Gobi bear abundance and inter-oases movements, Gobi Desert, Mongolia

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Abstract: Brown bears (*Ursus arctos*) inhabit much of the northern hemisphere, including portions of North America, Europe, and Asia. Whereas northern populations generally are healthy, their distribution becomes fragmented and conservation status more tenuous in their southern range. Many fragmented populations across southern Asia are poorly understood, and abundance and distribution data are minimal. One such population contains the Gobi bear, a brown bear surviving in the Great Gobi Strictly Protected Area of southwestern Mongolia. The number of bears in this area was assumed to be low, without data-based abundance estimates. Whereas bears frequent 3 oases complexes, it was not known to what extent bears moved or bred among these complexes, which span approximately 300 km. As part of a larger science-based conservation effort, we conducted a DNA-based mark–recapture population survey in 2009 to estimate abundance, inter-oases movements of individual bears and geneflow, and genetic variability. We placed barb-wire hair-collection sites surrounding 13 supplemental feeders at most water sources within the 3 oases complexes: Atas–Inges, Shar Khuls, and Tsagaan Bogd. During 5 sessions throughout spring and summer, we collected 600 bear hair samples and genotyped 205 samples at 12 variable microsatellite loci (from 24). We identified 21 individual bears (14 M and 7 F) 48 times and developed a mark–recapture population estimate of 22 bears (95% CI = 21–29). Estimates of mean detection probability were 0.27 (SE = 0.09, CI = 0.13–0.49) and 0.51 (SE = 0.063, CI = 0.39–0.64) for female and male bears, respectively. One female and 4 males were sampled at 2 oases complexes and 3 males were sampled at all 3 oases complexes. The genetic variability (heterozygosity) was low compared with other brown bear populations. We suggest this population is isolated from other bear populations and is likely critically endangered with fewer than 40 individuals.

Key words: brown bear, DNA, Gobi bear, Gobi desert, mark–recapture, microsatellite genotyping, Mongolia, *Ursus arctos*

DOI: 10.2192/URSUS-D-15-00001.1 ***Ursus 26(2):129–142 (2015)***

South of the contiguous Eurasian brown bear (*Ursus arctos*) population that spans northern Europe and Russia, there are several isolated populations (Fig. 1). Whereas the status of the continuous population across northern Eurasia is reasonably good (Least Concern, International Union for Conservation of Nature [IUCN] 2015 [The World Conservation Union] Red List website: http://www.iucnredlist.org/details/41688/0), in the southern portions of the species' range a number of small fragmented populations

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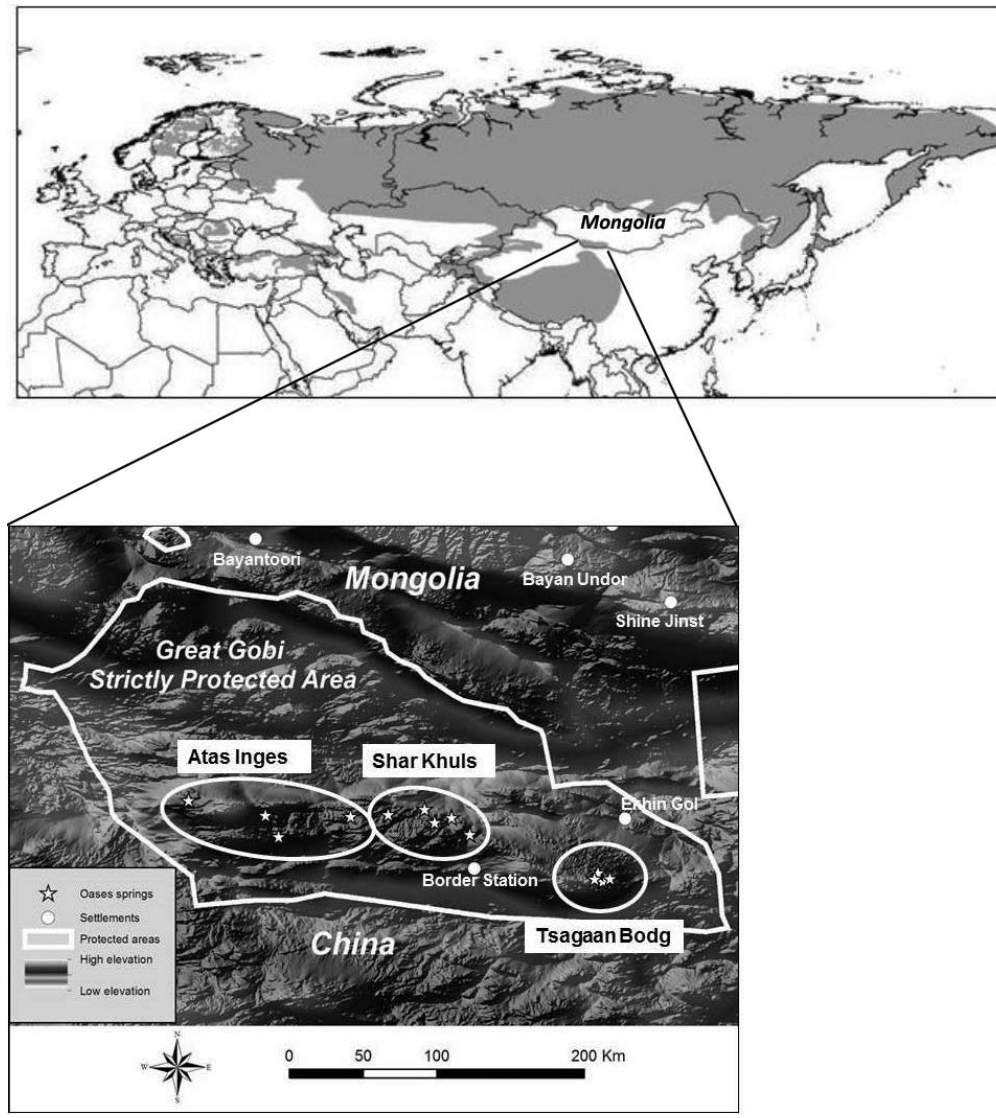

