Year End Descriptive Epidemiology Report: Bovine TB Epidemic in the England Edge Area

Delivery Area: Southern
County: Oxfordshire

YEAR END REPORT FOR 2017
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1. Executive Summary

a. There were three notable clusters of which two continued from 2016 (Deddington/Somerton in the north, presumed wildlife sourced and previously active, and Henley-on-Thames in south-east of the county). A new cluster with a novel spoligotype (NT: 7-5-5-4*3-3.1) occurred near Thame and the Buckinghamshire border.
b. The Henley cluster and new cluster at Chinnor could represent a significant spread of the presumptive wildlife infected area towards the Buckinghamshire Edge Area.
c. Incidence risk remains the same since 2016 from 14.6. to 14.4 in 2017 (actual breakdown numbers – from 53 to 51).
d. The proportion of breakdowns attributed to purchase of infected cattle has reduced compared to 2016. Of 41 OTFW breakdowns, 20 were attributed to wildlife source, 5 to residual infection and 3 undetermined, leaving 13 cases with purchase of infected cattle as the source. The proportion of OTFS breakdowns compared to previous years was similar.
e. Results from the Defra-funded found dead badger survey conducted in 2016-2017 by the University of Surrey were not available at the time of writing. Wild deer are widespread and hunting for game may provide some passive surveillance.
f. 44% of all breakdowns were still detected by non-routine testing suggesting that increasing from annual to six monthly testing (as of January 2018) might speed up detection.
g. Number of reactors per breakdown has increased this year from nine to 20 per breakdown. This may be due to increased use of interferon-gamma testing and spread of infection within herds.
h. Key drivers of the epidemic – presumed increased infected wildlife in 2017 and cattle movements i.e. two thirds of breakdowns attributed to purchase of cattle involved cattle from the HRA.
i. The increased number of Approved Finishing Units (AFUs), from four at the end of 2016 to eight in total by 2017, channelled riskier cattle into a controlled environment and may have helped mitigate the risk from purchased cattle into the county.
j. The risk to the Low Risk Area (LRA) was from cattle movements from Oxfordshire and more long-term, spread of infection front, associated with presumed infected wildlife, eastwards.
k. The risk from the High Risk Area (HRA) was from continued movement of infected cattle, and presumed infected wildlife into the county.
l. Forward look: a new local TB Eradication Group for Oxfordshire, Buckinghamshire and Berkshire and use of the TB Advisory Service (TBAS) should help promote farm biosecurity, drive changes in purchasing behaviour and increase knowledge of badger ecology. Potential employment of other wildlife initiatives such as the Badger Edge Vaccination Scheme (BEVS2) and badger control licences will help reduce the wildlife reservoir of infection.

2. Introduction

A key action in the implementation of the Government’s objective to achieve Officially Bovine Tuberculosis Free (OTF) status for England by 2038 was to recognise the different levels of TB in different parts of the country and varying the approach to control accordingly. To this end three bTB management areas or zones have been established. Between 2013 and 2017, the county of Oxfordshire straddled the Edge and High Risk Areas of England (see Appendix 1). This report describes the epidemiology of bovine tuberculosis (bTB) in the Edge area of central and eastern Oxfordshire. The Edge Area has a low but recently rising incidence of infected herds and control efforts are seeking to slow down and reverse geographic spread, and reduce the incidence rate, with the aim of obtaining OTF status for this area as soon as possible.

3. Cattle industry in the Edge Area of Oxfordshire

There is a mixture of beef suckler, dairy, and fattening units. Many dairy units have disappeared reverting to suckler beef herds in Oxfordshire. However, relatively high concentrations of large dairy farms still exist in south-west Oxfordshire (partially in the Edge Area but mainly in the Oxfordshire HRA). The majority of the fattening units in Oxfordshire source cattle from the HRA, particularly the South West of England, through markets or directly from farms, with a smaller number purchased locally from farms and Thame market (Oxfordshire).
There are a few large finishing units, some of which are AFUs, providing weekly quotas to abattoirs of cattle finished from buildings to fulfil supermarket contracts. More applications for Approved Finishing Units (AFUs) were received in 2017 to avoid the extra testing and restrictions associated with TB breakdowns, increasing the total in the county from four in 2016 to eight in 2017.

The ‘orange’ market at Cirencester has provided a valued outlet for bTB restricted cattle into AFUs across the south. Some pedigree cattle breeders are located within the county providing pedigree breeding cattle for the whole country. There are a handful of organic farms, both dairy and beef.

