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

Regional Office: South East. Counties in the Edge: Buckinghamshire, Oxfordshire (part county), Berkshire, Hampshire and East Sussex (part county).

Year-end report for 2015

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Executive Summary

a. The ‘Edge Area’ was established in January 2013 and was later incorporated into the Government’s strategy to achieve Officially Bovine Tuberculosis Free (OTF) status for England by 2038. It has a low but recently rising incidence of infected farms and is divided into three regions for reporting purposes. This report describes the bovine tuberculosis (bTB) epidemic in the South East Region of the Edge Area.

b. Dairy herds are few in number with predominance in Hampshire. The many finishing units and two local markets, Thame and Hailsham, channel HRA cattle into the South East (SE) Edge. There are more small herds (less than 50 cattle) in Hampshire and East Sussex.

c. Over the last 10 years, numbers of TB breakdowns have generally increased in all SE Edge counties except for Buckinghamshire and more recently, Hampshire. This increase is apparently mainly attributable to the establishment of endemically infected areas. The geographical distribution of breakdowns appears to reflect either the increased cattle density, and/or the high level of purchased cattle from the HRA in the north, and likely establishment of endemic infection in wildlife in the central part of the region where cattle density is low but a disproportionate number of breakdowns occur.

d. The total number of new breakdowns in 2015 compared to 2014 (95 breakdowns in 2015 & 99 in 2014) has remained about the same, although the temporal distribution of breakdowns has changed from the majority being in the first half of the year in 2014 to a more even distribution throughout the year in 2015. The most likely explanation for the 2014 distribution is that in the first half of 2014 many herds had not been tested within the previous 12 months resulting in a back log of breakdowns to be disclosed. With the removal of this factor from the 2015 testing campaign one might have expected a reduction in breakdowns. However, this has not been seen, possibly explained by the apparent expansion of wildlife infected areas in the SE Edge, which has generated more breakdowns. In all counties in the SE Edge, except East Sussex, breakdowns were associated with larger herd size; dairy herds were most likely to become infected (highest incidence), except in Berkshire.

e. On a county level, comparing 2015 with 2014, the number of breakdowns and the incidence (risk of becoming infected) has almost doubled in East Sussex, while in Buckinghamshire, Oxfordshire and Berkshire both have remained almost the same. Hampshire has had noticeably fewer breakdowns, 13 fewer (35%) breakdowns compared to 2014, and the incidence has fallen. In Oxfordshire and East Sussex, the ratio of OTFW to OTFS has changed dramatically from the previous roughly equal proportions in both counties, to almost 2:1 for Oxfordshire and 1:15 for East Sussex. This has proved hard to explain. Incidence is lowest in Buckinghamshire, which is on course to qualify for EU OTF status by 2025 if measures are introduced to prevent spread of infection, particularly from wildlife, from Oxfordshire.

f. The predominant genotype of *M. bovis* isolates from cattle in the SE Edge central area is 10:a; county characteristics are:

- Oxfordshire: Infected area mostly 10:a, now covering half of the county, straddling the Edge/HRA boundary, and across towards the Buckinghamshire border. The new cluster disclosed late in 2015, north of Henley-on-Thames on the Buckinghamshire border is of concern. Pockets of 17:a and 9:d are present to west of Oxford (mainly HRA).
- East Sussex (Edge): no genotypes were identified from the 2015 breakdowns; the HRA part is affected by two main genotypes 9:1 and 13:a divided by the River Ouse. Relatively stable and little evidence of spread. OTFW:OTFS ratio 1:15 – unusual and possibly explained by infections caught earlier compared to 2014 or proportion not bTB. HRA – continued activity 8 to 10 breakdowns per year.
- Buckinghamshire breakdowns are few and primarily originate from purchase of infected cattle, and in this respect the county has much in common with the LRA. However, one area of the county close to the Oxfordshire border is likely to have infected wildlife.

