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Comparing urban and wildland bear densities with a DNA-based capture-mark-recapture approach

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Abstract: California's black bear (*Ursus americanus*) population has tripled over the last 3 decades, causing an increased incidence of human–bear conflicts, many of which now occur in urban areas. Consequently, it is imperative that bear managers have the ability to monitor population parameters in both wildland and urban environments to help manage bears. Capture-mark-recapture (CMR) methods using uniquely typed genetic samples (DNA) collected via hair-snares have been widely used to monitor bears in wildland areas. However, we are unaware of researchers applying this technique to bears occupying urban areas. We implemented a multi-year DNA-based CMR study to compare bear densities between an urban area and a nearby wildland area. We deployed hair-snares for 6 weekly capture occasions during June and July, 2011 and 2012. We uniquely typed DNA from snared hair follicles using 14 microsatellite loci and 2 sexing loci. We coupled unique identification with robust-design closed-capture models and model averaging in Program MARK to estimate abundance. We identified 41 and 62 individual bears on the urban and wildland study areas, with average densities of 3.8 and 1.8 bears/10 km^2, respectively. Our data support the hypothesis that bears can occur at greater densities in urban areas. Based on these results, we recommend using DNA-based CMR methods to monitor populations of bears in urban areas, but we suggest increasing the density of sampling locations to account for greater bear densities. Furthermore, we contend that DNA-based CMR can also estimate survival, recruitment, rate of population change (λ), and identify movement patterns by incorporating additional survey years.

Key words: American black bear, California, DNA-based capture-mark-recapture, hair-snare, population estimate, robust design, urban bear, *Ursus americanus*

During the latter part of the twentieth century, the abundance of black bears (*Ursus americanus*) increased in many states (Karanth et al. 2011), and California was no exception. According to statewide estimates derived from age-at-kill data, California's black bear population during 1982 was <15,000 and increased to 35,000 by 2011 (California Department of Fish and Wildlife 2012). While these estimates reflect the statewide situation, the models that derive these estimates are inadequate to estimate smaller-scale population abundance because some of the models' assumptions are violated at such scales (Fraser et al. 1982, Fraser 1984, Coster et al. 2011). California Department of Fish and Wildlife (CDFW) biologists have documented black bears residing in places the bears historically never occurred and have recorded increases in abundance in places black bears historically were at low densities. Furthermore, bears occupying urban areas are

typically not harvested due to ordinances that prohibit hunting within city limits. Therefore, urban bear populations are not represented in modeled statewide population estimates.

Human–bear conflicts are increasing in urban areas as urban development, recreation in black bear habitat, and bear populations all continue to increase. Habituated bears living in and around urban environments take advantage of anthropogenic resources (i.e., acting food-conditioned) and are a major concern to wildlife managers and the general public who live with bears in their community (Beckmann and Lackey 2008, Baruch-Mordo et al. 2011, Merkle et al. 2011). It has been well documented that these bears can be a threat to public safety and inflict major property damage (Baruch-Mordo et al. 2008, Herrero et al. 2011). Less documented, but equally important to wildlife managers, is the fact that urban landscapes can negatively affect the health of wildland bear populations by functioning as a sink in a source-sink dynamic (Beckmann and Lackey 2008, Hostetler et al. 2009). Extensive efforts across North America are being made to manage human–bear conflicts and, more recently, studies have begun to evaluate the effects of urban environments on bear spatial use (Beckmann and Berger 2003*a*, Lyons 2005), activity patterns, and ultimately, population health (Beckmann and Berger 2003*a*, Baruch-Mordo et al. 2014).

Both ecological theory and human–bear conflict patterns have indicated a generalized hypothesis that density of bears occupying urban areas can be greater than density of bears occupying wildland areas. In one of the few studies on urban bear density, GPS-collared black bears occupying urban areas had greater densities and different sex ratios relative to GPS-collared bears in nearby wildland and rural environments (Beckmann and Berger 2003*b*, Beckmann and Lackey 2008). However, GPS-collaring studies are invasive, and marking animals is unacceptable to some members of the public. To make informed decisions about urban bears, managers and policy makers need reliable and cost-effective demographic and abundance estimates that are non-invasive and more accepted by the public (Thompson et al. 1998, Williams et al. 2002).

A common method of monitoring bear populations to obtain small-scale population parameters is to employ DNA-based capture-mark-recapture (CMR) techniques from systematically collected hair samples (Mowat and Strobeck 2000, Kendall and McKelvey 2008, Robinson et al. 2009). Collecting hair samples with hair-snare devices is non-invasive and does not require physically marking animals (Kendall and McKelvey 2008). The CMR monitoring methods can provide estimates of vital rates, such as survival, immigration, and emigration (Pederson et al. 2012), which can be used to monitor bear population dynamics as well as help determine if small-scale survey areas are serving as sinks, sources, or refuges.

