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Testing hair sampling on power poles as a potential method for DNA identification and monitoring of brown bears

Alexander Kopatz[1], Paul E. Aspholm[1], Anja Rudolph[2], Hans Geir Eiken[1], Julia Schregel[1], Siv Grete Aarnes[1], Camilla Tobiassen[1] and Snorre B. Hagen[1]

[1] Bioforsk – Norwegian Institute for Agricultural and Environmental Research, Svanvik, Norway
[2] University of Leipzig, Institute of Biology, Leipzig, Germany

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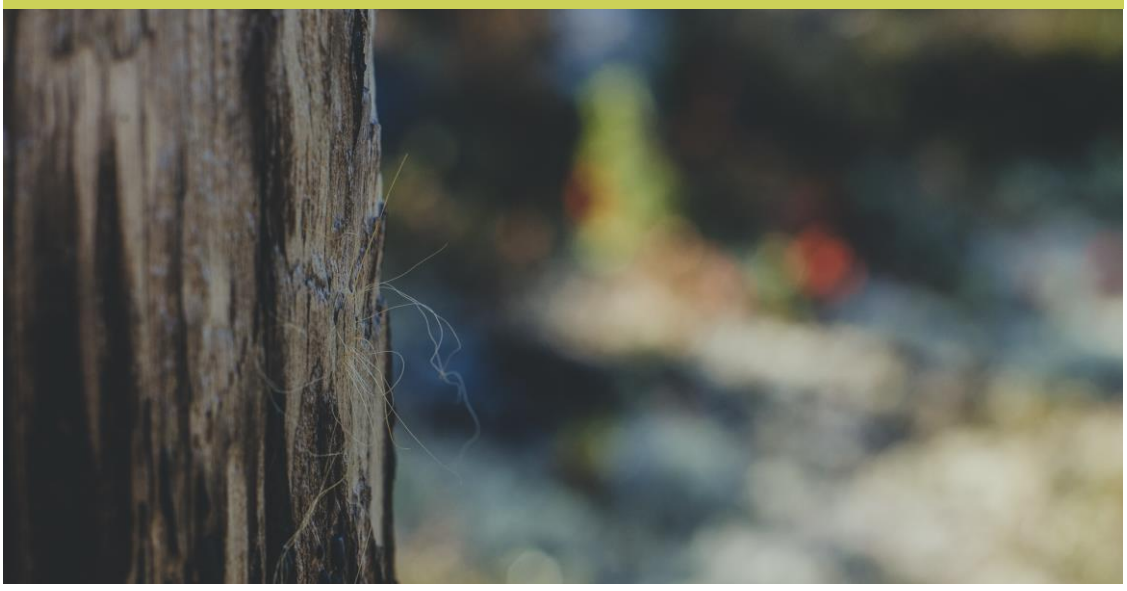

Brown bear hair on a power pole in Pasvik, Norway. Photo: Alexander Kopatz.

Main Office
Frederik A. Dahls vei 20,
N-1432 Ås
Tel.: +47 40 60 41 00
Fax: +47 63 00 92 10
post@bioforsk.no

Bioforsk Soil and Environment
Svanhovd
N-9925 Svanvik
Tel.: +47 464 13 600
Fax: +47 78 99 56 00
svanhovd@bioforsk.no

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Authors: Alexander Kopatz[1], Paul E. Aspholm[1], Anja Rudolph[2], Hans Geir Eiken[1], Julia Schregel[1], Siv Grete Aarnes[1], Camilla Tobiassen[1] and Snorre B. Hagen[1]

[1] Bioforsk – Norwegian Institute for Agricultural and Environmental Research, Svanvik, Norway

[2] University of Leipzig, Institute of Biology, Leipzig, Germany

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Abstract: Genetic methods based on sampling of feces and hairs to study brown bears have become the method of choice for many wildlife researchers and managers. Feces and hairs are the most common sample material for DNA identification of individual bears. While the collection of feces and hairs in the field is carried out in an opportunistic manner, hair-trapping can be applied systematically at specific locations. We have here tested a novel systematic method based on hair sampling on power poles. The method relies on the specific behavior of bears to mark, scratch, bite and scrub on power poles, and by this also leave some hairs behind. During late summer and autumn we have investigated 215 power poles in the Pasvik Valley and sampled 181 hair samples in 2013 and 57 in 2014. A total of 17.3% of the samples collected in 2013 and 12.3% in 2014 were positive on brown bear DNA. Our success rates are comparable to other studies, however, DNA quality/content in the hair samples was generally low. Based on other studies, the method could be improved by sampling during spring and early summer and to use shorter frequencies of 2 to 4 weeks between each sampling. Based on our results and previous studies, we can conclude that this sampling technique should be improved by the development of a more accurate and frequent sampling protocol. Hair sampling from power poles may then lead to improved potential to collect valuable samples and information, which would be more difficult to collect otherwise.

