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A modification of the hair-trapping method for surveillance of problematic bear activity close to a farm — a case study from the Pasvik Valley in Norway

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Human–bear conflicts occur frequently in the Pasvik Valley, Norway. We used a variant of the hair-trapping method with higher densities of traps (2.5 × 2.5 km grid) to detect brown bears moving near human settlements and livestock. We distributed 20 hair traps for one month close to a farm with frequent observations of grazing bears. The study area consisted of one area close to the farm, and one adjacent area without settlements. We collected 85 hair samples and identified 13 different individuals by STR analysis. In the farm area, we detected 4 different males once, and a female that was detected in both areas. In comparison, nine bears (2 males and 7 females) were detected for more than one week in the area without settlements, suggesting lower roaming activity. Conclusively, hair trapping has the potential to survey bears at specific locations of importance to the wildlife management.

Introduction

The major cause of human–bear conflicts is depredation of livestock, but also attacks on humans occur. As the elusive nature of brown bears makes them difficult to monitor, reports of observations, tracks, feces, and killed livestock are key sources of information for local wildlife management and authorities (Linnell *et al*. 1999, Breck 2004, Graham *et al*. 2005, Baker *et al*. 2008). Genetic methods combined with noninvasive sampling of feces and hairs allow identification of individuals across large areas (*see* e.g. Taberlet *et al*. 1997, Bellemain *et al*. 2005, Schregel *et al*. 2012). De Barba *et al*. (2010a) used opportunistic sampling of hair and feces to confirm damages for compensation caused by brown bears. However, the yield of random sampling methods, such as hair and feces collection in the field may vary, and could lead to insufficient number of samples. Therefore, the application of systematic and baited sampling methods has been suggested, especially in areas and under conditions where opportunistic sampling is not feasible (Kendall & McKelvey 2008). Further, it has been shown in numerous cases that for gaining more efficient results, management decisions should be based also on additional evidence; e.g.

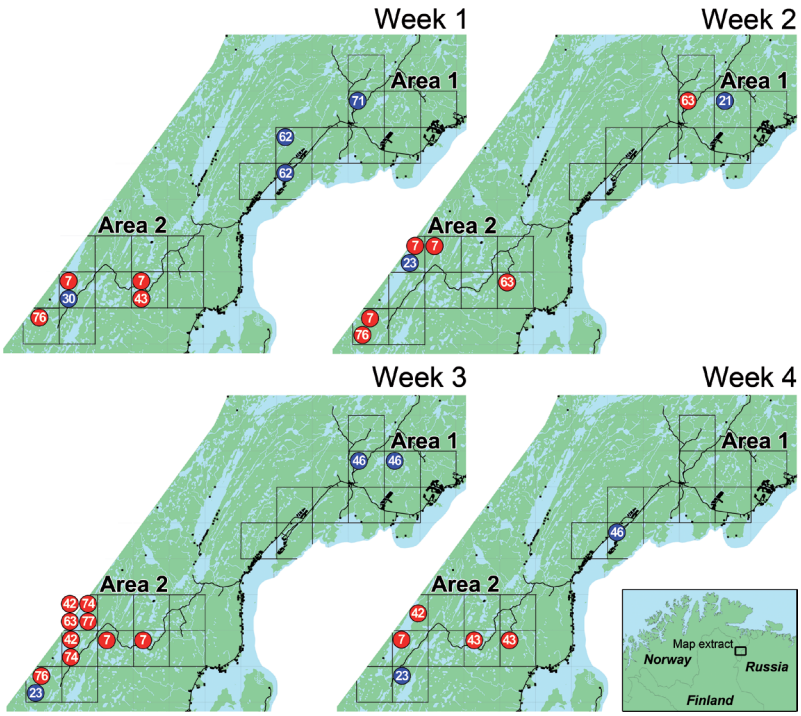

Fig. 1. Brown bears identified per 2.5 × 2.5 km grid per week near a farm in area 1, and in control area 2 without human structures in the Pasvik Valley, Norway. Each bear is represented by a circle, identity number and sex (red = females, blue = male). Human settlements (farms, houses, cabins) are shown as black squares and roads as black lines.

DNA collected at the scene of an incident (Eichmann *et al*. 2004, Blejwas *et al*. 2006, Sundqvist *et al*. 2008, Frosch *et al*. 2011).

Hair traps for bears were developed in the 1990s for systematic large-scale monitoring (Woods *et al*. 1999, Mowat & Strobeck 2000), and have been applied since then to investigate and monitor populations within defined areas (*see* e.g. Kendall *et al*. 2009, De Barba *et al*. 2010b). We believe that this method can also be used to detect and identify brown bears at specific locations that are of importance for management decisions, e.g. near livestock and human settlements. The Pasvik Valley in Norway has a small, stable population of brown bears (~10 bears/1000 km^2, *see* Schregel *et al*. 2012), and human–bear conflicts occur frequently. In this case study, we applied a 2.5 × 2.5 km grid of hair traps to detect the occurrence of bears in the close vicinity of a farm. This specific farm was of concern both to the owners and the local wildlife management as observation of at least two brown bears grazing in close proximity to the main buildings had been reported. We performed an intensive hair trap study to assess the bear situation around that farm and used the results to evaluate the potential future usage of the method for the wildlife management.

