International Union of Game Biologists XXVIII Congress

August 13-18, 2007 Uppsala, Sweden

Published by:

Searching for a new method to count wild boar: Problems associated with non-invasive tissue sampling in the field and laboratory

Presenter: <u>Ms. Cornelia Ebert,</u> Wildlife ecology, Research Institute of Forest Ecology and Forestry, Hauptstrasse 16, D-67705 Trippstadt, Germany. *cornelia.ebert@wald-rlp.de*

Authors:
C. Ebert, D. Huckschlag, K. Kolodziej, T. Schikora, H.K. Schulz, U. Hohmann
Research Institute of Forest Ecology and Forestry, Trippstadt _ Institute of Environmental Sciences, University of Koblenz-Landau Institute for Ecology, Evolution and Diversity, University of Frankfurt/ M

Abstract: Population estimates of wild boar remain difficult because of their complex social structure, nocturnal activity pattern and preference of dense vegetation. Thus traditional methods [e.g. aerial surveys, hunting bag analysis or classical capture-mark-recapture (CMR) approach] often provide highly biased data or are limited to minimum densities. In this context, the genetical analysis of non-invasively obtained tissue samples allows the collection of less heterogenic data with minimal animal manipulation yielding robust and less biased population estimates. Two different sampling strategies were tested since 2005 in a 4.000 ha area of the Palatinate Forest situated in southern Germany: "hair catchers" made of barbed wire stretched around baiting places and scat collection along transects. Effectiveness and practicability of the two strategies were evaluated via video and telemetry observation. Video observation revealed the different behaviour of the wild boars regarding the hair catchers, while telemetry data was used to validate the required transect density for scat sampling. We found that hair sampling provides highly heterogeneous results concerning the sampling probability of individual animals. Scat collection was problematic concerning sample size and DNA-quality. Further improvements of field protocols and DNA- preservation with the aim to increase the number of successfully sampled and genotyped individuals via scat collection will be presented.
For hair and scat, genotyping has been tested using 12 microsatellites, of which 7 proved to be suitable. Genotyping success of both tissue types will be discussed.

Keywords: Hair; Scat; Genotyping; Population estimate; CMR