



## Spatially explicit modeling of animal tuberculosis at the wildlife-livestock interface in Ciudad Real province, Spain



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### ABSTRACT

Eurasian wild boar (*Sus scrofa*) and red deer (*Cervus elaphus*) are the most important wildlife reservoirs for animal tuberculosis (TB) caused by the *Mycobacterium tuberculosis* complex (MTC), in Mediterranean Spain. These species are considered to play an important role in the transmission and persistence of MTC in cattle in some regions; however the factors contributing to the risk of transmission at the wildlife-livestock interface and the areas at highest risk for such transmission are largely unknown. This study sought to identify geographic areas where wildlife-livestock interactions are most likely to occur and to characterize the environmental and management factors at this interface contributing to persistence, incidence, and occurrence of TB on cattle farms, in one of the provinces with higher TB prevalence in Spain, Ciudad Real. We used spatially explicit, ecological niche models to evaluate the importance of factors such as wildlife demographics and hunting management, land use, climatic, and environmental variables as well as TB status in wildlife for TB breakdown (model 1), persistence (model 2) and new infection (model 3) on cattle farms and to generate high resolution maps of predicted TB occurrence to guide risk-based interventions. Models revealed that land use, particularly open area and woodland, high wild boar TB prevalence, and close proximity to fenced hunting estates were the most important factors associated with TB infection on cattle farms. This is the first time that local TB prevalence in wild boar for individual hunting estates has been significantly associated with TB occurrence on cattle farms at a local scale. Prediction maps identified two areas with high likelihood of TB occurrence in the southwest and northwest of the province where wildlife-livestock interactions and TB occurrence are highly likely and where TB preventative and mitigation strategies (e.g. targeted vaccination, increased biosecurity, etc.) should be prioritized. Methods and results of this study were aimed to inform the implementation of risk-based interventions to better prevent and control TB at the wildlife-livestock interface, a necessary step for the successful eradication of TB in cattle in Spain.

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### 1. Introduction

Animal tuberculosis (TB) is a disease of livestock, wildlife, and humans, with significant health and economic impacts around the world. It is caused by the *Mycobacterium tuberculosis* complex (MTC), which includes *Mycobacterium bovis* and *Mycobacterium caprae* (Palmer et al., 2012; Martínez-López et al., 2014). Transmission occurs both directly through respiratory and oral contact and indirectly through fecal and oral secretions, especially at

shared food and water sites (Menzies and Neill, 2000; De Garine-Wichatitsky et al., 2013). A compulsory national eradication program in Spain has been in place for over 30 years and consists of testing and culling cattle (Reviriego Gordejo and Vermeersch, 2006). The program has successfully reduced TB herd prevalence in cattle from 12.0% in 1987, to 1.7% in 2008 nationally (Gortázar et al., 2011). However recently progress has stalled and national prevalence decreased only from 1.7% only to 1.3% by 2011 (García-Saenz et al., 2014; Martínez-López et al., 2014). This plateau in TB eradication Spain is mostly associated with the persistence of disease in a few high-prevalence regions (Vicente et al., 2013; Martínez-López et al., 2014), mostly located in south-central Spain (SCS) (Gortázar et al., 2011). From 2007 to 2011, 35.8% of farms in Ciudad Real

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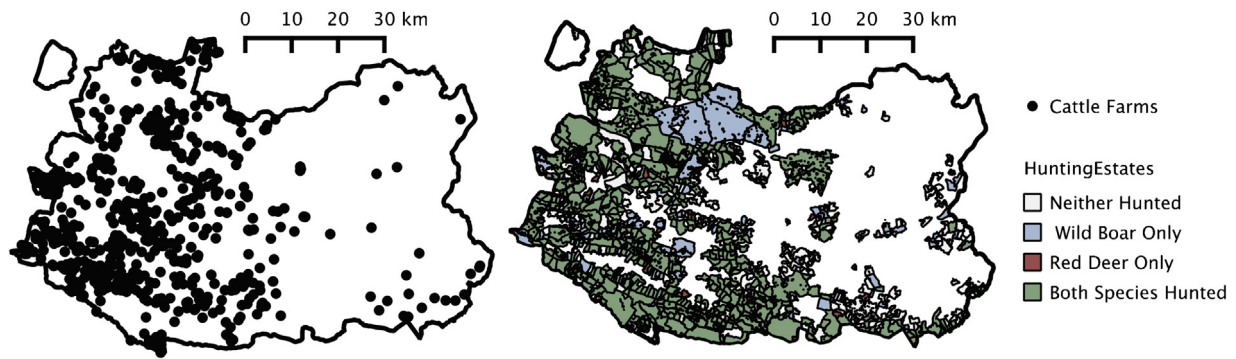


Fig. 1. Maps of the locations of (a) farm centroids and (b) hunting estates in Ciudad Real province. Hunting estates are classified by the animals they hunted during 2007–2011.

