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Management of wild boar and red deer populations in Germany by using non-invasive population estimates for calibrating harvest rates

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In Germany, as in many other parts of Europe, forest dwelling ungulates are usually regulated by means of hunting. But reliable data on population sizes are lacking in most cases, which would be helpful for calibrating hunting success in terms of population regulation. Within this framework non-invasive genetic population estimation approaches represent a promising tool for ungulate management. We developed and tested a non-invasive genetic approach for wild boar (*Sus scrofa*) and red deer (*Cervus elaphus*) population estimation based on faeces collected from free ranging populations in south western Germany. Through genotyping of faecal samples a capture-mark-recapture based modelling of population size has been conducted. In the study area, a state hunting ground of 10.000 ha in size, the applied hunting regime intends to reduce wild boar and red deer populations as a measure to diminish forest damage (red deer) and to control diseases (classical swine fever, wild boar). A comparison of the resulting spring population densities based on genotyping faeces showed that harvest was merely able to take approx. 50 % of assumed reproductive output for red deer and only approx. 35 % of assumed reproductive output for wild boar. Thus the current hunting practice has been denounced as an ineffective regulating tool. Reliable population estimates can be used as a calibrating tool to adjust hunting practice.