Department for Environment, Food and Rural Affairs

TB surveillance in wildlife in England

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Overview

TB surveillance was conducted in badgers in nine badger control areas in the High Risk Area[1] of England in 2016, and in both badgers and deer in one potential Hotspot[2] in the Low Risk Area[1] in 2017 where badgers were suspected of involvement in a cluster of cattle TB cases. These exercises showed the presence of TB in badgers in all ten areas. However the two sets of results are not directly comparable to each other given differences in sampling strategy and testing protocol.

Genetic analysis indicates that the *M. bovis* bacteria found in badgers were usually similar to those found in cattle in the locality. The genetic analysis of these badger isolates will be continued. Whole genome sequencing will be carried out and combined with other ongoing research as whole genome sequencing of *M. bovis* isolates becomes the default method of genetic analysis. More insights on the spatiotemporal relationships of infection between the cattle and badgers may become available as this work progresses.

An update on TB surveillance in wildlife in Eastern Cumbria, Low Risk Area

A cluster of bovine TB herd breakdowns has emerged in the Low Risk Area of England in Eastern Cumbria, southeast of Penrith. A potential Hotspot area has been declared and cattle, non-bovine animals and wildlife have been subjected to enhanced bovine TB surveillance since September 2016. Current investigations have concluded that disease is most likely to have been introduced by cattle imported from Northern Ireland. The transmission route of *M. bovis* to many of the local cattle cases was unclear, with cattle contact not considered to be a possible route of infection in some of the cattle cases. Infected badger carcasses have been found in this area. An update of the results are contained in this section.

Collection of ‘found dead’ badger and wild deer carcasses is ongoing in the east Cumbria Low Risk Area. Carcasses are submitted for post mortem, with tissues taken in an attempt to culture *M. bovis*.

[1] The High Risk (HRA) and Low Risk Area of England (LRA) was established on 1st January 2013, and is part of the Strategy for achieving Officially TB Free (OTF) status for England by 2038

[2] A potential hotspot area is an area in England or Wales of enhanced surveillance around TB breakdowns with confirmed disease of uncertain origin emerging in a region of historically low TB incidence.

To date a total of 35 badger carcasses have been collected. Three badgers have been confirmed as *M. bovis* positive; 29 have tested negative. Results are pending from the remaining three carcasses. The current sample size is too small to accurately estimate the prevalence of infection in the badger population in the area. All six deer submitted have been negative.

Genotyping has been conducted on *M. bovis* isolated from the three positive badger carcasses. The badgers all had the 17:z genotype which has previously not been identified in Great Britain. This is the same genotype that has been linked to the cluster of bovine TB herd breakdowns in this area, and evidence from whole genome sequencing suggests that this genotype is from Northern Ireland, most likely brought in through the import of infected cattle. As this genotype is not found anywhere else in Great Britain, this suggests that there has been transmission from the local cattle population into the wildlife.

In order to understand the extent of infection in the wildlife in this part of the Low Risk Area, APHA is continuing to test carcasses that are reported through the Defra Rural Service Helpline (0300 200 301).

TB surveillance in badgers in cull areas

In 2016 a sample of cage-trapped badger carcasses was collected from the nine areas undergoing their first or fourth year of culling. Tissues were taken and cultured in an attempt to isolate *M. bovis*, the bacterium which causes bovine TB. Carcasses were examined for visible lesions suspicious of TB. Infected badgers were found in all nine areas sampled. Most of the isolates collected had genotypes typical of those seen in local cattle. Further results can be found in this section.

The goal of this surveillance was to take the opportunity to understand more about TB in badgers in the high risk area of England, as it had been many years since regular surveillance was carried out. The second goal was to develop methods of tracking any changes in TB prevalence which could inform exit strategies, such as when it could be optimal to switch to vaccination as has been proposed in Ireland.

As expected, infected badgers were found in all areas (Table 1). Initial genetic analysis of *M. bovis* isolates from 46 infected badgers showed that one badger (from Gloucestershire) had a novel *M. bovis* genotype not seen previously in cattle but which may have evolved from the common and widespread genotype 17a.

The other 45 isolates had typical *M. bovis* genotypes also found in cattle. The locations of these 45 isolates were then compared with the defined geographical

"home-ranges" for genotypes frequently seen in cattle[3]. Two badger isolates from Dorset had a rare genotype which does not have a defined home-range. Of the remaining 43 isolates, three were out of home-range (one in Herefordshire, two in Gloucestershire).

The second goal of tracking prevalence was unsuccessful. The method of collection proved unsuitable for determining the prevalence. Due to the high volume of badgers collected across a short period of time, it was necessary to freeze carcasses prior to sampling which is known to reduce the diagnostic sensitivity of tissue culture.

In addition, 83% of collected carcasses had moderate to severe decomposition which further affected the sensitivity of culture (Table 2). The degree of carcass decomposition was associated with the delay between dispatch and delivery of carcasses to the processing centre. Finally there was bias in the geographic distribution of sampled carcasses in the year 1 areas. This reflects differences in the deployment and initial success of cage-trapping in different parts of an area as most of the sampled carcasses were collected in the first two weeks of culling. As a result of these limitations it is not meaningful to calculate the prevalence of TB in this sample of badgers as we cannot accurately determine the effect of these factors on how representative the sample is, or the effect on diagnostic sensitivity.

In 2017 a smaller scale carcass collection exercise was carried out to see if the speed of transporting carcasses could be improved to reduce levels of decomposition. Blood sample collection for serological testing was also trialled as a potentially more efficient method to assess prevalence. No results from these exercises are yet available.

[3] See Chapter 7 of the "Bovine tuberculosis in Great Britain in 2016 TB: explanatory supplement to the annual report" for more information on genetic home-ranges. https://www.gov.uk/government/publications/bovine-tb-epidemiology-and-surveillance-in-great-britain-2016

Table 1 Summary of data from 2016						
Area	Carcass condition (degree of autolysis)				Evidence of infection	
	Severe	Moderate	Mild	Not recorded	*M. bovis* cultured[1]	Visible lesion(s) only[2]
Area-1	14	29	10	17	4	5
Area-2	1	41	24	2	4	2
Area-4	40	54	15	18	4	3
Area-5	48	47	8	21	1	8
Area-6	33	62	16	7	8	4
Area-7	30	62	17[3]	18	6	4
Area-8	29	54	19	18	2	1
Area-9	39	50	15	18	9	4
Area-10	29	57	18	14	8	9

[1] Confirmed infections, [2] Suspected infections [3] One further sample yielded a culture of acid fast bacilli. However, a diagnosis of *M. bovis* could not be confirmed.

Table 2 *M. bovis* recovery according to degree of autolysis			
Autolysis	Total	*M. bovis*	
		n	%
Mild	142	10	7.04
Moderate	456	26	5.70
Severe	263	6	2.28
Not recorded	133	4	3.01

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