

Investigating Potential Role of Deer as Vectors of Bovine Tuberculosis in England and Its Policy Implications

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Summary

Wild deer is considered as a potential vector of bovine tuberculosis (bTB) in the United Kingdom, yet the details of deer-to-cattle transmission mechanism is largely unknown. This study investigates the geographical association between deer species and the bTB incidence rates among cattle herds across England. The outcome of this study suggests that spatial distributions of deer population and bTB herd breakdown share common geographical patterns. This was confirmed through statistical testing using both global as well as local spatial statistics. It suggests that the exposure of cattle herds to wild deer population may be facilitating the spreading of bTB.

Keywords: bovine tuberculosis, deer, epidemiology, spatial autocorrelation

1. Introduction

Wild deer populations are on the rise across the UK, both in their volume and their range (Ward, 2005). This trend has led to the heightened risk of wild deer to act as spatial and temporal vectors in transmitting an epidemic such as bovine tuberculosis (bTB). In the context of bTB, badgers are generally accepted as the most common maintenance host for *M.bovis* to cattle, which in turn causes bTB infection, and inter-species transmission between deer and badger has been also confirmed (Ward *et al.* 2009). Yet, the details of the deer-to-cattle transmission mechanism of *M.bovis* bacteria remain largely unexplored (Menzies, 2008). The highly varied manifestations of bTB incidences in cattle and wild animals across the world are testament to the complex and highly locally specific spatial processes that characterise the epidemiology of bTB.

Current debate on bTB is politically driven, and it could benefit from a geographical perspective to confirm the ways in which bTB is transmitted and how they are spread across space and time. This study aims to investigate from the geographical perspective the potential role of deer as transmission vectors of bTB. It uses a previously unexplored geo-spatial data to carry out geo-spatial analysis on the distribution patterns of deer and bTB cases. Investigating how deer affects the process will help illuminate the mechanism of inter-species transmission and add insights into policy making on possible intervention against further spread, possibly through deer vaccination or culling. It also compares the pattern of distribution for bTB breakdown ratios aggregated using different areal units to see what works effectively in identifying the spread of bTB.

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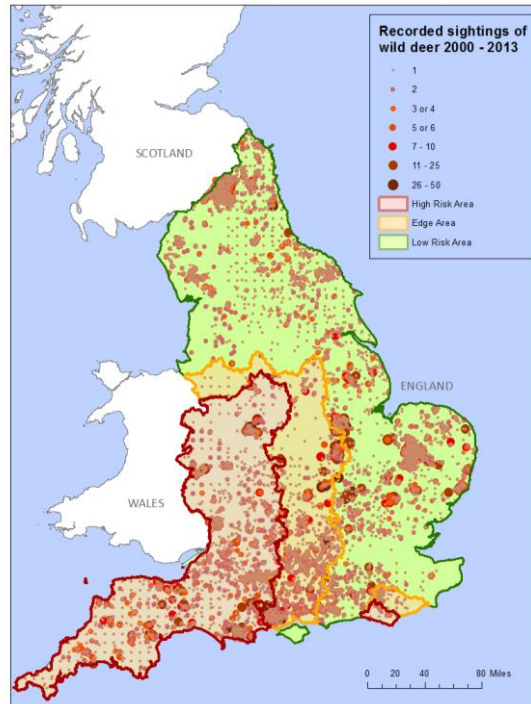


Figure 1: Recorded sightings of all species of wild deer in England (2010 – 2013), superimposed over the low bTB risk area, the edge area and the high risk area as defined by DEFRA.

2. Data

The study collected geographical data on bTB herd breakdown and deer sightings across England. UK cattle herds and their bTB statuses were supplied by the Animal & Plant Health Agency (APHA) (formerly known as AHVLA). The data were aggregated at the parish level, and also by areal units defined by major roads and railroads. Data on sightings of different deer species came from (1) the National Biodiversity Network (NBN) which covers sightings with a grid reference (mostly in 6 or 8 digits) from 2010 to 2013, and (2) British Deer Distribution Survey (BDS) which offers more comprehensive records of the individual locations for each sighting up to 2011. **Figure 1** shows the geographical locations from both datasets. The green, amber and red zones respectively show the low bTB risk area, the edge area and the high risk area, as defined by DEFRA.

