

Extended Abstract

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Non-invasive scat sampling for use in wild boar (*Sus scrofa*) population size estimation - evaluating a field method

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Introduction: Population estimation is an important task for the management of wild boar, in particular with respect to the epidemiological role wild boar play in the transmission of the classical swine fever (ARTOIS et al. 2002). In research for methods that enable to obtain reliable data and are less biased than most traditional approaches (e.g. hunting bag analysis or traditional mark-recapture), strategies based on non-invasive genetic sampling yield promising results in several species (PIGGOTT & TAYLOR 2003). The most commonly used tissue sources are hair and scat. After individual identification of samples via genotyping, a modified capture-mark-recapture approach can be applied for population estimation. For wild boar, a pilot study revealed that hair sampling at baited stations is not practicable. Alternatively, scat sampling along transects was tested in the field. Scat sampling trials were conducted during two years in a forested area in south western Germany. Results of these field trials are presented, main focus lying on practicability and sampling efficiency.

Methods: All scat sampling trials were carried out between December 2006 and January 2008 in the same study area situated in south western Germany. The study area is covered with forest to approx. 90%. Wild boar occur in the whole sampling area and are hunted in most parts. The annual harvest in the state-hunting areas between 1999 and 2006 averages 2.7 individuals per km² (range: 1.14 to 5.23 animals per km² and year, REIS 2006). Wild boar scat was collected along 16 transects of approx. 7 to 8 km length each. Transects were installed parallel to each other in direction from north to south (overall length: 104 km). Per day, 8 transects were searched for scat, hence all transects were searched every 48 hours. Each transect was searched 6 times in total during 2-3 weeks. Whole samples were stored deep frozen (-19 ° C) in sealed plastic bags. Genotyping of samples was carried out in the laboratories of the University of Koblenz-Landau, Germany (details: KOLODZIEJ et al. 2008). In the trials carried out in winter 2007/8, Adaptive Cluster Sampling (THOMPSON 1990) was applied in combination with the strip transects in order to increase sample size. Based on the genotyping results, population sizes were calculated using program CAPTURE (WHITE et al. 1978). Because the population can not be assumed to be closed, population densities have been calculated with a buffer of 1000 m around the study area, which corresponds to the radius of an average 95% MCP-home range of wild boar radiotracked in the study area (EBERT, unpublished data). Thus, the area used for density calculation corresponds to 5200 ha.

Results: In trial A, 141 samples were found (table 1). Of these, 89 were genotyped successfully, representing 74 individual animals. Three of the sampled wild boars were resampled twice and six were resampled once (an additional three were resampled within one sampling day, which is not included in the estimate). With comparable sampling effort, trial B1 and B2 yielded considerably higher sample sizes (table 1), i.a. due to Cluster sampling. However, the recapture rate in trial B1 did not increase compared to trial A. This reflects in the confidence interval of the population estimate, which in both cases is fairly large (table 1).

Table 1: Results of three scat sampling trials carried out in the same 4000 ha- study area (see also KOLODZIEJ et al. 2008)

	Trial A (Dec. 2006)	Trial B1 (Dec. 2007)	Trial B2 (Jan. 2008)
N samples	141	326	515
Samples /km	0.23	0.53	0.83
% of samples obtained via Cluster Sampling	-	23.90	34.95
N wild boar sampled (resampled)	74 (12)	121 (23)	-
Population estimate: Model Mh Chao (95% CI)	426 (219 – 934)	757 (427 – 1444)	-
Population density (N/km ²), (95% CI)	8 (4 – 18)	15 (8 – 28)	-
Hunting bag in study area/year	160	360	

Discussion: Scat sampling efficiency can be considerably increased by applying Adaptive Cluster sampling in combination with strip transects. However, the higher sample size can not be explained by the Cluster Sampling alone. Thus, other reasons, e.g. an increase in population size from year 2006/7 to 2007/8, seem to contribute to the sample. An indication for this is the increase in hunting bag between the two sampling years with similar hunting effort (table 1). Furthermore, the recapture rate does not increase between trials A and B1, which would have improved the population estimate. The broad confidence intervals of the population estimates indicate that higher recapture rates – and consequently an even higher sample size – are necessary in order to obtain a more accurate estimate. Furthermore, until now the possibility of an overestimation of the population due to edge effects or due to genotyping errors can not be ruled out and require further investigations (see KOLODZIEJ et al. 2008). Compared to other studies (as reviewed in HEBEISEN et al. 2008), the population densities (table 1) range among the highest, especially when considering the relatively poor habitat.

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