Fig. 1. Eurasian brown bear distribution with fragmented populations across the southern distribution and the Gobi population. Inset is our study area within the Great Gobi Strictly Protected Area in southwestern Mongolia, including the oases complexes (ovals) and springs (stars).

have either an unknown or a suspected threatened or endangered conservation status where they persist. Research focusing on several of these populations is limited but growing, (Pakistan: Bellemain et al. 2007, Newaz 2007; Turkey: Can and Togan 2004, Ambarlı 2012; India: Sathyakumar 2006; Nepal: Aryal et al. 2010; Japan: Sato et al. 2004, Sato and Endo 2006), although few data-based abundance estimates exist (Bellemain et al. 2007, Ambarlı 2012).

One isolated brown bear population exists in the Gobi desert of southwestern Mongolia. The Great Gobi Strictly Protected Area (GGSPA; Fig. 1), covers 45,918 km^2 and is home to a small remnant population of brown bears, referred to as "mazaalai" or Gobi bears, by Mongolians. Based on track surveys, that population has been anecdotally estimated at between 15 and 30 individuals by several authors between the 1960s and 1990s (see reviews within Batsaikhan et al. 2004, McCarthy et al. 2009). They are isolated to the north, east, and west by a low-density herder-based population with scattered villages or small towns. The closest bears to the north extend

into northern Mongolia from Russia in a few locations and are 500–800 km away. Also, the Russian brown bear population extends into western Mongolia through eastern Kazakhstan approximately 500 km away. South into China, the proximity of brown bears is less certain. As recently as the 1970s, a now-extirpated population of Gobi bears may have existed adjacent to, and within 100 km of, the current population (Batsaikhan et al. 2004, McCarthy et al. 2009). Because of the present suspected low population size, restricted range, and limited available habitat of Gobi bears, long-term persistence of the species will be a challenge that will likely require effective conservation efforts.

Gobi bears are confined to 3 oasis complexes in the GGSPA of southwestern Mongolia and use approximately 15,500 km^2 within the area. They are rarely observed and data about their biology, ecology, and behavior are sparse. There is little available information regarding factors that limit their numbers; and efforts to promote their recovery, including re-population of any part of their former range, are problematic. Research to provide a better understanding of Gobi bears is crucial to devising appropriate and timely conservation measures.

Most, or all, bears in the GGSPA likely frequent $\geq$1 of the supplemental feeding stations positioned at the infrequent water sources that occur in each of the 3 oases complexes: Atas–Inges, Shar Khuls, and Tsagaan Bogd (M. Batmunkh, personal communication; Fig. 1). Each oasis complex consists of multiple springs where surface water exists and feeder stations have been placed to supplement bear forage. These feeder stations present an excellent opportunity to collect DNA from Gobi bear hair. McCarthy et al. (2009) collected hairs from Gobi bears and used 3-locus microsatellite genotypes and sex to identify 8 individuals in 2 oases complexes.

As part of a larger cooperative international research effort to understand Gobi bear ecology and assess and improve the species' conservation status, we conducted a DNA-based population survey to estimate population size, movement patterns, genetic diversity, and isolation status. Our objective was to collect DNA samples from hair to identify individuals and estimate their numbers using mark–recapture estimation methods (Woods et al. 1999, Proctor et al. 2010). Further objectives were to use capture histories to identify movements between springs and oasis complexes, assess inter-oases geneflow, and estimate genetic diversity relative to other brown bear populations in the world.

The Gobi bear is listed in the Mongolian Red Book of Endangered Species; this categorization was validated by the bear's designation as Critically Endangered (C2a(i)&D1) in the November 2005 Mongolian Biodiversity Databank Assessment Workshop (Clark et al. 2006). The results from this survey will be the basis for status assessment within the IUCN Regional Level Red List process (IUCN 2012).

Methods

Field methods

This survey was based on a mark–recapture method using hair sampling and DNA genotyping of individual bears and their capture histories over several capture sessions (Woods et al. 1999, Proctor et al. 2010). We defined our study area as the portions of the GGSPA that contained oases complexes (i.e., water sources). Because these are the places where GGSPA rangers and managers observe bear tracks regularly, we thought all (or almost all) bears frequent these oases at some point during the non-denning season because they are the only reliable water sources available in the GGSPA. We varied our sampling design from the usual systematic grid of sampling cells (Woods et al. 1999) because of logistical constraints and because these isolated water sources attract most, if not all, large mammals living in the area. We therefore used the oases as locations for hair sampling sites. We constructed hair-snare DNA sites at 13 springs that exist within the 3 oases complexes (Fig. 1). Hair-snare sites consisted of a single strand of barbed-wire placed 50 cm above the ground surrounding a feeder station. Before our effort, feeder stations had been present for $\geq$10 years as part of a government program to supplement bear foraging resources. Supplemental feed was composed of livestock pellets and distributed once in April–May and more rarely in September. Feed at the stations was usually depleted within 3 weeks of distribution; however, bears continued to occasionally visit feeder stations throughout the remainder of their active season. The supplemental food had similar nutritional and energy content to that of the wild foods these bears eat (H. Reynolds, unpublished data). As bears entered the wire enclosure, they left a hair sample on the wire. In addition, it is well-known that bears in other areas use tree rubs (Kendall et al. 2009); therefore, we also placed barbed wire on several trees at a

few springs to collect additional hair samples. Several of these trees had evidence of previous rubbing activity by bears. We set up hair collection sites in 2008 and collected hairs throughout the spring and summer as a pilot survey and to allow cautious bears to get used to the wire. In 2009 we carried out a formal mark–recapture population estimate by collecting hair during each of 5 collections sessions: 28–30 March, 17–20 April, 25 April–3 May, 4–8 June, and 12–14 July. Sampling session length varied ($\bar{x}$ = 24 days) from consistent intervals because we used GGSPA rangers to collect samples in several sessions during their regular park-monitoring rounds. Hair samples were placed in paper envelopes and air-dried at room temperatures until analysis. Relative location of samples and their proximity to one another along the barbed wire were noted to allow for sub-sampling in the lab.

