Temporal sampling frame selection in DNA-based capture–mark–recapture investigations

Michael T. Wegan[1,4], Paul D. Curtis[1], Raymond E. Rainbolt[2], and Beth Gardner[3]

[1]*Department of Natural Resources, Cornell University, Ithaca, NY 14853, USA*
[2]*Fish & Wildlife Management Program, US Army, Fort Drum, NY 13602, USA*
[3]*Department of Forestry and Environmental Resources, North Carolina State University, Raleigh, NC 27695, USA*

Abstract: Capture–mark–recapture (CMR) population parameter estimation utilizing DNA analysis from remotely-collected hair samples to identify individuals and generate encounter histories has become the standard methodology for estimating abundance of American black (*Ursus americanus*) and grizzly bear (*U. arctos*) populations. However, few published studies have examined the time frame for efficiently collecting high-quality hair samples. Our objectives were to examine several measures of hair trapping success and sample quality, such as DNA amplification rates and the mean number of black bear hair samples collected per trap visit, from hair-snare samples collected in 2 non-overlapping, multi-interval sampling frames conducted during 2005 and 2006 at Fort Drum Military Installation in northern New York. Through our data analyses and a review of 12 other bear CMR studies using remote hair sampling, we emphasize that temporal sampling frame is a crucial consideration in study design. To avoid biased population estimates and to use financial, personnel, and temporal resources effectively, hair sampling should be conducted during late spring and early summer.

Key words: American black bear, capture–mark–recapture, genetic sampling, hair, population estimation, temporal sampling frame, *Ursus americanus*

Capture–mark–recapture (CMR) population parameter estimation using DNA analysis of remotely-collected hair samples to identify individuals and generate encounter histories is a ubiquitous tool in bear population ecology research and management (Garshelis 2006, Proctor et al. 2010). DNA-based CMR has proven attractive due to its ability to generate larger sample sizes for arguably less financial or personnel resource expenditures than conventional capture–recapture methods (Woods et al. 1999, Tredick et al. 2007). The literature offers myriad refinements of DNA-based CMR sampling and estimation processes, such as quantifying and incorporating genotyping errors into population parameter estimates (Paetkau 2003, McKelvey and Schwartz 2004, Lukacs and Burnham 2005, Roon et al. 2005, Dreher et al. 2007) and refining existing and exploring new estimation procedures (Boulanger and McLellan 2001, Miller et al. 2005, Gardner et al. 2009, Gardner et al. 2010). Testing alternative hair

trapping devices (Beier et al. 2005, Boulanger et al. 2006, Robinson et al. 2009) and sub-sampling protocols (Tredick et al. 2007, Dreher et al. 2009, Laufenberg 2010) also have been investigated. Others have explored moving traps between trapping sessions (Boulanger et al. 2006) and manipulating sampling grid size (Boulanger et al. 2004).

Although researchers have not focused much effort on understanding the implications of temporal sampling frame selection of DNA-based CMR, it may have significant impacts on sample quality, numbers of samples collected, and, ultimately, parameter estimation bias. Proctor et al. (2010) suggested that the temporal sampling frame of their hair snaring efforts targeted a period of annual shedding for grizzly bears (*Ursus arctos*) in the late spring–early summer. This suggests that 2 basic assumptions underlie their motivation: (1) annual molting occurs in the late spring–early summer in bears; and (2) barbed-wire enclosures obtain more samples or samples of higher quality from bears during this period of molting than in other 'non-shedding' periods (i.e., loose hair is more easily

[4]Present address: Wildlife Division, Michigan Department of Natural Resources, East Lansing, MI 48823, USA; weganm@michigan.gov

collected by the barbed-wire than firmly-rooted hair). Although both assumptions seem reasonable, neither has been validated in the literature. Indeed, any empirical evaluations of seasonal molting in ursids are scarce. However, as serum prolactin levels and lengthening photoperiod have been shown as major factors in initiating spring molting in mammals (Rougeot et al. 1984, Martinet 1992), and prolactin was found to peak in spring in captive black bears (*U. americanus*, Tsubota et al. 1995), it may be reasonable to deduce that molting in temperate North America occurs from spring through mid summer. This is supported by the findings of Rogers (1980) and Schwartz et al. (2003), which surmise through direct observation and a review of literature, respectively, that the molting period ends by late July or early August. Belant et al. (2005) noted a steady decline in the quantity of hair samples per trap over 4 trap sessions as the summer progressed on their Stockton Island study area. The reduction in success may have been due to sampling continuing into the post-molt period, but they did not comment on this possibility. Ultimately, the effects of sampling during the spring molting period compared to mid-late summer or fall on sample quality and number of samples collected are speculative, as data-driven analyses focused on these effects have heretofore not been conducted.

