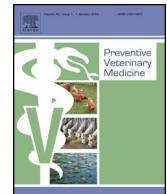




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Farm-level risk factors for the occurrence, new infection or persistence of tuberculosis in cattle herds from South-Central Spain

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ABSTRACT

Eradication of tuberculosis (TB) in cattle is a priority in the EU. However, and despite the resources invested, TB eradication is still a goal yet to be accomplished. As a consequence, the identification of risk factors contributing to TB transmission and persistence is key to a better understand and, ultimately, more cost-effectively control and eradicate this complex zoonotic disease worldwide. This study aimed to identify the factors contributing to the TB occurrence, new infection, and persistence in one of the most TB-prevalent regions in the South-Central part of Spain (SCS), Ciudad Real (CR), and for which high quality and detailed information on cattle and wild ungulate demographics, management, and sanitary status was available for up to 5 years (2007–2011). Multilevel logistic modeling was used for this purpose. Results of this study revealed that the risk for TB (occurrence, new infection, and/or persistence) in cattle herds from CR is related to TB-persistence on farm in previous years, extensive production systems (beef and bullfighting being more risky than dairy) and large farm in terms of cattle number. Also, the presence and proximity of fenced hunting estates (which are usually intensively managed) significantly contributed to the risk of TB occurrence and persistence in CR. This association suggests that wild ungulates may play a role as TB-reservoirs and transmit TB to cattle in the CR, a region where TB is endemic and is associated with extensive farming of beef cattle. To the best of author's knowledge this is the first study to (i) evaluate the wild ungulate-domestic interface at a farm level using detailed information over an extensive region and period of time (2007–2011) and (ii) to identify a direct association between TB in cattle and the proximity and management practices of wild ungulates. Methods and results presented here may support policies to better prevent and control TB in the SCS and in other regions/countries with similar epidemiological conditions.

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1. Introduction

Tuberculosis (TB), caused by *Mycobacterium tuberculosis* complex (MTC), particularly *Mycobacterium bovis* and *Mycobacterium caprae*, is a zoonotic bacterial disease that affects a wide range of domestic and wild species all over the world (Alexander et al., 2002; Palmer, 2007; Humblet et al., 2009; Smith et al., 2011). Although TB eradication has

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been a major objective for developed countries in the last decades, this goal has yet to be realized (Reviriego Gordejo and Vermeersch, 2006; Schiller et al., 2011). Despite the enormous resource allocation and investment for TB eradication, some countries such as the United Kingdom (UK) (particularly in the South West of England) are experiencing an increase in endemic TB, whereas, in other countries, such as France or Germany, it is an emerging disease problem (Schiller et al., 2011; DEFRA, 2012; <http://www.bovinetb.info/>).

In Spain, the overall TB-tendency is a slow decrease in herd prevalence, but some regions have higher (>3%) prevalence despite the intensive and costly (€34.7 million during 2011) eradication program in place (MAGRAMA, 2012). TB is especially prevalent in South Central Spain (SCS), where wild ungulates, particularly Eurasian wild boar (*Sus scrofa*) and red deer (*Cervus elaphus*) play an important role as TB reservoirs (e.g. Vicente et al., 2006; Gortázar et al., 2011a). Tuberculosis in Eurasian badgers (*Meles meles*), which has also been reported in Spain since 2008, is not a factor for TB transmission to cattle in Southern Spain (Sobrino et al., 2008; Balseiro et al., 2011). However, recent research suggests that TB transmitted by badgers should be explored more fully as a reservoir for cattle TB in Spain (Payne et al., 2012). In Spain, recent BTB research has been mainly focused on molecular epidemiological studies and on the assessment of the role of wildlife species as reservoirs of BTB (e.g. Aranaz et al., 2004; Gortázar et al., 2005; Parra et al., 2005). One study (Allepuz et al., 2011) explored the spatial variation of BTB risk of being positive, new positive or persistently positive, as well as the risk of eliminating BTB in positive herds throughout Spain (from 2006 to 2009), showed that persistence of BTB positive herds, and herds located in the central, western, and southwestern part of the country had a higher risk of TB exposure. The authors suggested that two different kinds of underlying factors could be related to the risk of new BTB positive herds or to the persistence of BTB positive herds: (i) short-latency factors such as changes in the surveillance system, the diagnostic procedures, personnel involved in BTB testing or inspection of field activities, or (ii) factors that are constant, such as contact with infected wildlife, herd management or herd size. A specific approach to areas where factors designated as (ii) above may predominate is needed to identify associations for TB exposure in cattle (Rodríguez-Prieto et al., 2012). It is important to note that in the Mediterranean farming habitats across southern Iberia there is a trend for private livestock farms to become hunting estates (Delibes-Mateos et al., 2009), where wild and domestic ungulates congregate in the same geographic area. Interactions between wildlife and livestock create risks for disease transmission (Phillips et al., 2003; Kuiken et al., 2005), which increase when animals congregate and share resources (Miller et al., 2003; Wobeser, 2009).