The majority of cattle are grass fed whilst outside, with some supplementation for dairy cows and young stock. Fattening cattle on large units are often fed with blends of grass and maize silage and by-products from the human food industry. Use of mineral licks at pasture is variable although where used, almost all are accessible to badgers. There is a trend towards lesser dependence on maize silage as conserved winter forage compared to recent years.

![Figure 1: Proportion of herds of different sizes in Oxfordshire](image1.png)

**Figure 1** Proportion of herds of different sizes in Oxfordshire

![Figure 2: Cattle numbers by type in Oxfordshire](image2.png)

**Figure 2** Cattle numbers by type in Oxfordshire
4. Overview of the TB epidemic in the Edge Area of Oxfordshire

a. History of TB in the Edge Area of Oxfordshire

Established and Emerging Infected Areas

Prior to 2004, breakdowns in Oxfordshire were all attributed to purchased infection, cleared quickly and rarely reoccurred. Thereafter, breakdowns started to appear in significant numbers in the Faringdon area just west of the Edge area in south Oxfordshire bordering Gloucestershire – a high incidence area. Initially these breakdowns were of several genotypes including 17:a, 17:b, 17:e, 74:a and 10:a (genotypes prevalent in Wiltshire, Gloucestershire and this area of Oxfordshire). From 2010, breakdowns have mostly changed genotype to 10:a – probably a reflection of the increasing prevalence of this genotype in the wildlife, and possibly affected by repeated years of flooding in this low lying area adjacent to the River Thames which may have displaced wildlife populations and encouraged migration into the area of wildlife infected with 10:a.

Since 2014 when reports were started for the Edge area, new areas of probable wildlife sourced infections for 10:a appeared north, east and south-east of the Faringdon area – initially appearing as isolated clusters but later joining up with this area to the west of Oxford as new breakdowns have occurred filling in these gaps. Some areas remained clear, represented as irregularities or fingers of no endemicity extending into this mapped endemic area. Closer examination of some of these revealed very low cattle dense areas and therefore an absence of ‘sentinel’ animals for assessing infection in wildlife.

In 2015 and 2016, a cluster of breakdowns appeared in the Henley-on-Thames area of genotype 10:a and closely related genotypes. Uncertainty remained whether this was related to infected wildlife as many of the farms also had a history of purchase from 10:a areas. However, if wildlife associated, this represented a sudden large spread of the infected area of about 20km from the previous years’ mapped endemic areas and was adjacent to the border with the south of Buckinghamshire, then a very low incidence county.

In addition to endemicity caused by 10:a, there has been accumulating evidence for genotype 9:d and spoligotype 17 in the mid latitude of Oxfordshire.

The rising incidence of TB in the county over recent years has been attributed to purchase of infected cattle and spread of infection in badgers.
b. Geographical distribution of bovine TB cases (new and ongoing breakdowns) in the Edge Area of Oxfordshire

The geographical distribution of bTB cases (new and ongoing breakdowns) in the Edge Area of Oxfordshire is shown in Figure 3.
Continuing the trend of previous years, the distribution of breakdowns has advanced eastwards. New clusters of breakdowns with presumptive wildlife source occurred in addition to established clusters near the HRA border (black square). The new and developing clusters appearing further eastwards were:

- **Deddington-Somerton area (green circle)** in the north of the county,
- **Henley-on-Thames (blue circle)** in the south east corner of the county
- and a new and recent isolated cluster in **Chinnor (orange circle)** in the east corner of the county very close to Buckinghamshire with an undetermined genotype (NT:7-5-5-4*-3-3.1 - likely to be a mutation of 10:a). Three new breakdowns sharing the same mutation (NT) with no links between them or contiguous contact, suggesting infected wildlife involvement (three more in 2018 - not genotyped yet).

The established areas of bTB in the west of the county remained in the highest cattle dense areas in the north of the county near Banbury and Epwell and the south west of the county where there is a concentration of large dairy herds.

From 2018, when the county becomes wholly Edge Area, these clusters west of the county will join clusters in HRA of the county which all have the same epidemiology and should be managed in the same way.

![Oxfordshire Epi map - May 2018](image)

**Figure 4.** Oxfordshire cattle breakdowns attributed to wildlife sources plotted 2000 to 2017. 3km radius included to suggest area affected in line with radial testing policy. Dark grey = genotype 10:a.
Main genotype 10:a – The predominant genotype of *M. bovis* continues to be 10:a in Oxfordshire, mirroring the presumptive wildlife endemic area illustrated by the dark grey areas shown in Figures 4 and 5. In the former, the bright green triangles with hatched grey 3km discs demonstrate 2017 10:a breakdowns attributed to wildlife covering new areas: Banbury, Epwell and south west Oxon. Also attributed now to wildlife with 10:a was a portion of the Henley cluster and the Somerton cluster.

