Spatial distribution of wild boar population abundance: Basic information for spatial epidemiology and wildlife management

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A B S T R A C T

The Eurasian wild boar (*Sus scrofa*) is growing in numbers and has been expanding its distribution in Europe from some decades ago. This increasing trend, in some circumstances, leads to conflicts involving several sectors, among others, agriculture damages, conservation problems and health risks. The disease-related conflicts are especially relevant; wild boar was raised as a potential host for numerous pathogens provoking economic losses to the livestock industry. In a wildlife management context, reliable indicators of wild boar abundance at large spatial scales are highly demanded. Thus, our main aim was to handle hunting bag data available for the 2006–2007 to 2009–2010 hunting seasons in order to develop a predictive model able to account for wild boar abundance in overall mainland Spain. For modelling, the response variable was the number of wild boars annually hunted per 100 km^2 in each hunting estate, as a well-established wild boar abundance index. Using data for 6280 hunting estates (∼44% of the study area), and 21 ecogeographical predictors (geography, climate and land cover), we modelled the species abundance by means of generalized linear models with a negative binomial distribution. Three analytical approaches were comparatively assessed, which differed in how the five bioregions considered in the Spanish Wildlife Disease Surveillance Scheme were considered in modelling. In terms of predictive performance on independent datasets, the approach in which five independent models were adjusted (one per bioregion) achieved the highest scores. These models were used to predict wild boar abundance in overall mainland Spain by using UTM 10 × 10 km squares (*n* = 5245) and municipalities (*n* = 8050) as territorial units, in order to enhance the representativeness of the model at national scale and their usefulness in epidemiological studies, respectively. The pattern for wild boar abundance obtained in this study enlarges the knowledge of this species in mainland Spain. The analytical procedure developed here is valuable in itself, and it can be considered to model the spatial patterns of wild boar – or other relevant species – elsewhere, which is information highly demanded for wildlife managers in general and epidemiologists in particular.

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1. Introduction

The Eurasian wild boar (*Sus scrofa*) has experienced a notable growth during the last decades in Europe, both in terms of population abundance (e.g. Sáez-Royuela and Tellería, 1986) and distribution range (e.g. Apollonio et al., 2010). The causes of its expansion are likely related to an elevated ability for occupying a wide range of habitats (e.g. Abaigar et al., 1994; Acevedo et al., 2006; Schley and Roper, 2003), its prolific reproduction (e.g. Ruiz-Fons et al., 2006) and a generalized increment of food and shelter availability for this species, which was mediated, at least in Mediterranean environments, by the abandonment of the rural areas and the traditional land uses (e.g. Acevedo et al., 2011; Merli and Meriggi, 2006), and the hunting management (Putman et al., 2011). Currently, this species is the most widespread and – generally – also the most abundant wild ungulate in Europe (Apollonio et al., 2010). But this increasing trend, in some circumstances, leads to conflicts involving several sectors, among others, traffic accidents (Lagos et al., 2012), agriculture damages (Herrero et al., 2006), conservation problems (Bueno et al., 2009) and health risks (Gortázar et al., 2007, 2010).

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The relationship between host abundance and health status has been found in numerous studies (e.g. Anderson et al., 1981). High density of wild animals (overabundance situations, *sensu* Caughley, 1981) allows an increase in the transmission of some diseases that can affect not only the fitness of the overabundant species, but also public health and livestock health, as well as the conservation of emblematic species (e.g. Gortázar et al., 2010). In this context, our target species, the wild boar, become a potential host for numerous pathogens (e.g. Ruiz-Fons et al., 2008a), most of them related to shared-diseases (Gortázar et al., 2007). Thus, wild boar has the potential to interfere with the eradication programmes of diseases in livestock. For instance, wild boar is the most important wildlife reservoir of bovine tuberculosis in the Iberian Peninsula (Gortázar et al., 2012), and its population abundance was identified as a relevant risk factor promoting higher prevalences both in wildlife (Vicente et al., 2007) and, at some extent, in cattle (Boadella et al., 2012a). Classical swine fever, the major disease causing economical losses to the pork industry, can be another example. Wild boar may play an important role in the epidemiology of this disease since they can act as a reservoir for the virus and can be a potential source of infection to domestic pigs (e.g. Aubert et al., 1994; Boklund et al., 2008; Laddomada, 2000). Reviewing this disease in wild boar, Artois et al. (2002) linked the wild boar population density to the number of cases and the virus persistence. Similarly, wild boar contact with Aujeszky's disease virus (ADV) remains stable in time in the Iberian Peninsula even after significant reduction of ADV prevalence in domestic pigs (Boadella et al., 2012b), and direct relationships were suggested between wild boar population abundance and ADV prevalence (Acevedo et al., 2007; but see Ruiz-Fons et al., 2008b). This illustrates the increasing risk wild boar pose in the final stages of ADV eradication in pigs, mainly in situations of high wild boar population density.