In recent years, many risk factors for TB occurrence at an individual/animal, herd and regional/international level have been identified (see Humblet et al., 2009 for a comprehensive review). As an example, in the UK and New Zealand, some studies described the association between movement of animals, herd size, management practices and/or badger presence and TB occurrence (Gilbert et al.,

2005; Porphyre et al., 2008; Gopal et al., 2006). Similarly, a recent Belgian study described the previous (i.e. historical) occurrence of TB in the herd, proximity of an outbreak, cattle density and cattle movements as main risk factors (Humblet et al., 2010). Proximity and contact with wildlife species has been suggested to play an important role in TB transmission (Humblet et al., 2010; Allepuz et al., 2011; Rodríguez-Prieto et al., 2012), and was reinforced when the same MTC spoligotypes of cattle was identified in some wildlife species (Aranaz et al., 1996; Gortázar et al., 2005).

In Spain there is still a lack of knowledge and controversy regarding (1) the risk primary factors that contribute to TB transmission and spread under the different and, complicated, epidemiological scenarios; (2) the role different wildlife species play in TB maintenance and transmission to domestic animal populations; and (3) the most cost-effective control and eradication measures that should be implemented, given the apparent lack of effectiveness of some of the strategies currently in place (MAGRAMA, 2012; Reviriego Gordejo and Vermeersch, 2006).

The study presented here is intended to explore the potential risk factors for TB occurrence, new infections and persistence in cattle farms from one of the most problematic and TB-prevalent regions in SCS, the Ciudad Real (CR). We were particularly interested in evaluating the factors associated TB in cattle at the wild ungulate-domestic interface.

2. Methods

2.1. Study area

We performed the study in CR (37°13'48" N to 39°31'43" N in latitude; 2°25'54" W to 6°34'06" W in longitude; area of 19,813 km²). This province is flanked by two important mountainous zones, the Toledo Mountains to the North and Sierra Morena to the South, which are contiguous with the Guadiana river valley, a fragmented Mediterranean agriculture habitat (Fig. 1). Ciudad Real is a high ungulate dense area, comprised of cattle and small ruminant farms, hunting estates, and natural protected areas. Big game hunting is practiced in Mediterranean forests/scrublands (primarily oak trees *Quercus* spp.), that are interspersed with typical agroforestry systems called "dehesas" (savannah-like habitats, 3.1 million ha in Spain; Moreno and Pulido, 2008) that are mainly devoted to livestock farming. In this region, red deer and wild boar (and fallow deer to a lesser extent) may exist as 'managed' populations which remain within large fenced hunting estates, and these wild ungulates are maintained at high densities with supplementary feed provided. In contrast, 'unmanaged' wild ungulate populations occur in open (i.e. no fence) estates where they are free-ranging and not managed for hunting with no supplementary feeding. In summary, a complex epidemiological scenario exists in CR, with coexistence of wild and domestic ungulates under diverse management practices and is one of the provinces that has traditionally high levels of TB herd prevalence and incidence in Spain (Allepuz et al., 2011; MAGRAMA, 2012). For that reason, and because detailed

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