g. Infection in wildlife was first observed in Oxfordshire from 2004 and then spread to Hampshire and West Berkshire. In the latter this is believed the main source of infection for cattle herds, while in the former two counties about half of the breakdowns are attributed to a wildlife source. Wildlife infection is probably very rare in Buckinghamshire and no breakdowns are attributed to this; similarly wildlife infection is believed low in the East Sussex Edge, although it has been present in the HRA of East Sussex for over 25 years.

h. Evidence of infection in wildlife in the SE Edge Area is largely circumstantial, historic, and with samples matching cattle genotypes, although recent testing of badgers near Oxford revealed infection in some animals. The Badger Edge Vaccination Scheme was put on hold in late 2015 due to the ongoing problems with the supply of licensed Badger BCG from Denmark and the wilder global shortages of human BCG vaccine. Infection in other domestic species in the SE Edge in 2015 was limited to two further cases in cats in the ongoing ‘Newbury cluster’ (total now 16), believed infected after exposure to infected wildlife.

i. Most breakdowns in the SE Edge Area are detected through routine annual skin testing of herds. However, slaughterhouse surveillance finds 25% of all OTFW breakdowns, and in Oxfordshire increasing (though small) numbers are detected by check tests following resolved breakdowns, suggesting the increased frequency of testing in this county which is being considered could be useful. There are few ‘recurrent’ breakdowns in the SE Edge, mainly occurring in Hampshire, Oxfordshire and western half of Berkshire, and most likely associated with reinfection from a wildlife source. A single recurrent case in Buckinghamshire was thought to be from residual infection in the herd.

j. The highest impact/burden of bovine TB infection in the SE Edge falls on farms in Berkshire, Hampshire and Oxfordshire where persistence and reinfection from wildlife are believed responsible for higher numbers of reactors.

k. Key drivers of the epidemic in the SE Edge are believed to be wildlife infection in Hampshire, Oxfordshire and West Berkshire, and purchase of infected animals elsewhere, with insufficient evidence to make conclusions about East Sussex.

l. The SE Edge area poses serious risk to the bTB Eradication policy both from the expansion of infected areas within it towards the LRA, and from continuing opportunities for the introduction of new disease from the HRA. It is possible that without additional controls the wildlife infected area could expand to reach the LRA within 5 years. Hailsham and Thame markets are a potential conduit for higher risk cattle into LRA, however the introduction of compulsory post movement testing in April 2016 should help to mitigate the risk of spread of bTB with these cattle.

m. There are clear risks to the SE Edge from the HRA: cattle purchased from herds in the HRA was believed responsible for 18% of all 2015 breakdowns, and there is evidence of spread of wildlife endemic areas from the HRA into clean areas with the introduction of new genotypes. Large farm enterprises spanning the HRA and Edge Area, e.g. heifer rearing, and the introduction of HRA cattle into Edge commons grazing both pose additional risks.

n. Controls focused only on cattle herds are unlikely to reduce numbers or spread of infected areas and effective mitigation of wildlife exposure routes are needed. According to APHA case vet investigations, the commonest most likely risk pathway is exposure at grazing – probably the most difficult to achieve separation between badgers and cattle. However, this should be caveated by a possible widespread failure to consider sufficiently other risk pathways involving wildlife, such as contamination of feed stores and contact during housing. The Badger Edge Vaccination Scheme had no significant impact with such poor uptake. Extrapolating from this is the risk that there will be no or too few applications for badger culling licences. Repeated IFN-gamma herd tests have diminishing returns in persistent breakdown herds where exposure cannot be controlled and have now been limited (May 2016).
1. Introduction

The Government published its strategy to achieve Officially Bovine Tuberculosis Free (OTF) status for England by 2038 in 2014. A key action in its implementation was to recognise the different levels of bTB in different parts of the country and varying the approach to control accordingly. To this end three management areas were established in 2013 (see Appendix 1). This report describes the epidemiology of bovine TB in the South East region of the Edge Area. The Edge Area sits within the annual testing area of England, creating a zone of increased surveillance between the High Risk Area which has a much higher incidence of bTB and the Low Risk Area where bTB is approaching eradication. It has a low but recently rising incidence of infected farms. 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.