Sammendrag: Genetiske metoder basert på innsamling av ekskrementer og hår for å studere bjørner er blitt førstevalget for mange forskere og naturforvaltere. Ekskrementer og hår er det vanligste prøvematerialet for DNA-identifisering av individuelle bjørner. Innsamling av ekskrementer og hår i felten blir utført på en opportunistisk måte, mens hårfelle-metoden kan anvendes systematisk innenfor spesifikke områder. Vi har her testet en ny systematisk metode basert på innsamling av hårprøver fra høyspentstolper. Metoden er basert på den spesielle adferden til bjørner med å markere, klore, bite og klø seg på stolpene, og på denne måten også etterlate seg hår. I gjennom sensommeren og høsten undersøkte vi 215 høyspentstolper i Pasvikdalen og samlet inn 181 hårprøver i 2013 og 57 i 2014. Totalt gav 17,3 % av hårprøvene i 2013 og 12,3 % hårprøvene i 2014 positivt utslag på bjørn-DNA. Vår suksessrate er sammenlignbar med andre studier, men DNA kvaliteten/innhold i hårprøvene var generelt lavt. Basert på tidligere studier så kan metoden forbedres ved å samle inn prøver om våren og tidlig sommer og med å ha kortere hyppighet på 2 til 4 uker mellom hver innsamling. Basert på vårt resultat og tidligere studier så kan vi konkludere med at innsamlingsteknikken bør forbedres ved å utvikle en mer nøyaktig og hyppigere innsamlingsprotokoll. Hårprøver fra høyspentstolper kan da øke potensialet for å samle verdifulle prøver og informasjon som det kan være vanskelig å få tak i på annen måte.

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Godkjent / Approved

Snorre B. Hagen (Sign.)

Prosjektleder / Project leader

Alexander Kopatz (Sign.)

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Abstract

Genetic methods based on sampling of feces and hairs to study brown bears have become the method of choice for many wildlife researchers and managers. Feces and hairs are the most common sample material for DNA identification of individual bears. While the collection of feces and hairs in the field is carried out in an opportunistic manner, hair-trapping can be applied systematically at specific locations. We have here tested a novel systematic method based on hair sampling on power poles. The method relies on the specific behavior of bears to mark, scratch, bite and scrub on power poles, and by this also leave some hairs behind. During late summer and autumn we have investigated 215 power poles in the Pasvik Valley and sampled 181 hair samples in 2013 and 57 in 2014. A total of 17.3% of the samples collected in 2013 and 12.3% in 2014 were positive on brown bear DNA. Our success rates are comparable to other studies, however, DNA quality/content in the hair samples was generally low. Based on other studies, the method could be improved by sampling during spring and early summer and to use shorter frequencies of 2 to 4 weeks between each sampling. Based on our results and previous studies, we can conclude that this sampling technique should be improved by the development of a more accurate and frequent sampling protocol. Hair sampling from power poles may then lead to improved potential to collect valuable samples and information, which would be more difficult to collect otherwise.

1. Introduction

Non-invasive genetic sampling of brown bears (*Ursus arctos*) or other rare and elusive mammals within restricted areas has become favored by numerous wildlife researchers and managers during the last decade to assess the genetic and demographic parameters of populations. Biological samples are collected in the field and used for identification of animals with the help of the DNA contained in the sample (Taberlet et al. 1997; Waits and Paetkau 2005; Schwartz et al. 2006; Kendall et al. 2009). Feces and hairs are the most common source material for DNA in bear monitoring and research and are widely utilized, e.g. in the national brown bear monitoring scheme of Norway (see Aarnes et al. 2013) and Sweden (Kindberg et al. 2011).

Bioforsk Svanhovd has conducted numerous studies in non-invasive genetic sampling and also applied hair trapping to detect brown bears in different areas in Norway, and in collaboration with our national (Norwegian State Nature Inspectorate) and foreign partners, in Finland and Russia (see e.g. Kopatz et al. 2011, 2012a and 2013). Here, we test another, systematic, non-invasive genetic sampling method, which does not involve the set-up of hair traps, and therefore may lower the effort needed to collect brown bear samples in the field from the population living in the Pasvik Valley, Finnmark, Norway (Schregel et al 2012). The power poles in the Pasvik Valley (Fig. 1) are treated with a distillate of tar, called creosote, which serves as a protection against rotting and insect damage. The strong smell of this creosote and the frequent and exposed appearance of the poles seem to attract bears, a circumstance that has been used in a previous study in Greece to obtain hair samples (Karamanlidis et al. 2007 and 2010). Marking behavior has been reported occasionally and some hair samples from bears have been collected previously at power poles in the Pasvik Valley by the Norwegian State Nature Inspectorate (Magne Asheim, Steinar Wikan and Rolf Randa, pers. comm.). By using the species specific behavior of bears to mark, scratch, bite and scrub on these wooden poles, it might be possible to collect hair samples more systematically and without disturbing the brown bear (Karamanlidis et al. 2007 and 2010). As several factors may influence the preservation of the DNA contained in a hair sample, such as habitat and environmental conditions (see e.g. Murphy et al. 2007), we aim to test the efficiency of this sampling technique for the sampling of this bear population in the far north of Europe.

