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Short communication

Pine marten *Martes martes* and red fox *Vulpes vulpes* sign indices in Scottish forests: population change and reliability of field identification of scats

David Baines, Nicholas Aebischer, Allan Macleod & John Woods

The range and abundance of the pine marten *Martes martes* and red fox *Vulpes vulpes* are considered to have increased in the Scottish Highlands in recent decades. In 2009, we resurveyed 11 forests surveyed for predators in 1995, together with an additional five forests. Our survey techniques followed those used in 1995. In all, we used DNA analysis to identify 414 mammal scats, representing 30% of the scats collected and identified in the field as being from either fox or marten. Of these, 77% of scats had been identified correctly by two field observers, with no difference between the individual observers. However, of the scats incorrectly identified, there was a bias towards identifying marten scats as fox scats. We used DNA confirmation to obtain correction formulae for scats identified in the field as fox or martens. The corrected marten sign index had increased 3.9-fold since 1995 and the fox sign index had increased 2.2-fold in the 11 forests surveyed in both years.

Key words: Martes martes, pine marten, predation, predator management, red fox, scats, Vulpes vulpes

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Numbers and distribution of several predator species in Scotland, including both pine marten *Martes martes* and red fox *Vulpes vulpes*, declined during the 19th and early 20th centuries. This decline followed habitat loss and intensive culling by gamekeepers (Langley & Yalden 1977), whose objective was to conserve game birds, particularly red grouse *Lagopus lagopus scoticus,* for shooting (Tapper 1999). Legal protection of martens in 1988 allowed them to recover much of their former range and abundance (Tapper 1999), but the marten is still rare in Scotland, with only an estimated 3,500 adults, representing at least 95% of the British population (Birks 2002). Reduced predator management by fewer gamekeepers (McGilvray 1995) has probably resulted in fewer martens being killed, and may also have resulted in increases in foxes. Records of martens culled by gamekeepers before 1988 provided information on distribution and abundance (Langley & Yalden 1977). Since their protection, assessments of marten status have largely been dependent on systematic searches for scats, despite concerns over the general reliability of scat surveys, and in particular, the relationship between scat abundance and population density (Birks et al. 2004).

In 2009, we repeated a survey for signs of predators that was originally undertaken in 11 forests in 1995. Our objectives were to determine the reliability of field identification of mammal scats through follow-up DNA analysis and to determine whether marten

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and fox signs had increased between the surveys. We also discuss the implications of changes in marten and fox numbers on capercaillie *Tetrao urogallus*, a declining grouse species in Scottish forests (Ewing et al. 2012).

Material and methods

Forest selection

Martens can be a major predator of capercaillie clutches (Summers et al. 2009) and fox abundance can be negatively associated with capercaillie breeding densities and breeding success (Kurki et al. 1997, 2000). Thus, we selected study forests that currently support, or have recently supported, regionally important numbers of breeding capercaillie. Eleven forests which were originally surveyed for predator indices in 1995 (Baines et al. 2004) were resurveyed in 2009. We surveyed five additional forests in 2009, also supporting capercaillie, to increase the number of scat samples for DNA analysis and to provide baseline data for future surveys (Table 1). These 16 forests comprised a range of types including ancient Scots pine *Pinus sylvestris* forests that are no longer commercially logged and commercial Scots pine plantations and mixed species plantations primarily of larch *Larix* spp. and spruce *Picea* spp., logged on 40 - 80 year rotations. Their sizes ranged from 100 to 5,800 ha, averaging 1,900 ha (SD = 1,790) and did not differ significantly between surveys. The study forests also exhibited a geographical range, with a maximum distance between forests of 160 km, which encompassed several Special Protection Areas that include capercaillie as a qualifying interest, as well as core and peripheral parts of the perceived pine marten distribution (Balharry et al. 1996).