Concern about sample quality and number is rooted in the desire to avoid incorporating error in encounter histories, which may bias demographic estimates (Lukacs and Burnham 2005). Poor sample quality can result in several types of error: (1) failure to produce any samples that successfully amplify when ≥1 sample was collected; (2) failure to identify all individuals that visited a hair trap when >1 sample was collected; or (3) the creation of a genotype which does not occur in the sampled population (Woods et al. 1999). The former 2 errors may become more prevalent if few samples are available per trap where ≥1 sample was collected, as few opportunities at a low amplification rate inherently result in a depressed probability of identifying an individual in a recorded visit. This phenomenon was noted by Mowat and Strobeck (2000), as they failed to identify any individual at 15 of 155 (9.6%) trap checks in which ≥1 hair sample was collected on their Alberta study site due to both poor sample quality and low number of samples per trap visit. Although these metrics can have significant effects on estimates, the relationship between

them and collection during shedding and non-shedding periods has not been evaluated via analysis of remotely-collected hair sampling data. The objective of our investigation was to address this paucity through the examination of several metrics of hair-trapping success from data collected in both the spring molt and post-molt, mid-late summer period for black bears in 2005 and 2006 on Fort Drum Military Installation in northern New York. We also evaluated 12 peer-reviewed CMR studies using similar sampling techniques to explore patterns in temporal sampling frames. Through these approaches, our objective was to examine the importance of considering temporal sampling frame to avoid biased population parameter estimates and utilize financial, personnel, and temporal resources effectively.

Study area

The study area was a 16,327 ha contiguous area on Fort Drum Military Installation in northwestern New York, USA (Fig. 1). The majority of the study took place in the Eastern Ontario Plains Ecoregion, which has a mix of forest types with white oak (*Quercus alba*) and northern red oak (*Q. rubra*) dominating savannah areas along with white pine (*Pinus strobus*), lowbush blueberry (*Vaccinium angustifolium*), blackberry (*Rubus fruticosus*), raspberry (*R. idaeus*), bush honeysuckle (*Diervilla lonicera*), and whorled loosestrife (*Lysimachia quadrifolia*). Other forest habitats include northern mixed forests of sugar maple (*Acer saccharum*), hemlock (*Tsuga canadensis*), and quaking (*Populus tremuloides*) and bigtooth aspen (*P. grandidentata*), as well as deciduous lowland forests which are predominantly sugar maple, oak (*Quercus* spp.), and American beech (*Fagus grandifolia*; US Army Garrison Fort Drum 2011). An extensive network of palustrine wetlands is present throughout the study area. The study area had a mean elevation of 208 m with a range of 150–263 m (US Army Garrison Fort Drum 2011). There is no permanent human habitation on the study area, but temporary bivouac areas were established for military training activities during the study.