A pilot study, conducted in 2013 in the Pasvik Valley, tested whether the power pole sampling technique could be efficient under local conditions (Fig. 2). One person walked along the power line in the Upper Pasvik Valley twice and collected a total of 181 hair samples from the poles, of which 25 did not have hair-bulbs (which contain the DNA), resulting in 156 hair samples used for DNA analysis. Of these, 23 (17.3%) samples were positive and were used for genetic identification. The hair samples collected in the first round in August 2013 most probably consisted of hair left during several years prior to the study while the hair samples from the second round were less than one month old (see Results and discussion).

Given the difficulties in monitoring and studying an elusive animal such as the brown bear, acquiring sample material from known locations without substantial effort involved may be an efficient sampling technique. Therefore, we conducted a follow up study and sought to answer the following questions:

- Is this method sufficient in providing enough biological material (hair) of good quality?
- Since power poles are usually more exposed to weather: do the samples contain enough DNA for individual identification and can they be used for monitoring purposes?
- Is this method efficient?
- At which frequency should the power poles be checked and samples collected?
- Could the number of samples collected and the results of the genetic analysis be improved by special modifications of the method?

2. Materials and methods

Study area

The study area was located in the Pasvik Valley, Finnmark, in northern Norway (for a detailed description see Schregel et al. 2012). This study focused on power poles just north of and inside the Norwegian area of the tri-lateral hair trapping project in the Pasvik Valley (Smith et al. 2007; Kopatz et al. 2011). The power poles were located in a line with a maximum distance of ca. 100 m. The poles are officially marked and registered with successive numbers by the electricity company. In the study area the poles covered the numbers from 596 to 811 (north towards south), virtually mainly along county road no. 885. Mostly, the power line consists of single poles, occasionally of two poles. Nevertheless those had a single registration number and were registered as pole A (main pole incl. the registration number) and B (the other, secondary pole). The area around the power line consists of arctic and boreal ecosystems in a mosaic of peat land and forest with Scots pine (*Pinus silvestris*) and downy birch (*Betula pubescens*).

Sample collection

In our pilot study in 2013, all power poles from pole no. 596 to 811 had been investigated (Fig. 2). Here, we applied the same approach, since the poles were picked clean and sampled along the power line in one sampling session, over the period 22.09.-11.10.2014 (Fig. 3). Each hair bale on a pole was considered a separate sample. The hair was collected into a paper envelope and each sample was labelled with a sample number, date, pole number and name of the collector. The envelopes were stored in a dry, dark and cold room in the laboratory until subsequent genetic analysis, immediately after completion of the field work.

Molecular analysis

The samples were analyzed using a validated DNA-analysis for brown bears (Andreassen et al. 2012) at the genetic laboratory of Bioforsk in Svanhovd based on eight genetic markers (STRs: Mu05, Mu09, Mu10, Mu23, Mu50, Mu51, Mu59 and G10L). Sex determination was based on the X- and Y-specific DNA sequences of the amelogenine gene (Kopatz et al. 2012a).

3. Results and discussion

In autumn 2014 we collected a total of 57 hair samples from power poles (see Fig. 3) of which 7 (12.3%) were positive for DNA. However, 6 of these positive samples did not contain enough material for DNA amplification and therefore genetic identification of the originating individual was not possible. For a single sample, a comparison with our DNA database of known brown bears in the area identified bear FI43/MO3 at pole 783. However, the quality of the sample material as a whole was low (Appendix 1). A total of 19 (33.3%) samples did not contain hair roots. All poles and their locations with hair are shown in figure 3.

Marking and rubbing behavior of bears is still poorly understood. However, the few studies investigating such behavior reported that marking and rubbing was often associated with the mating season (Green and Mattson 2003; Karamanlidis et al. 2007), as it has been also reported from other carnivore species (Schmidt and Kowalczyk 2006). Further, previous studies suggested that mainly male bears tend to mark during mating season (Burst and Pelton 1983; Rogers 1987). However, based on our results from 2013, one female bear was particularly active at marking on power poles (Appendix 2) and this individual (FI43/MO3) has been identified at one power pole in 2014 (see above). It has been reported earlier that female bears with cubs may also visit power poles (Karamanlidis, unpublished results).

In the following the results and discussion to the main questions of this study and in comparison with the results of our 2013 pilot study (Appendix 2):

3.1 Is this method sufficient in providing enough biological material (hair) of good quality?

In 2013, a total of 181 hair samples were collected (Fig. 2) in two turns (7.8-21.8. and 24.8.-17.9.2013). Of those, 25 samples did not have a hair-root. 156 hair samples were used for DNA analysis. 23 (17.3%) were positive and were used for DNA identification. Notable is the increase in genotyping success at the second turn of sampling 24.8.-17.9.2013 (see Appendix 2). This can be most probably explained by the fact, that the samples collected during the second visit of the poles were less than one month old and therefore have not been exposed to the environment longer than four weeks. In 2014 we collected a total of 57 hair samples and 7 (12.3%) showed a positive result for DNA. However, the amount of DNA was not enough for good quality amplification and identification.