Other genotypes (referring to Figures 4 and 5 (probable wildlife sourced breakdowns) – spoligotype 17 and genotype 9:d are represented as orange and lime green circles respectively for all years, and 2016 breakdowns represented by pentagons). Historically there was a narrow band running from west to east midway at the level of Oxford attributed to wildlife infection involving spoligotype 17 and genotype 9:d. Spoligotype 17: 1 case 17:a north Oxford was attributed to wildlife in 2017 (orange disc with red triangle) and three cases of 17:b - at least one near oxford attributed to wildlife in 2017. Genotype 9:d: one case attributed to wildlife in 2017 in southwest Oxford (green disc red triangle). 9:d can mutate to 10:a but not the other way around, suggesting 9:d pockets of endemic bTB remain.

Further probable wildlife sourced breakdowns include: one case of 10:u near Berkshire (pink disc with blue triangle), one case of 130: south of the Somerton cluster which maybe a local mutation of 10:a (two historic cases nearby) (purple disc blue triangle) and a new cluster on the Buckinghamshire border with a new unclassified local genotype (NT:7-5-5-4*-3.1) in an area with no history of suspected wildlife infection pre-2017 (yellow hatched discs with pink triangles).

Some breakdowns may represent wildlife movements across the county border into Oxfordshire: several cases of 10:a, three cases of 10:7-5-6-4*-3 near the Warwickshire border (similar cases on other side although purchase cannot be ruled out) and 74:a in the HRA where the same genotype has occurred in the adjoining counties of Gloucestershire and Wiltshire on the other side of the county border.

One unexplained breakdown with 9:b (home range of Wales) was the first ever case in Oxfordshire, in a closed herd of 1000 dairy cattle with a history of 9:d and 10:a since 2010.
Figure 5. Overview of probable wildlife genotype areas in Oxfordshire, Buckinghamshire, Berkshire and Hampshire.
5. Descriptive epidemiology of bovine TB in the Edge Area of Oxfordshire

Level of Bovine TB

![Graph showing monthly breakdowns]

**Figure 6** 2017 monthly distribution of breakdowns showing OTFS (Orange) and OTFW (Blue)

![Graph showing annual incidence risk]

**Figure 7** Annual Incidence Risk (%) over last four years

The incidence risk, calculated as the probability of OTF herds experiencing a TB breakdown in the year when tested, was similar to the previous year. There were 31 breakdowns in 2015, which increased to 53 in 2016 with a small decrease to 51 in 2017.

The neighbouring HRA of Oxfordshire (realigned as part of the Edge Area from January 2018), has remained stable over the past few years with 19 breakdowns in 2014, 24 in 2015, 24 in 2016 (15 OTFW and 9 OTFS) and 23 in 2017 (18 OTFW and 5 OTFS). It is likely that the addition of this part of the county will increase the overall county incidence next year when Oxfordshire becomes fully Edge Area. In 2017 the number of breakdowns in the HRA was just under half the number in the Edge Area but with only 30% of the cattle herds compared to the Edge Area.
Comparing 2017 to 2016, further cases within two clusters identified in 2016 add more credence to there being wildlife involvement: i) Somerton cluster: six breakdowns were grouped around Deddington (south of Banbury). Two of these were probably due to purchasing infected cattle and the remainder infected from local wildlife. Several breakdowns in this area have previously been attributed to wildlife. ii) Henley cluster: occurred in the south east corner of the county around Nettlebed (north west of Henley-on-Thames). Several of these could be related to cattle purchases. However, several involved the main Oxfordshire genotype (10:a) which suggests that wildlife infection also had to be considered as a likely source, especially when no direct purchase link could be established.

If wildlife was implicated, this would represent a large movement in the presumptive wildlife infected area towards the Buckinghamshire border. This hypothesis is even more evident in 2017 when another separate cluster at Chinnor, north of the M40 in the east of the county appeared near the Buckinghamshire (Edge Area) border. Several cases were not linked by cattle movements or contacts, but share the same genotype. This means the most likely link was the movement of local wildlife. One breakdown holding has been completely closed (only artificial insemination was used for breeding) for over ten years.