Laboratory methods

Genetic analyses were carried out at the Wildlife Genetics International laboratory in Nelson, British Columbia, Canada, by O. Tumendemberel. Wildlife Genetics International has extensive experience in analyzing bear hair samples of low DNA quantity and quality from barbed-wire sampling techniques and follows protocols outlined in Woods et al. (1999) and Paetkau (2003). Samples were transported to Wildlife Genetics International with appropriate Convention on International Trade in Endangered Species permits from Mongolia and Canada.

Samples were sub-sampled to reduce lab costs because individual bears often leave multiple hair samples at a site per visit. We used 2 criteria to exclude samples prior to extraction. First, samples with no guard-hair roots and <5 underfur hairs were set aside on the basis of quality. Only 6 samples containing <10 underfur hairs were analyzed, and the success rate for these was 0%. The second criterion for exclusion was to limit the number of samples to be analyzed from a given collection site-session. The maximum was 4 extractions for sites with <8 samples, 5 extractions for sites with 8–10 samples, and ≥50% with >10 samples.

We extracted DNA using QIAGEN's DNeasy Tissue kits following the manufacturer's instructions (QIAGEN, Venlo, Netherlands; http://www.qiagen.com/). We used 10 guard-hair roots where available. When underfur was used, we extracted DNA from clumps of whole underfur rather than from clipped individual roots. We expected low marker variability because of suspected low genetic diversity. We therefore put considerable effort into marker selection before starting the analysis of individual identity. For this purpose we selected higher quality samples (generally extracted from ≥10 guard-hair roots) that were collected at different times and places, and screened them with 25 microsatellite markers. From this effort we identified 12 markers that were sufficiently variable for use (G1A, G10B, G1D, G10L, G10M, G10P, G10U, MU23, MU51, MU59, P07, and CXX110; Ostrander et al. 1993, Taberlet et al. 1997, Paetkau et al. 1998a, Breen et al. 2001, Proctor et al. 2002, Bellemain and Taberlet 2004), resulting in 13 total usable markers when we added the amelogenin gender marker (Ennis and Gallagher 1994; Table 1).

Table 1. Measures of marker variability, including the observed frequency of the most common allele (Max f, A = no. of alleles) for Gobi bears of Mongolia, 2009. Sample sizes are as per the final results (marker selection was done with smaller sample sizes). Differences between expected heterozygosity (H_E) and observed heterozygosity (H_O) were not significant at any marker.

Marker	*N*	H_E	H_O	A	Max f
G10B	22	0.54	0.59	3	0.64
G1D	22	0.75	0.82	4	0.32
D1a	22	0.62	0.68	3	0.52
I45P07	22	0.61	0.64	3	0.50
MU51	22	0.51	0.50	3	0.64
MU23	22	0.60	0.68	3	0.50
MU59	22	0.51	0.55	2	0.50
G10L	22	0.38	0.41	2	0.75
G10M	22	0.46	0.41	2	0.66
G10P	22	0.46	0.32	2	0.66
G10U	22	0.51	0.55	3	0.59
CXX110	22	0.51	0.64	2	0.55
G10O	16	0.51	0.44	2	0.53
Msut-6	20	0	0	1	1
G1A	21	0	0	1	1
G10H	19	0	0	1	1
G10C	19	0	0	1	1
CPH9	19	0	0	1	1
MU50	18	0.26	0.28	3	0.86
G10X	19	0	0	1	1
144A06	16	0	0	1	1
D123	16	0	0	1	1
Msut-2	16	0.18	0.19	2	0.91
MU26	16	0	0	1	1
CXX20	20	0	0	1	1
$\bar{x}$		0.29	0.30	1.92	0.77

The 13 markers were completed in 2 single sequencer lanes, so the first and second pass involved 6 and 7 microsatellite markers respectively. After the first pass, we removed samples with high confidence scores for <3 of 6 markers. This cull was necessary

to the efficiency and accuracy of our process; it eliminated the samples with the lowest success likelihood and highest potential of genotyping error. All remaining samples with incomplete genotypes went on to one or more rounds of re-analysis.

Error-checking involved replication of one mismatch (MM), 2MM, 3MM, and 4MM pairs as detailed in Paetkau (2003) and replication of any genotypes represented by only one sample. Mismatches are pairs of genotypes that are identical except for 1 allele (1MM), 2 alleles (2MM), or more. These paired samples are potentially from the same bear and often only differ because of an error in the genotyping process. Replicating these close genotypes allows them to be verified and errors eliminated (Paetkau 2003). This process is an excellent and resource-efficient method for minimizing or eliminating genotyping errors that would result in "false" identification of individual bears (see Kendall et al. 2009). The probability that 2 individuals had identical genotypes at our 13 markers was best considered by looking at potential siblings (Woods et al. 1999, Paetkau 2003). We therefore calculated this probability (Psib) for each individual in the population after removing each individual's genotype being calculated for their Psib calculation to remove bias in the generated allele frequencies. At the end of the error checking and the individual identification processes, one sample from each identified individual was rerun at the 7 most variable loci to verify there were no bears created through genotyping error.

Population estimation

Population estimates were generated assuming population closure during the survey. Closure violation occurs when bears leave or enter the study area during the sampling process and tends to positively bias population estimates because some bears may not be available for capture and therefore might be captured only once. Given the Gobi bear distribution, movement pattern data collected from Global Positioning System (GPS) collars, and the fact that no records of Gobi bear sightings or sign have been verified outside of their present distribution since the 1970s in either China or regionally in Mongolia, we had strong evidence that the population was closed. Our population estimate represents the number of bears using the oases and springs of the presently known distribution of Gobi bears.

