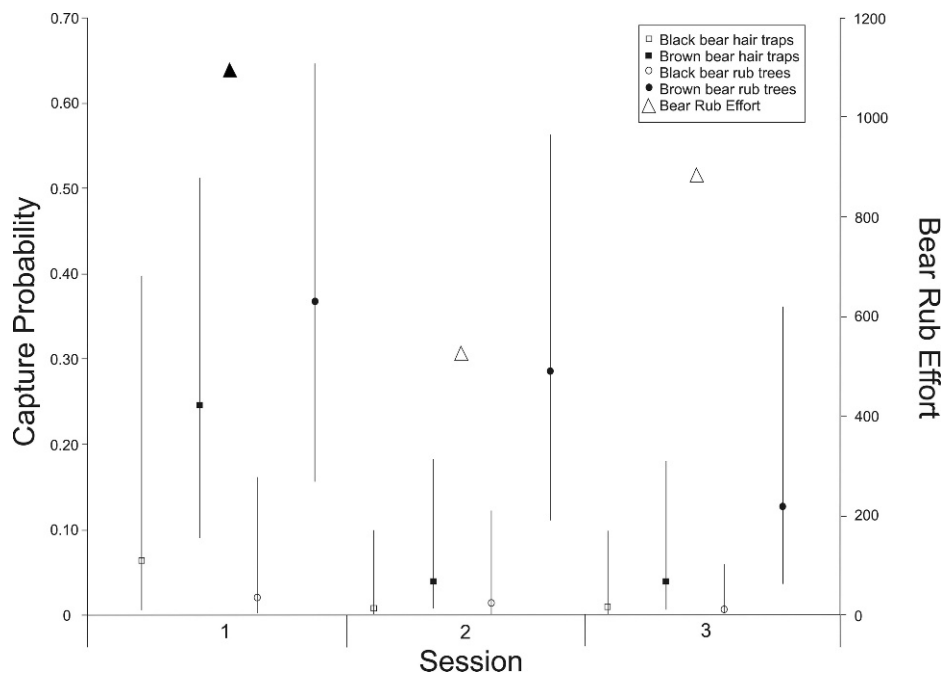


Fig. 2. Capture probabilities and 95% confidence intervals from the best model for black bears and Asiatic brown bears by method from Jun to Aug 2008, Zabolochenaya watershed, Primorski Province, Russia. Bear rub effort was the cumulative number of days between hair collections for each tree surveyed by session.

included individual capture heterogeneity varying on the intercept, and time varying on the slope, but was weakly supported (i.e., $\Delta AIC_C > 6$; Burnham and Anderson 2002). Our SECR model estimated brown bear density as 3/100 km² (95% CI: 1.4–4.8). Due to sparse black bear detection data, models did not converge. In order to compare density estimates, we divided the abundance estimates from the Huggins (1991) models by the buffered and naïve areas of the watershed, which were assumed to have zero error. The brown bear density calculated for the MMDM-buffered watershed was 1.8 bears/100 km² (95% CI: 0.9–2.8), the ½ MMDM-buffered watershed was 2.7 bears/100 km² (95% CI: 1.3–4.1), and the unbuffered watershed density estimate was 4.6 bears/100 km² (95% CI: 2.3–6.9; Fig. 3).

Discussion

Estimates

By testing the NGS methods in the field and evaluating capture–mark–recapture models, we have provided a step toward better abundance estimates of brown and Asiatic black bears in the RFE. The capture probabilities for brown bears resulted in

abundance and density estimates with reasonable precision for a pilot study (CV = 26% and 28%, respectively), but it is worth noting that Pollock et al. (1990) recommended a CV of <20% for most management decisions. Bear rubs had greater success in detecting brown bears, although the end of our sampling season may have coincided with the shift in seasonal habitat (Seryodkin, unpublished data) as suggested by the decline in capture probabilities despite increases in sampling effort.