To manage populations of bears that use urban areas, biologists as well as city planners must ascertain how urban bear population dynamics compare to adjacent wildland populations. Further, monitoring bears in urban areas is essential to provide baseline data for evaluating impacts of management actions (e.g., aversive conditioning using non-lethal hazing techniques, bear translocation, and food removal via anti-bear garbage devices) on bear density and vital rates. Our main study objective was to compare black bear densities within the 2 main landscape types in the eastern Sierra, urban and wildland. We tested the hypothesis that bear density would be greater in our urban study area than our wildland study area. To this end, we conducted a multi-year DNA-based CMR using hair-snares for 2 study areas that were similar, aside from urban development and human population density.

Study area

Mono County, California, USA is situated along the eastern Sierra Nevada mountain range, occupies approximately 7,884 $km^{2,}$ and has a low density of people, with approximately 2 people/km^2 (U.S. Census Bureau 2010*a*). Most bear habitat is confined to the mountainous region located along the eastern escarpment of the Sierra Nevada. The bear habitat east of the Sierra Nevada to the Nevada border is in the Great Basin Desert, which is considered low-quality bear habitat. The predominant land type in Mono County is considered wildland or rural, defined as geographic areas containing <2,500 people (U.S. Census Bureau 2010*b*). The other main land type is urban, defined

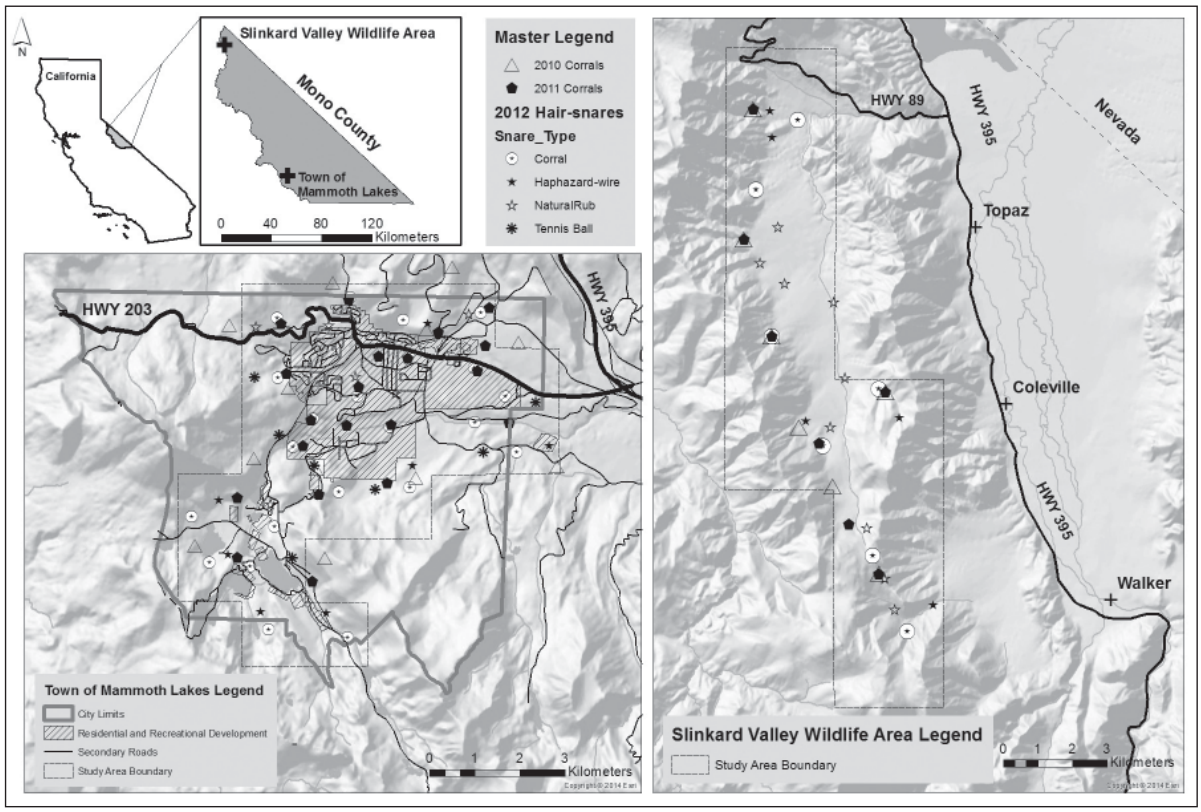

Figure 1. Location of study areas and distribution of hair-snares for a DNA-based capture-mark-recapture study of black bears in Mono County, California, USA, 2011–2012.

as geographic areas containing 2,500–50,000 people (i.e., communities; U.S. Census Bureau 2010*b*). We established 2 study sites in Mono County, the first of which was the Town of Mammoth Lakes (TML), representing an urban study site, and the state- and federally-owned Slinkard Valley Wildlife Area (SVWA) represented the wildland study site (control; Figure 1).