Methods

In 2005, we established an array of hair traps (*n* = 26) across the study area in an approximation of a 3-km x 3-km grid (Fig. 1). We constructed barbed-wire enclosures similar to those described in Woods
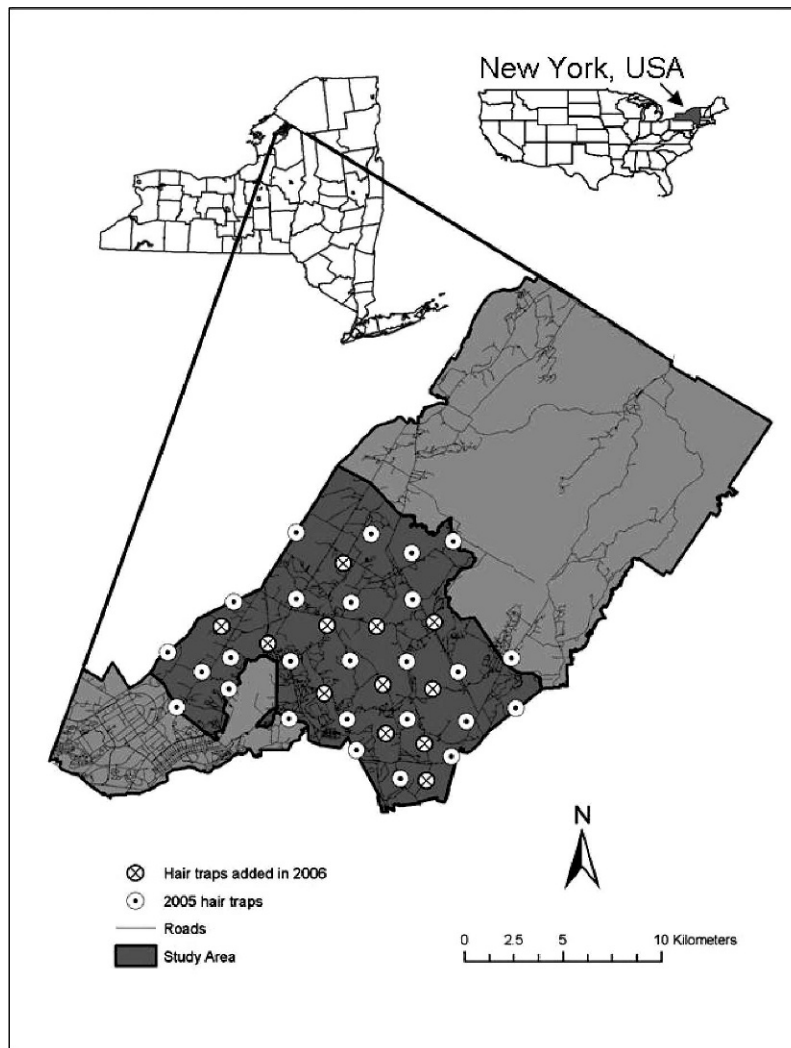
Fig. 1. Fort Drum Military Installation in northern New York, USA, and hair trap sites used during 2005 and 2006 for a study of black bears. All sites were active for 8 sampling sessions in 2006, whereas only traps represented by dotted circles were active for 6 sessions in 2005.

et al. (1999); however, we hung 2 strings of double-stranded, 4-point barbed-wire, one at ~25 cm and one at ~60 cm. In 2006, we increased trap density by adding 12 traps within the existing array in a fashion that approximated uniform spacing (Fig. 1).

The protocol for collecting hair samples was identical in 2005 and 2006. We checked and rebaited each trap with 0.45 kg of raw bacon and 1 half-opened 170 g can of sardines every 7 days. From anecdotal evidence, we perceived that the bear population was dense enough to elicit a high number of visitations and produce more hair samples than we were capable of processing due to budgetary

constraints if a persistent, non-consumable bait was used. Therefore, we suspended the baits ~1.5 m above ground so that they were likely to be consumed by bears, reducing the probability of further visitation at that trap in the trapping interval. In 2005, sampling occurred over 6 weeks in mid–late summer (31 Jul 2005–11 Sep 2005). In 2006, we conducted the survey over 8 weeks in the late spring–early summer (1 Jun 2006–28 Jul 2006). At the conclusion of each sampling interval, we placed each sample in individually labeled manila coin envelopes and stored them at room temperature with desiccant and limited light exposure before shipment to

Wildlife Genetics International in Nelson, British Columbia, Canada after the respective trapping seasons. Prior to analysis, we culled all samples with <1 guard hair root or <5 underfur roots. We did not attempt to analyze these samples due to insufficient genetic material. This prescreening process removed all samples with unreasonably low likelihoods (~10%) of producing a usable genotype (David Paetkau, Wildlife Genetics International, Nelson, British Columbia, Canada, personal communication, June 2011). We used QIAGEN's DNeasy Tissue kits (QIAGEN, Valencia, California, USA) as instructed by the manufacturer to extract genetic material from samples. Microsatellite genotyping and assignment of samples to individuals was performed as described in Paetkau (2003) at 6 commonly used microsatellite markers: G10L, G1D, G10P, G10M, G10J, and MU59 (Paetkau 2003).