In this report bTB incidents (usually referred to as ‘breakdowns’) which are strongly suspected (‘OTFS’) and fully confirmed (‘OTFW’) are presented separately in recognition of the Edge Area characteristic of adjoining both the High and Low Risk Areas (HRA and LRA) in which the predictive value of positive tests differ. That is, while OTFS breakdowns are very likely to truly be infected with bTB, this likelihood decreases as the overall level of disease decreases, so OTFS breakdowns in the LRA are less likely to be truly diseased. This is discussed further in Appendix 3. Note that due to the timing of this report, all data are derived directly from the transactional database ‘Sam’ and so will differ slightly from the data to be published later this year in the annual bTB reports for England, for which the data have been reviewed to remove duplicates and correct errors.

The use of such data also means that the incidence measure in this report is derived by calculating the number of new breakdowns per 100 herds tested, while the measure used in the annual reports is adjusted for the effect of variable frequency of testing by measuring the number of breakdowns per 100 herd years ‘at risk’. This has little effect on the comparison within an area, but improves the comparability of incidence between areas.

2. Cattle industry in the Edge Area of the South East

The South East (SE) Edge contains about 2,600 herds with about 260,000 cattle.

All SE Edge counties have a similar mixture of cattle enterprises of varying sizes but because of variations in land quality and historical trading arrangements there are local concentrations of particular types such as a higher proportion of dairy cattle in Hampshire compared to other Edge counties in the region.

Medium to large finishing Units concentrated in north Oxfordshire and north Buckinghamshire purchase cattle mostly from markets from a wide geographical area including the HRA. Some have converted to AFUs (Approved Finishing Units) mitigating the risk of TB spread.

Thame market which lies on the border between Oxfordshire and Buckinghamshire, channels cattle mostly for fattening from the local area which includes some Oxfordshire HRA and endemic Edge and disperses them mostly locally including some LRA farms.

Hailsham (East Sussex) market trades in locally sourced cattle (approximately 40 mile radius) that originate mostly from East Sussex (HRA & Edge) and part of West Sussex (LRA) posing a risk of TB dispersal into LRA (West Sussex) and Edge (East Sussex) through cattle movements.

There is still movement of breeding cattle from the HRA into the Edge although purchasing behaviour is gradually changing with more caution exercised.

The risk posed by fattening cattle of spreading TB is probably much less than breeding cattle on a case by case basis because of shorter lifespans, but the high numbers traded make them significant.

Hampshire and East Sussex have proportionately higher number of herds of less than 50 cattle, something that may have reduced the number of breakdowns in these counties.
3. History and geographic distribution of bovine TB in the South East Edge

a. History

The epidemic curve in Figure 3 shows a progressive increase in TB incidents over the last ten years in all counties except for Buckinghamshire which has remained more or less stable. Looking at each year separately, a seasonality to incident numbers can be seen, something that has historically been more associated with most convenient testing times when cattle are housed rather than timing of TB infection.
Figure 3: Epidemic curve for SE region – number of bovine TB incidents each month from 2006 to 2015.
b. Geographical distribution of bovine TB breakdowns (new and ongoing) in the South East Edge

Figure 4: Geographical distribution of breakdowns in 2015 (excluding East Sussex) and showing genotypes where available, with animal density inset in top left hand corner.

Distribution of breakdowns in figures 4 and 5 are the combined effect of several factors notably, i) cattle density particularly noticeable in north Oxfordshire and Buckinghamshire (referring to the small inset), ii) likely endemic wildlife infection with particular reference to the central portion of figure 4 where cattle...
density is the lowest but a disproportionate number of breakdowns occurred, and iii) purchasing which particularly affects finishers – again northern section of figure 4.

![Image: Geographical distribution of breakdowns in the East Sussex Edge area.](image)

**Figure 5: Geographical distribution of breakdowns in the East Sussex Edge area.**

Note that no genotypes are available because only one case was culture positive, and too recently for genotyping results to be included in this report.