Figure 8: Herd size frequency distribution (top) and Herd size frequency distribution for breakdowns only (bottom)
As for previous years, breakdowns showed a predilection for larger herd size. Figure 8 shows that breakdowns are almost evenly distributed across the herd-size categories compared to the frequency distribution of non-TB affected herd according to herd size - which shows a steady decrease in numbers as herd size increases.

**Figure 9: County cattle distribution according to type**

**Figure 10: Breakdowns according to industry sector**

Figures 9 and 10 suggest a predilection for dairy herds, even though they only represent about 8% of cattle herds in the whole county. However, this effect is probably mostly due to size of herd rather than a sector association. Suckler herds remain the vast majority of herds with breakdowns in Oxfordshire.
Risk pathways for bTB infection

The most likely risk pathways for bTB infection in OTFW and OTFS breakdown herds in the Edge Area of Oxfordshire are shown below in Figures 11 and 13, respectively. The attribution of risk pathways for each breakdown was based on evidence from disease report investigations carried out by case vets.

Figure 11 Distribution of infection sources in 2017 for Oxfordshire OTFW breakdowns (n=41)

Figure 12 Distribution for origin of purchased cattle in OTFW breakdowns of purchase origin (n=13)
Figure 13 Distribution of infection source in OTFS breakdowns

Figure 14 Comparison with 2015 and 2016 OTFW breakdown numbers attributed to purchase and wildlife.

Figure 14 illustrates the most likely reasons for the changes in incidence in Oxfordshire between 2015 and 2017. There was a marked increase in purchased source and wildlife source in 2016 compared to 2015. However, in 2017, OTFW herds, which comprised 80% of the new breakdowns (compared to 72% in 2016), show that the purchase of infected cattle have contributed much less to the increased incidence compared to the previous year.

Figures 11 to 13 show that OTFW breakdowns attributed to wildlife are the primary source of infection in Oxfordshire - wildlife source accounting for 47% of confirmed cases, whereas purchased source for only 31% of the cases (mainly purchases from HRA).

OTFS data for source in 2015 is not available and in 2016, 80% of OTFS breakdowns were most likely purchased. In 2017 this number was reduced to 50%. OTFS breakdowns do not have a genotype identified which adds a level of uncertainty, making case vets more reluctant to conclude wildlife as a source.

In conclusion, although the incidence in 2017 was similar to 2016, the attribution for source of infection has changed making infected wildlife the primary source of infection in Oxfordshire.
No breakdowns were attributed to contiguous cattle-to-cattle spread, but this was considered as a low likelihood possibility source in a few cases when neighbouring farms shared the same genotype. This is the case with the 130: cluster and less likely the NT cluster where anecdotally there was no contact between cattle on adjacent farms.

An increased number of cases are now attributed to residual cattle infection from a previous TB breakdown. There were none in 2016 and 13% in 2017, although figures in 2016 may not have fully accounted for this source. This would be due to ongoing repeated breakdowns in this county with a high proportion of all breakdowns having had previous histories of TB (31 out of 51 breakdowns). This is much more evident in the HRA of Oxfordshire where interferon-gamma testing is not routinely deployed to clear herds of TB.

Figure 15 shows the distribution of probable infection source by sector, with the attributed source of infection being clearly associated with the need to purchase cattle. Most of the fatteners were attributed to cattle movements whereas almost all of the dairies were attributed to wildlife. Sucklers had an even spread attributed to both.

![Figure 15 Probable source of infection according to Herd Type (OTFW and OTFS)](image)

**Role of other species**

**Badgers and other wildlife**
An absence of any recent data for *M. bovis* infection in any wildlife continues to add some uncertainty to any conclusions for wildlife being the source for cattle infection, which are made by a process of elimination of other source pathways.

The two suspected cases of TB in wild deer reported in 2017 were both negative for *M. bovis* on culture. It is important to inform farmers of the statutory obligation to report any suspicious lesion in deer. The Defra-funded found dead badger survey was undertaken in Oxfordshire and other counties of the Edge Area in 2016 and 2017 by the University of Surrey. Results are still pending at the time of writing.

**Other domestic species**
None reported in 2017.
Detection of cases

As in 2016, 56% (27 cases in total) of all Oxfordshire breakdowns were detected by routine annual tests – a proportion that was the same for both OTFW and OTFS cases (Figure 16). Four of these (two in OTFW and two in OTFS) involved a failed retest of an inconclusive reactor detected at the annual test. 12% (six cases) were detected by pre-movement tests (PRMT), 10% at the post-breakdown twelve month test (12M) (five cases) and 9% by slaughterhouse post mortem examination and 6M test after a concluded breakdown (four cases each).