Urban study site

The urban study site was located within the TML community (city limits 60 km^2), located at the base of the Mammoth Mountain Ski Resort, and elevation range was 2,200–2,700 m. We reduced the study area to the 44-km^2 area within the city limits where there was the highest presence of humans, anthropogenic resources (e.g., trash), and anthropogenic structures (e.g., campgrounds, resorts, and cabins). The study area had 8,234 year-round residents (U.S. Census Bureau 2010*b*) and 1.5 million visitors during the spring and summer, which was the same time bears were most active (Town of Mammoth Lakes 2007). The average housing density within the study area was 219 housing units/km^2 (U.S. Census Bureau 2010*b*). Hunting was prohibited within the 60-km^2 city limits of TML. The TML study area has a long history (>3 decades) of habituated and food-conditioned bears living and hibernating within city limits (California Department of Fish and Wildlife, unpublished data).

Vegetation types within the study area included fragmented patches of mixed conifer forest dominated by Jeffrey pine (*Pinus jeffreyi*), interspersed with montane chaparral including currant (*Ribes* spp.), manzanita (*Arcostaphylos* spp.), bitterbrush (*Purshia tridentata*), aspen (*Populus tremuloides*), and willow (*Salix* spp.; Mayer and Laudenslayer 1988). In addition to residential and commercial development within the study area, there were also interspersions of open green-ways for recreational use, a large network of hiking and biking trails, 2 golf courses, 9 campgrounds, 5 lodges, and the Eastern Sierra Valentine Reserve (0.63 km^2), which is a field research station administered by the University of California, Santa Barbara. Access in the reserve is restricted for the general public.

Wildland study site

The SVWA study site encompassed 70 km^2

of CDFW and U.S. Forest Service public land. Elevation ranged between 1,800 m and 2,550 m. There were no permanent residents within the study site, and the nearest communities were located approximately 9 km east of the center of SVWA. The combined population size for those communities was 1,266 in 2009 (U.S. Census Bureau 2010*b*). There was little human use in the area, and vehicle access to SVWA was prohibited to the public. Bear hunting was allowed in the SVWA from late August to the end of December, but not during our survey period.

Vegetation included big sagebrush (*Artemisia tridentata*), antelope bitterbrush (*Purshia tridentata*), pinyon pine (*Pinus monophylla*), aspen, mixed-conifer forest dominated by Jeffrey pine and white fir (*Abies concolor*), and irrigated pasture (Mayer and Laudenslayer 1988). There was a variety of both hard and soft-mast crops, including pinyon pine, snowberry (*Symphoricarpos rotundifolius*), Sierra plum (*Prunus subcordata*), elderberry (*Sambucus* spp.), bittercherry (*Prunus emarginata*), wild rose (*Rosa woodsii*), and Sierra currant (*Ribes cereum*). In addition, numerous permanent and intermittent creeks flowed in canyons in the study site.

Methods

Field methods

We surveyed bears during June and July, 2011–2012. To reduce geographic closure violations of the CMR models, we used ridgelines as boundaries of the SVWA assuming these geographic barriers would help reduce bear movement in and out of the study area (Boulanger et al. 2004*a*). The TML study area was surrounded by ridgelines to the north and west and the Great Basin Desert to the south and east.

The optimal grid cell size for surveying bears with hair-snares is the average size of a bear's home range so that each bear has the opportunity to encounter a hair-snare (Mowat and Strobeck 2000, Boulanger et al. 2004*a*). Because we did not have an estimate of home-range size in our study areas, we determined cell sizes for our sampling grid based on estimates of the home ranges of urban and wildland bears in nearby study areas (Beckmann and Berger 2003*a*). The Beckmann and Berger (2003*a*) study areas were in similar ecoregions and were located 30–80 km from our wildland study area. While oversampling may be inefficient, it does not result in bias (White et al. 1982). However, undersampling (i.e., grid cell too large) can lead to density estimates that are biased low because some bears are missed (Boulanger et al. 2004*a*). Consequently, we reduced cell sizes to be smaller than average home range size estimated in the Beckmann and Berger (2003*a*) study to avoid undersampling and to reduce bias in our sampling design.

For TML in 2011, we could not use a grid system because of the spatial distribution of private property that allowed access. Instead, we established a 2-km^2 circular buffer around each hair-snare (n = 20) such that the entire urban study area was covered with minimal overlap. Some overlap occurred due to the spatial distribution of private property access and to protect against under-sampling. By the 2012 TML field season, we secured adequate private property access and switched to 2-km^2 grid cells (n = 22; Figure 1). In SVWA, we used 10-km^2 grid cells (n = 7) for 2011 and 2012 field seasons (Figure 1). We used a smaller grid cell size in TML compared to SVWA because previous studies have found bears have smaller home range sizes and space use when there is a high-density food source (Beckmann and Berger 2003*b*, Beckmann and Lackey 2008, Baruch-Mordo et al. 2014). All hair-snares were set up within each grid cell in close proximity to bear sign (e.g., tracks, scat, and tree scratches), near a food source, or in travel corridors.