Predator indices

Within each forest, we searched vehicle tracks for mammal scats (Lockie 1964). Trails and tracks can provide higher numbers of scats than random searches (Güthlin et al. 2012) and were selected for this purpose. Track lengths searched varied from 6.0 to 11.0 km (mean: 9.3 km ± 1.6 (SD)). We resurveyed all routes from the original 1995 survey. Observers walked tracks five times; initially during a clear-up round in the second half of April to count and remove all scats, and then twice in both May and June (middle and end of the month). Two different observers (Allan Macleod & John Woods) collected all scats in the field in 2009, but neither observer participated in the original 1995 survey. Observers simultaneously scanned both sides of vehicular tracks for scats at a slow walking pace. All scats were initially classified as 'fox', 'marten' or 'other species' in the field before characteristic elements of their morphology had been altered by handling.

Table 1. Predator indices in relation to region and forest type in 1995 and 2009. Forest types are: 1) open canopy as in native pinewoods; 2) mature Scots pine plantation, canopy sufficiently open for some dwarf shrubs; 3) mixed species plantation with closed canopy, often with some clear-felled areas and restocked ground. Values for fox and pine marten are mean scats 10 km^{-1} day^{-1} x 100 and excluding the clear-up round. Numbers of scats in each forest and year are given in parentheses. A dash (-) indicates that data were not collected.

			Fox		Marten	
Forest	Region	Forest type	1995	2009	1995	2009
Abernethy	Strathspey	1	(8) 9.3	(36) 57.5	(6) 7.0	(139) 221.9
Allean	Perthshire	3	-	(33) 54.6	-	(19) 31.4
Craigmore	Strathspey	2	(12) 13.4	(19) 36.2	(4) 4.5	(83) 158.3
Darnaway	Moray	3	(7) 8.7	(28)45.5	(29) 36.0	(24) 39.0
Drummond Hill	Perthshire	2	(6) 9.0	(15)25.1	(32) 47.8	(24) 40.2
Dupplin	Perthshire	2	(1) 1.8	(19) 43.9	(2) 3.5	(0) 0
Gask	Perthshire	3	(33) 60.5	(36) 86.1	(1) 1.8	(2) 4.8
Glen Tanar	Aberdeenshire	1	(4) 4.9	(8) 14.9	(0) 0	(50) 93.3
Glenmore	Strathspey	2	-	(29) 29.2	-	(19) 53.0
Inverlaidnan Hill	Strathspey	3	(5) 11.0	(2) 5.4	(12) 26.5	(4) 5.4
Kinveachy	Strathspey	1	(6) 11.1	(7) 17.2	(14) 25.9	(13) 31.9
Littlewood	Aberdeenshire	1	(11) 19.8	(78) 141.1	(0) 0	(0) 0
Morangie	Easter Ross	3	-	(63) 105.7	-	(72) 120.8
Novar	Easter Ross	3	-	(8) 12.1	-	(31) 46.9
Pannanich	Aberdeenshire	2	-	(3) 6.4	-	(20) 42.8
Rothiemurchus	Strathspey	1	(6) 8.1	(3) 5.7	(0) 0	(16) 30.3

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We extracted DNA from 414 scats, representing 30% of all scats collected, to verify their originator. A positive identification of DNA was obtained for 311 (75%) of the 414 scats. These included: 1) 217 scats that could not be confidently allocated to species using field characteristics (low certainty), 2) 88 scats where the field workers had a high certainty of correct identification as either pine marten or fox, and 3) six scats that were neither marten nor fox. The scats sent for DNA analysis were a randomly selected subset from within each certainty category.

Correcting the field identification

Assuming that the scats identified by DNA analysis were a representative sample of the scats identified in the field, it was possible to correct the numbers of scats identified as fox and marten in the field as follows. Let i_f be the fox identification rate, i.e. the probability that a fox scat will be correctly attributed to fox in the field, and i_m the marten identification rate. Then $1 - i_f$ is the probability of misidentifying fox as marten, and $1 - i_m$ the probability of misidentifying marten as fox. Let O_f and O_m be the observed numbers, and T_f and T_m the true numbers, of fox and marten scats, respectively. Observed and true numbers are linked by the relationships $O_f = i_f T_f + (1 - i_m) T_m$ and $O_m = i_m T_m + (1 - i_f) T_f$. Reversing these relationships provided the correction formulae that allow T_f and T_m to be estimated from O_f and O_m in the following way: $T_f = (i_m O_f - (1 - i_m) O_m) / (i_f + i_m - 1)$ and $T_m = (i_f O_m - (1 - i_f) O_f) / (i_f + i_m - 1)$.