A previous study utilizing bear rubbing behavior on power poles to collect hair samples, had success rates of 25% if the hair was exposed for more than 4 weeks to the environment, while hair samples collected within a 4 week window showed DNA success rates of 78% to 82% (Karamanlidis et al. 2010). Further, high success has been reached from hairs collected during mating season and early summer (Karamanlidis et al. 2010). Genetic studies using natural rub trees to collect bear hair reported a success rate of 15.1% (Stetz et al. 2010). The yield of hair may be increased with the use of barbed wire wrapped around the pole from 0 to 3 meters height (Karamanlidis et al. 2010)

The more successful results of previous studies using power poles may suggest that a large part of the samples collected in this project most probably have been older than 4 weeks (see above). This is supported by our observations that most hair samples consisted of single, rootless, often bleached out hairs. Further, our sampling was conducted late in the year, in autumn, several months after mating season. Power poles should be sampled in spring and early summer to investigate if the numbers and success rates would increase, as

described in other studies (Karamanlidis et al. 2007 and 2010). Samples from 2013 which have been at the power poles for not longer than 4 weeks showed a substantial increase in genotyping success (see above and Appendix 2).

3.2 Since power poles are usually more exposed to weather: do the samples contain enough DNA for individual identification and can they be used for monitoring purposes?

Power poles are rather exposed to all weather conditions, such as sun light, rain, snow and wind. Long time exposure of biological samples, such as hairs and feces, to UV light in combination with fluctuating temperatures and humidity cause the degradation of the DNA molecules and therefore a genetic analysis can be unsuccessful (Murphy et al. 2007). Previous studies using biological samples of different exposure times showed that samples older than a few weeks did not contain enough DNA for extraction and amplification (Karamanlidis et al. 2010).

Overall, our success rates are comparable to other genetic studies using hair remaining after rubbing and marking. However, sampling time should be adjusted to take place earlier in the year, preferably in spring and summer during mating season. Furthermore, sampling should be done more frequently in order to minimize the period samples are exposed to the environment and thus to increase DNA yield and genotyping success (Karamanlidis et al. 2010).

3.3 Is this method efficient?

The brown bear is elusive and collecting biological samples from such a species usually requires experienced personnel (e.g. to distinguish feces) or detailed information on bear activity (e.g. by direct observations) and habitat (feces collection, hair trapping, rub trees) as well as logistics (e.g. hair traps). Here, sampling at power poles may present a simplification: power poles are at known and fixed locations and are usually comparably easy to access.

Walking and sampling along the power line, as described above (see Material and methods), took about 22.5 man hours in 2014. This means 2.5 hair samples were collected per man hour. This is comparably more than for feces collected opportunistically in the field and hair samples from hair snares, which are collected at a rate of 0.2 samples per man hour on average (see Kopatz et al. 2012b). It is important to mention, though, that purpose and goal of a study may vary and so far no method can substitute the other (Kopatz et al. 2012b). The costs of the genetic analysis of the samples remain the same as for feces or other samples. Based on previous studies, the number of samples may be increased by more regular checks and visits to collect samples during late spring and summer (see Karamanlidis et al. 2010). Overall, this sampling method may have large potential to collect valuable samples and information, that otherwise would be much more difficult to acquire.

3.4 At which frequency should the power poles be checked and samples collected?

Based on our results and previous studies (see Karamanlidis et al. 2010), power poles should be checked from late May to early August (during spring and early summer; mating season) at an interval of at least two weeks. This is the period used successfully also to check and collect hair samples at hair snares (see e.g. Kendall et al. 2008; Kopatz et al. 2011) for which success rates for positive DNA identification were between 64% and 77% (Kopatz et al. 2011).

Karamanlidis et al. (2010) reported success rates of 78% to 82% when samples were collected during that particular time of the year and within a four week sampling interval.

3.5 Could the number of samples collected and the results of the genetic analysis be improved by special modifications of the method?

A single turn to check the power poles in Pasvik, especially that late in the year, does not seem to deliver the best results. If this method is to be implemented, it requires a simple but strict sampling scheme in terms of the period at which the method is used as well as at which intervals power poles are revisited. The sampling protocol should be adjusted to the experience of previous studies and local knowledge. According to which, a sampling period from May to August, with two to three revisits after two weeks could deliver the highest success rates in DNA identification (see also Karamanlidis et al. 2010).

Fig. 1: Power pole in the Pasvik Valley, Norway. Every pole is registered by its unique number. Photo: Alexander Kopatz.

