Original Research

A novel approach to mapping and calculating the rate of spread of endemic bovine tuberculosis in England and Wales

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ABSTRACT

A mathematical method for estimating the endemic status of bovine tuberculosis (bTB) in cattle in England and Wales has been developed.

6.25 km² hexagonal cells were used as the base resolution. Maps were produced for overlapping two-year periods spanning 2001/03 to 2009/11. Distance from a farm to the ten nearest 'Officially Tuberculosis Free status – Withdrawn' incidents within the same time period was measured. Endemic areas were defined as those hexagons containing farms where the 3rd nearest incident occurred within 7 km. Temporal spread of endemic bTB was estimated by creating a contour map displaying the spread of endemic bTB over the two-year periods, and using boundary displacement to calculate the rate of spread across each hexagon. A rate was obtained for ~2300 cells and varied between 0.04 km and 15.9 km per year (median = 3.3 km per year). This work will enable further analysis of the factors associated with this expansion.

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1. Introduction

A disease can be defined as endemic when it is constantly present in a population (Thrusfield, 2007) and persists without being reintroduced from outside (Segen, 2006). Although the numbers of herds and cattle affected by bovine tuberculosis (bTB) in England and Wales have increased epidemically since the 1980s, closer study reveals substantial areas that are affected by persistent bTB, which should more accurately be considered endemic.

It is evident from time-series maps of the spread of bTB produced using annual surveillance data that the major mode of spread of endemic bTB in England and Wales is by expansion along the edges of existing endemic areas; only rarely do isolated outbreaks become new foci of endemic disease (for example see Fig. 2 in Defra, 2011). In order to characterise the spread of endemic bTB, we first need to develop a definition of endemicity in this context, and then identify the areas which are defined as endemic and map their expansion.

This is the first time that such an approach has been taken to investigate the spatial epidemiology of bTB. Historically, the progression of bTB has been illustrated by mapping disease frequency such as incidence and prevalence or the density of animals that react to bTB testing (AHVLA, 2013). Although these maps provide valuable information about the spatial distribution of bTB, they do not discriminate between endemic disease and localised outbreaks which are unlikely to persist. Identification of

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the areas where bTB is endemic will allow better targeting of interventions to control the spread of the disease.

Developmental work explored various approaches to defining endemicity for bTB. We considered approaches using classical measures of incidence such as number of incidents per number of herds or herds tested within a grid cell; and attempts to specify for endemic disease were made by incorporating criteria such as confirmation of disease and recurrence of bTB. It was found that an approach based on proximity to confirmed disease helped eliminate sporadic incidents likely to be the result of long distance cattle movements and was therefore likely to produce the best estimates of the location of truly endemic disease.

We report a new and generally applicable mathematical method for predicting the endemic status of bTB in cattle for localities and times, and demonstrate how this method can be used to map endemic bTB and calculate the rate at which the endemic areas are expanding in England and Wales.

2. Methods

2.1. Data handling and map production

Data describing bTB testing and incidence were obtained from surveillance data recorded in the Animal and Plant Health Agency's VetNet database for nine 24 month intervals from 1st September to 31st August (to begin and end at a time when tests were least frequent) and spanning 2001/03 to 2009/11 using Microsoft Access 2003. Geographic data were processed and maps were produced in ArcGIS 10.0 (ESRI, 2011). Custom scripts were written in Python 2.6 (Python Software Foundation, 2012).

2.2. Spatial resolution

A custom script was used to generate hexagonal grids with cell sizes of 6.25 km^2 and 25 km^2. Advantages and disadvantages of hexagonal grids relative to square grids have been reviewed by Birch et al. (2007). Square grids are far more widely used than hexagonal grids, possibly because raster data and smaller grid cells can easily be aggregated into lower resolution grids. Whilst hexagonal grids are less practical in the context of data processing, they minimise the distance between points within the same cell, and all pairs of neighbouring cells share an equal length of edge, meaning that neighbouring hexagons are readily adaptable to smoothing.

2.3. Defining endemicity

Endemicity was defined in three steps. Firstly, measures related to the two key criteria of endemicity, disease presence and disease recurrence were assessed. Secondly, a range of candidate definitions of endemicity were identified to provide a new measure. Thirdly, it was necessary to identify a clear and communicable mapping solution to allow the proposed definitions to be understood, assessed and calibrated through expert and non-specialist stakeholder knowledge. The geo-processing workflow is included in the Supplementary information.

Incidents of bTB are classified as either 'Officially Tuberculosis Free status – Suspended' (OTF-S) or 'Officially Tuberculosis Free status – Withdrawn' (OTF-W). OTF-W status is obtained once disease has been confirmed at post mortem, either by the presence of lesions or through microbiological culture of the causative organism *Mycobacterium bovis.* Only OTF-W incidents were considered in the calculation of endemicity as using a more inclusive measure of 'any incident' did not discriminate between areas of sporadic and isolated disease and likely endemic areas.

Within each of the 24 month time periods, the distances from each farm holding to the nearest ten OTF-W incidents were calculated. Data were averaged by 6.25 km^2 and 25 km^2 hexagon cell and then mapped for rapid comparison of each measured distance.

From these maps it was possible to visually define a number of candidate definitions of endemicity using a combination of different distance thresholds (3, 5, 7 or 10 km) to ranked nearest incidents (1st to 10th). Examples include 10 km from the 2nd nearest OTF-W incident, or 3 km from the 3rd nearest OTF-W incident.

After investigating the outlying areas of endemicity as defined by our candidate definitions and comparing them with data from VetNet, distance to the 3rd nearest OTF-W incident was shown to be the most reliable measure of endemicity. This definition suitably omitted areas where the disease was likely to have been seeded by long distance cattle movements.

Discussions with social science collaborators revealed that maps using contour lines were more likely to be understood than hexagon values which tended to obscure patterns at farm or parish level. A series of interpolated contours showing the expansion over time of the endemic area for selected distance thresholds to the third nearest OTF-W holding were produced to communicate the results. These were generated from the hexagonal cell values using an inverse distance weighting (IDW) interpolation.

Significant efforts were made to ensure the maps were clear to all non-specialist stakeholders: only expansion (rather than contraction) was shown, towns and major roads were added to help identify locations, and colours were optimised to avoid implying risk. These maps were then used in consultation with expert Veterinary Officers (VOs) as part of the validation process outlined in the next section.

2.4. Validation of the definition of endemicity used for the maps

To assist with validation of the geospatial definition of endemicity and to determine the appropriate distance threshold to use to create the contour polygons, two methods of validation were used. The first approach consisted of a focus group in collaboration with social scientists in which VOs with local knowledge of bTB spread were consulted to obtain their view of how endemic bTB is spreading in their areas. They were shown four versions of the