Of the four breakdowns detected at slaughter, two were sucklers, one dairy and one an AFU. As in 2016, over 25% of OTFW herds had a previous confirmed breakdown during the last three years (10% 12M and 9% 6M tests as above detected at post-breakdown tests).

The 44% of breakdowns not detected by routine herd testing reinforces the importance of these other active surveillance methods in this county although introduction of six-monthly testing in 2018 will help detect infection earlier at routine testing increasing the proportion of breakdowns detected by routine herd testing and hence decreasing the dependency on unplanned surveillance.

Burden of Bovine TB

![Figure 17 Oxfordshire Edge total annual reactor numbers 2015 to 2017](image)
Using numbers of reactors removed as a proxy for a measure of the burden to the taxpayer of bTB in Oxfordshire, 266 reactors were removed in 2015 (192 interferon gamma), 451 in 2016 (234 interferon gamma) and more than double - 1032 in 2017 (778 interferon gamma- a large increase on interferon gamma reactors).

On an individual breakdown level, the number of reactors taken per breakdown has increased from 9 in 2015 and 2016 to 20 in 2017. Since there is no increase on the number of breakdowns from 2016 (53) to 2017(51) this suggests the spread of TB within a herd under breakdown testing has doubled from previous years. This also correlates with a higher number of OTFW breakdowns in 2017 (41/51=80%) compared to 2016 (38/53=71%)

Figure 18 Oxfordshire Edge reactors per breakdown and per 1000 animal tests 2014 to 2016

Key drivers of the Bovine TB epidemic in the Oxfordshire Edge

Cattle Movements
Over 30% of breakdowns in 2017 were still attributed to the purchase of infected cattle - two thirds being from the HRA. This accounted for most breakdowns in fatteners, but less than half of those in sucklers compared to previous years.

Residual Infection
The change compared to 2016 is in the number of breakdowns attributed to wildlife source and residual infection - 47% due to wildlife source and 13% residual. Also the number of reactors per breakdown has increased - doubling from last year. The level of infection within herds has increased and the proportion of new breakdowns of OTFW status also seems to be increasing – something observed over the past few years within the South East as the level of endemicity rises within certain counties. The number of residual infections are due to breakdowns with repeated infections which are now suspected to be caused by infected cattle remaining in the herd at the end of the previous breakdown.

Infected Wildlife
Excluding those associated with purchase of infected cattle, the gradual spread of breakdowns over the previous 14 or so years in an eastwards direction from the Gloucestershire border has been reported previously and is thought to be caused by infected wildlife. However, new areas may be appearing in the south east of the county, formerly considered clear of endemic wildlife infection. New genotypes are being detected in presumptive wildlife sourced cases around the county.
Monitoring of wildlife (badgers and deer) may provide more certainty, although it is likely from the picture over the past few years that prevalence in wildlife may be low and difficult to detect from a survey unless large numbers are tested (i.e. large sample sizes are used).

6. Summary of risks to the Low Risk Area and any mitigating factors

Spread of the presumptive wildlife infected area eastwards towards the LRA counties is the most serious long-term risk to the future possible OTF status of the LRA. The Henley and Chinnor clusters illustrate this risk. If these are confirmed areas of wildlife infection, then the infection front is approaching the LRA over a much larger area.

Movement of cattle from Oxfordshire to the LRA mainly through local markets has become more risky with the increase in incidence risk in 2016. Breeding cattle are likely to pose most risk to receiving herds because of their longer lives and wider contact with other cattle groups at destination farms. Voluntary private interferon-gamma tests as an additional pre-movement test provides significant mitigation. Compulsory post-movement testing now provides extra mitigation for all cattle movements into the LRA.

Summary of the risk to the Edge Area from the High Risk Area

Two thirds of breakdowns attributed to purchase of cattle involved cattle from the HRA. The increasing number of AFUs in Oxfordshire in 2017 mitigates this risk by channelling these cattle into a controlled environment. Current rules only permit the establishment of AFUs without grazing in the Edge Area.

Presumptive spread of infected wildlife from the HRA has continued, increasing the likely areas of endemicity. The number of genotypes involved has risen making the spatial pattern much more complex than a few years ago when apart from some diversity immediately adjacent to the Gloucestershire border, there was only one genotype, 10:a..