**Established and Emerging Infected Areas**

Prior to 2004, breakdowns in Oxfordshire, Berkshire, Buckinghamshire, and Hampshire were all attributable to purchased infection, cleared relatively quickly and rarely reoccurred. However, over the ensuing years, probable endemic wildlife infected areas have appeared as detailed below. These areas have spread into the Edge area especially from 2010 affecting Oxfordshire, West Berkshire, and Hampshire. Although the East Sussex endemic area (HRA) has existed for 25+ years, the East Sussex Edge Area does not appear to have any clear wildlife endemicity yet, whilst the situation in Buckinghamshire is unclear.

The history of purchased infections brought many different genotypes into the area. However, only 10:a and 10:u seemed to have become firmly established from an infection front moving eastwards from Gloucestershire and Wiltshire. Some cattle breakdowns in 2015 now suggest that other genotypes have become established probably prior to 2015.

For this report, presumptive wildlife endemicity has been characterised by the presence of one or more of the following:

- wildlife source for cattle infection by elimination of other risk pathways
- interlocking pattern of contiguous breakdowns with the same genotype without neighbouring cattle to cattle contacts nor purchased sources
- persistence (cattle breakdowns of over 18 months duration)
- steady ongoing pattern of low numbers of annual reactors suggestive of wildlife to cattle transmission

**A) Berkshire:** Breakdowns occurred in the west half of the county. There are now two endemic genotypes in the county: 10u and 10a (see figure 6). 10:u was first reported in 2008 as a new genotype disclosed near Newbury, Berkshire. Since then, this genotype has been associated with breakdowns across a large area of West Berkshire and North Hampshire with alpacas and a large cluster of cats infected.
Another cat case in 2015 with genotype 10u has added to the portion of the ‘Newbury Cat Cluster’ located in a housing estate near Newbury. Greenham Common adjacent to this housing estate continued to have breakdowns in the cattle present during 2015. Two ‘persistent’ dairy breakdowns (i.e. infected for more than 550 days) with 10u are located in West Berkshire. There has been some geographical expansion of the area eastwards.

Figure 6: Projected wildlife endemic areas for genotypes 10u (lilac areas) and 10a (grey areas)
Created by plotting 3km circles around all breakdowns believed to be of local origin including alpaca, wild deer and cat cases. Spread from 2008 onwards illustrated by colour-coding the start year of each breakdown.

It is clear from historic isolates obtained from wild deer with *M. bovis*, and a handful of cattle breakdowns, that 10a has also been circulating in this area for a time, but to a lesser degree (see figure 6). Phylogenetic comparison between 10u and 10a indicate two SNP (Single Nucleotide Point) changes between them, and it is most likely that 10u has evolved from 10a in this area (see phylogenetic analysis figure 21). Compared to 10u, spread of 10a over 2015 has been more noticeable, particularly north of the M4 in the vicinity of the A34 involving a cluster of five breakdowns. These include one persistent dairy case where 10u had been isolated previously associated with young cattle grazed in the 10u endemic area west of Newbury but later in 2014 in the same breakdown, 10a was found in a cow group grazed only at the main farm near Hampstead Norrys situated about 16km away from the Newbury grazing. This illustrates how within one enterprise, cattle grazing extends over large geographical distances and different genotype endemic areas.

**B) Buckinghamshire:** Six out of 13 breakdowns in 2015 (OTFW + OTFS) were clearly of purchased origin. Of the remainder, two were classed as residual from previous breakdowns and five as obscure. The failure to recover *M. bovis* in culture from the five OTFS ‘obscure’ breakdowns meant these breakdowns could not be genotyped, so limiting the potential for identifying the source. Of the six OTFW breakdowns, five were purchased and one residual.
In general, Buckinghamshire has continued to behave like LRA counties with the majority of breakdowns attributed to purchase of infected cattle. However, an area of Buckinghamshire close to the Oxfordshire border, east of Bicester in the north, where the endemic area of Oxfordshire has advanced most eastwards appear likely to have infection in local wildlife probably badgers. For example, reviewing previous historic breakdowns, further genotype information has excluded the original explanation for a Buckinghamshire case near Bicester in 2014 of being contiguous spread, and because it was in a relatively closed herd and genotype was the Oxfordshire 10a, the most likely explanation was a wildlife source. This herd broke down again in 2015 but was OTFS. This represents the first tentative wildlife sourced infection in Buckinghamshire albeit only about 3km from the western border with Oxfordshire.