We used the Huggins closed-capture model (Huggins 1991) and heterogeneity mixture models (Pledger 2000) in Program MARK (White and Burnham 1999; MARK Version 7.1, www.phidot.org/software/mark/, accessed 19 Nov 2013). Examination of our capture and recapture patterns suggested that we consider capture probability variation due to time and sex as covariates in our suite of competing models. We therefore developed and tested models assuming no covariates, sex alone, time alone, and sex and time together, additively and as interactions. We also developed 2 heterogeneity mixture models (Pledger 2000). We compared models using the small-sample-size–corrected Akaike's Information Criteria (AIC_c; Burnham and Anderson 2002). We considered models to be supported by the data if their Delta AIC_c scores were <2.0. To account for model uncertainly, we model-averaged our population estimates based on AIC_c weights relative to support for the best model with the lowest AIC_c score. We calculated log-based confidence intervals (White et al. 2002) on model-averaged estimates. Estimates of variances for combined-sex estimates were obtained from the variance–covariance matrix of model-averaged estimates.

We did not use the recently developed Spatially Explicit Capture Recapture models (Efford 2004) that are designed to estimate density because all evidence suggested that we sampled the full extent of the inhabited area of bears, and therefore there was minimal chance of movement to or from or focal study area during the period in which sampling occurred. Furthermore, our sampling strategy was linked to the unusual study area; we sampled all known water springs in a desert with vast areas of unsuitable habitat where these oases likely attract all large mammals.

Spatial analysis

We used capture histories combined with spatial sampling locations to map the extent of individual bear movements within a Geographic Information System. This information allowed us to explore inter-oases movements of individual male and female bears. We also used the software program Genetix (Belkhir 1999) to explore genetic clustering due to fidelity to any one oasis complex. Genetix is a powerful clustering algorithm that does not rely on population-specific allele frequencies and thus does not rely on large sample sizes to detect genetic similarities. Genetix uses allele sharing and multidimensional Factorial Correspondence Analysis (Benzecri 1973, She et al. 1987, Proctor et al. 2012) and provides an objective exploration into groupings of similar

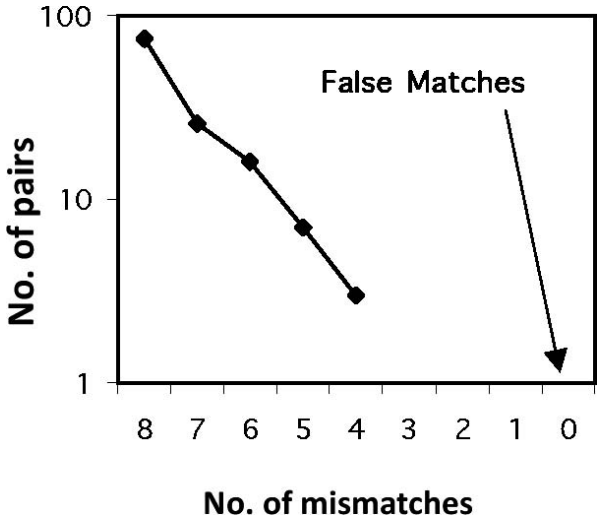

Fig. 2. Plot of mismatching genotypes between paired individuals of sampled Gobi bears after the error-checking process, Gobi Desert, Mongolia, 2009. The graph indicates that the closest 2 individual bears' genotypes differ at 4 alleles, suggesting a very low probability of our data set containing a bear created through genotyping error.

genotypes without a priori assumptions of group membership.

Results

Sample collection and genotyping

In 2009 we collected 600 hair samples of sufficient quality for attempted analysis; 308 were extracted after sub-selection and rejection for having too few hairs. Ninety-nine yielded poor results on the first pass and were discarded as were 4 mixed samples (>1 bear). Ultimately, 205 were successfully genotyped. After re-analyzing all paired genotypes that had 1MM, 2MM, 3MM, and 4MM, our final data set contained no pairs of genotypes with fewer than 4MM, indicating that we likely had no "false" bears due to genotyping error (Fig. 2). Between scoring errors, loading errors, and amplification errors associated with remotely collected hair samples, 24 alleles were changed after reanalysis during the error checking process resulting in a per locus error rate of 0.09%.

We identified 21 individuals in 2009 (7 F and 14 M). One female that was not identified in 2009, was identified in our 2008 pilot study. The mean number of samples per individual male bear was 14.1 (SE = 2.98) and 4.8 (SE = 1.36) per individual female bear, and 1 individual was represented by only 1 sample. The highest individual probability of 2 siblings having an identical genotype at our 13 markers (including sex) was 0.00087 (Appendix SI), which translates into a 1 in 1,153 chance of 2 siblings having identical genotypes and thus going undetected as 1 bear. The expected heterozygosity of the Gobi bear was 0.29, and this is close to the lowest values recorded for any population of *U. arctos* in the world (Table 2).

Table 2. Genetic variability of Gobi bears relative to other *Ursus arctos* bears.

Study area	Heterozygosity	No. of alleles/locus
Pyrenees Mountains, Spain[a]	0.25	1.7
Gobi	0.29	1.9
Kodiak Island, Alaska[b]	0.30	2.1
Pakistan[c]	0.49	3.3
Yellowstone, USA[d]	0.56	4.9
S Selkirks, Canada[e]	0.54	4.3
Scandinavia, Europe[f]	0.66	5.8
Southern Canada[b]	0.68	6.4
Northern Canada[b]	0.78	7.4

[a]Taberlet et al. (1997).
[b]Paetkau et al. (1998b).
[c]Bellemain et al. (2007).
[d]Proctor et al. (2005).
[e]Miller and Waits (2003).
[f]Waits et al. (2000).