Under a wildlife management framework in general, and an epidemiological perspective in particular, reliable estimates for wild boar population abundance at large spatial scales are highly demanded in order to establish bases on which management schemes for both the species and the potential diseases can be sustained (Ostfeld et al., 2005). It is well known that wild boar population abundance is not easily estimated because of their complex social structure, nocturnal activity pattern and preference for dense vegetation (e.g. Cahill et al., 2003). So, indirect methods – i.e. methods in which signs of species presence (and no direct counts of animals) are used to estimate population abundance/density – were widely developed and used for this species. These methods include hunting bags analysis (Boitani et al., 1995), pellet counts (Vicente et al., 2004; Acevedo et al., 2007) and, more recently, capture–recapture approaches – for instance, by means of noninvasive genetic sampling (Ebert et al., 2010). The effort required to apply each method is highly variable and it determines their applicability to be used at large spatial scales. On the one hand, generally as sampling effort requirements increase, the method applicability at larger spatial scales decreases (Acevedo et al., 2008). On the other hand, for epidemiologists and wildlife managers, methods requiring little time, cost, and labour are preferred over more demanding methods (e.g. Acevedo et al., 2007). Thus, to estimate wild boar population abundance at large spatial scales, hunting bags statistics are the most recommendable cost-effective and suitable option (Acevedo et al., 2006; Honda and Kawauchi, 2011; Sáez-Royuela and Tellería, 1986), since information is available, and this method only requires efforts to systematically register and centralize the information into a database (see Rodríguez-Prieto et al., 2012).

Unfortunately, national/international harmonized programmes to centralize useful information for wild mammals monitoring – as hunting bag statistics – are not yet available (but see www.aphaea.eu). For instance, hunting bag data in Spain are recorded at regional level, but raw data digitalized at hunting estate
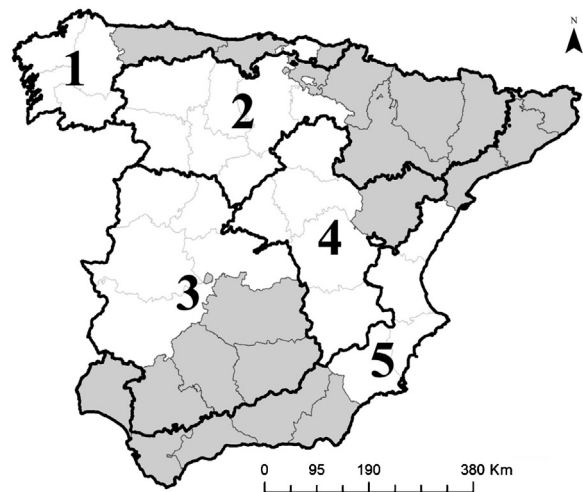

Fig. 1. Mainland Spain, with a division into five large bioregions according to the Spanish Wildlife Disease Surveillance Scheme (Internal report to the Spanish Ministry of Agriculture 2008). Provinces considered in this study are showed (in grey).

level are only available for some regions (e.g. Acevedo et al., 2011); in others only summaries at regional level are produced (e.g. Bosch et al., 2012). In this context, we aimed to manage and process the hunting bag data available for the 2006–2007 to 2009–2010 hunting seasons to develop and validate a predictive model accounting for wild boar abundance in overall mainland Spain. The spatial distribution of wild boar abundance at large spatial scale is highly demanded information potentially useful to understand the spatial epidemiology of shared-diseases, and to identify areas at higher risk for the emergence of undesirable overabundance situations leading to economical and ecological conflicts.

2. Material and methods

2.1. Study area

The study area was mainland Spain. This is situated in southwest Europe and covers 493,518 km^2 (nearly 85% of the Iberian Peninsula). Mainland Spain is divided into 47 provinces grouped in 15 autonomous communities (regions) which are the administrative units in terms of hunting regulation. Spain is a heterogeneous territory in habitat terms which determines patchy distributions and abundances of wildlife.

Based on habitat features and/or wildlife management, mainland Spain can roughly be divided into five bioregions (Fig. 1) according to the Spanish Wildlife Disease Surveillance Scheme (Internal report to the Spanish Ministry of Agriculture 2008). These bioregions were established in basis to environmental characteristics and, from an epidemiological perspective, the wild species communities and their peculiarities. Muñoz et al. (2010) described the most relevant characteristics of these bioregions. From the perspective of our target species, high abundances are achieved in Atlantic Spain (bioregion 1; Acevedo et al., 2009), distribution ranges of the species are expanding in Northern-Plateau and now is only locally abundant (bioregion 2; Acevedo et al., 2006), intensive hunting management schemes have contributed to high density populations in South-Central Spain (bioregion 3; Acevedo et al., 2007), but only moderate densities occur in the Interior mountains (bioregion 4; Acevedo et al., 2006), and, finally, wild boar is abundant mainly in the northern and southern ends in the South and East coast (bioregion 5; Rosell, 1998).