Figure 7: Overview of endemic areas in Oxfordshire, Berkshire and Buckinghamshire showing 4 genotypes.

Historically, there have been clusters of breakdowns around Aylesbury particularly to the north and south-west of the town. Most were attributed to purchased infection. In both of these clusters of cases, there has been a confirmed breakdown which has not been directly attributable to purchased infection. However, further investigation has concluded that the genotypes isolated could be attributed to a historic purchase on each premise which has then spread within the herd. Continued observation of this area has shown no evidence of local wildlife infection.

C) Hampshire: The apparent 10:u wildlife endemic area in west Berkshire extends over the border into northern Hampshire right down to Andover. A few breakdowns during 2015 have reaffirmed this infected area – see figures 6 & 7. Another 10:u cat case occurred in northern Hampshire in 2015. Genetic analysis
would be interesting to confirm whether this is more closely related to the previous Hampshire case than the Greenham cluster in Berkshire close to Newbury (see phylogenetic analysis figure 21).

There was a cluster of historic 10:a breakdowns and wildlife (2006 to 2014) where the three counties of Wiltshire, Berkshire and Hampshire join. This included a wild roe deer found in 2006 between Andover and Newbury, and about 5km from where 10:u was first isolated, supporting the hypothesis that 10:a was present in the area prior to the appearance of 10:u. No additional 10:a cattle breakdowns attributed to wildlife have occurred in 2015 in this area. However, a cluster of three breakdowns close to Andover in 2015 all involving finishers were determined as most likely wildlife sourced (see figure 6). The fact that these farms purchase cattle from other premises including those in the HRA, adds a significant uncertainty to the likelihood of a wildlife source. However, analysis of source farms has not found 10a either from history of breakdowns at the source farms or their local geographical area. If these breakdowns are the result of local wildlife infection, they suggest a significant expansion of the infection front towards the south of Hampshire. OTFS breakdowns may also suggest this direction of expansion.

Purchased cattle resulted in fewer genotypes (9a, and 11b) imported into the county compared to 2014 when a higher number of genotypes including 9:d, 9:f, 11:a, 15:a and 17:a were isolated. This may reflect a general change in buying behaviour in Hampshire. Genotype 9f was isolated from a slaughterhouse case traced back to a genuinely closed dairy herd near Winchester with no known links to and some 28km from Dorset, the main homergane. Previous breakdowns of the same genotype in the county which were of likely purchase origin have not been close enough geographically to suggest contiguous spread either. The nearest case was on the outskirts of the New Forest, south-west of Southampton, 27km away: Exploration of evidence for the involvement of deer in long distance spread includes the disclosure of a roe deer infected with genotype 9d in the north of the county in 2010 about the same distance (25+km) from its homergane, Wiltshire. However there have been no cattle breakdowns of this genotype at that time or since in the area and roe deer are territorial so travel over such a distance is not typical behaviour, so this seems an unlikely risk pathway for the genotype 9f slaughterhouse case. Fallow deer range extensively and infection spreading in badgers is also a possibility, however no sampling has been carried out and their infection status is unknown so this case remains unexplained. The forthcoming badger survey in the Edge Area may throw more light on this possibility.

Another explanation may be an error in identifying the source farm as there was limited evidence of infection on farm the animal was traced back to - two skin severe only reactors & 16 IFN-g reactors at the first short interval test, all with no visible lesions, out of over 550 cattle and cleared at the subsequent test. This level of positive tests could be explained by the estimated 97% specificity of the gamma test which could result in this number of ‘false positives’.

