Department for Environment, Food and Rural Affairs

An update on TB surveillance in wildlife

September 2019

Contents

Summary

In the February 2018 TB surveillance in wildlife publication[1], information was provided about a small scale carcass collection exercise carried out in 2017. The purpose of this was to test the feasibility of collecting and transporting carcasses for post mortem and taking blood samples in the field. The samples were not tested for TB.

The exercise confirmed that carcasses could be successfully collected and transported, so the complete sampling methodology was piloted in two areas, Area 32 – Cumbria and Area 29 – Gloucestershire in 2018. The post mortem results showed that infection was present in the badger population in both areas, and genotypes were typical of those found in the local cattle populations. Further research is required on the blood collection methodology before it can be used for surveillance in wildlife in cull areas on a wider scale.

Area 32 – Cumbria

Background

A potential 'hotspot' area[2] (HS21) was declared in east Cumbria in the Low Risk Area of England during 2016. This was due to the emergence of a cluster of breakdowns associated with *Mycobacterium bovis* genotype 17:z. This genotype had not previously been identified in Great Britain, and investigations concluded that this was most likely introduced by cattle imported from Northern Ireland.

The novel genotype in this area provides clear evidence that local spread of TB is occurring. Whilst cattle contact was identified as the transmission route for some of the breakdowns, others were unclear. Infected badger carcasses with the same genotype as the cattle breakdowns were found also in the area[1].

From the index case in November 2014 to 24 July 2019, there has been a total of 39 outbreaks across 33 premises associated with genotype 17:z.

Infection in badgers

Following the declared potential hotspot protocol, enhanced surveillance of found-dead wildlife was initiated in September 2016. Carcasses were collected and tested for *M. bovis* by post mortem and tissue collection for culture. The initial results of this surveillance in

[1] Defra (2018) TB surveillance in wildlife in England. https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/787588/tb-surveillance-wildlife-england-2017.pdf

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

found-dead wildlife was published in February 2018[1] and further information was provided in September 2018[3]. As of 19 July 2019, three *M. bovis* positive badgers have been identified of the 62 collected[4]; eight deer carcasses have been collected, one was unsuitable for sampling, the other seven were negative. APHA is continuing to test found-dead badger and deer carcasses in HS21 reported via the Defra Rural Service Helpline (03000 200 301).

As published in December 2018[5], 602 badgers were removed from the Area 32-Cumbria during the 2018 cull operations. Of these, 205 were controlled shot and 397 cage-trapped. A publication in March 2019[6] described the surveillance carried out by APHA on the cage-trapped badgers from the area. It was reported that a small number of culture results were still pending. As an update, 41 out of 369 tested badgers (11.1%) were positive, all with the genotype 17:z. The prevalence in the central minimal infected area (MIA)[7] was 21% (38/181) and 1.7% (3/175) in the outer buffer. The remaining thirteen carcasses from parcels that span both the MIA and outer buffer were negative.

As part of the surveillance, Whole Genome Sequencing (WGS) was carried out on all *M. bovis* isolates from cattle and badgers. As of August 2019, there were 22 unique genetic sequences (or clades) found in Area 32 (Fig 1) of which:

- three clades were found in both species, including Clade A which is the most likely ancestor of the epidemic and which all the other clades are descended from,
- fifteen clades were found in badgers only,
- four clades were found in cattle only.

There are two samples pending and a further three samples which cannot be completed due to poor sequence quality.

There are less sequences available from cattle, possibly due to the increased frequency of cattle surveillance (to six-monthly whole-herd testing) which should be removing infected animals earlier and thus before they have developed visible lesions and can be easily cultured.

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[3] Defra (2018) Setting minimum and maximum numbers of badgers to be controlled in 2018: Advice to Natural England, Annex B: Summary of Area 32-Cumbria. https://www.gov.uk/government/publications/advice-to-natural-england-on-setting-minimum-and-maximum-numbers-of-badgers-to-be-controlled-in-2018

[4] Three further cultures are pending

[5] Defra (2018) Summary of badger control operations during 2018. https://assets.publishing.service.gov.uk/government/uploads/system/uploads/attachment_data/file/765439/badger-control-monitoring-2018.pdf

[6] Defra (2019) TB surveillance in badgers during year 1 badger control operations in eastern Cumbria, Low Risk Area. https://www.gov.uk/government/publications/bovine-tb-surveillance-in-wildlife-in-england/tb-surveillance-in-badgers-during-year-1-badger-control-operations-in-eastern-cumbria-low-risk-area-2018#fn:3

[7] Minimal Infected Area; the location of the infected badgers, associated farms and contiguous breakdown areas, plus a radius of the estimated average social group territory based on main sett distribution

The presence of shared sequences across the two species provides more evidence that possible cattle-badger and/or badger-cattle transmission is occurring in the area. However, direction of transmission cannot currently be inferred from this data.