We used the corral hair-snare design adapted from Woods et al. (1999). To entice bears to go over or under the single strand of barbed wire, we placed a non-consumable lure (0.5 L) in the center of each hair corral on a pile of course woody debris. We also sprayed lure on a rag and hung the rag 4 m above the center of each hair corral as an aerial attractant. We randomly assigned a particular lure on the first visit each year, and then rotated lures systematically for each sampling occasion to increase visitation with the novelty of a new scent.

In 2012, in addition to the corral hair trap, we added alternative hair-snares in both study areas to increase recapture rates and reduce capture heterogeneity following Boulanger et al. (2008; Figure 1). In TML, we added 1

alternative hair-snare to each cell and we added 2 alternative hair-snares in SVWA following recommendations of Boulanger et al. (2008) and Kendall and McKelvey (2008). For alternative hair-snares, we modified bear rubs as described in Kendall et al. (2009) and used 2 hair-snare designs we developed. We named 1 hair-snare design the haphazard-wire hair-snare. For the haphazard-wire hair-snare, we wrapped barbed wire around multiple branches of a single tree (e.g., pinyon pine and juniper) and placed a perforated metal box in the center of the tree. Bear lure was secured in the box to entice the bear to snag its hair on the barbs when investigating the lure. The second hair-snare design was a single-catch design we named the tennis ball hair-snare. The tennis ball hair-snare design consisted of a 15-cm-diameter, 61-cm-long pipe attached vertically to the base of a tree or fence post. Bear lure was injected and then sealed into a tennis ball. The tennis ball was placed in the bottom of the pipe. When a bear reached into the pipe to obtain the lure-filled tennis ball, it snagged its hair on gun brushes and barbed wire. Lure-soaked rags were hung in the vicinity of both the haphazard-wire and tennis ball hair-snares as an aerial attractant. See Fusaro et al. (2017) for more details on the alternative hair-snare designs.

During each field season, we collected hair samples and replenished the lure at each hair-snare once every 7 days for 6 weeks. We used this sampling interval to minimize violations with demographic and geographic closure for closed population models as well as to reduce sample exposure to ultraviolet light and moisture, which degrade DNA (Kendall and McKelvey 2008). All samples with >5 bear hairs were collected. To reduce analyzing samples from the same individual multiple times during the same session, we analyzed the samples with the most hairs when bears left multiple samples on adjacent barbs (Tredick et al. 2007). In addition, we eliminated obvious non-target species samples (e.g., deer) in the field. Hair samples were collected with sterilized hemostats and put in individual coin envelopes. Barbs that contained hair samples were sterilized with a flame to prevent residual DNA mixing with future samples. The envelopes were stored at room temperature in airtight containers with desiccant beads until DNA extraction.

Laboratory methods

Following methods from Brown et al. (2009), we determined species, individual identity, and gender of bears through analysis of DNA extracted from the follicles of the hair samples. Fourteen nuclear microsatellite loci were used to define unique individuals: G1A, G10B, G10C, G10H, G10o, G1D, G10L (Brown et al. 2009), A107, A002, B001, D103, D112, D116, and D118 (Meredith et al. 2009). Gender was assigned using AME and SRY markers (Xu et al. 2008, Pagès et al. 2009).

In addition to collecting hair samples for CMR, we also collected opportunistic hair samples from known bears year round from both study areas, as well as other areas of Mono County when they became available. These samples were collected from trapped, depredation (i.e., euthanized for defense of life or property), roadkill, and hunter-harvested bears. We used the reference database of local DNA samples to define allele frequencies and help determine the probability of identity $P_{(id)}$ and probability of identifying siblings $P_{(sib)}$ values by accounting for the population structure of the local bear population (Mills et al. 2000).

Extensive effort was put forth to reduce genotyping errors. Consensus genotypes were analyzed using Microsatellite Toolkit (Park 2001) and Genalex (Peakall and Smouse 2012) software. We scored genotypic data twice, by 2 people blind to the reads of the other, to ensure correct and consistent allele calls. We ran all DNA samples ≥3 times to check for consistency, and each plate of DNA included both negative and positive controls for quality assurance. We checked expected heterozygosities at all loci for deviations from Hardy-Weinberg equilibrium to ensure the absence of null alleles and significant allelic dropout. Samples that did not successfully amplify a bear genotype after the first round of testing were re-extracted (if there was sufficient sample remaining) and tested again. Samples that only amplified specific alleles at G1A and SRY loci were identified as *Canis* spp. based on known canine DNA profiles. Mixed samples occurred when hair from multiple bears was snagged on the same barb at the same time. We discarded the mixed

samples because we could not genetically differentiate the individual bears from those samples (i.e., >1 allele at multiple loci; Roon et al. 2005).