Pocket of wildlife infection cannot be ruled out in the areas bordering Wiltshire and Dorset. In 2003, bovine TB was isolated in wildlife in the south-western aspects of the New Forest National Park close to the Dorset border in a roe deer and a fox suggesting wildlife endemicity there. However, evidence for breakdowns in cattle caused by grazing in the New Forest common over the years has been scant with most breakdowns being attributed to purchased cattle.
D) Oxfordshire:

Historically, this county has had an established infected area since 2004. At this time, breakdowns started to appear in significant numbers in the Faringdon area just west of the Edge Area in south Oxfordshire bordering Gloucestershire – then and still, 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 10a. Since 2014 when reports were started for the Edge area, new areas of probable wildlife sourced infections for 10a have appeared north, east and south-east of the main area – initially appearing as isolated clusters but later joining up with the main area to the west of Oxford as new breakdowns have occurred filling in these gaps. Some areas remain clear, represented as irregularities or fingers of no endemicity extending into this mapped endemic area. Closer examination of some of these reveal very low cattle dense areas where the absence of cattle means there is no ‘sentinel’ for assessing infection in wildlife.

During 2015, this presumptive infected wildlife area for genotype 10a has expanded marginally in an eastwards direction in the north of the county near Bicester and has almost reached the Buckinghamshire

Figure 8: Oxfordshire - Projected wildlife endemic area for genotype 10:a
Created by mapping 3km radii around breakdowns assessed as wildlife sourced and showing progression from 2000 with the county border as the western limit for Oxfordshire but contiguous with the wildlife endemic areas of Gloucestershire and Wiltshire. 3km chosen as being consistent with radial testing policy. Edge area represented by red boundary and pink hatching. Black hatched areas represent additions in first and second 6 months of 2015 to the 2014 report which alter the boundaries of the area. (SE GIS Team)
The area in the south of the county that overlaps with the county border, has almost joined with the new Berkshire endemic area centred around the cluster of five breakdowns discussed above for Berkshire.

Towards the end of 2015, a breakdown north of Henley-on-Thames and on the county border with Buckinghamshire has been concluded as most likely wildlife sourced. There is evidence of significant spread within this 180 head suckler herd with 14 skin reactors, 10 with visible lesions, disclosed at the first short interval test. The spoligotype was 10, genotype pending at time of writing. If this was wildlife sourced, it would represent a significant jump and spread of the infected area of over 20km, something not observed previously in the SE Edge area. Early indicators in 2016 are that this may not be the only farm affected in an area which extends into Buckinghamshire. However, recent disclosure of different genotypes suggests that breakdowns may not be related to each other.

Within the county, two smaller genotype infected areas appear to exist within the 10a area – 17a and 9d. Genotype 17a has affected a small number of farms in the HRA of Oxfordshire (2009 and 2013) and in 2015 one in the Edge area, all located close to Faringdon – reflecting a probable extension of the homorange over the county boundary from Wiltshire. Genotype 9d has been isolated from a cluster of three breakdowns in 2014 and 2015 - two in the HRA and one in the Edge. They extend in a straight line starting about 6km from the Wiltshire border near Faringdon in an eastwards direction covering 25km and terminating about 5km from the outskirts of Oxford. The homorange for the genotype is also the county of Wiltshire. This is a marked difference to what has been seen for the gradual creeping spread of genotype 10a over a 12 year period. A hypothetical explanation may be connected with movements of infected fallow deer which cover much larger distances compared to badgers. However, there has been a history of purchases associated with 9d five to six years previously in the area close to Oxford which might be connected with the case in the Edge area and a possible wildlife sourced case in 2010/11 close to the middle case of the cluster, both providing evidence of historical 9d in the area rather than a naïve sudden introduction.

E) East Sussex: In the HRA of East Sussex encompassing about 100 cattle keepers, two genotype endemic areas exist: 13:a (116 breakdowns in last 14 years), unique to the area east of the River Ouse with a concentration in the parish of Lewes, and 9:l (9 breakdowns in last 14 years) west of the river (see figure 9). 9:l has been seen more commonly in Devon.