Population estimate

In 2009, we captured 21 bears 48 total times (Table 3) and captured bears in all 5 sessions. The pattern of newly identified individuals by session was 3, 9, 2, 5, and 2 bears in sessions 1–5 respectively. The spread of bear captures (least and most) was 3 bears in session 1 and 17 in session 4, suggesting the presence of variation of the probability of detection across sessions.

The most supported Huggins closed model contained sex and session as additive covariates and was the only model with a ΔAIC_c <2.0 (Table 4). This model indicated sex-specific detection probabilities but similar temporal patterns of capture probability across sessions. There was minimal evidence of heterogeneity variation as modelled by heterogeneity mixture models. Behavioral response models did not converge, presumably because of sparse data. Our model-averaged abundance estimate was 22 bears (8 F and 14 M) with a 95% confidence interval of 21–29 (Table 5). Estimates of mean detection probability were 0.27 (SE = 0.09, CI = 0.13–0.49) and 0.51 (SE = 0.063, CI = 0.39–0.64) for female and male bears, respectively.

Table 3. Recapture summary for males (M), females (F), and both sexes of Gobi bears sampled in 2009 in the Gobi Desert of Mongolia. 1× indicates the number of bears captured 1 time, 2× indicates the number of bears identified 2 times, etc.

	M	F	Both sexes
Bears identified	14	7	21
Captures	37	12	48
1×	2	3	5
2×	4	3	8
3×	6	1	6
4×	1	0	1
5×	1	0	1

Spatial capture results

DNA from hair samples of Gobi bears was collected at all sampled springs within the 3 oases complexes. Eight males and 3 females were sampled at 4 springs within the Atas–Inges oasis complex. Ten males and 3 females were sampled within 5 springs within the Shar Khuls oasis complex and 6 males and 2 females were sampled at 4 springs within the Tsagaan Bogd complex (Fig. 3). Females were sampled from 10 of 13 springs and at all 3 oases complexes (Fig. 3a). DNA from a single individual female was captured at springs within both the Atas–Inges and Shar Khuls complexes, confirming female movement between the complexes (Fig. 3b). Multiple males were captured at all sampling sites except one spring with only one capture (Fig. 3c). Three males were captured at both Atas–Inges and Shar Khuls oases complexes (Fig. 3d). One male was captured at Shar Khuls and Tsagaan Bogd complexes (Fig. 3d). Three males were captured at all 3 oases complexes (Fig. 3d). We found no clustering using the Genetix Program of individuals based on capture location within oases complexes (Fig. 4), which indicates little breeding fidelity within any one oasis complex.

Discussion

This survey is the first rigorous data-based population estimate of the Gobi bear. Our estimate of 21–29 bears makes the Gobi bears of Mongolia one of the smallest isolated *U. arctos* populations in the world. The low genetic diversity corroborates observations by GGSPA personnel that this population is totally isolated from other *U. arctos* bears. The combination of very low numbers and the population's isolation confirm that this population is at risk of extirpation. These results informed a recommendation that this population be considered Critically Endangered by a recent assessment using the IUCN Red List Criteria at Regional and National Levels (IUCN 2012).

Gobi bears may live in one of the most extreme desert environments of any *U. arctos* population on earth (Schaller et al. 1993). This northern (43° latitude), high-elevation (800–2,700 m) desert experiences extreme heat (+45°C), cold (−35°C), and dryness with <100–200 mm of precipitation annually. As such, Gobi bears may retain important genetic variation (from a global perspective) related to their ability to survive in the harsh environmental conditions presently existing in the Gobi Desert. Also, they have one of the lowest recorded levels of genetic diversity in bear populations in the world. However, actual issues related to inbreeding depression in wild bear populations have been rare. On-site examinations by experienced veterinarian specialists from Mongolia and North America are planned in the near future to assess the potential of reproductive issues that might contribute to any inbreeding depression.

Population size is one of the most powerful predictors of persistence (Berger 1990, Shaffer et al. 2000, Reed et al. 2003). Populations with fewer than 50–100 adults are at high risk of extirpation (IUCN

Table 4. Model-selection results of Huggins closed models to estimate population size of Gobi bears, Gobi Desert, Mongolia, 2009. Small-sample-size–corrected Akaike Information Criteria (AIC_c), the difference in AIC_c values between the *i*th model and the model with the lowest AIC_c value (ΔAIC_c), Akaike weights (w_i), and number of parameters (K) are presented.

Model	AIC_c	ΔAIC_c	w_i	K	Deviance	Model likelihood
p(sex[a] + [b]session)	128.95	0.00	0.76	6	93.48	1
p(session)	131.61	2.66	0.20	5	98.39	0.2642
p(sex * [b]session)	134.80	5.85	0.04	10	89.85	0.0535
p(sex)	142.87	13.92	0.00	2	116.14	0.0009
p(.)	145.05	16.11	0.00	1	120.40	0.0003
Π^{c}_{i}(.) Θ^{c}_{1}&Θ_2(.)	148.35	19.40	0.00	3	119.50	0.0001
π_i(sex) Θ_1&Θ_2 (sex)	151.12	22.17	0.00	6	115.65	0

[a] "Sex" indicates sex-specific detection probability.
[b] "*" indicates an interaction effect and a + denotes an additive effect.
[c] "π" and "Θ_1&Θ_2" indicate heterogeneity mixture models.

Table 5. Model-averaged abundance estimates (weighted by Akaike wt) for the Gobi bear, Gobi Desert, Mongolia, 2009. Estimates are based on models listed in Table 4.

Sex	Estimate	SE[a]	mt + 1[b]	CI[c] low	CI high	CV[d]
F	8	1.41	7	7	15	17.8%
M	14	0.53	14	14	17	3.7%
Total	22	1.50	21	21	29	6.8%

[a]SE is standard error.
[b]mt + 1 is the no. of animals sampled.
[c]CI is confidence interval.
[d]CV is coefficient of variation.