We refer to the set of samples which amplified at all 6 microsatellite loci as $S = \sum s_t$, where s_t is the number of successfully amplified samples at the tth sampling session for $t = 1, 2,…, T$ weeklong intervals. We pooled all insufficient samples and those that failed to amplify and noted the set as $F = \sum f_t$, where f_t is the number of samples collected at the tth sampling session that did not successfully amplify. Therefore, $S + F$ is the total number of samples across all trapping sessions and $s_t + f_t$ is the number of samples collected at the tth sampling session.

We coupled the 2005 and 2006 datasets to create a reconstructed 14-week sampling sequence from 1 June–11 September. Weeks 1–8 represent the 2006 sampling season and weeks 9–14 represent the 2005 sampling season. We developed several measures of effectiveness of trapping effort that may be influenced by the timing of sampling: weekly amplification rates, r_t, and weekly mean number of hair samples per known trap visit, $\overline{h}_t$. For week t, let x_t be the number of traps at which we collected ≥1 sample and $x_t = x_{ts} + x_{tf}$, where x_{ts} is the number of traps at which we gathered ≥1 sample and ≥1 individual was identified by genotype and x_{tf} be the number of traps at which we collected ≥1 sample but none successfully amplified. Also, let v_t be the number of known visits to traps during the tth week, generated from the successfully genotyped data, plus x_{tf}. By counting the number of times each genotyped individual visited traps in the same week and adding the number of traps at which bear hair was collected but failed to produce a successful sample (i.e., assume one bear visited the site during the week), we calculate v_t as the minimum known number of times bears visited our traps in the week. Then, $r_t = s_t / (s_t + f_t)$ x 100 and $\overline{h}_t = s_t + f_t / v_t$. Further, $p_t = 1 - x_{ts} / x_t$, where p_t was the probability that no individual was successfully genotyped at a trap at which we collected ≥1 hair sample. This is an important metric because p_t is the apparent error incorporated in encounter histories due to poor sample quality and low sample numbers. The other error created by these factors, failure to identify all individuals that visited a site when >1 sample was collected, cannot be quantified as the data set does not provide the necessary information to reveal the instances we failed to identify all bears that visited a trap during a given sampling interval. We also established these values on a monthly basis, denoted by the subscript "$_m$" rather than "$_t$". We assumed that yearly differences in bear susceptibility to sampling via hair traps were negligible and used a simple linear regression to model the relationship between time (the 14 sampling sessions) and r_t and $\overline{h}_t$. While we did not perform formal tests on the monthly statistics, they provide insight on a greater temporal scale that takes advantage of greater sample sizes.

We also reviewed a 12 article subset of pertinent peer-reviewed literature selected through keyword searches of multiple electronic databases with combinations of the terms *Ursus*, hair, genetic, DNA and population estimation. Article selection criteria required that: (1) black or grizzly bear population ecology or a methodological derivative (e.g., sub-sampling, trap spacing, incorporation of genotyping error) was of primary interest; (2) barbed-wire traps as described in Woods et al. (1999) were used; (3) genetic analysis of remotely collected hair samples was the primary identifier of individuals; and (4) the investigation occurred in North America. Because we attempted to discern patterns and effects of sampling timing, these criteria constrained our literature review to rigorous inquiries with similar methods and goals. We discuss the implications of reported temporal sampling frames from the reviewed articles and the effects of sub-sampling and prescreening in light of the observed trends in our data collected at Fort Drum Military Installation in 2005 and 2006.

Results

We retrieved ≥1 hair sample at 141 (29.9%) of 472 trap-check opportunities (i.e., number of traps x

Table 1. Weekly and monthly results from genetic sampling of black bear hair at Fort Drum Military Installation, New York, USA, 2005 (26 hair traps monitored) and 2006 (38 hair traps monitored). For weekly (t) and monthly (m) measures, r was the percent of samples that successfully amplified, $\bar{h}$ was the mean number of samples collected per known visit, x was the number of traps where ≥ 1 sample was collected, p was the weekly probability that ≥ 1 sample successfully amplified from a trap at which ≥ 1 sample was collected.

