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Effects of culling Eurasian wild boar on the prevalence of *Mycobacterium bovis* and Aujeszky's disease virus

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ABSTRACT

Worldwide, failure to eradicate a disease in livestock has sometimes been related to wildlife reservoirs of infection. We describe the effects of Eurasian wild boar (*Sus scrofa*) abundance reduction through increased culling on the prevalence of two chronic infectious diseases, tuberculosis (TB) and Aujeszky's disease (AD), in a region of South-central Spain (SCS). The two infections studied responded differently to an approximately 50% reduction of wild boar abundance. Wild boar TB prevalence remained stable in control sites, whereas it decreased by 21–48% in treatment sites. In one treatment site, the annual wild boar abundance was positively correlated with the annual percentage of skin test reactor cattle. In another treatment site, red deer (*Cervus elaphus*) *M. bovis* infection prevalence decreased after culling wild boar. No significant effect of wild boar culling on wild boar ADV seroprevalence was found. The reduction in wild boar TB was achieved despite no alternative *M. bovis* host being included in the culling strategy. We advocate that culling could become a part of integrated control strategies including habitat and game management changes and vaccination, contributing to increase their success likelihood, or reducing the total expenses.

1. Introduction

Failure to eradicate a disease in livestock has sometimes been related to wildlife reservoirs of infection (e.g. Delahay et al., 2002; Corner, 2006). Therefore, there is a need to develop strategies aimed at controlling infectious disease agents in wildlife reservoirs (Wobeser, 2002; Gortazar et al., 2012). Together with vaccination, selective culling of infected animals after systematic testing is a key tool for disease control in livestock. In situations in which a wildlife reservoir is suspected to be a barrier to disease control in livestock, wildlife culling is often considered (Gortazar et al., 2007). The main aim of culling as an approach to managing disease in wildlife populations is to reduce the density of infected animals and hence diminish opportunities for transmission (Ward and Smith, 2012). However non density-dependent demographic and behavioral factors influence pathogen dynamics, and subsequently the outcome of management interventions (e.g. Carter et al., 2007; Davidson et al., 2009; Sparklin et al., 2009). Herein, we analyze the effects of culling Eurasian wild boar (*Sus scrofa*) on the maintenance of two chronic infectious diseases: tuberculosis (TB) and Aujeszky's disease (AD).

In some south-central regions of Spain, bovine TB (*Mycobacterium bovis*) remains at high herd prevalences, particularly in beef and bullfighting cattle the ones with higher infection rates (Allepuz et al., 2011). In these regions, cattle are commonly raised free-range and thus

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share habitat with wild ungulates, which show *M. bovis* infection prevalences up to 50% (Gortazar et al., 2008). Aujeszky's disease virus (ADV) serum antibody prevalence (seroprevalence) in wild boar in south central Spain (SCS) is also high (over 40%) and maintained over time (Boadella et al., 2012). Although AD is currently controlled in Spanish domestic pigs, the wild boar situation could eventually represent a threat to the success of the eradication program (Boadella et al., 2012). Therefore, information on how to reduce the high TB and AD prevalences in SCS wild boar populations is needed.

Culling native wildlife is an unpopular strategy and has to be time-flexible optimized to be efficient and sustainable (Bolzoni and De Leo, 2007). Despite this, culling has been a common tool to attempt to control infectious diseases in wildlife populations, including TB in different countries worldwide (Krebs et al., 1997; Caley et al., 1999; Corner et al., 2011).

Worldwide, little is known about the impact of culling free-ranging *S. scrofa* populations on their exposure to pathogens. Culling of the Eurasian wild boar in its native range for TB or AD control has never been reported. Some feral pig control took place in parts of the Northern Territory of Australia as a means of TB surveillance, though removal of infected cattle and buffalo largely controlled the problem (McInerney et al., 1995). Control of classical swine fever (CSF) by shooting wild boar has been attempted in France, Germany and Italy. There is evidence that this measure was much less effective than expected (Laddomada, 2000). Due to the ecological elasticity of the wild boar (i.e. increased turnover due to compensatory reproduction which enhances disease persistence), the population may be quickly re-established and the threshold level for infection die-out may not be reached after culling (Guberti et al., 1998; Artois et al., 2002; EFSA, 2009).