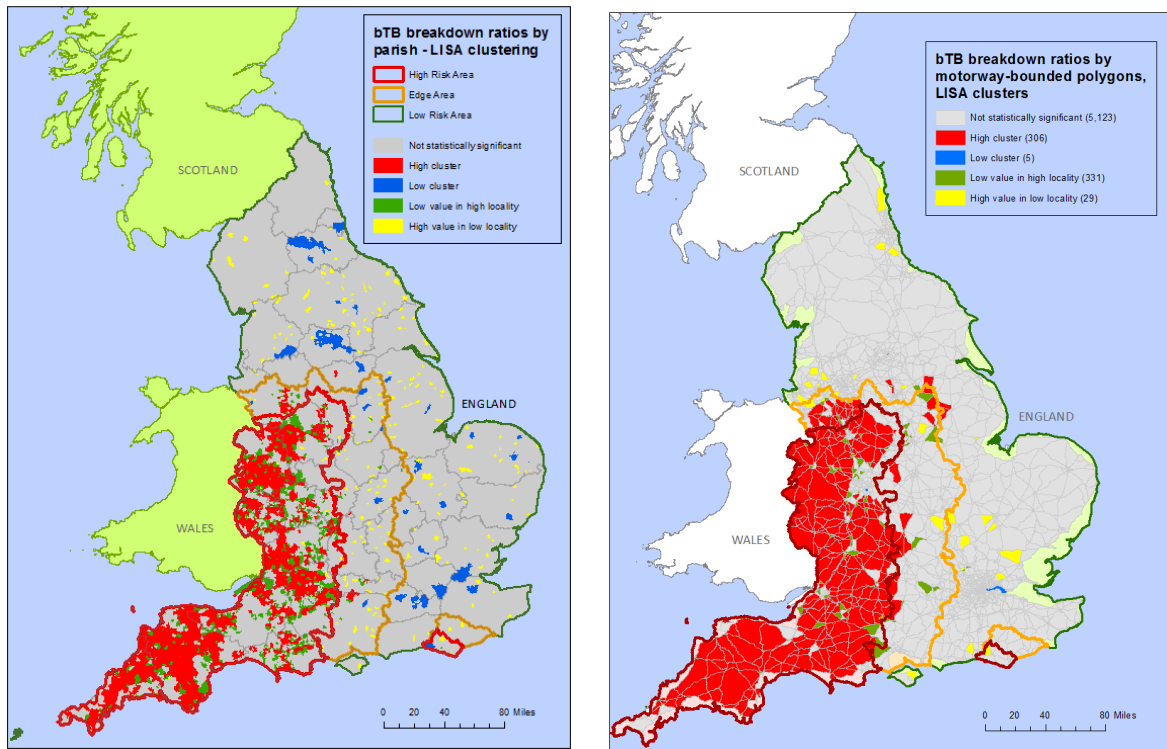
3. Analysis

In order to investigate the spatial association between the deer population and the cattle bTB breakdown ratio and also to identify a more detailed depiction of the bTB breakdown ratios, we carried out global and local analyses of univariate and bivariate spatial autocorrelation.

Application of global Moran's I on bTB breakdown ratios at the parish level revealed statistically significant spatial autocorrelation (Moran's I = 0.339, P value = < 0.001), with four types of localised clusters detected by Local Moran's I statistic (**Figure 2(a)**). It shows that areas of high bTB breakdown ratios (highlighted in red) occur almost exclusively within the high risk area. A few 'spills' found in the edge area (e.g. the high-high polygons around Sandbach and Knutsford, Cheshire, and Newbury, Hampshire) could be an early sign of expansion of the disease.

In contrast, **Figure 2(b)** shows LISA for average bTB breakdown ratios by zones bound by major roads and railroads. While the patterns shown in the two figures are similar, **Figure 2(b)** makes onward spillage more visible, and it also identifies a cluster around the north-east front line of the edge area, which may be due to MAUP. However, it also suggests that the boundaries of high/edge/low risk areas

defined by DEFRA are broadly correct but may need updating for the purpose of rendering a detailed understanding, especially if bTB breakdown continues to spread.



(a)

(b)

Figure 2: Local Moran's I analysis of bTB breakdown ratios by (a) parish for England, and (b) by areas bound by major roads and railroads.