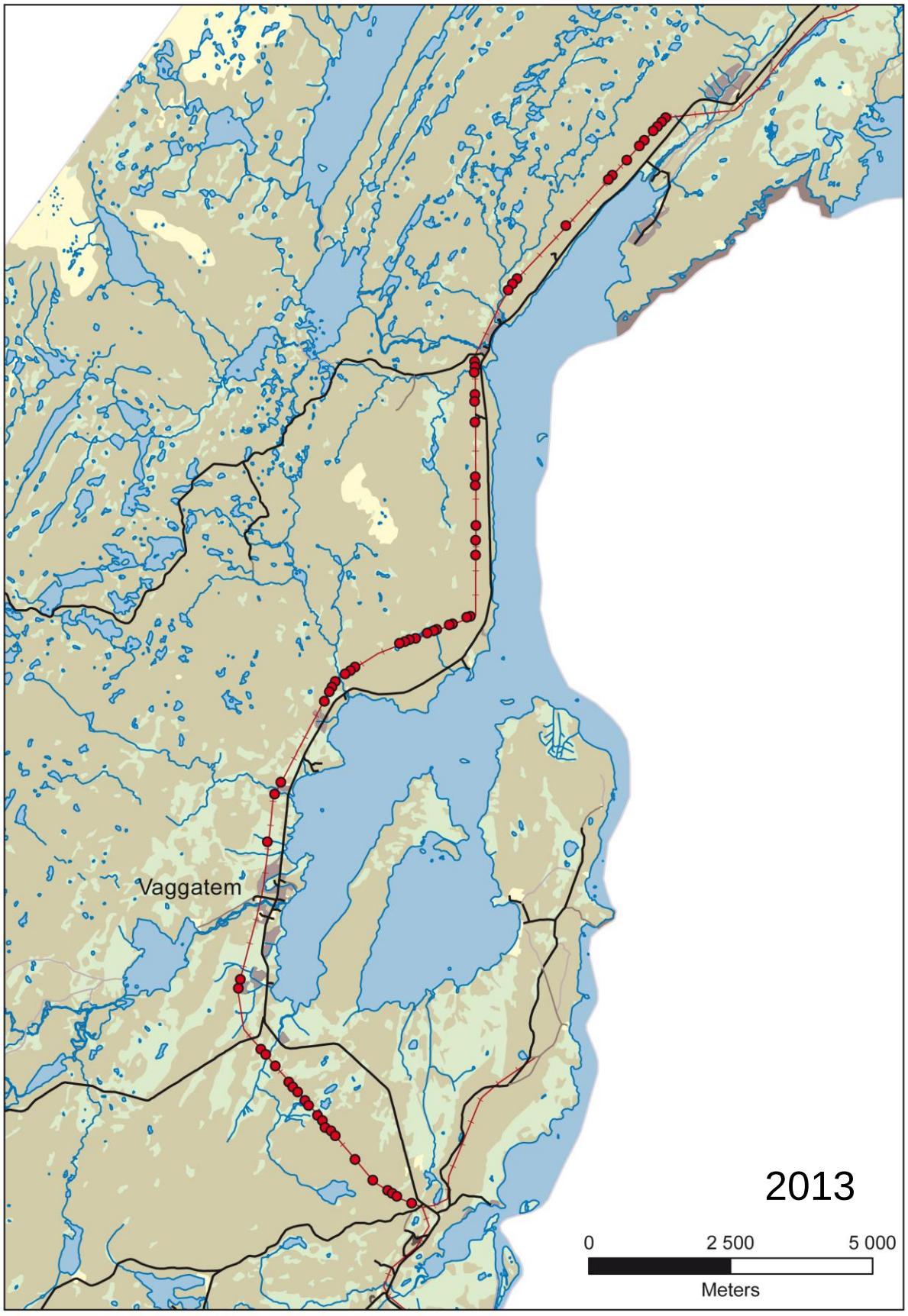

Fig. 2: Hair samples collected in 2013 at power poles in the Pasvik Valley, Norway. The power line is represented as red line and poles with hair samples are shown by a red circle.

Fig. 3: Hair samples collected in 2014 at power poles in the Pasvik Valley, Norway. The power line is represented as red line and poles with hair samples are shown by a red circle.

4. Conclusive remarks

We tested the collection of hair samples at power poles to monitor brown bears in the Pasvik Valley. After sampling in 2013 and 2014 we can conclude:

- Hair sampling at power poles is a simple method which does not require special knowledge or large effort. The locations of power poles are usually known and easy to access.

- Power poles are used by some brown bears for marking and scratching. Previous studies indicate strong association with such a behavior during mating season.

- From 215 power poles investigated, we collected 181 hair samples in 2013 and 57 hair samples in 2014. Some samples collected in 2013 most probably originated from several years in the past. Success rates were 17.3% in 2013 and 12.3% in 2014. However, DNA content was generally low.

- Our success rates are comparable to other studies. However, sampling was not conducted during spring and early summer, when higher success rates have been reported by other studies.

- Sampling should be conducted in intervals of a maximum of 4 weeks, preferably within 2 weeks, as it has been shown to be successful during hair-trapping. Studies showed that the success rates for genetic analyses of biological samples decreased substantially if the sample material was exposed for longer than 4 weeks to the environment.