Since wild boar abundance is a known TB and AD risk factor (Gortazar et al., 2006; Vicente et al., 2007), we hypothesized that culling would reduce the infection or the prevalence of both diseases, particularly among the younger age classes whose rapid turnover make age-specific prevalence rates a proxy for incidence (Wobeser, 1994). To challenge this hypothesis, we used information on three instances where SCS wild boar populations were reduced by different means. The aims of this observational study were (1) to quantify the changes of TB and AD prevalence after increased wild boar culling in three sites of SCS; (2) to compare TB and AD prevalence between sites with an intervention and sites without intervention; and (3) to assess the potential association between wild boar abundance reduction and the TB status of sympatric host species such as cattle, red deer (*Cervus elaphus*) and fallow deer (*Dama dama*).

2. Material and methods

2.1. Study sites

South-central Spain is unique by having a growing hunting industry in a Mediterranean ecosystem (Acevedo et al., 2007). This region is characterized by severe summer droughts and an intense management of game species (mainly red deer and wild boar) by fencing and feeding. However, high densities and high disease prevalences (including TB) also occur in protected areas in the absence of management for hunting, possibly because of the over-abundant wild ungulate populations (Gortazar et al., 2008). These factors promote the aggregation of animals at watering sites, for example, facilitating contact between individuals and among species. This study included 13 sites within SCS where data was available from 2000 to 2011. Ten sites were used as controls and three as treatment sites. Study sites were chosen on the basis of (1) previous knowledge of their management characteristics and (2) a representative range of management practices. Sampled sites had different characteristics and included both protected areas and hunting estates and ranged in size from 723 to 54,252 ha (Table 1). Information on wild boar abundance was available for 10 sites (9 controls and one treatment site, site 8) through the presence frequency of wild boar faecal droppings on transects (FBII; Acevedo et al., 2007). In a second treatment site (site 4) this information was not available, but direct wild boar counts converted into kilometric abundance indices (KAI) were available, instead (http://www-rbd.ebd.csic.es/Seguimiento/mediobiologico.htm). Due to access restrictions, no abundance information was available for the remaining treatment site (site 9) and one control site.

Treatment sites had a substantial reduction in wild boar abundance. Site number 4 (54,252 ha) implemented a more intense and year round wild boar culling strategy in 2008 by shooting, due to high TB prevalences reported in this species (Gortazar et al., 2008). Site 8, a private fenced estate of 723 ha, reduced wild boar abundance commencing in 2005 by hunting all the available wild boar (through increased drive hunts and stand hunting during the hunting season) with the purpose of eliminating the entire wild boar population. Site 9 (2690 ha) started to capture and move to an adjacent estate all females and part of the young wild boar in 2005 in order to raise only large trophy males. Sympatric ungulate species were not subject to increased harvest in any of the treatment sites.

Data on the prevalence of TB-compatible lesions in red deer were available for 8 control sites. Lesion prevalence constitutes a good proxy for TB prevalence in red deer, although sensitivity and specificity is unknown (Vicente et al., 2006; Carta et al., 2012). Both for sites 4 and 8, data on TB-compatible lesions and *M. bovis* culture prevalences were available for sympatric ungulate species. Additionally in site 4, data on the TB skin testing results of cattle (Gortazar et al., 2008), was available for the period 1994–2011. Cattle skin testing sensitivity and specificity are estimated at 84% and 97%, respectively (de la Rua-Domenech et al., 2006).

2.2. Animal sampling

Data on 2428 hunted wild boar sampled for routine sanitary surveillance from 2000 to 2011 was obtained (Table 2). Sex was known for 2289 animals (1192 females, 1097 males). Age-classes of biological meaning (according to reproductive and social status) were defined. Based on