



Original Research

Spatio-temporal variability of bovine tuberculosis eradication in Spain (2006–2011)



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ARTICLE INFO

Article history:

Received 25 July 2013

Revised 14 May 2014

Accepted 6 June 2014

Available online 19 June 2014

Keywords:

Bovine tuberculosis

Space–time analysis

Risk factor analysis

Spain

INLA

ABSTRACT

In this study we analyzed the space–time variation of the risk of bovine tuberculosis (bTB) in cattle between 2006 and 2011. The results indicated that at country level, there were no significant temporal changes between years, but, at county level bTB evolution was more heterogeneous. In some counties, between some years, the prevalence and the incidence of the disease was higher as compared to the global rate in the rest of the counties of Spain.

The analysis of potential risk factors indicated that both, a large number of movements from counties with high incidence (>1%), and presence of bullfighting cattle herds increased bTB risk. Red deer abundance, number of goats and number of mixed cattle–goat farms were not significantly associated with the prevalence/incidence of bTB.

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1. Introduction

Bovine tuberculosis (bTB) is a chronic infectious disease of cattle (including all *Bos* species, and *Bubalus bubalus*) and bison (*Bison bison*) caused by any of the disease-causing mycobacterial species within the *Mycobacterium tuberculosis*-complex (Anon, 2013). Cattle are mainly affected by *Mycobacterium bovis* and *Mycobacterium caprae* which can also affect other domestic and wild animals as well as humans (Aranaz et al., 2004; De la

Rua-Domenech et al., 2006). Due to its zoonotic nature and the high economic impact in livestock production, eradication of bTB in the EU is the final target (Reviriego and Vermeersch, 2006) through the development of bTB eradication programs.

In Spain, the first official bTB testing was performed in 1950 in a dairy herd in the north of Spain, but it was not until 1993 when most dairy and beef herds were included in the national control program. During the application of this program, mainly based on intradermal tuberculin testing (IDT) and culling of reactor animals, the cattle herd prevalence has decreased from 5.9% in 1993 to 1.3% by the end of 2011 (Anon, 2012). Despite that important progress, during the last 12 years, the herd prevalence in Spain has only declined from 2.5% in 2000 to 1.3% in 2011, and the herd incidence has been fluctuating between 0.8% and 1.0%.

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Spatio-temporal disease mapping models are a useful tool to describe the pattern of diseases and to identify regions with unusual levels of disease, time trends or both (Meliker and Sloan, 2011; Schrödle and Held, 2011). Moreover, space–time models can contribute to the assessment of the stability of the risk of infection, which cannot be evaluated just by spatial models (Abellan et al., 2008). When analyzing the observed counts of disease within different areas for a sequence of time periods, four groups of components can be considered (Lawson et al., 2003): (i) the spatial structured component: due to area-specific risk factors such as contact with infected wildlife, (ii) the unstructured spatial component: due to characteristics of the farms within the counties (e.g., herd size or livestock rearing practices), (iii) the temporal component: due to time risk factors such as national changes in the national eradication program, and finally (iv) the space–time component: due to time-area specific risk factors, such as changes between years in the counties due to new personnel, diagnostic procedures or movements of animals. These different levels of variability can be accounted for by the use of multilevel (i.e., hierarchical) models (Beale et al., 2008). Moreover, the decomposition of the risk variability by using different (and appropriate) random effects allows the formulation of hypotheses about the role of factors potentially related to the risk of infection at different levels.

In a previous analysis of the variability of the geographical risk of bTB infection across Spain, it was evidenced that counties located in the central and south of Spain had a risk more than three times higher than the rest of the country (Allepuz et al., 2011). However, in that study the temporal evolution of the disease across areas was not assessed. Furthermore, specific explanatory variables were not included in the model so their relationship with the risk of bTB could not be quantified.

The objective of the present work was to analyze the space–time variation in the risk of bTB in Spanish cattle between 2006 and 2011, and to identify factors related with the variability of the risk of infection.

2. Materials and methods

2.1. Data management

For the period 2006–2011, annual data at county level, of the total number of herds stratified by type (dairy, beef or fighting bulls), disease status (i.e., herds that became positive/new positive), number of cattle-goat mixed herds, number of goat farms and animal movements, were provided by the Spanish Ministry of Agriculture, Food and Environment (MAGRAMA).

The abundance of red deer (*Cervus elaphus*) in Spain was obtained from Acevedo et al. (2010) at Universal Transverse Mercator (UTM) $10 \times 10 \text{ km}^2$ grid cells. This variable was aggregated at county level by calculating the average abundance of the different cells that intersected with the county. This data aggregation was carried out through Quantum GIS (Quantum GIS Development Team, 2012) by joining the attributes based on their spatial location.

For each year, three variables related to animal movement were created by using R version 2.15.1, (R Development Core Team, 2008) and the 'statnet' package (Handcock et al., 2003): (i) in-degree at county level, i.e., the number of contacts that a given county received from other counties (ii) in-degree at herd level, i.e. the number of movements that a given herd from a given county received (including intra-county movements), and (iii) weighted in-degree, i.e. the total number of cattle received by a given herd in a given county (including animals from intra-county herds).

In addition, for each of these movement-related variables, a differentiation was made between high risk movements (e.g., in-degree from counties with an incidence $>1\%$), and low risk movements (e.g., in-degree from counties with an incidence $\leq 1\%$), resulting in a total of six explanatory variables.

Even though all information was provided on an annual basis, all explanatory variables were included into the model as fixed effects, which imply that the value of each of these variables remained the same during the years.

Moreover, in order to avoid problems derived from non-linear relationships with the dependent variable and the possible concurrency between explanatory variables and random factors (Saez M.; Personal communication), all explanatory variables were categorized before including them in the model. For this purpose, a reclassification into four categories following their quartile distribution was carried out. In the cases of red deer abundance and number of mixed cattle-goat farms, as their first quartile was zero, they were also divided into four categories, but the first one included all the zeroes, and the remaining values were divided into terciles. In addition, as half of the values of bullfighting cattle were zeroes, this variable was included as dichotomous (absence and presence). The distribution of the explanatory variables after categorization is shown in Table 1. Figs. 1 and 2 show the spatial distribution of the categorized explanatory variables included in the model.

2.2. Model specification

We assumed that the total and the new bTB positive herds at county level followed a Poisson distribution centered on λ_{ij} and γ_{ij} , respectively, being i the county (i.e., $i = 1$ to 483) and j the year (i.e., $j = 2006$ to 2011):

$$\lambda_{ij} = P_{ij} \times H_{ij}$$

$$\gamma_{ij} = I_{ij} \times H_{ij}$$

where, P_{ij} and I_{ij} are the prevalence and incidence respectively, and H_{ij} the total number of herds, in each county and year.

Due to the hierarchical structure of the data (i.e., space, time and space–time), a generalized linear mixed model (GLMM) approach was implemented (Zuur et al., 2009). Within the Poisson regression and GLMM context, \hat{P}_{ij} and \hat{I}_{ij} were parameterized as a function of random and fixed effects:

$$\hat{P}_{ij} \text{ or } \hat{I}_{ij} = \exp(\beta_0 + S_i + \text{eta}_i + g_i + \text{psi}_{i,j} + Z\beta)$$

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