Data analysis

The total number of marten and fox scats found in each forest over the four visits in May and June, but excluding those found on the clear-up round, were divided by the exposure period in days (i.e. the time interval between the end of the clear-up round and the final visit) to calculate scats per day. To adjust for differences in transect route length between forests, the number of scats per day was divided by the transect length. The indices were presented as scats 10 km^{-1} day^{-1}, which we then multiplied by 100 for ease of presentation. Subsequent analyses addressed whether marten and fox sign indices had changed in the same suite of forests since 1995 using Poisson regression (generalised linear models with Poisson error, log link) adjusted for overdispersion, with marten or fox scat as the dependent variable, $\log_e$ transect length*time interval as an offset and forest and year as factors. This analysis was done twice, initially on uncorrected mammal indices and then repeated with corrected indices derived from the DNA analysis on scats collected in 2009. We assumed the 2009 correction factors would apply to the 1995 data.

Results

DNA verification of scats

Of the 311 positive DNA samples, the observers identified 116 as fox and 195 as pine marten. The DNA analysis demonstrated that there were also scat samples for domestic dog *Canis familiaris* (3), hedgehog *Erinaceus europaeus* (2) and wild cat *Felis sylvestris* (1). These scats accounted for only 2% of the scat samples, and we have not considered them further. Of the remaining 305 scats, 236 (77%) were correctly identified by the observers. A total of 69 scats positively identified through DNA were misidentified in the field, with an equal split between the two observers (Table 2). Of the 69 scats, 64 were misclassified as fox in the field when they were

Table 2. Scats misidentified in the field in relation to subsequent DNA confirmation according to species (fox or pine marten) for each of the two observers (AM = Allan Macleod; JW = John Woods) in each field assigned identification certainty category.

	Both observers		Observer AM		Observer JW	
	No. wrong	%	No. wrong	%	No. wrong.	%
All scats	69		36		33	
Field - fox, DNA - marten	64	93	32	89	32	94
Field - marten, DNA - fox	5	7	4	11	1	6
High certainty	6		6		0	
Field - fox, DNA - marten	5	83	5	83	-	
Field - marten, DNA - fox	1	17	1	17	-	
Low certainty	63		30		33	
Field - fox, DNA - marten	59	94	27	90	32	94
Field - marten, DNA - fox	4	6	3	10	1	6

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Table 3. Predator indices, (means ± 1 SE) from 11 forests surveyed in both 1995 and 2009. Mammal indices are scats 10 km^{-1} day^{-1} x 100 and excluding scats from the clear-up round. Corrected mammal indices are given in parentheses.

	1995		2009	
Predator	Forests with sign	Abundance index	Forests with sign	Abundance index
Red fox	11 (100%)	15.9 ± 5.2 (12.2)	11 (100%)	43.5 ± 12.2 (27.4)
Pine marten	8 (73%)	15.3 ± 5.5 (19.0)	9 (82%)	57.3 ± 21.8 (73.4)

actually marten. Misclassification of marten as fox was broadly consistent between the two observers ($\chi^2_1 = 0.79$, $P > 0.1$). Whilst 116 of the sampled scats in the field were identified as fox, DNA confirmation found that only 52 (~ 45%) of those were actually from fox, plus an additional five scats misidentified as marten in the field, giving a total of 57 confirmed fox scats. Conversely, 195 scats were classified as marten in the field, but 254 were confirmed by DNA analysis (195 plus the 64 misidentified as fox, minus the five misidentified as marten, which were actually fox). This gives identification rates of $i_f = 52/57 = 0.912$ for fox and $i_m = 190/254 = 0.748$ for marten. This means that if no martens are present at a site, 8.8% of scats would be identified in the field as originating from marten. Inverting the identification rates into correction formulae gives: $T_f = 1.133\ O_f - 0.382\ O_m$ and $T_m = 1.382\ O_m - 0.133 O_f$.