	Jun 2006				Jul 2006				Aug 2005				Sep 2005	
	1	2	3	4	5	6	7	8	9	10	11	12	13	14
No. samples	23	30	60	72	84	40	55	27	21	8	10	15	15	15
r_t (%)	100	93.3	95	97.2	85.7	77.5	83.6	85.2	61.9	62.5	50	53	20	73.3
$\bar{h}_t$	2.56	3.33	2.31	3.13	3.36	1.82	2.12	1.93	2.63	2.00	2.50	1.88	1.88	2.14
v_t	9	9	26	23	25	22	26	14	8	4	4	8	8	7
x_t	7	7	14	15	19	15	19	11	6	5	4	7	8	4
p_t	0	0	0	0	0	0.07	0.05	0.09	0.33	0	0.50	0.29	0.62	0
No. samples		185				206				54				30
r_m (%)		96.2				83.5				57.4				46.7
$\bar{h}_m$		2.76				2.36				2.25				2.00
v_m		67				87				24				15
x_m		43				64				22				12
p_m		0				0.05				0.27				0.42

number of trapping sessions). We collected a total of 481 samples, 84 in 2005 and 397 in 2006. Through our prescreening process, we removed 33 samples (6.9%) deemed to contain insufficient genetic material. The mean number of samples collected per week was 33.9 (SD = 24.47). The rate of successful amplification at 6 microsatellite loci over all weeks was 83.2%, but ranged between 100% and 20% by week (Table 1). Samples sizes, especially in 2005, were low for several weeks, as we collected ≤ 26
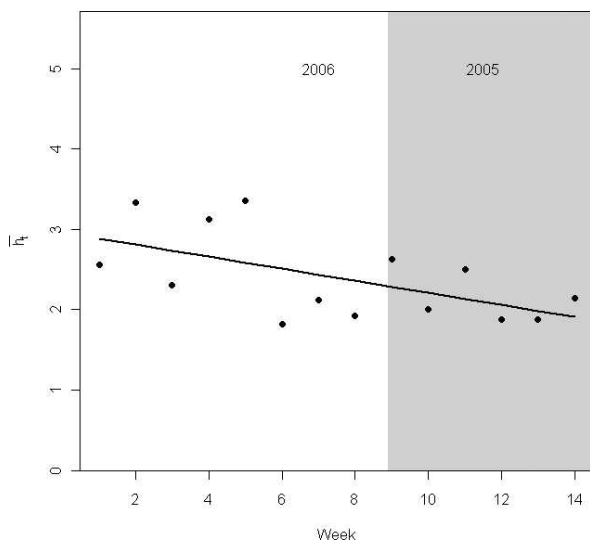

Fig. 2. Weekly mean number of black bear hair samples collected per known trap visit ($\bar{h}_t$) in 2005 and 2006 at Fort Drum Military Installation in northern New York, USA.

samples in half ($n = 7$) of the trapping sessions. Week was a significant predictor for both mean number of hair samples per known trap visit, $\bar{h}_t$, ($P = 0.03$, $R^2_{adj} = 0.34$; Fig. 2) and weekly amplification rate, r_t, ($P < 0.01$, $R^2_{adj} = 0.64$; Fig. 3), suggesting that the mean value declined as season grew later for each metric. The rate of failure to successfully genotype a bear where ≥ 1 sample was collected during the tth sampling period, p_t, increased at a significant rate as the season progressed ($P = 0.02$, $R^2_{adj} = 0.31$; Fig. 4).