- Barbed wire around poles may increase the amount of hair and samples collected.

- A strict sampling protocol should be developed in collaboration with all partners (Bioforsk, Norwegian State Nature Inspectorate, Fylkesmannen and other groups of interest e.g. locals).

- Overall, this sampling technique should be improved and may hold further potential to collect valuable samples and information, which would be more difficult to collect otherwise.

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Appendix 1. Hair samples collected at power poles in the Pasvik Valley, Norway in autumn 2014 and the results of their genetic analysis. Samples are sorted by the power pole registration number (* = Quality assurance reported low DNA content).

Pole No. - Sample	Date	Sample No.	DNA analysis	Notes
599-1	20.09.2014	14NH177	Negative	No hair roots
599-2	20.09.2014	14NH178	Negative	
599-3	20.09.2014	14NH179	Negative	
599-4	20.09.2014	14NH180	Negative	
599-5	20.09.2014	14NH181	Negative	
599-6	20.09.2014	14NH182	Negative	
599-7	20.09.2014	14NH183	Negative	
599-8	20.09.2014	14NH184	Negative	
601-1	20.09.2014	14NH185	Negative	No hair roots
606-1	20.09.2014	14NH186	Negative	
606-2	20.09.2014	14NH187	Negative	
606-3	20.09.2014	14NH188	Negative	
640-1	20.09.2014	14NH189	Negative	No hair roots
640-2	20.09.2014	14NH190	Positive	
640-3	20.09.2014	14NH191	Negative	No hair roots
640-4	20.09.2014	14NH192	Negative	
674-1	26.09.2014	14NH213	Negative	No hair roots
674-2	26.09.2014	14NH214	Negative	
674-3	26.09.2014	14NH216	Negative	
677-1	26.09.2014	14NH211	Negative	
677-2	26.09.2014	14NH212	Negative	
681-1	09.10.2014	14NH233	Negative	No hair roots
694-1	01.10.2014	14NH193	Negative	No hair roots
694-2	01.10.2014	14NH194	Negative	No hair roots
694-3	01.10.2014	14NH195	Negative	No hair roots
697-1	01.10.2014	14NH210	Negative	
697-2	01.10.2014	14NH217	Negative	
700-1	01.10.2014	14NH196	Negative	No hair roots
700-2	01.10.2014	14NH197	Negative	No hair roots
701-1	01.10.2014	14NH204	Negative	No hair roots
701-2	01.10.2014	14NH205	Negative	
701-3	01.10.2014	14NH206	Negative	
701-4	01.10.2014	14NH207	Positive	
701-5	01.10.2014	14NH208	Negative	No hair roots
701-6	01.10.2014	14NH209	Negative	
703-1	01.10.2014	14NH201	Negative	
703-2	01.10.2014	14NH202	Negative	
703-3	01.10.2014	14NH203	Negative	
707-1	01.10.2014	14NH198	Negative	No hair roots
707-2	01.10.2014	14NH199	Negative	No hair roots
712-1	01.10.2014	14NH200	Positive	
747-1	11.10.2014	14NH234	Negative	No hair roots

Pole No. - Sample	Date	Sample No.	DNA analysis	Notes
766-1	21.10.2014	14NH254	Negative	
783-1	23.09.2014	14NH229	Positive	**FI43/MO3***
784-1	23.09.2014	14NH226	Negative	No hair roots
784-2	23.09.2014	14NH222	Negative	
786-1	23.09.2014	14NH218	Positive	
786-2	23.09.2014	14NH219	Negative	
786-3	23.09.2014	14NH220	Positive	
786-4	23.09.2014	14NH221	Negative	
786-5	23.09.2014	14NH223	Negative	
789-1	23.09.2014	14NH228	Positive	
792-1	23.09.2014	14NH224	Negative	No hair roots
792-2	23.09.2014	14NH225	Negative	No hair roots
792-3	23.09.2014	14NH227	Negative	
806-1	21.10.2014	14NH255	Negative	
806-2	21.10.2014	14NH256	Negative	

** Quality assurance reported low DNA content.*

Appendix 2. Hair samples collected at power poles in the Pasvik Valley, Norway in summer and autumn 2013 and the results of their genetic analysis. Samples are sorted by the power pole registration number (* = Quality assurance reported low DNA content).