Material and methods

Study area, study design and sampling

The study was carried out in 2008 in the Pasvik Valley, Finnmark County in Norway at approximately 70°N and 30°E (Fig. 1). The area consists of arctic and boreal ecosystems in a mosaic of peatland and forest with Scots pine (*Pinus silvestris*) and downy birch (*Betula pubescens*).

We established two adjacent study areas with a total size of 125 km^2. Area 1 was located in a sparsely inhabited area in close proximity to an active cattle farm, houses and cabins (*see* Fig. 1). In 2008, prior to the study, several observations of bears, tracks and feces had been reported from this area, and at least one observation of two brown bears close to the main building of the cattle farm was confirmed (M. Asheim, State Nature Inspectorate, Norway, pers. comm.).

Area 2 was located near study area 1, and chosen as the closest area with similar characteristics to area 1, but without human settlements and with lower human activity (Fig. 1).

Hair traps were placed in a geographical grid as described previously by others (cf. Kendall *et al*. 2009). In addition, we carried out weekly inspections and renewal of the scent lure and used increased density of hair traps by dividing both study areas into a meshed 2.5 × 2.5 km grid (Fig. 1). In total, we distributed 20 hair traps, ten in each study area. The enclosure-type hair traps were made of barbed wire placed 40 cm above ground around the lure. The lure was placed in the middle of a pile of wood or moss and consisted of 1.5 liters of mixed fermented fish and aged cattle blood. Hair trapping period lasted from 13–14 August to 9–10 September 2008. Contrary to the reference studies, we did not translocate the hair traps within the square. Hair samples were collected into paper envelopes and stored in a dark, cool place until subsequent DNA analysis.

Molecular analysis

We used the DNeasy Tissue Kit (Qiagen) and followed the manufacturer's instructions to extract DNA from the hair samples. All DNA samples were genotyped using six dinucleotide markers (Short-tandem-repeats, STRs) developed for bears: G1A, G10B, Mu05, Mu09, Mu15 and Mu26 (Paetkau & Strobeck 1994, Paetkau *et al*. 1995, Taberlet *et al*. 1997), plus one marker for sex determination using the primers SE47 (Yamamoto *et al*. 2002) and R143 (5´-AGGTGGCTGTGGCGGCA-3´). PCR and the fragment analysis were performed as described by Kopatz *et al*. (2012). The probability of identity of each sample was calculated with the software Gimlet ver. 1.3.3 (Valière 2004). The uniqueness of the DNA profiles was verified by expanding the analysis of the identified individuals to 13 markers: G1D, G10L, Mu10, Mu23, Mu50, Mu51 and Mu59 (Paetkau & Strobeck 1994, Paetkau *et al*. 1995, Taberlet *et al*. 1997). The analysis of the markers, the average probability of identity and the average probability of sibling identity were done as described by Andreassen *et al*. (2012).

Data analysis

The individual data of the bears detected in both areas were used to test for differences between the two study areas. We evaluated the data based on graphical comparisons of the weekly number of bears caught/trap/area. In addition, we assessed the overall activity of the bears by summing the weekly number of bears caught/trap/area for the whole study period. This yielded a number (total number of bear visits/hair trap during the study), which was compared between the two study areas using general linear models (GLMs) as implemented in the statistical package R (R Development Core Team 2008). As our data consisted of counts of bear visits (i.e. whole numbers), we specified the statistical model using a log link and Poisson's distribution (i.e. log-linear model). This was done by specifying 'family=Poisson' in the GLM formulae in R (R Development Core Team 2008). The analysis was repeated for males and females separately to identify potential differences between the sexes. In all cases, standard diagnostic plots were used to check model assumptions.

Results

In total, we collected 85 hair samples from 12 different traps. On average, 4.25 samples were obtained per trap/month. The traps in area 1 (near the farm) captured fewer samples (22 hair samples), than the traps in area 2 (63 samples). The number of samples collected was highest during week 3 in area 2 (22 samples) and lowest during week 4 in area 1 (one sample; *see* Table 1). Brown bear DNA was detected from 74 samples (87%; n_{total} = 85), out of which 90% (67 samples) were successfully genotyped. As a result, 13 different bears were identified; seven females and six males. We detected five different bears in area 1 (four males and one female; Fig. 1). In the first week, we detected first two males (bear no. 62 and 71), then in the second week one male (bear no. 21) and one female (bear no. 63), and during the following two weeks one more male (bear no. 46). In area 2, we found in total 9 different individuals (seven females and two males), and all were detected more than once. Five of the bears were

sampled within three of the four weeks (Fig. 1). One female (bear no. 63) was identified in both areas (*see* week two; Fig. 1), while none of the males found in area 1 were detected in area 2.