We selected 12 peer-reviewed articles from those that matched our criteria. Within these investigations, findings from 17 study areas were discussed; the sample sizes reported here are subsets of the study areas unless otherwise specified (Table 2). Hair samples from 10 of the study sites were culled in sub-sampling protocols. Only 2 used a pre-screening process similar to ours. Sub-sampling procedures and pre-screening reduced the number of samples analyzed to cut the cost of laboratory work (Boersen et al. 2003; Tredick et al. 2007; Clark et al. 2010). These processes precluded calculation of overall amplification rates because many samples that may have successfully produced a genotype were not analyzed. Furthermore, 3 investigations that did not employ these procedures estimated grizzly bear population parameters and could not discern between black bear and grizzly bear samples that were insufficient for analysis. Thus, amplification rates were not available because the total number of grizzly bear samples was unknown. Therefore, we
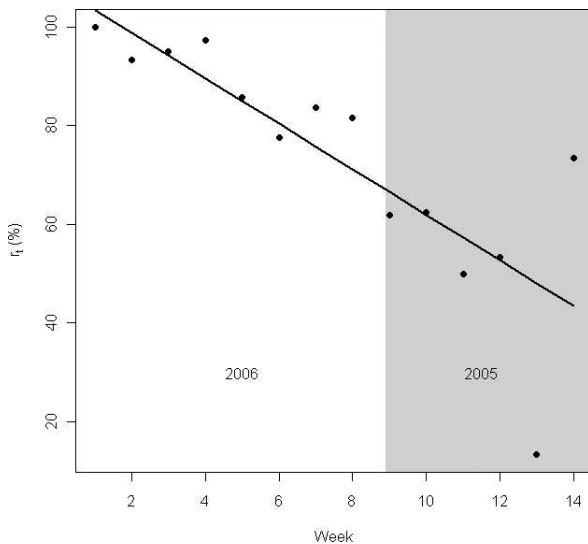
Fig. 3. Weekly rate of successful DNA amplification of black bear hair samples at 6 microsatellite loci (r_t) at sites where ≥1 sample was collected in 2005 and 2006 at Fort Drum Military Installation in northern New York, USA.

Fig. 4. The weekly rate of failure to successfully genotype any individual at a trap at which we collected ≥1 hair sample (p_t) in 2005 and 2006 from black bear hair samples collected at Fort Drum Military Installation in northern New York, USA.

did not attempt to link amplification success to sampling time for these investigations.

The temporal sampling frame at 15 study sites was reported, sometimes only by month. We compared the frequency distribution of the number of times each month was listed in these investigations' sampling frames and the observed monthly rate of failure to collect a sample that successfully genotyped at a trap at which we collected ≥1 hair sample (p_m) from our data in Table 1 (Fig. 5). The most frequently sampled month was July; 13 of the 17 listed sampling frames occurred in that month. Only 3 studies continued into September but sampling continued into November in 2 investigations (far past of the expected spring molting season).

Discussion

By combining hair-trap data from 2005 and 2006 at Fort Drum, we developed a reconstructed time series. We assumed that no factors significantly affected yearly patterns in bear susceptibility to being sampled by barbed-wire hair traps and that amplification rates and mean hair samples per trap visit were reliable indicators by which to measure this susceptibility. In focusing on these data, we avoided the confounding issue of variation in annual and seasonal food availability and its effect on
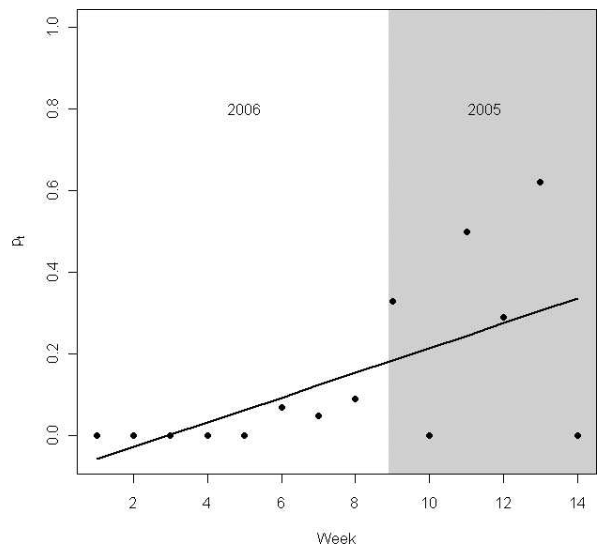
visitation rates (Noyce and Garshelis 1997). Further, we assert that our prescreening process established a minimum threshold that excluded only samples that were unlikely (i.e., ~10% probability of successful amplification) to produce a full genotype and that our calculations of amplification rates were unlikely to significantly differ had we attempted extraction of extremely low quality samples. As we only removed 33 samples through prescreening, the expected 3–4 additional samples that would have amplified were insufficient to change our findings significantly.