Pole No. - Sample	Date	Sample No.	DNA analysis	Notes
599-1	07.08.2013	BH0064	Negative	
599-2	07.08.2013	BH0065	Negative	
599-3	07.08.2013	BH0066	Negative	
599-4	07.08.2013	BH0067	Negative	
600-1	07.08.2013	BH0068	Negative	
600-2	07.08.2013	BH0069	Negative	
601-1	07.08.2013	BH0070	Negative	
602-1	07.08.2013	BH0071	Negative	
602-2	07.08.2013	BH0072	Negative	
604-1	24.08.2013	BH0195	Negative	
604-2	24.08.2013	BH0196	Negative	
605-1	24.08.2013	BH0197	Negative	
605-2	24.08.2013	BH0198	Negative	
605-3	24.08.2013	BH0199	Negative	
608-1	24.08.2013	BH0200	Negative	
608-2	24.08.2013	BH0201	Negative	
611-1	24.08.2013	BH0202	Negative	
611-2	24.08.2013	BH0203	Negative	
612-1	24.08.2013	BH0204	Negative	
612-2	24.08.2013	BH0205	Negative	
622-1	24.08.2013	BH0206	Negative	
633-1	31.08.2013	BH0225	Negative	
634-1	31.08.2013	BH0226	Negative	
634-2	31.08.2013	BH0227	Negative	
635-1	31.08.2013	BH0228	Negative	
635-2	31.08.2013	BH0229	Negative	
648-1	08.08.2013	BH0073	Negative	
649-1	08.08.2013	BH0074	Negative	
650-1	08.08.2013	BH0075	Negative	
653-1	08.08.2013	BH0076	Negative	
653-1	10.09.2013	BH0297	Negative	
653-1	10.09.2013	BH0298	Negative	
653-2	08.08.2013	BH0077A	Negative	
653-2	08.08.2013	BH0077B	Negative	
653-3	08.08.2013	BH0078	Negative	
653-4	08.08.2013	BH0079	Negative	
654-1	08.08.2013	BH0080	Negative	
654-2	08.08.2013	BH0081	Negative	
658-1	08.08.2013	BH0082	Negative	
666-1	09.08.2013	BH0088	Negative	
666-1	10.09.2013	BH0299	Negative	
668-1	09.08.2013	BH0089	Negative	

Pole No. - Sample	Date	Sample No.	DNA analysis	Notes
668-1	10.09.2013	BH0300	Negative	
674-1	09.08.2013	BH0090	Negative	
674-2	09.08.2013	BH0091	Negative	
674-3	09.08.2013	BH0092	Negative	
674-4	09.08.2013	BH0093	Negative	
674-5	09.08.2013	BH0094	Negative	
677-1	09.08.2013	BH0095	Negative	
677-2	09.08.2013	BH0096	Negative	
677-3	09.08.2013	BH0097	Negative	
679-1	09.08.2013	BH0098	Negative	
679-1	10.09.2013	BH0301	Negative	
679-2	09.08.2013	BH0099	Negative	
679-3	09.08.2013	BH0100	Negative	
690-1	14.08.2013	BH0107	Negative	
690-2	14.08.2013	BH0108	Negative	
690-3	14.08.2013	BH0109	Negative	
690-4	14.08.2013	BH0110	Negative	
690-5	14.08.2013	BH0111	Negative	
690-6	14.08.2013	BH0112	Negative	No hair roots
690-7	14.08.2013	BH0113	Negative	
691-Nr4-1	24.08.2013	BH0194	Negative	
693-1	14.08.2013	BH0114	Negative	
693-1	12.09.2013	BH0302	Negative	
693-2	14.08.2013	BH0115	Negative	
693-3	14.08.2013	BH0116	Negative	
694-1	14.08.2013	BH0117	Positive	
694-10	14.08.2013	BH0126	Positive	**FI43/MO3***
694-11	14.08.2013	BH0127	Negative	
694-2	14.08.2013	BH0118	Negative	
694-3	14.08.2013	BH0119	Positive	
694-4	14.08.2013	BH0120	Negative	
694-5	14.08.2013	BH0121	Negative	
694-6	14.08.2013	BH0122	Negative	
694-7	14.08.2013	BH0123	Negative	
694-8	14.08.2013	BH0124	Positive	**FI131***
694-9	14.08.2013	BH0125	Negative	
696-1	14.08.2013	BH0128	Negative	
696-2	14.08.2013	BH0129	Negative	
697-1	14.08.2013	BH0130	Negative	
697-1	12.09.2013	BH0303	Negative	
697-2	14.08.2013	BH0131	Negative	No hair roots
698-1	14.08.2013	BH0132	Negative	
700-1	14.08.2013	BH0133A	Negative	
700-1	14.08.2013	BH0133B	Negative	
700-2	14.08.2013	BH0134	Negative	
700-3	14.08.2013	BH0135	Negative	
701-1	14.08.2013	BH0136	Negative	