7. Assessment of effectiveness of controls and forward look

The incidence of bTB has remained the same since 2016, but the epidemiological picture has become more complex. This may not favour the long-term objective of OTF status in Oxfordshire for 2025. The whole of Oxfordshire will become part of the Edge Area in 2018. Eradication of TB will require some form of wildlife control as well as tighter control of cattle movements from farms in the HRA and Edge Area. Early detection of infection through more frequent surveillance testing of herds, alongside the use of interferon-gamma testing for breakdowns in the whole county, will help reduce the likelihood of leaving residual infection within breakdown herds that regain OTF status.
Appendix 1: Overview of risk and surveillance areas of England and Edge Area objectives and controls

1.1 Policy objectives for the Edge Area:
Short to medium term:
   a. slow down geographic spread
   b. maintain crude herd incidence of OTFW breakdowns <2% overall by 2019
   c. begin to reduce the incidence rate

Longer term:
   d. reduce geographic spread of bTB and push the Edge Area boundaries westward
   e. reduce OTFW herd incidence to <1% by 2025
   f. attain OTF status (incidence of indigenous OTFW herd breakdowns <0.1) for the lowest incidence counties in the Edge Area.

1.2 Key Control Measures
Surveillance
   a. enhanced herd test coverage (annual)
   b. extend targeted surveillance to 3km around new OTFW breakdowns in Cheshire and Derbyshire (radial testing), with six month follow-up
   c. found dead badger survey close to completion in 2017

Management of cases ('breakdowns')
   a. increased sensitivity of breakdown herd testing:
      - OTFS breakdowns to pass two short interval tests at severe interpretation to regain OTF status
      - mandatory IFN-g parallel testing in OTFW
   b. enhanced epidem. investigation and data analysis
   c. information sharing - location of breakdown herds

Figure A1: Bovine TB risk and surveillance areas of England effective since January 2013, as set out in the Government’s Strategy for Achieving Officially Tuberculosis-Free Status for England (from TB hub)
Appendix 2: Cattle industry in the Edge Area of the region

Number of cattle premises by size band in the Edge Area of the region at 1 January 2015 (RADAR Cattle book 2008 (or most current update))

<table>
<thead>
<tr>
<th>Cattle per premises</th>
<th>1-50</th>
<th>51-100</th>
<th>101-200</th>
<th>201-350</th>
<th>351-500</th>
<th>501+</th>
<th>All</th>
<th>Mean</th>
<th>Median</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number of premises</td>
<td>221</td>
<td>95</td>
<td>92</td>
<td>52</td>
<td>28</td>
<td>18</td>
<td>509</td>
<td>126</td>
<td>65</td>
</tr>
</tbody>
</table>

Number of Approved Finishing Units (AFUs) registered in the Region’s Edge Area of Oxfordshire: Eight in total, of which four were approved in 2017 representing a marked increase in the number of applications received in 2017. Only one TB isolation unit was approved in a TB breakdown holding

Common land in the Region’s Edge Area of Oxfordshire:
Port Meadow & Wolvercote Common: This is a relatively small common with half a dozen graziers and only used from spring to autumn. One cattle keeper who leases common rights brings animals from Herefordshire (in the HRA) which increases the home range of cattle beyond the local vicinity. The common lies adjacent to the River Thames and floods each year during the winter. This may make it an unfavourable habitat for resident wildlife of bTB significance.

Cattle/Herd purpose:

<table>
<thead>
<tr>
<th>Beef</th>
<th>Dairy</th>
<th>Dual purpose</th>
<th>Unknown</th>
<th>Total</th>
</tr>
</thead>
<tbody>
<tr>
<td>Number</td>
<td>%</td>
<td>Number</td>
<td>%</td>
<td>Number</td>
</tr>
<tr>
<td>Cattle</td>
<td>44193</td>
<td>68.9</td>
<td>16760</td>
<td>26.1</td>
</tr>
</tbody>
</table>
## Appendix 3: Summary of the Edge Area regional headline cattle TB statistics