Previous studies have had success with concurrent or complementary NGS sampling methods for CMR analysis (Dreher et al. 2007; Gervasi et al. 2008; Kendall et al. 2008, 2009; De Barba et al. 2010). The capture of 13 brown bears and 17 black bears in a short time and in a small study area suggests moderate success of the NGS methods. However, a single capture season represents a snapshot in time and modeled estimates are not definitive. Capture probability variation is modeled within the limits of available data and sample size, and within a single year of sampling, geographic closure violation may be a major contributing factor to this variation (Boulanger and McLellan 2001, Boulanger and Himmer 2004). For example, McCall (2009) found

Table 7. Spatially explicit mark–recapture models for brown bears from program DENSITY for the Zabolochenaya watershed, Primorski Krai, Russia, sampled from June to August 2008.

Model ^a	No. parameters	AIC _c	Δ AIC _c	Model weight	Deviance	$\hat{D}^b$	
						per km ²	SE
$g(\cdot)\sigma(\cdot)$	2	197.88	0	0.965	172.481	0.0311	0.0086
$g(h)\sigma(t)$	5	204.54	6.66	0.034	165.774	0.0307	0.0085

^a h = individual capture heterogeneity, t = time, σ = sigma detection parameter, g = intercept.

^b $\hat{D}$ = density estimate

that a single year abundance estimate of a 3-year study was biased by >200%, presumably caused by a berry crop failure that resulted in bears moving greater distances.

We were able to assume demographic closure based on our short sampling season, but our closed-population models suffered from geographic closure violation as evidenced by the lack of convergence in the black bear SECR model. The permeable barriers and low topographical relief of the SABZ probably contributed to geographic closure violation, which was also evidenced from the decline in bear rubbing from June to August. As our objective was to evaluate the performance of 2 NGS methods, we defined the study area based on telemetry data

suggesting that bears typically reside in low elevation areas during our sampling timeframe and then expand and move their home ranges to higher elevations following seasonal food resources (Seryodkin, unpublished data). Thus we attempted to minimize geographic closure violation and reduce the impacts of known migration for the majority of our sampling period. The brown bear SECR model estimate was within a reasonable range of the density estimates from the MMDM and $\frac{1}{2}$ MMDM buffered watersheds, suggesting that the mean distance correction, by species, improved the approximation of the effective sampling area. Other studies have found that density calculated by the MMDM-buffered sampling area are typically overestimated