Predator indices

Considering data from the 11 forests surveyed in both years, nine forests had signs of pine marten in 2009, compared with eight in 1995 (Table 3). There was an apparent mean 3.7-fold increase in marten scats ($F_{1,10} = 8.39$, $P = 0.016$) and a 2.7-fold increase in fox scats ($F_{1,10} = 14.34$, $P = 0.004$) based on field identification. After correction for misidentification of both the 1995 and 2009 samples, the increases were 3.9-fold for marten scats ($F_{1,10} = 8.04$, $P = 0.018$) and 2.2-fold ($F_{1,10} = 3.13$, $P = 0.11$) for fox scats.

Discussion

Using DNA analysis to check the field identification of fox and marten scats, we found that 23% of scats were misidentified in the field, with a bias towards identifying marten scats as fox scats. Using corrected scat indices, we found a 3.9- and a 2.2-fold increase in marten and fox sign index, respectively, since 1995. Marten and fox sign indices were derived solely from scat collections along forest tracks. Although tracks provide higher numbers of scats than random or transect searches, estimates between tracks show greater spatial variation and their temporal repeatability is uncertain (Güthlin et al. 2012). Consequently, their use in deriving either estimates of abundance or population size can be limited and open to different interpretation (Webbon et al. 2004). Scat deposition and decay rates are likely to differ according to diet-related differences in defecation rates and seasonal and habitat differences in deposition (Davison et al. 2002) and can be confounded by differences in persistence times due to weather (Laing et al. 2003). That said, many of these potential biases were mitigated by standardising survey timing and duration so that scat abundance was compared only within one season, on one substrate type, within forest habitats only and within one geographic area. By enforcing these conditions as tightly as possible and using the same sampling regime, both in terms of timing of survey and the tracks themselves, we consider that in comparing the 1995 and 2009 surveys we generally compared changes in abundance as opposed to changes in activity. However, with only two data points (1995 and 2009), it is difficult to be sure that the changes reflect a true trend rather than merely between-year variation. Supportive data suggesting a true increase in martens are provided by increases in annual scat indices at Abernethy, one of our study forests (Summers et al. 2004, 2009). Furthermore, an independent data set of fox indices derived from the number killed on over 300 sporting estates in Scotland has increased by 150% (95% CL = 50-262) between 1961 and 2009 (Aebischer et al. 2011). However, similar data were not available for martens. The apparent increase in martens is likely to reflect a recolonisation of much of the former range following their legal protection (Balharry et al. 1996). The precise relationship between predator numbers and scat density is unlikely to be linear and hence our reported magnitudes of increase in marten and fox sign indices may not equate to the same levels of increase in abundance. This may particularly be true if track-marking behaviour using scats is a

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feature of highly territorial populations at relatively high densities (Balharry et al. 1996). More recently, genotyping of marten hair samples has allowed identification of individuals and estimation of population densities (Mullins et al. 2009). Although not conducted as part of our study, we recommend incorporation of this technique for any future surveys.

A potential bias not overcome was the one of observer error, both in detection rates and assigning the scat originator. Given the 14-year gap between surveys, different observers had to be used, but a DNA check on scat originator, allowing a comparison of observer accuracy, was performed in 2009. Such DNA analyses from scats have shown considerable scope for misidentification when only scat field characteristics are taken into consideration, even by recognised topic experts (Davison et al. 2002).

Management implications

Our study demonstrated that observer error in identifying scats is frequent, even amongst experienced field observers. We recommend that identification of representative samples of scats be confirmed by DNA analysis. Changes in scat indices may not be a reliable indicator of population change, therefore, future studies should ideally be accompanied by genotyping of hair or faeces to allow identification of individuals and estimation of population densities. Knowing the latter may be vital when considering management to help declining species of conservation concern such as the capercaillie. At one of our study forests, martens limited hatching success of capercaillie clutches (Summers et al. 2009). With low breeding success causing declines (Moss et al. 2000), it is unknown whether existing levels of predation can be sustained. A greater appreciation of the factors that determine predator abundance may be necessary to inform conservationists and forest managers alike whether more funding for legal fox control, together with a licensed removal of protected martens, may help reverse the decline in capercaillie.

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