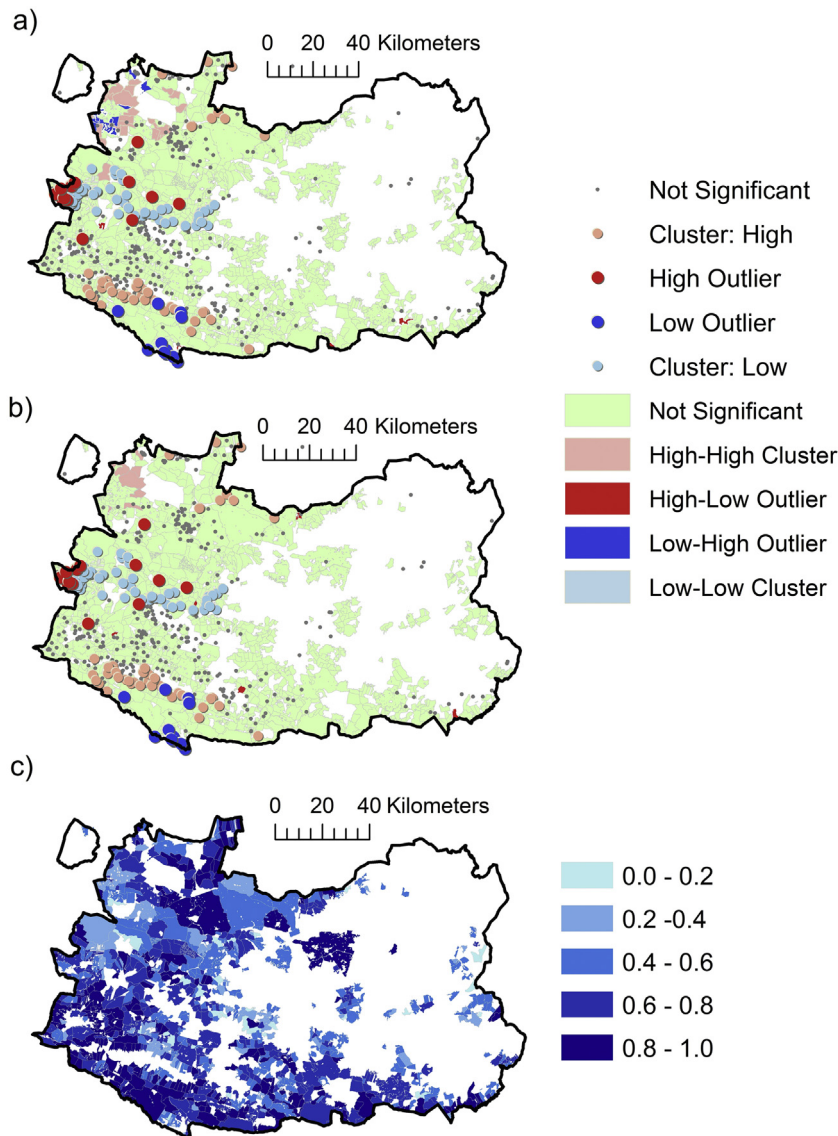


Fig. 2. Local Moran's I cluster analysis for total TBL prevalence from 1998 to 2015 for wild boar (a) and red deer (b) overlaid with a local Moran's I cluster analysis for persistence farms between 2007 and 2011 (a and b). Points represent the analysis of farms and polygons are of hunting estates (wildlife). Farms and estates not part of clusters are included as non-significant values. (c) Predicted TB prevalence by necropsy in wild boar from the TB model. Darker areas represent areas of higher predicted prevalence.

province, which is located in SCS, were positive in one or more years (Martínez-López et al., 2014), and at least 50% of positive farms were newly positive (i.e. negative in the prior year) (García-Saenz et al., 2014). A major factor for the persistence of TB is believed to

be wildlife reservoirs, especially Eurasian wild boar (*Sus scrofa*) and red deer (*Cervus elaphus*) in SCS Mediterranean habitats (Gortázar et al., 2012; Vicente et al., 2013).

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