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Is targeted removal a suitable means for tuberculosis control in wild boar?

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ABSTRACT

We assessed the suitability of targeted removal as a means for tuberculosis (TB) control on an intensely managed Eurasian wild boar (*Sus scrofa*) hunting estate. The 60 km^2 large study area included one capture (treatment) site, one control site, and one release site. Each site was fenced. In the summers of 2012, 2013 and 2014, 929 wild boar were live-captured on the treatment site. All wild boar were micro-chipped and tested using an animal side lateral flow test immediately after capture in order to detect antibodies to the *Mycobacterium tuberculosis* complex (MTC). The wild boar were released according to their TB status: Seropositive individuals onto the release site (hunted after summer), and seronegative individuals back onto the treatment site. The annual summer seroprevalence of antibodies to the MTC declined significantly in live-captured wild boar piglets from the treatment site, from 44% in 2012 to 27% in 2013 (a reduction of 39%). However, no significant further reduction was recorded in 2014, during the third capture season. Fall-winter MTC infection prevalence was calculated on the basis of the culture results obtained for hunter-harvested wild boar. No significant changes between hunting seasons were recorded on either the treatment site or the control site, and prevalence trends over time were similar on both sites. The fall-winter MTC infection prevalence on the release site increased significantly from 40% in 2011–2012 to 64% in 2012–2013 and 2013–2014 (60% increase). Recaptures indicated a persistently high infection pressure. This experiment, the first attempt to control TB in wild boar through targeted removal, failed to reduce TB prevalence when compared to the control site. However, it generated valuable knowledge on infection pressure and on the consequences of translocating TB-infected wild boar.

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1. Introduction

The primary means to control non-vector borne infections shared with wildlife include preventive actions, host population control and vaccination (Gortázar et al., 2015). However, wildlife disease control often consists of an intervention in natural ecosystems and is, as such, controversial (Artois et al., 2001).

One potential socially acceptable wildlife disease control strategy that is employed as an alternative to random culling (also called population control) is selective culling. Selective culling is similar to the test and cull schemes used with domestic animals. These schemes are, however, expensive, and their feasibility depends on access to the animals, the availability of convenient sensitive and specific diagnostic tests, the prevalence of the infection and the spatial distribution of the target population (Gortázar et al., 2015). Random and selective culling strategies are more likely to succeed in isolated populations than on large geographical scales, and the results will probably consist of a certain reduction in disease prevalence in the wildlife host and in the domestic host targeted, rather than in the total eradication of the infectious agent. The success of a culling scheme will also depend on the attributes of the specific infectious agent targeted (Boadella et al., 2012).

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In the Iberian Peninsula, intense Eurasian wild boar (*Sus scrofa*) management is characterized by supplementary feeding, fencing and translocation, often including piglet weaning in an attempt to reduce piglet mortality. Increased densities and aggregation cause a high prevalence of infection by members of the *Mycobacterium tuberculosis* complex (MTC), which are the causative agents of animal tuberculosis (TB) (Acevedo et al., 2007; Vicente et al., 2013). In this context, it has been shown that random wild boar culling may contribute to reducing wild boar TB prevalence, with positive effects on sympatric ruminants (Boadella et al., 2012). However, given that wild boar have an economic and cultural value for the hunting community in Spain, an intensive random culling program is unlikely to be supported (Boadella et al., 2012; Cowie et al., 2015). In addition, the recent development of an animal side lateral flow test that detects MTC antibodies in wild boar serum (Boadella et al., 2011) provided the opportunity to selectively cull infected wild boar, thereby enabling a more targeted approach to control, which would also be more acceptable to the hunting community (Cowie et al., 2015).

Rather than culling, we assessed the suitability of targeted removal as a means to carry out TB control on intensely managed wild boar hunting estates. We hypothesized that selectively removing seropositive wild boar from one hunting estate and harvesting them by hunting on the release site would result in a progressive decrease in TB prevalence as compared to a control site. We also expected that culling by hunting would counteract the adverse consequences of releasing seropositive animals onto the release site.