CMR analysis

We constructed an encounter history for each bear uniquely identified during the study. For both study areas and each year, we grouped the data into 3 14-day encounter occasions due to low sample sizes and recapture rates (<10%; Settlage et al. 2008). We pooled encounter occasions 1–2, 3–4, and 5–6. We used the Pradel formulation of the Huggins (1989, 1991) robust-design model. Because there was only 1 year between the 2 closed-capture sessions, there was a single estimate of apparent survival (φ) and discrete rate of population change (λ); thus, we only modeled initial capture (p) and recapture (c) probabilities. We tested 6 a priori models to evaluate potential differences between p and c by year (yr) and year and encounter occasion (yr + visit), as well 2 models with no temporal effects (constant or "." model). The models with visit account for potential capture differences between lures, which were switched from visit to visit, as well as other differences in capture probability due to weather, behavior, or other short-term temporal factors. We used the same models as Dreher et al. (2007) and Boulanger et al. (2008) except that all hair samples collected from alternative hair-snares were pooled as the final encounter occasion, with a unique estimate, for 2012 following Boulanger et al. (2008) and Kendall et al. (2009). We model-averaged population estimates and calculated log-based confidence intervals using the model-averaged variance and the minimum number of bears genetically identified (Lukacs 2010).

We recognize the different alternative hair-snare designs likely had different capture probabilities, and grouping the capture data can induce capture heterogeneity. Further, capture heterogeneity based on differences in sex and individuals is a concern with DNA-based CMR studies (Pollock et al. 1990, Boulanger et al. 2004*b*, Pederson et al. 2012). We tested the importance of heterogeneity by reconstructing the top models (models within 2 ΔAICc units from top model) with heterogeneity included using the Huggins-Pledger closed-capture full heterogeneity model with a mixture of 2 capture probabilities (Pledger 2000).

We estimated effective trapping area using home range size estimates from a nearby study in similar habitat types (Beckmann and Berger 2003*a*). We used the core (50%) home range estimates for both sexes combined and added 1 standard deviation to estimate home range size, which yielded effective trapping area size estimates of 12.9 km^2 and 131.1 km^2 for the urban and wildland bears, respectively. We created buffers of the estimated home range size around every hair-snare location for each area and year using the buffer tool in ArcGIS™ 10.2 (ESRI® Olympia, WA, USA). We then dissolved all the buffers into 1 polygon, and these polygons were used as the effective trapping areas. This approach is similar to typical effective area approaches that add half the width of an average home range or half the mean maximum distance moved as a buffer around a trapping area (Williams et al. 2002).

For each study area, we calculated density by dividing estimated abundance by the effective trapping area. We used the Delta method (Seber 1982) to estimate the variance of the density, which included the uncertainty in both abundance and effective trapping area (White et al. 1982). We used a Z-test to compare differences in densities between study areas for each year.

Results

We analyzed a total of 368 hair samples and identified a total of 131 individual bears throughout our study sites. Twenty-eight of the 31 known bear DNA samples collected opportunistically were genotyped successfully in the lab. These samples were used as a reference for the samples collected by the hair-snares. None of the known bears identified from opportunistically collected hair samples were identified during the CMR surveys. A reasonably low $P_{(id)}$ is <0.01 (Waits et al. 2001) and $P_{(sib)}$ is <0.05 (Woods et al. 1999). The $P_{(id)}$ for all samples we used for CMR was $\leq 1.1e^{8}$. The $P_{(sib)}$ for all the samples we used for CMR was $\leq 1.2e^{4}$. Hence, we were confident in our ability to distinguish between individual bears from DNA collected by hair-snares.

We analyzed 175 hair samples in the urban

Table 1. Model selection results from a Huggins closed-capture robust-design analysis for black bear populations in 2 study areas in Mono County, California, USA, June and July, 2011–2012.

