

**ESTIMATING RED DEER (*Cervus elaphus*) POPULATION SIZE BY GENOTYPING FAECES:
A NON-INVASIVE APPROACH**

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Some ungulate species are of conservation concern, whereas others are under heavy harvest pressure. Reliable data on population sizes are lacking in most cases. Non-invasive genetic population estimation approaches represent a promising tool for ungulate management.

We developed and tested a non-invasive genetic approach for red deer (*Cervus elaphus*) population estimation based on faeces collected from a free ranging red deer population in south-west Germany. In the study area, increasing harvest rates of >1 per km² and year in combination with increasing levels of browsing and bark peeling damages indicate a considerable increase of the red deer population within the last years. During 10 days, 1128 faeces samples were collected in a forested study area of 100 km². After DNA extraction, a real-time PCR was carried out for all faeces samples to determine the amount of target DNA. Further genotyping using 8 microsatellite markers was carried out only for samples with a sufficiently high content of red deer DNA. The analysis yielded 398 reliable consensus genotypes which correspond to 247 different red deer individuals. We calculated population size estimates for both sexes separately using the programs MARK and CAPWIRE. For the calculation of population densities, we augmented the transect grid by a seasonal male red deer home range radius to account for the fact that the study area is not geographically closed. The resulting population densities (1.24 (0.98 – 1.95) male and 1.92 (1.35 – 3.84) female red deer per km²) can be used to evaluate and adapt red deer management measures (see Hohmann et al., this Symposium).