All metrics of hair trapping success deteriorated from June through September in our study. Although sample sizes were low during several weeks, we observed a significant effect of time as the percent of samples that amplified at 6 microsatellite loci declined from sampling sessions 1–14. The mean number of hair samples collected per known trap visit also declined over the 14 sampling periods. Consequently, the measurable rate of error in encounter histories, p_t, increased as the season progressed from molting to post-molting periods. Fluctuations of p_t are likely functions of small sample size, but generally the first half of the sampling frame (weeks 1–7) produced high probabilities of collecting a sample that amplified and mean numbers of samples that amplified per visited trap. This is confirmed with the observed steady

Table 2. Peer-reviewed investigations that used barbed-wire traps to remotely collect hair samples from grizzly or black bears in North America.

Reference	Study area	Sampling year	Sampling frame	Pre-screening[a]	Sub-sampling
Woods et al. (1999)	Golden, British Columbia	1996	10 Jun–23 Jul	unknown	N
Mowat and Strobeck (2000)	Selkirks, British Columbia	1996	19 Jun–9 Aug	unknown	Y
	Alberta	1996	18 Jun–14 Aug	unknown	N
Boersen et al. (2003)	Tensas, Louisiana	1999	27 Jul–2 Nov	>10	Y
Triant et al. (2004)	Inland and Coastal Louisiana	1999	Summer	$\geq$5	N
Belant et al. (2005)	Apostle Islands, Wisconsin	2002	26 Jun–13 Aug	$\geq$5	N
Mowat et al. (2005)	Selkirks, British Columbia–see Mowat and Strobeck (2000)				
	Prophet, British Columbia	1998	25 May–1 Aug	unknown	Y
	Yellowhead, Alberta	1999	19 May–9 Jul	unknown	N
	Parsnip, British Columbia	2000	30 May–2 Aug	unknown	Y
	Bowron River , British Columbia	2001	2 Aug–22 Sep	none	Y
Dixon et al. (2006)	Northern Florida	2002–03	May–Nov	unknown	Y
Dreher et al. (2007)	Lower Peninsula, Michigan	2003	22 Jun–26 Jul	$\geq$5	Y
Tredick et al. (2007)	St. Johns, Florida	2001	Jun–Aug	$\geq$5	N
	Pocosin Lakes National Wildlife Refuge, North Carolina	2002	Jun–Aug	$\geq$5	N
Kendall et al. (2009)	Northern Continental Divide Ecosystem	2004	15 Jun–18 Aug	$\geq$1 guard hair roots or $\geq$5 underfur roots	Y
Tredick and Vaughan (2009)	Coastal North and South Carolina	2001–04	Summer	>5	Y
Clark et al. (2010)	White River National Wildlife Refuge, Arkansas	2004–07	Jun–Aug	$\geq$1 guard hair roots or $\geq$5 underfur roots	Y

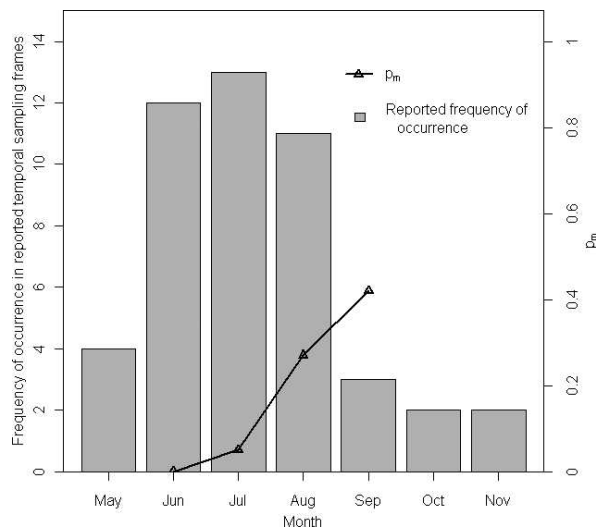[a]Minimum number of roots in any hair sample for genotyping analysis to be attempted.

Fig. 5. The frequency of months in reported temporal sampling frames from Table 2 and the monthly rate of failure to successfully genotype any individual at a trap at which we collected $\geq$1 hair sample (p_m) for black bear hair samples collected at Fort Drum Military Installation in northern New York, USA.

increase in the monthly rates of error incorporation, p_m. Overall, our analysis indicated that a late spring and early summer sampling frame was best for both hair sample numbers and quality of samples, which may influence population parameter estimates. As suggested by Proctor et al. (2010), our highest sustained success rates coincided with an annual molting period of black bears in the early spring–late summer, after which the incorporation of error in encounter histories due to poor quality samples became problematic. We suspect hair sample quality and quantity are enhanced during the spring molt as hairs are loose and highly susceptible to being plucked with root bulbs intact by barbed-wire.