2012); therefore, the Gobi bear's long-term prospects represent a challenge and are likely dependent on informed and effective management. *U. arctos* is a species characterized by long lives (20–30 yr) and slow reproductive rates (Miller 1990); therefore, there is time to implement management to avoid extirpation. Several management strategies are already in place, including the supplemental feeding program. We do not review a comprehensive list of management recommendations here, except to mention the need for a long-term strategy to increase the number of bears. In that regard, we have no evidence that current bear numbers represent the ecological carrying capacity for the occupied habitat. However, in the absence of evidence for excessive human-caused mortality, it is possible these bears are near or at carrying capacity in their occupied range. Therefore, we do not know whether efforts to increase bear numbers within the existing occupied habitat would be successful. We suggest that consideration be given to the idea that bear numbers be increased through expanding their current range, either by extending their current occupied habitat or by establishment of a second nearby population (possibly to the pre-1970 distribution) that might be connected through occasional movements, or both. We have a limited understanding of the history of the isolation of this population (Batsaikhan et al. 2004) except from reports by GGSPA rangers that bears occupied potentially 2 adjacent mountain ranges (within 100 km) as late as the 1960–1970s (McCarthy et al. 2009). The persistence of this small isolated population would be enhanced by the presence of a second, nearby population, similar to the small Deosai populations in the Himalayan Mountains of Pakistan, where inter-area movements enhance their genetic and demographic health (Nawaz et al. 2008). In the case of the Gobi bear, natural connectivity with current populations in northern and western Mongolia is highly unlikely because of the great distances involved (hundreds of km). Efforts to establish a second adjacent population would have to overcome several obstacles. A second nearby population may have the potential to be started through natural dispersal, or even population augmentation or re-colonization from an outside source. Because local habitats are extreme, augmentation from another source population raises the question of potential negative effects of outbreeding (Tallman et al. 2004). To avoid that issue, we recommend that priority consideration be given to managing for increased bear numbers within the GGSPA by expanding their occupied range and studying the potential for the establishment of a movement corridor to adjacent suitable habitat to encourage natural or assisted dispersal for establishment of a second population. We also recommend that the Gobi bears be assessed for evidence of inbreeding depression (as mentioned previously), and if it is found, some form of genetic augmentation be considered (Hogg et al. 2006). The trade-offs between inbreeding and outbreeding effects would need to be weighed (Tallman et al. 2004).

Whereas we likely captured almost the entire population that uses the sampled oases complexes, our best-supported model suggested that there was a difference in the capture probabilities between the sexes. This pattern was also evident in the difference in the number of samples per individual, on average, between males and females. Less encouraging was the fact that in 2008 and 2009 we captured only 8 females, which suggests there may be fewer than 10 females in the population. Populations with this few number of females likely face threats from stochastic (chance) demographic events (e.g., disease, low productivity) and the potential effects of inbreeding. However, observations from remote cameras and capture efforts for radiocollaring from our larger project on these bears indicate that reproduction is occurring. Direct observation of successful reproduction was observed within the population by research personnel (12 observed offspring over 10 yr; O. Tumendemberel, personal observation). Furthermore, we surmise that survival in this extreme environment is complex and challenging. Captive breeding efforts to augment this population likely will not be effective because bears often spend 2–4 years with their mothers learning habitat necessities (including locations of important food patches and water sources, and survival mechanisms in human encounters), particularly in less productive ecosystems (Nawaz et al. 2008). It would be