Model[a]	*K*	AIC_c	ΔAIC_c	w_i	Deviance
Urban study area (Town of Mammoth Lakes)					
1. *p*(.)=*c*(.) (Diff. Alt. *p*=*c*)	4	276.252	0	0.497	267.607
2. *p*(yr)=*c*(yr) (Diff. Alt. *p*=*c*)	5	277.987	1.735	0.209	267.003
3. *p*(.) *c*(.) (Diff. Alt. *p*=c)	5	278.439	2.187	0.166	267.455
4. *p*(yr+visit)=*c*(yr+visit)	6	281.232	4.980	0.041	267.832
5. *p*(.)=*c*(.) (Diff. Alt. *p*=*c*) hetero[b]	8	282.187	5.935		263.705
6. *p*(.)=*c*(.)	3	282.403	6.151	0.023	276.022
7. *p*(yr+visit) *c*(yr+visit)	9	282.810	6.558	0.019	261.652
8. *p*(yr) *c*(yr) (Diff. Alt. *p*=*c*)	7	282.861	6.608	0.018	266.962
9. *p*(yr)=*c*(yr)	4	282.979	6.727	0.017	274.334
10. *p*(.) *c*(.)	4	284.465	8.213	0.008	275.820
11. *p*(yr) *c*(yr)	6	287.364	11.112	0.002	273.964
Wildland study area (Slinkard Valley Wildlife Area)					
12. *p*(.)=*c*(.)	5	637.607	0	0.326	627.099
13. *p*(yr)=*c*(yr)	7	638.904	1.297	0.171	623.938
14. *p*(yr+visit)=*c*(yr+visit)	8	639.332	1.725	0.138	622.080
15. *p*(.)=*c*(.) (Diff. Alt. *p*=*c*)	6	639.498	1.891	0.127	626.780
16. *p*(.) *c*(.)	6	639.680	2.073	0.116	626.962
17. *p*(yr)=*c*(yr) (Diff. Alt. *p*=*c*)	8	641.159	3.552	0.055	623.907
18. *p*(.) *c*(.) (Diff. Alt. *p*=*c*)	7	641.735	4.128	0.041	626.770
19. *p*(.)=*c*(.) hetero[b]	9	643.210	5.603		623.631
20. *p*(yr) *c*(yr)	10	643.356	5.749	0.018	621.409
21. *p*(yr+visit) *c*(yr+visit)	14	646.259	8.652	0.004	614.406
22. *p*(yr) *c*(yr) (Diff. Alt. *p*=*c*)	11	646.459	8.852	0.004	622.102

[a] Key to model notation: *K* = no. of parameters; AIC_c = Akaike Information Criterion corrected for small sample size; ΔAIC_c = difference between the model listed and the AICc of the best model; w_i = model weight based on model AICc compared to all other model AICc values; *p* = capture probability; *c* = recapture probability; yr = year as a categorical variable; visit = encounter occasion as a categorical variable; "." = constant across year and encounter occasion; Diff. Alt. = there was a difference in capture rate for the fourth encounter in 2012 where the alternative hair-traps were pooled; hetero = a Pledger 2 mixture model to account for trapping heterogeneity.
[b] Heterogeneity model was not included in model averaging; therefore, model weights were not shown in this table.

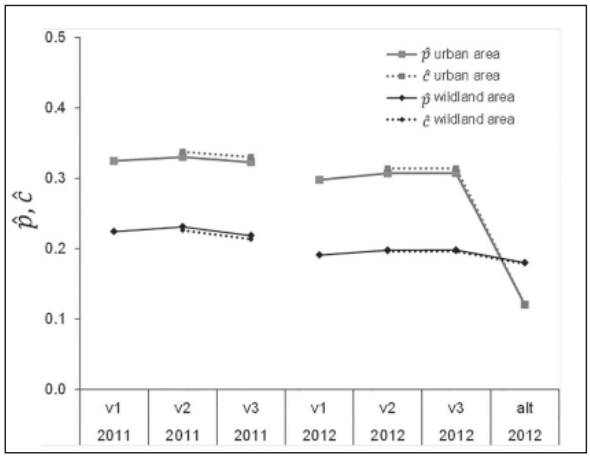

Figure 2. Model-averaged estimates of capture ($\hat{p}$) and recapture ($\hat{c}$) probabilities for 2 black bear populations in Mono County, California, USA based on data from hair sampling. Hair-snares were set for 6 weeks during June and July, 2011–2012. Weeks 1 and 2, 3 and 4, and 5 and 6, respectively, were pooled into visits 1, 2, and 3. For 2012, v1–v3 represents encounters with hair-snares and alt represents $p = c$ for the alternative hair-snares combined for v1–v3. Error bars are not shown for figure clarity (see Table 2).

study area (71 in 2011 and 104 in 2012). Genotyping success was 48% for the 2011 CMR hair samples and 80% for the 2012 CMR hair samples. We identified 41 individual bears during the study period, including 15 females, 25 males, and 1 unknown sex.

We collected 162 hair samples in the wildland study area (62 in 2011 and 100 in 2012). Genotyping success was 87% and 90% for the 2011 and 2012 CMR hair samples, respectively. We identified 62 individual bears during the study period, including 22 females, 38 males, and 2 unknown sex.