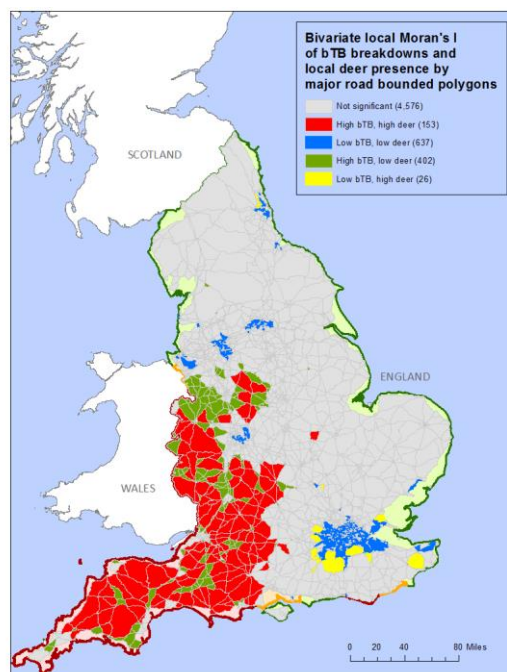


Figure 3: Bivariate LISA for average bTB breakdown ratios and deer sighting counts by areas bound by major roads and railroads.

In order to examine the geographical association between deer sightings counts and the bTB breakdown ratios, bivariate LISA was carried out. **Figure 3** shows the result of bivariate analysis that examines the similarity and difference in the spatial patterns of bTB herd breakdown ratios and local deer sightings. The areal units used in the bivariate LISA analysis were those bound by major roads and railroads, as the individual parishes were too small a scale for the deer data. It is also based on the hypothesis that major roads and railroads act as a barrier that restricts the movement of deer. In this instance, deer sightings and bTB breakdown ratios show association both globally as well as locally. Like the univariate analysis, the global autocorrelation is significant, and some patterns emerge at the local level. Some of the notable patterns found include the Low-High ‘corridors’ (green areas where low counts of deer sightings is observed but the bTB breakdown ratios are high), and the low-low polygons in London (blue areas) surrounded by areas of ‘low bTB and high deer’.

In **Figure 3**, a significant association between bTB and deer (shown in red) is found mainly in the high risk area as defined by DEFRA, which suggests that there is a certain level of contact between domestic cows and wild deer. There is also a cluster of areas of ‘high bTB and low deer sightings’ around the upper boundary of the high risk areas (shown in green). This, however, does not necessarily suggest the absence of deer population in these areas, as it may be simply due to insufficient number of reports on deer sighting. Another notable point is that there is hardly any areas with statistical significance to show ‘low bTB and high deer sightings’ (in blue) other than those surrounding London, and this is despite that there are clusters of high deer sightings counts across England (**Figure 1**). From **Figure 2**, we can surmise that the reason for the distinct lack of the blue areas is because many areas already saw some rise in bTB breakdown ratio. Based on the hypothesis stated above, it points to the danger that future contact between wild deer and domestic cows may facilitate the spread of bTB in these areas.

4. Discussion

In this study, we collected and aggregated detailed deer sighting data from multiple sources to carry out geographical analysis for the purpose of investigating the association between bTB incidences and deer population. The results suggest that these two distributions indeed share common geographical patterns, especially when aggregated to areal units confined by physical barriers of major roads and railroads that are likely to be restricting deer’s movements. The study also shows the spillover of the bTB spreading outside the current boundary of the high risk area and even beyond the edge area (red areas in **Figure 3**). Given that areas with low risks of bTB and low deer sightings (blue areas in **Figure 3**) are found only in London and around a limited parts of England, there is a potential risk of further spread of bTB across wider areas of England, infused by the contact between deer population and cattle herds.

These are preliminary results and are prone to some limitations, including the use of deer sighting data as a proxy for their distribution pattern, whilst the bTB data covers only a limited time span. The analysis also focus on the association between deer and bTB only, and it may yield further insights if other mammal species such as badgers were included in the study. Further analysis is currently ongoing, with which we hope to overcome these limitations.

5. Acknowledgements

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6. Biography

Naomi Carvey is a Data Analyst who works in the Conservation Science department at the Royal Botanic Gardens, Kew. She recently graduated from the MSc GIS programme at Birkbeck, University of London. Her research interest mainly revolves around environmental data, GIS and data presentation.

Shino Shiode is Senior Lecturer at Birkbeck, University of London where she serves as Director of the GIS programme. Her area of expertise extends to spatial epidemiology, geography of crime, as well as development of theory and methods for spatial analysis.

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7. References

Menzies F (2008). Tuberculosis in deer: Another piece in the unfinished *Mycobacterium bovis* jigsaw. *The Veterinary Journal*, 175, 287-288.

Ward A I (2005). Expanding ranges of wild and feral deer in Great Britain. *British Deer Society Mammal Review*, 35, 165-173.

Ward A I, Smith G C, Etherington T R, Delahay R J (2009). Estimating the risk of cattle exposure to tuberculosis posed by wild deer relative to badgers in England and Wales. *Journal of Wild Life Disease*, 45, 1104-1120.