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Analysis of the spatial variation of Bovine tuberculosis disease risk in Spain (2006–2009)

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ABSTRACT

In this study we explored the spatial variation of Bovine tuberculosis (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 by means of hierarchical Bayesian models. The results of the models showed that the risk of infection (positive or new positive herds), persistence and elimination was lower in counties located in north and north-eastern of Spain, and in the Balearic and Canary islands than in the rest of the country. In some counties the risk of positivity was high during the four years of study, whereas there were others where the risk of positivity was high only in some of the years. With regard to the risk of persistence of BTB positive herds, counties located in the central, western and south-western part of the country had a higher risk in the three studied periods. This study has identified some specific areas of increased BTB risk in Spain, information that is useful for disease management.

1. Introduction

Bovine tuberculosis (BTB) is a chronic disease of animals caused by *Mycobacterium bovis* (*M. bovis*), a member of the *Mycobacterium tuberculosis* complex (Smith et al., 2006). *M. bovis* is widespread throughout the globe and, due to its zoonotic nature (Acha and Szyfres, 2001) and the high economic impact in livestock production and in Animal Health policies, the eradication of BTB has been a major objective of farming communities and public health authorities

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over decades. In the European Union (EU) BTB has been an important issue since the European Economic Community (EEC) was constituted (Reviriego Gordejo and Vermeersch, 2006).

In Spain, between 1956 and 1964, the first legal initiative was established, with the culling of positive animals. Nevertheless, this measure did not succeed due to the high cost imposed onto the farmers. In 1965, thanks to government economical support the BTB control campaign began to be successful. This campaign was focused on dairy cattle and data obtained revealed an animal prevalence of around 20%. In 1986, when Spain became a member of the European Economic Community (EEC), national programs were reinforced and efforts were focused on increasing the testing coverage, including beef cattle. However, it was not until 1993, when the EU was established, that the BTB national eradication program included all dairy and beef cattle. Application of this program, which was mainly based on intradermal tuberculin testing of cattle and culling of reactor animals, decreased BTB prevalence from 5.9% in 1993 to 1.6% by the end of 2009. Despite these advances, BTB eradication has not yet been achieved and prevalence has remained between 1.6% and 1.8% (Anon., 2010a).

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 (Aranaz et al., 1996, 2004; Gortazar et al., 2005; Parra et al., 2005; Hermoso de Mendoza et al., 2006; Romero et al., 2008; Naranjo et al., 2008; Rodríguez et al., 2009). No epidemiological studies have attempted to describe and analyze the BTB situation in cattle herds throughout the country. In this study, we attempted to explore the spatial variation of the risk of BTB in cattle herds throughout Spain in different years, from 2006 to 2009. Such kind of studies can be carried out by the application of disease mapping methods. The objective of these studies is to provide an estimate of the true relative risk of a disease across a geographical study area in order to highlight areas of elevated or lowered risk, being useful for capture gradual regional changes (Best et al., 2005; Lawson et al., 2003; Ugarte et al., 2005). The standardized mortality/morbidity ratio (SMR) is the classic statistic used in representing disease risk when working with aggregated (e.g. county) data (Pfeiffer et al., 2008). This ratio is an estimate of the relative risk within each area (i.e. the ratio describes the odds of being in the disease group rather than the background group) (Lawson et al., 2003). It standardizes the data by re-expressing them as the ratio between the observed number of cases and the number that would have been expected in a standard population (Pfeiffer et al., 2008). National disease rate (indirect standardization) can be used to calculate the expected number of cases for each local area (Lawson and Williams, 2001). Standardized ratios are commonly used in disease map presentation, but they have some drawbacks. They are based on ratio estimators and hence can yield large changes in estimate with relatively small changes in expected value (Lawson et al., 2003). Sparsely populated areas with few (or zero) cases can generate extreme values; the variance of the standardized ratio is inversely related to the number of expected cases and therefore small populations will have large variability in the estimated rates. Moreover, these sparsely populated areas are often large administrative units, so they tend to dominate the map visually even though they produce the least-precise risk estimates (Elliot and Wartenberg, 2004). On the other hand, in spatial epidemiological studies, patterns indicating some dependence between the counts in neighbouring areas are frequently found (Richardson et al., 2004). This relates to the basic idea that locations close together in space often have similar values of outcome variables while locations far apart are often different (Lawson et al., 2003). To solve the problems associated with the overdispersion of the standardized ratios and to assess the amount of true spatial heterogeneity in order to detect areas of elevated or lowered risk, a variety of methods have been proposed (Lawson et al., 2003). For this study we have used a model-based relative risk estimation method based on Bayesian statistics and on a conditional auto regression (CAR) distribution for the spatial structure. This kind of models were proposed in the 1990s through the work of Besag et al. (1991), Clayton and Bernardinelli (1992) and Clayton et al. (1993) and are one of the most commonly used models for smoothing risks in disease mapping studies (Ugarte et al., 2005). The basic principle of Bayesian methods is that uncertain data can be strengthened by combining them with prior information (Pfeiffer et al., 2008). Within this approach, global or local (neighborhood) risk is taken as prior information and local estimates are smoothed towards the global average (where spatially unstructured heterogeneity predominates) or to the neighborhood average (where spatially structured heterogeneity predominates) (Clements et al., 2007). The model provides some shrinkage and spatial smoothing of the raw relative risk estimates that otherwise would be computed separately in each area. Such shrinkage gives a more stable estimate of the pattern of underlying risk of disease than that provided by the raw estimates (Richardson et al., 2004).

2. Materials and methods

2.1. Data

For the period 2006–2009, annual data by on the total number of herds, type of herd (beef, dairy and fighting bulls), BTB positive herds (i.e. total number of positive herds in a given year) and new positive herds (i.e. those herds negative to BTB the previous year that become positive during a given year) were provided, at county level, by the Spanish Ministry of Environment and Rural and Marine Affairs (MARM). Data at farm-level were obtained due to the implementation of the Spanish national BTB eradication program, annually approved by the European Commission for its financial support. In this context, any herd with a reactor to the single or comparative intradermal tuberculin test and/or γ-interferon test was considered a positive case of BTB (Anon., 2010b). Data was aggregated at county level by the official services of each autonomous community and send to MARM following quality standards included in Decision 2008/940/CE. Data validation was done at two levels: at county level and validation at national level. At this level, MARM validated all data sent