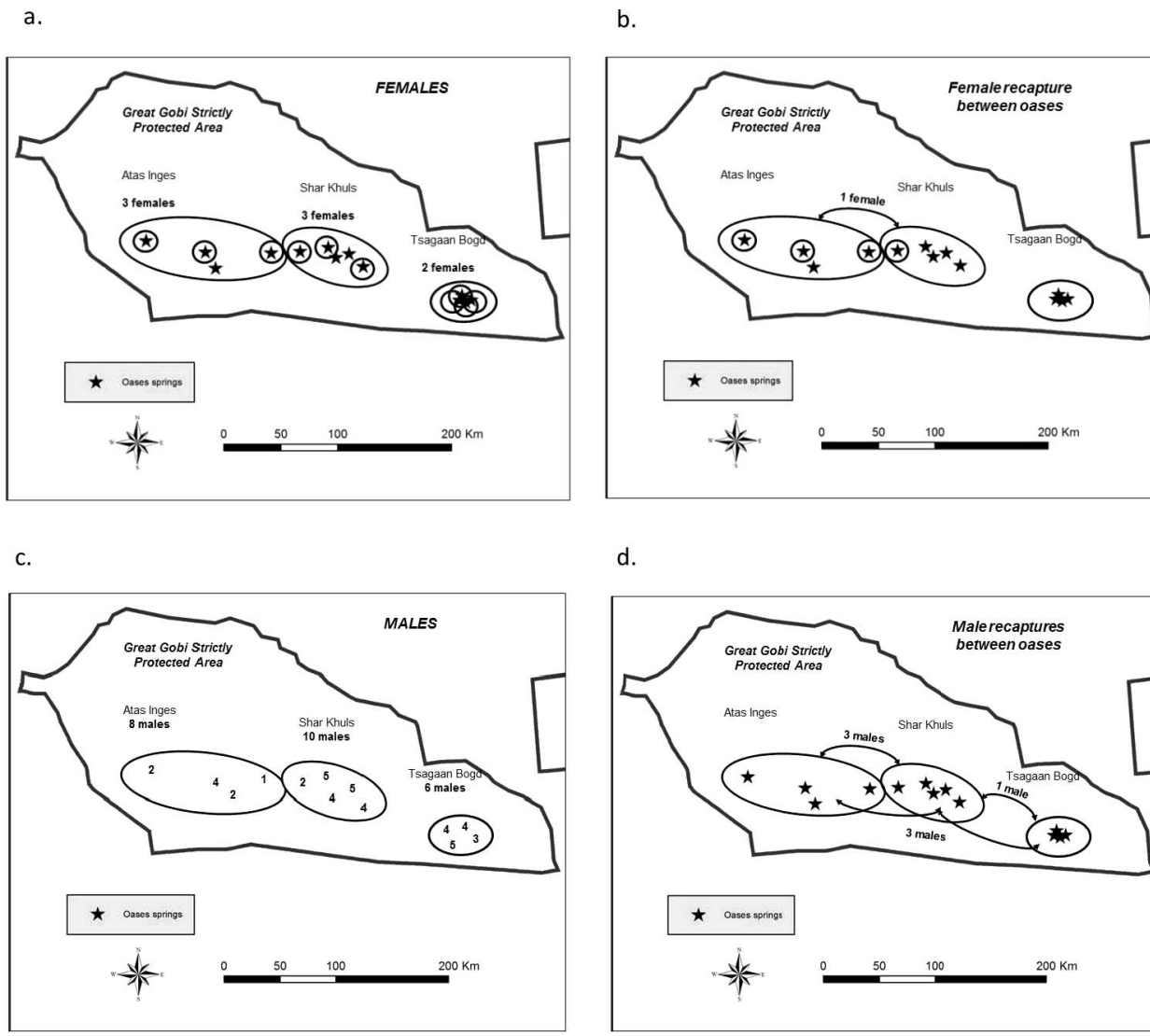

Fig. 3. (a) Summary of DNA captures of female Gobi bears sampled during the 2009 population survey by oases complex and spring, Gobi Desert, Mongolia, 2009. Stars in ovals indicate springs where female bears were DNA-captured. (b) One female Gobi bear's DNA capture locations between the Shar Khuls and Atas–Inges oases complexes during the 2009 population survey. Stars in ovals indicate springs where individual female bears were sampled. (c) Numbers of individual male Gobi bears sampled at oases springs during the 2009 population survey, and (d) Summary of male Gobi bear recaptures between oases complexes. Arrowed lines above the oasis complexes indicate movement by males between those complexes; lines below indicate movement of 3 male bears between all 3 oasis complexes. See details of specific individual's capture locations in Appendix SII.

detrimental if wild females were to be removed from the population for breeding, primarily because the population is so small. Without several years of learning from their mothers how to exploit sparse and dispersed food and water resources in this region, survival of any offspring released in this extreme and complex environment would likely be very low. Furthermore, success of carnivore reintroductions through captive breeding programs have a low success rate (Stamps and Swaisgood 2007, Jule et al. 2008).

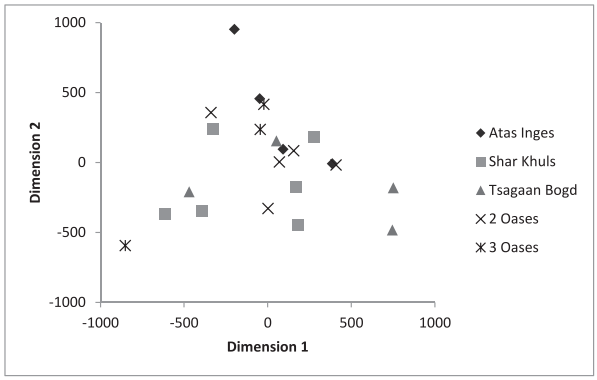

Fig. 4. Genetix plot demonstrating the lack of clustering of individual Gobi bear genotypes between any oases complex, Gobi Desert, Mongolia, 2009. These results indicate no breeding fidelity with any one oases complex. Plot is based on 22 individuals and 12 microsatellites.

Our capture probability and recapture rate was relatively high for a DNA-based mark–recapture study on bears (Boulanger et al. 2002, Mowat et al. 2005, Proctor et al. 2010), despite substantial variation in capture probability across sessions and between the sexes. Our support-weighted model-averaged abundance estimate alleviates potential issues concerned with model selection bias, providing confidence that our estimate likely is an accurate reflection of the number of Gobi bears using the oases.

There are several potential scenarios that may have contributed to a negative bias (low estimate) in our population estimate. First, the possibility exists that we did have 2 bears (potential siblings) with identical genotypes that we considered as 1 bear. If this were the case, it would mean our estimate was biased low, by $\geq$1 bear. However, the highest Psib value indicates this probability was very small at 1 in 1,157 individuals. Second, males may have a higher capture probability for various reasons, including that they may exclude females from using the supplemental feeders (Nevin and Gilbert 2005); thus, there may be more females in the population than we sampled. Our estimate of detection probabilities for females was 0.27 compared with 0.51 for males, potentially suggesting that exclusion or potential differences in movements of males and females created lower detection rates for females. Our GPS telemetry data, however, do not support this hypothesis because we have no evidence of males spending long periods of time at the feeder-sampling sites (H. Reynolds, unpublished data). Males, on average, left more samples than did females across 18 DNA surveys reported in Proctor et al. (2012), but the average mean difference was not as extreme as we found in this project. To further test whether males were excluding females from feeding sites (and thus, sampling sites), we recommend that future surveys provide secondary supplemental feeders with DNA sampling stations at several feeders, to reduce the possibility of female exclusion by males. By modelling sex-specific detection rates, we reduced heterogeneity bias in our population estimate due to differential detection rates, particularly given that heterogeneity bias is minimal when detection rates are high (Pollock et al. 1990). Third, a positive behavioral response could result in an overestimate of detection probabilities and a resulting negative bias in estimates. This scenario is unlikely because the feeders were in place long before our study occurred and therefore any change in detection probability after initial detection would have occurred when the feeders first were in place. The main source of variation in this case would be heterogeneity variation as previously discussed. Finally, it is possible that a few bears did not visit the water sources we sampled. Our study area is large and complex, and the possibility exists that an unsampled small spring exists that potentially could support a small number of bears.