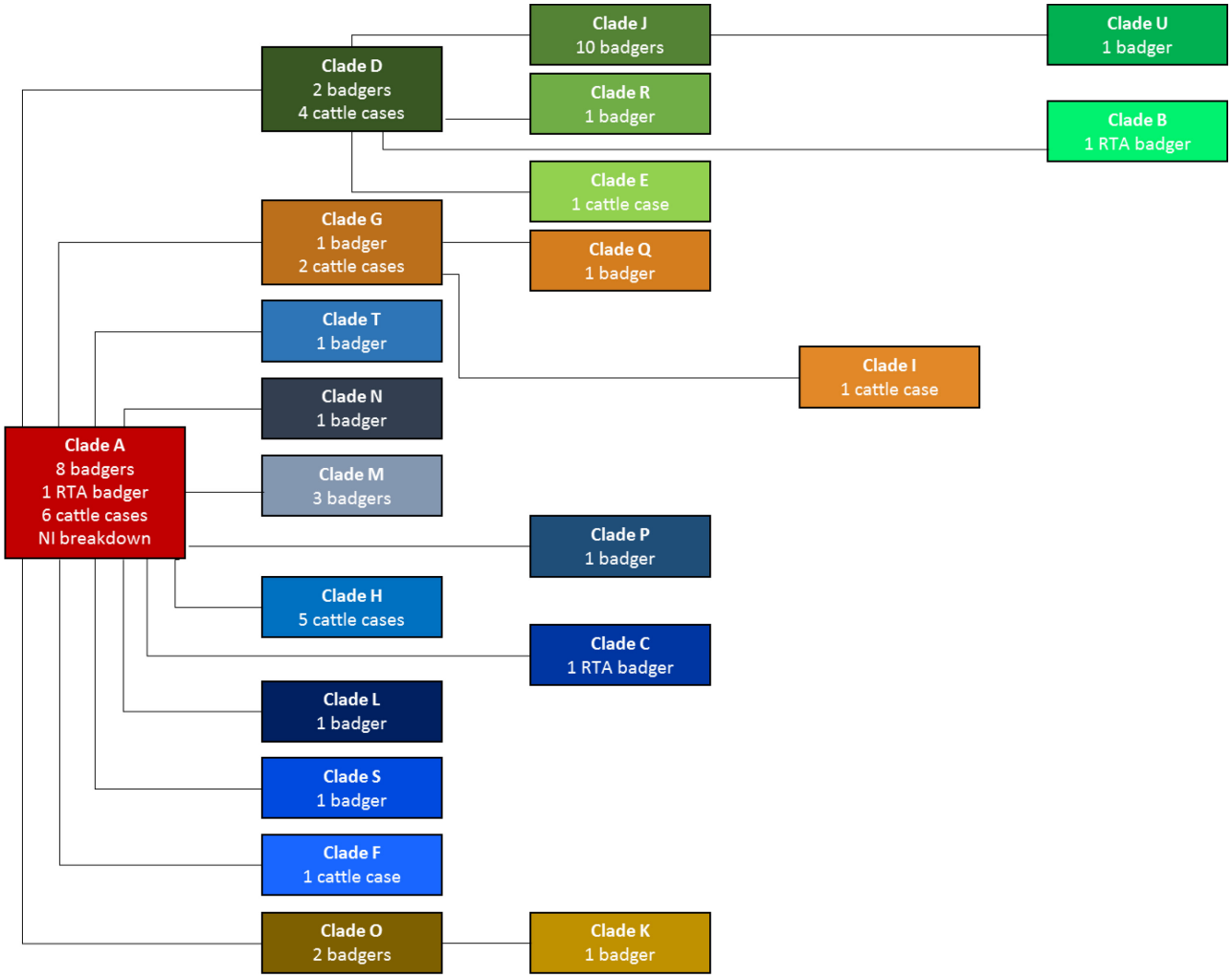

Figure 1. WGS tree for all *M. bovis* isolates from HS21, where Clade A (red) represents the original imported strain and each column represents a one SNP difference.

Area 29 – Gloucestershire

In 2018, a sample of cage-trapped badger carcasses and bloods were collected from Area 29 – Gloucestershire in the High Risk Area of England, which was undertaking its first year of culling. Post mortems were carried out, tissues taken and cultured in an attempt to isolate *M. bovis* and bloods were tested for comparison of novel test methods. Sampling of badgers in this area built on trials carried out in 2017 to improve collection of carcasses and explore possible blood sampling methods. This work was carried out at the same time as Area 32 – Cumbria. This means that carcasses collected from Area 29 were subjected to post mortem analysis on an opportunistic basis, so results may not represent the whole area.

In line with findings from the Randomised Badger Culling Trial – 17.7% of badgers tested in Area 29 (23/130) were positive for *M. bovis*. Genotyping of the *M. bovis* positive isolates was also carried out. Five genotypes; 17:a, 10:a, 74:a, 17:b and 9:g were identified, all of which were typical of the local genotypes in the cattle population in Gloucestershire, four within the local 'home-ranges' and one not.

WGS from the positive badgers (23) were analysed alongside the cattle sequences[8] available within 10km of the boundary of the cull area (189). Four badger isolates have WGS that are identical or very closely related to those of cattle isolates in the area. This suggests that transmission is occurring between the two populations, although the direction of transmission cannot be determined. A further 3 badger isolates have WGS that are identical or very closely related to each other, suggesting that transmission is occurring within the population.

APHA is conducting an evaluation of a serological test which, if successful, could provide a simple, cost efficient and effective method to take samples from all animals removed during badger control operations and then test a statistically significant and representative selection of the samples. The aim of the test is to detect anti-bodies in the blood which would confirm infection with *M. bovis*. The evaluation of the method and the test itself is only half-way through and the test is therefore not yet ready for deployment. There are no results which can be published at this time.

[8] from 2017 onwards

This publication is available at www.gov.uk/government/publications

Any enquiries regarding this publication should be sent to us at

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