### Herd-level statistics

<table>
<thead>
<tr>
<th></th>
<th>2017</th>
<th>2016</th>
<th>2015</th>
</tr>
</thead>
<tbody>
<tr>
<td>a. Total number of cattle herds live on Sam at the end of the reporting period</td>
<td>452</td>
<td>440</td>
<td>431</td>
</tr>
<tr>
<td>b. Total number of herd tests carried out in the period</td>
<td>716</td>
<td>663</td>
<td>757</td>
</tr>
<tr>
<td>c. Total number of OTF cattle herds TB tested during the period for any reason</td>
<td>354</td>
<td>362</td>
<td>383</td>
</tr>
<tr>
<td>d. Total number of OTF cattle herds at the end of the report period (i.e. herds not under any type of TB02 restrictions)</td>
<td>400</td>
<td>399</td>
<td>407</td>
</tr>
<tr>
<td>e. Total number of cattle herds that were not under restrictions due to an ongoing TB breakdown at the end of the report period.</td>
<td>424</td>
<td>408</td>
<td>417</td>
</tr>
<tr>
<td>f. Total number of new TB breakdowns detected in cattle herds during the report period</td>
<td>51</td>
<td>53</td>
<td>31</td>
</tr>
<tr>
<td>• OTF status suspended (OTF-S)</td>
<td>10</td>
<td>15</td>
<td>10</td>
</tr>
<tr>
<td>• OTF status withdrawn (OTF-W)</td>
<td>41</td>
<td>38</td>
<td>21</td>
</tr>
<tr>
<td>g. Of the OTF-W herd breakdowns:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>• Occurred in a holding affected by another OTFW breakdown in the previous three years?</td>
<td>10</td>
<td>10</td>
<td>unknown</td>
</tr>
<tr>
<td>• How many can be considered the result of movement, purchase or contact from/with an existing breakdown based on current evidence?</td>
<td>13</td>
<td>20</td>
<td>7</td>
</tr>
<tr>
<td>• New OTF-W breakdowns triggered by skin test reactors or 2xIRs at routine herd tests</td>
<td>22</td>
<td>19</td>
<td>12</td>
</tr>
<tr>
<td>• New OTF-W breakdowns triggered by skin test reactors or 2xIRs at other TB test types (forward and back-tracings, contiguous, check tests, etc.)</td>
<td>18</td>
<td>12</td>
<td>6</td>
</tr>
<tr>
<td>• New OTF-W breakdowns first detected through routine slaughterhouse TB surveillance</td>
<td>4</td>
<td>7</td>
<td>3</td>
</tr>
<tr>
<td>h. Number of new breakdowns revealed by enhanced TB surveillance (radial testing) conducted around those OTF-W herds (may not be applicable to every county in the Edge Area)</td>
<td>N/A</td>
<td>N/A</td>
<td>N/A</td>
</tr>
<tr>
<td>• OTF-S</td>
<td>n/a</td>
<td>n/a</td>
<td>n/a</td>
</tr>
<tr>
<td>• OTF-W</td>
<td>n/a</td>
<td>n/a</td>
<td>n/a</td>
</tr>
<tr>
<td>i. Number of OTF-W herds still open at the end of the period (including any ongoing OTF-W breakdowns that began in a previous quarter)</td>
<td>33</td>
<td>26</td>
<td>12</td>
</tr>
<tr>
<td>j. New confirmed (positive M. bovis culture) incidents in non-bovine species detected during the report period (indicate host species involved)</td>
<td>0</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

### Animal-level statistics (cattle)

<table>
<thead>
<tr>
<th></th>
<th>2017</th>
<th>2016</th>
<th>2015</th>
</tr>
</thead>
<tbody>
<tr>
<td>a. Total number of cattle tested in the period (animal tests)</td>
<td>81469</td>
<td>66760</td>
<td>66624</td>
</tr>
<tr>
<td>b. Reactors detected:</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>• tuberculin skin test</td>
<td>1032</td>
<td>451</td>
<td>266</td>
</tr>
<tr>
<td>• additional IFN-gamma blood test reactors (skin-test negative or IR animals)</td>
<td>254</td>
<td>217</td>
<td>74</td>
</tr>
</tbody>
</table>

---

1 In some cases there is minor variation (under 4) between the total number of breakdowns reported in the Year End Descriptive Epidemiology Reports for individual counties and the report on Bovine tuberculosis in England in 2017. These are due to differences in the breakdown case definition, where incidents first detected in late 2016 are included as 2017 breakdowns in the individual county reports; and where incidents occur in epidemiologically linked premises.
<table>
<thead>
<tr>
<th></th>
<th>Reactors per breakdown</th>
<th></th>
<th>Reactors per 1000 animal tests</th>
<th></th>
<th>Additional animals identified for slaughter for TB control reasons (DCs, including any first-time IRs)</th>
<th></th>
<th>SLH cases (tuberculous carcases) reported by FSA</th>
<th></th>
<th>SLH cases confirmed by culture of <em>M. bovis</em></th>
</tr>
</thead>
<tbody>
<tr>
<td>c.</td>
<td></td>
<td>20</td>
<td></td>
<td>9</td>
<td></td>
<td>8.58</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>d.</td>
<td></td>
<td></td>
<td>12.67</td>
<td>6.76</td>
<td></td>
<td>3.99</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>e.</td>
<td>Additional animals identified for slaughter for TB control reasons (DCs, including any first-time IRs)</td>
<td>0</td>
<td></td>
<td>2</td>
<td></td>
<td>5</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>f.</td>
<td>SLH cases (tuberculous carcases) reported by FSA</td>
<td>12</td>
<td></td>
<td>9</td>
<td></td>
<td>7</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>g.</td>
<td>SLH cases confirmed by culture of <em>M. bovis</em></td>
<td>10</td>
<td></td>
<td>7</td>
<td></td>
<td>4</td>
<td></td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
Appendix 4: Suspected sources of *M. bovis* infection for all the new OTF-W breakdowns identified in the report period