2. Material and methods

2.1. Study area

The study area, a 60 km^2 large private hunting estate, is divided into three sites. Each one is surrounded with game species-proof fencing, signifying that it is possible to differentiate the populations. There are no badgers (*Meles meles*) on the study site, and red deer (*Cervus elaphus*) TB prevalence is low (<5%). Wild boar MTC infection prevalence (based on culture) had been recorded since 2011 during the annual hunting events, resulting in a mean MTC infection prevalence of 57% (80 of 141 samples tested). In 2011, prevalence was similar on two sites (66–68%), but lower on the third one (37%). The details of hunting data per season from 2011 to 2014 are presented in Table S-1. We used this data as a basis to define one treatment site (30 km^2, initial prevalence 68%, captures and release of seronegative wild boar), one control site (17 km^2, initial prevalence 66%, no capture and testing), and one release site (13 km^2, initial prevalence 37%, release of seropositive wild boar; Fig. S-1).

2.2. Data collection and analysis

All animal handling was carried out by personnel from the hunting estate. In summer (May–September) 2012, 2013 and 2014, gamekeepers live-captured-recaptured a total of 929 wild boar (604 piglets, 325 older animals) by means of cage traps followed by safe physical restraining devices. All live-captured wild boar were micro-chipped and tested for antibodies to MTC using an animal side lateral flow ELISA (ChembioDPP Vet test, New York, USA). This test has: a running time of 20 min; a sensitivity close to 90% in adult wild boar, and a high specificity (90.4%) (Boadella et al., 2011). However, it has a lower sensitivity (61.5%) in the case of wild boar piglets (Che'Amat et al., 2015). Juvenile and adult wild boar were immediately released according to their TB status: Seropositive individuals onto the release site and seronegative individuals back into the capture area, with both sites being subjected to routine hunting in fall-winter.

Seronegative and seropositive piglets were separated and kept in captivity (weaning) until their release in November. Those individuals that re-tested as seropositives were again moved to the release sites, and seronegative individuals went back into the capture area (Table 1; Time-space schematic flow as in Fig. S-2). The aim of releasing seropositive animals onto the release sites was to keep them enclosed until the routine hunting season. This was expected to increase the chances of eliminating the infected animals by hunting, thereby producing a profit rather than the loss caused by culling.

Background data on wild boar abundance and spatial aggregation were obtained yearly in September, i.e., after the annual summer captures, by applying the method based on recording fecal dropping abundance and distribution on linear transects, as described in Acevedo et al. (2007) (Table S-2).

All hunter-harvested wild boar were sampled in fall and winter. Sex and age-class were recorded (age based on tooth eruption: yearling if borne that season; subadult if between 12 months and 2 years of age; adult if over 2 years of age). Pooled tissues were cultured for MTC as in Che'Amat et al. (2015).

Sterne's exact method was used calculate 95% confidence intervals (CIs) of apparent prevalence, while we used Fisher's exact tests (STATISTICA 9.0 software, version 7.1., StatSoft, Inc, www.statsoft.com) in order to compare prevalence figures for a given age class or site before and after management measures were implemented.

3. Results

Capture and release data for all years are described in Table 1. A total of 228 piglets and 182 older wild boar were captured on the capture site in summer 2012. While it was not possible to know the real number of wild boar present, this capture figure represents a confirmed minimum summer density of 13.67 wild boar per square kilometer in summer 2012. The annual summer seroprevalence of antibodies to the MTC declined significantly in live-captured wild boar piglets from the capture site, from 43.86% (±6.44) in 2012 to 26.74% (±6.34) in 2013 (a 39% reduction in seroprevalence). However, no significant further reduction was recorded in 2014 (33.33% ±7.12) during the third capture season. In older wild boar, the summer 2012 seroprevalence (70.3%) increased significantly to 85% in 2013, with no changes in 2014 (Fig. S-3).

Fall-winter MTC infection prevalence was calculated on the basis of culture results obtained from 345 hunter-harvested wild boar from all study sites (Fig. 1 and Table S-1). No significant changes between hunting seasons were recorded on either the capture site or the control site, and prevalence trends over time were similar on both sites. However, on the release site, the seasonal fall-winter MTC infection prevalence increased significantly in (subadult and adult) hunter-harvested wild boar, from 33.3% in 2011–2012 to 60.3% and 70.0% in 2012–2013 and 2013–2014, respectively (Table 1 and Fig. 1).

In total, 14 recaptures of originally seronegative wild boar were recorded on the capture site during the study period. Of these, 10 had tested negative at piglet age, and were re-tested one year later. Eight of these ten (80%) had already seroconverted. One piglet was recaptured two years later, and it had also seroconverted. Finally, three adults were negative at the first capture in summer 2012, and two had seroconverted two years later. A total of 17 additional recaptures (7 in 2013 and 10 in 2014) were of animals that had tested positive at the first capture. These had supposedly been translocated to the release sites, but were actually hunted or live-recaptured on the capture site.

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