Regarding a potential positive bias of our estimate, the 2 closest genotypes between individuals had 4 mismatches (genotypes were similar except at 4 alleles), providing evidence that we likely had no false individuals in our final data set. The other potential influence of male dominance at feeder stations is that some females may have been recaptured less because of exclusion (also discussed above as a negative bias if any females were excluded totally). However, we sampled 21 individuals and our estimate was 22 bears, which did not leave much room for our estimate to be positively biased. Although these small biases are certainly possibilities, they do not change our overall conclusion that there are likely fewer than 40 bears in the GGSPA using these oases complexes, rather than 60 or 100 bears.

There are several methods available for error-checking genotyping results (multiple tubes, Taberlet et al. [1997]: or systems combining multiple tubes and methods of Paetkau [2003], e.g., Schwartz et al. [2006]) and all are aimed at reducing biases in population estimates (Roon et al. 2005). The method we used, as detailed in Paetkau (2003), has been shown to be very effective in reducing errors to a trivial level (Kendall et al. 2009), while being very cost-effective.

This final point is particularly important for projects conducted in areas of the world where resources for wildlife research are scarce and efficient methods are a necessity.

We captured females and males at multiple springs and across oases complexes within the GGSPA. Our relatively high recapture rate allowed us to gain insights into the spatial use of the study area by both sexes, particularly the use of springs across several oases complexes by several individuals. This inter-oases use provides solid support to explain our result of no internal genetic structure within the Gobi bears between oases complexes. We conclude that inter-oases breeding was very likely occurring. These results suggest that management efforts to move bears between oases to enhance inter-oases geneflow would be unnecessary. Furthermore, 2 males were captured at oases that were approximately 280 km apart. Our GPS radiocollar data will provide a more detailed examination of home range size, but based on the pattern of DNA captures, the home ranges of several males will likely be in the range of 3,000–6,000 km^2. Home ranges of this size are consistent with ecosystems of low productivity (McLoughlin et al. 2000).

This project was designed to be integral to the ongoing Gobi Bear Project efforts to assess factors that may limit population size and distribution of Gobi bears. Included in these efforts are data collected by GPS telemetry, capture and examination of bears, diet analyses using scat to identify the breadth of forage items and identify key foods, assessing habitat use, mapping of important habitat areas including foraging areas and movement corridors, and determining other critical habitat requirements. Also, the GPS information can provide information on the relative time spent by individual bears at supplemental feeding stations, their frequency of use of springs and the habitat at oases complexes, and the amount of time bears go between spring visits for water intake.

Conservation implications

We also recommend that continued population monitoring be implemented. DNA-based monitoring efforts have been applied to brown bears in other studies (Boulanger et al. 2004) and are underway on other small threatened populations in other locations around the world (DeBarba et al. 2010). This effort may take 1 of 2 forms. The first is annual sampling with relatively low effort—because the DNA sites are somewhat permanent fixtures around feeding sites at oases springs, and rangers visit regularly, collecting samples would be relatively efficient. Combined with the use of remote cameras (also already deployed), additions of new individuals to the population could be monitored. A database of all genotypes of individual bears would allow documentation of new additions to the population (births) through identification of new genotypes. The disadvantage of this option is that it may be expensive to run many genotypes annually, to detect only a few new individuals. If the genotyping were done within a lab in Mongolia, that cost would be reduced. The second approach would entail a repetition of the full survey every 5–10 years. The disadvantage of this approach is that detecting a trend would be challenging because confidence intervals tend to overlap unless there are dramatic declines or increases in population size (Boulanger et al. 2003). However, in the absence of significant trend results, periodic abundance estimates can be informative, new individuals can be discovered, and lab costs could be amortized over the interval between surveys.

The conservation issues facing the Gobi bear population may be similar to other small, South Asian, isolated bear populations, including other species. Issues concerning establishment of a second nearby population will be ecologically, socially, and politically challenging to overcome in the Gobi and in other locations where such action may be relevant. In some cases, establishing inter-population connectivity to a neighboring population to promote demographic and genetic exchange may be possible where recent fragmentation might be reversed through management. However, in some cases, distances separating populations may be too far for this option to work. In addition to targeted management to reduce human-caused mortality, efforts to maintain or enhance food supplies may also be beneficial and establishment of a second nearby population may provide the best complementary option for long-term persistence. Different spatial configurations of isolated populations will likely require situation-specific solutions, including consideration for factors such as genetic and ecological similarities of source populations, the presence of available and suitable habitat to contain an additional population, social and political will for such endeavors, and the practicality of potentially moving bears between countries if required. Our study inferences cannot provide answers to all these questions, but highlight the need for their consideration in cases of small isolated

populations with little hope of natural connectivity with an adjacent population. The first step in assessing the need for any conservation actions is to determine population status (i.e., abundance, distribution, connectivity) as this project has done. Of course, an ecological and demographic understanding (diet, habitat use, mortality patterns) of any population under consideration will also be very useful, and our larger research effort is designed to gather that information.

Acknowledgments

We would like to thank the Mongolian Ministry of Environment, Green Development and Tourism for their cooperation and support in this project. We also thank the Mongolian Academy of Science Institute of General and Experimental Biology and the United Nations Development Program for their financial, personnel, and logistical support. We appreciate and would like to acknowledge the participants' field work (site set-up and hair collection), including B. Mijiddorj, E. Erdenekhuu, A. Buysentseteg, B. Maamba, S-O. Shar, H. Tsagdar, and the late D. Sharav. In addition to the substantial financial and in-kind project support provided by Gobi Bear Project team members and the Institute for Conservation Research of the San Diego Zoo, we received financial support from The Charles Engelhard Foundation, the International Association for Bear Research and Management, the Calgary Zoo, and Wildlife Genetics International. We also thank the *Ursus* Associate Editor, F. van Manen, and the manuscript reviewers for their suggestions, which improved this manuscript.

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Received: 30 December 2014
Accepted: 11 July 2015
Associate Editor: van Manen

Supplemental material

Appendix I. Microsatellite genotype data for 22 Gobi bears of Mongolia.

Appendix II. Summary of the number of male Gobi bears sampled during the 2009 population survey, by oases complex and spring.