Heterogeneity models did not converge properly for any models with time-specific estimates (e.g., p(yr)=c(yr)). We believe this was mainly due to our small sample sizes. However, the heterogeneity model did converge for the top models for both study areas and provided a basic evaluation of heterogeneity. There was no strong evidence for capture heterogeneity for either study area; the heterogeneity models were >5.6 ΔAIC units from the top model and had model weights of 0.02 and 0.03 for the urban and wildland study areas, respectively (Table 1). Heterogeneity models were not included in model averaging because MARK only model-averages over 1 class of models (e.g., either all models with heterogeneity or all models without heterogeneity) because of the parameter differences.

From the urban study area, there were 3 models with ΔAIC ≤ 2 that accounted for 87% of the total model weight (Table 1). These top models included support for a difference in capture rate for the fourth encounter in 2012 where the alternative hair-snares were pooled (i.e., Diff. Alt. p=c). Although the top model had constant capture and recapture probabilities, there was some support for a difference in capture rates between years (w_i = 0.21; Table 1). For the wildland study area, there were 5 models with ΔAIC ≤ 2 (Table 1), suggesting weak model differentiation for the wildland study area. Because there was model selection uncertainty, we used model-averaging for all estimates.

Model-averaged estimates of p ranged 0.30–0.33 (SE = 0.06–0.09) for the non-alternative hair-snares in the urban study area and 0.20–0.23 (SE = 0.05–0.06) for the wildland study area (Table 2; Figure 2). The capture and recapture probability for the alternative hair-snares was 60% lower than the average for the regular hair-snares in the urban area but was similar to the regular hair-snares in the wildland area (Table 2; Figure 2). Model-averaged φ was 0.60 (SE = 0.19, 95% CI = 0.23–0.88) for the urban study area and 0.40 (SE = 0.12, 95% CI = 0.19–0.65) for the wildland study area. We do not report model-averaged estimates of λ because they were poorly estimated, with 95% CIs that are too wide to be meaningful (e.g., 0.24–2.43 and 0.84–3.66).

Based on model-averaged abundance and effective trapping area, bear density (bears/10 km^2) for 2011 was 1.6 times greater in the urban study area ($\hat{D}$ = 2.7, SE = 0.6) than the wildland study area ($\hat{D}$ = 1.7, SE = 0.4), although densities did not differ significantly (P = 0.13). For 2012, bear density was 2.5 times greater in the urban study area ($\hat{D}$ = 4.8, SE = 0.8) than the wildland study area ($\hat{D}$ = 2.0, SE = 0.6), and the difference was significant (P = 0.003).

Discussion

Though much of the historic range of bears is still wildland, an increasing amount of bear historic range has become urbanized. In addition, there has been an increase in wildlife, including bears, living in urban areas (Gehrt

Table 2. Model-averaged estimates of abundance ($\hat{N}$) from a Huggins robust-design closed-capture model for 2 black bear populations in Mono County, California, USA, June and July, 2011–2012.

Study area[a]	Year	Effective trapping area (km^2)[b]	$\hat{N}$	SE	95% CI[c]		p	c	CV (%)
					Lower	Upper			
Urban	2011	74	20	4.5	17	29	0.32	0.34	22
	2012	94	46	7.5	39	58	0.31	0.31[d]	16
Wildland	2011	329	55	11.9	44	75	0.22	0.22	22
	2012	366	72	20.6	55	108	0.20	0.20[e]	29

[a] Urban study area was located in the Town of Mammoth Lakes, and Wildland study area was located in Slinkard Valley Wildlife Area.
[b] Effective trapping area was based on home range sizes from a black bear study in a similar nearby area (Beckmann and Berger 2003*b*).
[c] Log-based confidence interval.
[d] Session 4 (pooled alternative hair-traps) p and c = 0.12.
[e] Session 4 (pooled alternative hair-traps) p and c = 0.18.

et al. 2010). Here, we found bear density to be 1.6–2.5 times higher in the urban study area compared to the wildland study area. Our results are similar to previous studies, where bears in the urban–wildland interface lived at 3 times greater densities compared to bears in wildlands (Beckmann and Berger 2003*a*, *b*). Data from these studies support the theory that bears can occur at greater densities in urban areas; the high density of bears in urban areas such as TML has implications for bear population ecology and management. The increase in density is likely a result of bears being tolerant of each other when food resources are abundant (Beckmann and Berger 2003*b*), and urban areas may act as a refuge from hunting. However, we believe the main cause of the high density of bears in TML is a result of the anthropogenic resources available and not the lack of hunting in the urban area. Our survey did not occur during the bear hunting season, and only 12 bears were taken from all of Mono County in both 2010 and 2011 (California Department of Fish and Wildlife 2011, 2012), making it unlikely that hunting prior to our surveys had a large impact on the wildland area population. However, further research needs to be conducted to determine the cause of density differences between the urban and wildland study areas.