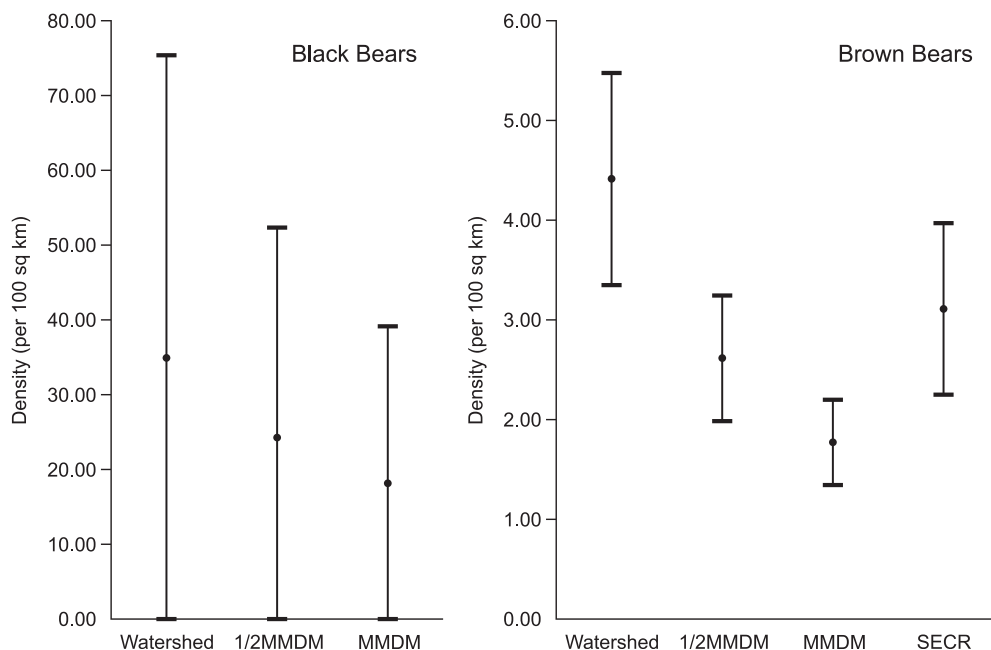


Fig. 3. Mean and standard error of density estimates using 4 density estimation methods for each bear species: spatially-explicit mark–recapture estimate from program DENSITY (Efford 2004), and closed-population model abundance estimates from Table 6 divided by the watershed boundary buffered by the (1) mean maximum distance moved by recaptured individuals (MMDM), (2) buffered watershed boundary by $\frac{1}{2}$ MMDM, and (3) the naïve area of the watershed.

relative to SECR model estimates (Soisalo and Cavalcanti 2006, Obbard et al. 2010), but our pilot study lacks the precision as well as the intention to test the hypothesis.

Capture probabilities of black bears were lower than of brown bears, which may have reflected behavioral differences. There was only a single black bear recapture on bear rubs and no recaptures from the hair traps; abundance estimates derived from such sparse datasets are unreliable (Boulanger et al. 2004). With little knowledge of interspecific interactions between the species and general behavior toward the hair traps and bear rubs, we may only speculate as to why there were a high number of black bears detected in the initial session and why only one of 19 hair trap events yielded samples from both species. American black bears may display avoidance behavior of brown bears (Herrero 1978, McLellan 1993) and have lower capture probabilities. Asiatic black bears may exhibit similar behavior, and in order to circumvent this, we would suggest more extensive geographic sampling into less optimal habitat areas. Sampling earlier in the season may also mitigate varying capture probabilities as a result of bears responding to seasonal food resources and from the weakened strength of the bait attractant during the mid-summer months of high precipitation. Trap shyness may also affect capture probabilities. Although Asiatic black bears rub less frequently than brown bears (Seryodkin 2006), previous studies have demonstrated improved accuracy and precision of estimates resulting from using multiple detection methods (Boulanger et al. 2008; Kendall et al. 2008, 2009; Stetz et al. unpublished data).

Wild boars were the only other species known to enter hair traps, and their hair was easily distinguishable in the field by its coarseness and color. Bear rub trees near a wallow were used by wild boars. Trees were also used by tigers for marking, although they tended to exhibit a strong selection toward leaning trees (Brahmachary and Dutta 1981, Smith et al. 1989, Protas et al. 2010), whereas bears are likely to find leaning trees as a physical barrier to rubbing (J. Stetz, personal observation).

We modeled abundance estimates using a strategy that allowed for the detection of species-specific behavioral differences by using species as a grouping variable. Site-specific abundance estimates have been obtained using a similar approach (Coster et al. 2011). By allowing capture probability to vary with time, we were able to detect the decline in captures

after the initial session. Our data supported species-dependent capture probabilities to both hair traps and bear rubs, although heterogeneity was difficult to model due to the sparseness of the data. Other studies have found that males and females exhibit behavioral differences that affect capture probabilities. For instance, differences in home-range sizes between sexes are expected to affect the frequency of site encounters (Boulanger et al. 2004). Female bears have also been found to rub less frequently than male bears overall (Rogers 1987; Kendall et al. 2008, 2009; Karamanlidis et al. 2010), but female capture probabilities have been observed to increase over the season (Kendall et al. 2008, 2009). Although we were unable to model sex-specific capture probabilities, the strong male bias detected by hair traps in both species have indicated that our 'snapshot' of the local bear population may not reflect the true resident bear population of the watershed.