<table>
<thead>
<tr>
<th>Most likely origin</th>
<th>Oxfordshire</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Prov.</td>
</tr>
<tr>
<td>Introduction (e.g. purchase) of infected animal(s)</td>
<td></td>
</tr>
<tr>
<td>Local - lateral spread from neighbouring holdings</td>
<td></td>
</tr>
<tr>
<td>• exposure to infected wildlife</td>
<td></td>
</tr>
<tr>
<td>• other farmed species</td>
<td></td>
</tr>
<tr>
<td>• recrudescence of residual infection from a previous TB breakdown</td>
<td></td>
</tr>
<tr>
<td>• infected human source</td>
<td></td>
</tr>
<tr>
<td>Undetermined/obscure</td>
<td></td>
</tr>
<tr>
<td>Other (explain)</td>
<td></td>
</tr>
</tbody>
</table>

NB – half points given to breakdowns where two risk pathways have been judged of equal likelihood (half point to each).

<table>
<thead>
<tr>
<th>Probability of introduced <em>M. bovis</em> infection</th>
<th>Likely (no secondary breakdowns detected)</th>
<th>Possible (no secondary breakdowns detected, but dataset incomplete)</th>
<th>Not likely (secondary spread has occurred)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Definite</td>
<td>1</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Likely</td>
<td>7</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Possible</td>
<td>2</td>
<td>6</td>
<td>0</td>
</tr>
<tr>
<td>Not likely (indigenous infection in the locality)</td>
<td>12</td>
<td>11</td>
<td>0</td>
</tr>
</tbody>
</table>

Appendix 5: Overview of the bTB Control Programme in this Region of the Edge Area

5.1 Edge Area Testing Policy

- Limited exemptions applied for interferon-gamma testing to some beef fatteners, including those converting to AFUs. These herds have not seen an increase in the number of slaughterhouse cases and only one breakdown was disclosed in one AFU via purchase.
- Some discretionary interferon-gamma testing has been applied to cases suspected of containing undisclosed TB before they were confirmed by post mortem/culture and specific epidemiological groups were targeted. Consideration for this to be applied more widely under risk assessment.
- No enhanced case management was carried out in the Edge Area of Oxfordshire - all persistent breakdowns were within the HRA (five persistent breakdowns since 2013).

5.2 Unusual bTB breakdowns
• None in the Edge Area except for a large dairy usually affected by 10:a and 9:d, disclosing 9:b in 2017 completely out of home range and never found in Oxfordshire. No purchase links or contiguous herds.
• HRA has had an explosive breakdown at the end of 2017 on a dairy of 1000 cattle with 200 skin reactors, 100 of those visibly lesioned at slaughter, in an endemic area close to Faringdon where several dairy herds have been infected with different genotypes over recent years reflecting likely multiple wildlife sources (10:a, 9:d, 17:a)

5.3 Other Testing Measures
• Overdue testing has been brought down to a very low level by working with the county local authority which is very pro-active in Oxfordshire.

5.4 Other Control Measures
• The South East TB Eradication Board has continued to meet and discuss initiatives such as holding a veterinary practitioner conference to increase knowledge about the local bTB situation, recognising that the private vet is key to bTB control.
• In 2017 with the National Farmers’ Union (NFU), APHA established a new TB Eradication Group for Buckinghamshire, Berkshire and Oxfordshire with the first meeting scheduled for March 2018.

APHA is an Executive Agency of the Department for Environment, Food and Rural Affairs and also works on behalf of the Scottish Government, Welsh Government and Food Standards Agency to safeguard animal and plant health for the benefit of people, the environment and the economy.