Comparable amplification rates for DNA-based CMR investigations were not reported in the reviewed articles. Sub-sampling and pre-screening processes were common, and these procedures excluded processing samples of low quality, possibly lessening the impact of temporal sampling frame selection. However, with declining sample quality and number of samples per visit ($\overline{h}_t$) in the mid to late summer, we observed a higher probability of missed capture events. The rate of failure to identify

an individual at a trap visited by a bear (p_m) increased every month from 0 in June to 0.42 in September. Sub-sampling and pre-screening processes may select for the highest quality samples available, but cannot effectively circumvent this error. If only samples of poor quality are available from a trap site and few samples are available per visit, hierarchical selection procedures will not increase the probability of those samples producing a viable genotype. The resultant probability of failure to record captures for late summer sampling may enhance bias that sub-sampling may inherently introduce into the estimation process (Tredick et al. 2007, Dreher et al. 2009, Laufenberg 2010). For low-density bear populations with low capture probabilities, this is especially troublesome, as CMR estimation processes are more easily biased by errors in encounter histories when capture probabilities are low (Lukacs and Burnham 2005).

According to the published articles we reviewed, most remote hair sampling occurred during a 3-month period, from June to August, and significantly declined in the fall. The data from Fort Drum do not provide coverage of all reported sampling periods, but still offers utility in evaluating the most frequently sampled months from the reviewed articles. Overall, most published articles' sampling periods coincided with our highest monthly measures of success in June and July, although 11 continued into August, which was suboptimal compared to the previous 2 months. The great variation in latitude and elevation in the locations of these projects may influence the timing of molt, but we feel confident in asserting that it would have tapered off on a population level by mid summer for all study sites (Rogers 1980, Schwartz et al. 2003).

Fall sampling, which took place in October and November at 2 study sites in the literature review, may take advantage of a secondary autumnal molting period which occurs in many mammals in response to decreased photoperiod and increased serum melatonin levels (Rougeot et al. 1984). Our data do not address this possibility, but high food availability in mid summer through fall may reduce capture probabilities (Noyce and Garshelis 1997, Boyce et al. 2001). Additionally, bear distribution may shift in the late summer and fall to localized areas of high food abundance (Raine and Kansas 1990, Wegan 2008, Nielsen et al. 2010). A major redistribution of the population during sampling, where some individuals leave the effective trapping area in search of these food resources, would violate the closure assumption in CMR studies. Caution should be taken, however, in extrapolating results from spring and mid summer sampling to other seasons, as movement patterns and bear distribution may significantly change seasonally.

Given both the empirical evidence and our knowledge of the life history of black and grizzly bears, we feel that late spring–early summer presents a confluence of opportunity when generally low food availability may heighten capture probabilities and, as we have shown, hair sample quality and quantity are very high. Sampling during this period coincides with spring molt and may reduce one source of bias in CMR studies using genetic analysis of remotely-collected hair samples to estimate bear population parameters. It also reduces the probability of violations to the closure assumption as long range bear movements may be less likely than in the late summer and fall, but produces results that may not be appropriate for inference about bear distribution and habitat use in other seasons.

Management implications

The remote collection of hair samples to generate demographic estimates for black and grizzly bears is an important tool for the establishment of meaningful and robust management and policy. The ubiquity of and reliance on this procedure necessitates that researchers seek to refine collection and estimation procedures to enhance confidence in the parameter estimates. By focusing the sampling effort on the late spring–early summer, errors in capture histories can be reduced, lessening the bias incorporated in population parameter estimates. These findings have the potential to significantly impact any type of study (e.g., bear habitat use, distribution, population parameter estimation) that samples bear populations through the remote collection of hair samples. The use of more robust biological information gained simply by focusing the temporal sampling frame on the spring molt of bears will allow wildlife managers to implement more defensible conservation policy with greater confidence.

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