From a management perspective, human–bear conflicts in TML have been a continuing challenge because of the juxtaposition of the communities' positive attitude toward living with bears in town with the need to minimize bear damage. Peine (2001) notes that it typically takes 10–25 years for communities to formulate policies for problem bears, and these often come after a human tragedy. While there have been no bear-related human fatalities yet in the TML, bears have become habituated, injured people, routinely break into vehicles and occupied and unoccupied homes, forage in unlocked dumpsters, and take fish stringers from fishermen (T. J. Taylor, California Department of Fish and Wildlife, unpublished report). Since 1996, TML officials have put substantial effort into reducing human–bear conflicts by enforcing local trash management ordinances, education, and employing hazing techniques (Peine 2001). In addition, CDFW biologists and wildlife officers spend 25–35% of their time, annually, mitigating human–bear conflicts in Mono County (T. J. Taylor, California Department of Fish and Wildlife, unpublished report). Most importantly, our results establish a population abundance baseline before any additional city-wide management actions are implemented. These data can be presented to city managers and allow for informed decisions regarding the best course of action when implementing nuisance bear mitigation practices.

We note there are several issues with our study. First, genotyping success for TML in 2011 was 32% lower than 2012, which may mean

the 2011 population estimate was biased low. In other words, we likely missed identifying individual bears because genotyping success was low. The small size of our study areas may have resulted in geographic closure violation. The sizes of the study areas were necessitated by logistics (urban area) and budget constraints (wildland area). Small study areas can result in high variance for abundance estimates (Boulanger and McLellan 2001) because population sizes are smaller and higher p is needed to produce precise estimates (e.g., White et al. 1982 recommend $p > 0.30$ when $N < 100$). In addition, abundance estimates for small areas may be biased because lures in small areas can draw bears in from outside the study area (Boulanger et al. 2004*a*).

We attempted to mitigate this bias by choosing study areas that were geographically isolated via ridgelines and surrounding marginal habitats (e.g., Great Basin Desert). In addition, as an index for movement in and out of our study areas, no bears identified from hair samples in the study areas were also identified outside of the study areas from the known bear hair samples we collected. Thus, we believe bias due to closure violation was minimal. However, while variance in the urban area was acceptable (i.e., CV of abundance estimate was <20%) once the cell size was reduced in 2012, variance of abundance estimates in the wildland area was high (i.e., CV >20%). It is likely TML was a large enough area, given the high density of bears, and p was high enough ($p = 0.31$) to satisfy closed capture assumptions and yield population size estimates that were accurate and precise. However, the wildland study area should be expanded to reduce the potential for bias. In addition, we need to determine a method to increase p such that it is high enough to reduce the CV to <20%.

Undersampling, which can result from cell sizes that are too large relative to home range use, will result in CMR estimates of population abundance and density that are biased low (White et al. 1982). However, oversampling, which can result from cell sizes that are too small, does not result in biased estimates, but is inefficient and unnecessarily expensive. Based on a pilot study in 2010, we determined the smaller cell size we used in the urban area was necessary to ensure we adequately sampled the bear population. The methods and results from the pilot study for the SVWA were akin to the 2011 and 2012 survey (Table 3). However, in TML, the corral hair-snares were set up using a 5-km^2 grid system. In addition, for logistical purposes, we did not set up hair-snares in the city center. As a result, in TML only 18 bear hair samples were collected during the 6-week sampling period, an insufficient quantity for our CMR analyses. Two corral hair-snares were activated for 2 weeks in the city center after the 6-week CMR. During those 2 weeks, 25 bear hair samples were collected. It became apparent that bears were seeking refuge in the city center and not leaving the city center on a regular basis. This, in addition to numerous reports of human–bear conflicts in the city center, led us to seek private property access in the center of town and reduce our cell sizes further to 2 km^2 for the subsequent 2011 and 2012 surveys.

Management implications

We found DNA-based CMR surveys an effective technique for monitoring small-scale populations of black bears, including urban populations. While hair-snare studies have been implemented in wildland and rural landscapes for black bears, we are unaware of any peer-reviewed studies that used hair-snares to estimate population parameters of black bears within urban areas akin to TML. Based on our results, we recommend using small grids in urban areas because urban bears tend to live at higher densities. To avoid undersampling, which results in population density estimates that are biased low, we advocate starting with grids that are denser than what would be used for adjacent wildland areas when home range data on the urban bears is not available. In addition, gaining knowledge of activity areas of urban bears and access to private land for hair-snares is also critical to increasing capture probability and obtaining reliable abundance estimates. Furthermore, surveying for longer periods of time and during different seasons would help determine the presence of temporal shifts in bear density within a community. With additional survey years, robust versions of CMR study designs can provide estimates of population vital rates, such as apparent

survival, finite rate of population change (λ), movement, and recruitment (Pederson et al. 2012). These data can be used to inform urban bear management decisions.

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