Thus, we recorded consistently more individuals in area 2 than in area 1 (Fig. 1). Log-linear models confirmed this pattern and showed statistically significant higher trap visiting activity by the bears in area 2 than in area 1 ($b = 0.9808$, SE = 0.3909, df = 18, $p = 0.0121$). However, separate analyses for males and females indicated considerable differences in the area use between sexes: significantly more trap visiting activity by female bears was detected in area 2 than in area 1 ($b = 2.996$, SE = 1.024, df = 18, $p = 0.00345$).

Discussion

We successfully used a modification of the hair-trapping method to detect the actual number of individual bears roaming in close proximity to a cattle farm (Pasvik Valley, Norway). The overall number of samples per trap as well as the success of DNA identification from hairs was similar to those in previous studies using hair trapping on a much larger scale (e.g. *see* Kendall *et al*. 2009, De Barba *et al*. 2010b). In spite of the small scale of the study, 13 different individuals were detected which indicates high local densities of bears within the study areas, especially when compared with studies of densities in a larger area of the same valley (*see* Schregel *et al*. 2012).

Based on reports of brown bear observations during the study period, the local wildlife management authority assumed that at least two individuals were roaming in the area around the farm (M. Asheim, State Nature Inspectorate, Norway, pers. comm.). However, our intensive hair trapping identified five different bears. Consequently, based on this new information, it might be difficult to justify the removal of a particular bear from that area.

An average bear density in the Pasvik Valley is comparable to that in other core areas of brown bears in northern Europe (Schregel *et al*. 2012). However, considering the size of our trapping area, we detected more bears than expected from the density estimates of the larger area. So far, there is no literature on the range of the scent lure; however, we assume that it is unlikely that it expanded beyond the grid borders. It is thus improbable that the traps attracted bears from outside the research area. It has been shown that brown bears in northern Europe are not distributed equally, and that especially females aggregate in a few core areas (Kojola *et al*. 2003). The relatively large number of female bears identified within a restricted area may indicate that our study areas were within a brown bear core reproduction area.

Our results indicate that bears seem to favor the neighboring and more pristine forests even though they are in close distance to the farm. It has been reported earlier that brown bears tend to avoid human settlements and structures (Nellemann *et al*. 2007, Steyaert *et al*. 2011) and our

Table 1. Number of samples and brown bears detected by hair traps per week in area 1 (near human settlements) and in area 2 (adjacent pristine area) in the Pasvik Valley, Norway.

	Week	Sampling period	No. of traps	No. of traps with hair	Total no. of samples	No. of unique bears	
						Female	Male
Area 1	1	13–20 Aug	10	3	11	0	2
	2	20–27 Aug	10	2	3	1	1
	3	27 Aug–3 Sep	10	2	7	0	1
	4	3–10 Sep	10	1	1	0	1
Area 2	1	14–21 Aug	10	3	12	3	1
	2	21–28 Aug	10	5	14	3	1
	3	28 Aug–4 Sep	10	5	22	6	1
	4	4–9 Sep	10	5	15	3	1

results supports to some degree these findings. In contrast to area 1 close to the farm, all identified bears in the adjacent more pristine area were detected almost every week, suggesting lower roaming activity. We obtained higher amount of samples and detected significantly more females in the area without settlements than in the area near the farm. Furthermore, mostly male bears were identified close to the farm. Even though the activity of bears near human structures seem to be male biased (Riley *et al*. 1994, Linnell *et al*. 1999, Saito *et al*. 2008) our study also identified one female near the farm.

Despite the possibility that not all brown bears in the area visited the hair traps due to individual behavioral response (Boulanger *et al*. 2006), the identified individuals close to the farm were different during almost every week. One individual was detected twice, during the last two weeks. Our results indicate that a small area restricted to the close vicinity around human infrastructure can be monitored by using intensive hair trapping. In conclusion, this more intensive hair-trapping method supplied additional and crucial information for the local wildlife managers.

Studies on wild and elusive large mammals such as the brown bear are often characterized by a small sample size. Results from such studies should be interpreted cautiously and general conclusions should be drawn carefully (Bissonette 1999). Here, we explored a new application of an established method under very specific and restricted conditions in the field. Furthermore, the generality of our pilot study may suffer from the small total number of bears identified and used for statistical comparison. Thus, future studies should preferably include both several pairs of farms and control areas (i.e. spatial replication) as well as cover several study years (temporal replication).

Due to its non-intrusive and non-rewarding nature for bears, hair trapping may be more easily justified and conducted than e.g. the immediate removal of bears, especially under conditions which require high ethical and political sensitivity, such as are likely to be required in situations of human–bear conflicts. Especially in regions of continual bear visits, more frequent checks of the hair traps for samples, e.g. every three to four days, might be feasible. Also immediate genetic analysis in a DNA laboratory to identify individuals would be very important for a prompt management action. Applying a monitoring approach, which delivers more precise and rapid information on the number and presence of bears in an area may influence the attitudes in the community in a positive manner (Ransom *et al*. 2012, Caudron *et al*. 2012).

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