The density of brown bears in the Primorski Province has been roughly estimated to be 1/100 km² (Seryodkin 2006). Therefore, our SECR results support previous local observations that the Zabolochennaya watershed is exceptional for brown bears relative to the overall average for the region. We were unable to compare the black bear Huggins abundance or SECR density estimates to the brown bear estimates due to very low precision, but other data sources suggest that brown bears and black bears occur in similar abundances within the RFE (Seryodkin et al. 2002). We urge caution in using our estimates beyond the scope of this pilot study, however, as differences in study design and size can render estimates incomparable across study areas (Smallwood and Schonewald 1998).

Evaluation of the methods

Collecting hair every 10–14 days was sufficient for successful DNA extraction of the hair samples; however, precipitation may have reduced the persistence and effectiveness of the scent lure in hair traps, thereby affecting capture success. Our lure was made with the best materials at hand, but could have been improved with the addition of rotten fish and blood as often used in similar studies. Unfortunately, we cannot ascertain whether capture probabilities were affected by the strength or content of the attractant.

Sub-selecting hair samples by visual inspection to target brown bears or black bears was not feasible, although methodical sub-sampling in the lab may reduce redundant analysis (Stetz et al. unpublished

data) and reduce genetic costs overall (Tredick et al. 2007). Because there was a higher failure rate of underfur samples, we suggest establishing a threshold for the number of hairs (>30) to improve cost efficiency. Furthermore, given a high variability of markers in both species (D. Paetkau, personal communication, 2012) our genetic analysis has indicated that 6 markers would be sufficient for assigning individual identity; however, more samples are needed to determine which markers would be appropriate.

Future work

Our pilot study results suggest that NGS methods can be applied to bear populations in the RFE and may qualify or improve existing population estimates. Advances in spatially explicit modeling analysis allow for more flexible sampling designs and improved capture probabilities than our study was able to achieve. Kendall et al. (2008, 2009) found increasing female capture probabilities in the fall season, and we may expect a similar pattern in the RFE. Setting additional sampling stations in less optimal habitat and lengthening the sampling season may also improve capture probabilities. In the more remote areas of the SABZ, bear rubs may become opportunistic sampling points if semi-permanent wildlife trails are not available.

In our study we targeted 2 bear species using the same sampling methods and analyses despite apparent behavioral and life history differences. The lack of geographic closure, however, seemed to prevent capturing the true population as indicated by the male capture bias, varying capture probabilities in both species, and the failed convergence of the black bear SECR model. There is still room for improvement of the NGS methods in the RFE, but our pilot study has established a baseline for future research. For example, we provide further support for using annual rub surveys for long-term population monitoring (Stetz et al. 2010) given our capture probabilities of brown bears on bear rubs were similar to or higher than previous studies in the Rocky Mountains of Canada and the United States (Kendall et al. 2008, Sawaya et al. 2012). Future research may adjust the spatial coverage, sampling time frame, and sampling intensity depending on the species while maintaining the approximate 2-week sampling schedule to minimize DNA degradation. Although black bears do not rub as frequently as brown bears, we recommend using both sampling methods at this time until one method may prove to be redundant or ineffective. The

use of bear rubs in our study was intended to simply augment hair trap data, but our modeling analysis established their necessity for exploiting behavioral differences between the species.

Finding the logistical and financial support to conduct further work will be problematic. Therefore, we suggest such methods could run concurrently with other studies requiring extensive fieldwork, for example, ongoing camera trap studies (Soutyrina et al. 2010). Neither bear species is a priority for international conservation organizations, and the regional wildlife management authorities so far do not have the resources for systematic population sampling, even though such information could improve harvest strategies. Therefore, developing the political and financial support for continued work will be an important first step to improving and expanding use of NGS survey techniques for bears in the Russian Far East.

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