Pole No. - Sample	Date	Sample No.	DNA analysis	Notes
702-1	14.08.2013	BH0137	Negative	
703-1	14.08.2013	BH0138	Negative	
703-2	14.08.2013	BH0139	Negative	No hair roots
703-3	14.08.2013	BH0140	Negative	
711-1	12.09.2013	BH0304	Negative	
711-2	12.09.2013	BH0305A	Negative	
711-2	12.09.2013	BH0305B	Positive	**FI43/MO3***
711-3	12.09.2013	BH0306	Positive	**FI43/MO3**
711-4	12.09.2013	BH0307	Positive	**FI43/MO3**
711-5	12.09.2013	BH0308	Positive	**FI43/MO3**
711-6	12.09.2013	BH0309	Positive	**Female, no ID**
712-1	12.09.2013	BH0310A	Negative	
712-1	12.09.2013	BH0310B	Positive	**Female, no ID**
712-2	12.09.2013	BH0311	Positive	**FI43/MO3**
712-3	12.09.2013	BH0312	Negative	
712-4	12.09.2013	BH0313	Positive	**FI43/MO3**
712-5	12.09.2013	BH0314	Positive	**FI43/MO3**
712-6	12.09.2013	BH0315	Positive	**FI43/MO3**
712-7	12.09.2013	BH0316	Positive	**FI43/MO3**
713-1	14.08.2013	BH0141	Negative	No hair roots
713-1	13.09.2013	BH0317	Positive	No ID
713-2	14.08.2013	BH0142	Negative	
713-2	13.09.2013	BH0318	Negative	
713-3	13.09.2013	BH0319	Positive	No ID
713-4	13.09.2013	BH0320	Positive	No ID
713-5	13.09.2013	BH0321	Negative	
713-6	13.09.2013	BH0322	Positive	No ID
713-7	13.09.2013	BH0323	Negative	
715-1	17.09.2013	BH0324	Positive	**FI43/MO3***
715-2	17.09.2013	BH0325	Positive	**FI43/MO3***
715-3	17.09.2013	BH0326	Positive	**FI43/MO3***
715-4	17.09.2013	BH0327	Positive	No ID
715-5	17.09.2013	BH0328	Negative	No hair roots
716-1	16.08.2013	BH0143	Negative	
717-1	16.08.2013	BH0144	Negative	
719-1	16.08.2013	BH0145	Negative	
719-2	16.08.2013	BH0146	Negative	
719-3	16.08.2013	BH0147	Negative	
719-4	16.08.2013	BH0148	Negative	
719-5	16.08.2013	BH0149A	Negative	
719-5	16.08.2013	BH0149B	Negative	
733-1	16.08.2013	BH0150	Negative	
735-1	17.09.2013	BH0329	Negative	No hair roots
735-2	17.09.2013	BH0330	Negative	No hair roots
739-1	16.08.2013	BH0151	Negative	No hair roots
765-1	06.09.2013	BH0230	Negative	No hair roots
766-1	06.09.2013	BH0231	Negative	

Pole No. - Sample	Date	Sample No.	DNA analysis	Notes
766-2	06.09.2013	BH0232	Negative	
766-3	06.09.2013	BH0233	Negative	
766-4	06.09.2013	BH0234	Negative	
776-1	19.08.2013	BH0152	Negative	No hair roots
777-1	19.08.2013	BH0153	Negative	
777-2	19.08.2013	BH0154	Negative	
777-3	19.08.2013	BH0155	Negative	
779-1	19.08.2013	BH0156	Negative	
779-2	19.08.2013	BH0157	Negative	
782-1	19.08.2013	BH0158	Negative	No hair roots
782-2	19.08.2013	BH0159	Negative	
782-3	19.08.2013	BH0160	Negative	No hair roots
783-1	19.08.2013	BH0161	Negative	
784-1	19.08.2013	BH0162	Negative	
784-2	19.08.2013	BH0163	Negative	
786-1	19.08.2013	BH0164	Negative	No hair roots
786-2	19.08.2013	BH0165	Negative	No hair roots
786-3	19.08.2013	BH0166	Negative	No hair roots
786-4	19.08.2013	BH0167	Negative	No hair roots
786-5	19.08.2013	BH0168	Negative	No hair roots
786-6	19.08.2013	BH0169	Negative	No hair roots
786-7	19.08.2013	BH0170	Negative	No hair roots
786-8	19.08.2013	BH0171	Negative	No hair roots
787-1	19.08.2013	BH0172	Negative	
787-2	19.08.2013	BH0173	Negative	
789-1	21.08.2013	BH0174	Negative	No hair roots
789-2	21.08.2013	BH0175	Negative	
790-1	21.08.2013	BH0176	Negative	
791-1	21.08.2013	BH0177	Negative	
791-2	21.08.2013	BH0178	Negative	
792-1	21.08.2013	BH0179	Negative	No hair roots
793-1	21.08.2013	BH0180	Negative	
793-2	21.08.2013	BH0181	Negative	
793-3	21.08.2013	BH0182	Negative	
798-1	21.08.2013	BH0183	Negative	
798-2	21.08.2013	BH0184	Negative	
802-1	21.08.2013	BH0185	Negative	
805-1	21.08.2013	BH0186	Negative	
806-1	21.08.2013	BH0187	Negative	No hair roots
806-2	21.08.2013	BH0188	Negative	
806-3	21.08.2013	BH0189	Negative	
807-1	21.08.2013	BH0190	Negative	No hair roots
810-1	21.08.2013	BH0191	Negative	
810-2	21.08.2013	BH0192	Negative	No hair roots
810-3	21.08.2013	BH0193	Negative	

** Quality assurance reported low DNA content.*