Figure 9: East Sussex HRA showing River Ouse as defining boundary between the two main genotypes, 9:l and 13:a

While the northern boundary for these genotypes appears to have been well defined in the past (apart from spread by cattle movements out of the area), in 2010, 13:a was isolated for the first time from both a cattle herd and a badger just north of the previous boundary, the A27 road and the associated railway line. Four breakdowns with genotype 13:c also unique to East Sussex have been recorded. A new genotype, 9:7-3-5-3*-3-3.1 was isolated for the second time ever, from a slaughtered animal in a West Sussex farm where it resided for only three weeks, having come from an East Sussex herd where it was born. The other isolation of this genotype was from a stored badger sample taken from the enclave area 18 years previously. This genotype is not very closely related to the usual East Sussex 9:1. It was also found in a geographically different location, with 9:1 only found to date west of the River Ouse, whereas 9:7-3-5-3*-3-3.1 was isolated from an animal originating east of the river and north of the A27 road.

The evolution and evidence of spread of the infected area, albeit quite limited, threatens the adjacent Edge area. However, there is no clear evidence of spreading wildlife endemicity from the HRA into the Edge. The
distribution of genotypes 9:l to the west of the River Ouse and 13a to the east has remained the status quo (figure 9). A recurrent case originally caused by animal movements involving genotype 13a in the Edge area near Haywards Heath appears to have caused infection in the adjacent LRA of West Sussex through animal and carcase movements. However, there is no evidence to date of consequent establishment of 13a in local wildlife either in West Sussex or the Edge Area near Haywards Heath, although these areas are under scrutiny.

Of the 16 breakdowns in 2015, only one was OTFW. This compares with nine in 2014 of which four were OTFW. The extreme 1:15 ratio of OTFW to OTFS has been very unusual. Unfortunately, veterinary resources in this geographical area have been too limited for an in depth investigation of this phenomenon, with many case investigations not carried out or documented. Therefore, it is not possible to provide interpretation with any degree of certainty. For one or two breakdowns, risk pathways for origin of infection have included wildlife which is more likely in one of the closed herd breakdowns. However, apart from four likely purchased infections, the rest remain undetermined as to origin. No culture was obtained from the OTFW case. So for all 16 breakdowns in East Sussex, no genotypes are available at the time of writing.

Possible explanations for the unusual OTFW to OTFS ratio might include:

a) A significant proportion are not bovine TB – something supported by the fact that this group of breakdowns did not behave in the same way as the rest of the Edge: much lower predisposition to larger herds (almost normal distribution), no recurrence, and case vets could not determine source. Possible alternatives: non-specific reactions caused by environmental mycobacterium or the area is behaving like an OTF area where false negatives are as a proportion of total tests carried out, more likely because the level of infection circulating is so low. However, with much trade linked to the HRA of East Sussex through the local market, Hailsham, this scenario is less likely. The fact that four of the 2015 breakdowns were most likely associated with purchases supports this.

b) Infections were too early in their development to be confirmed. This remains a possibility although it begs the question why has it not been seen in other Edge areas. However, compared to the previous year, it is likely that infections in general will have been caught much earlier as the inter-test interval has dropped and therefore is probably at least part of the explanation.

c) Testing operator problems associated with the new OV contract. Quality control procedures both within APHA and the service provider should have mitigated this risk, so this is unlikely.

d) Sampling problems of reactors at slaughter such as submission of insufficient tissue for culture. APHA uses a small number of slaughterhouses which are shared with all other regions. As this phenomenon has only been seen in East Sussex, this is unlikely to be the explanation.

e) Problems with culturing at the laboratory. As for (e), the same laboratories are used for the whole country so it would not explain why only one county would be affected.

Following a quiet spell during the first half of 2015, 8 breakdowns occurred in the adjacent HRA of East Sussex pushing the annual total very much in line with previous years although only one case was confirmed in 2015 (see figure 16). Therefore, what was beginning to be perceived as an increasing quiescence in the East Sussex HRA has not been supported by the evidence. Referring to figure 9, the HRA has remained remarkably stable and predictable over the years. However, a similar unusual ratio of OTFW to OTFS was seen in 2015 as in the Edge. This will be explored further in the annual report for England, which is published later in the year when more data are available.

Figure 10: HRA East Sussex – demonstrating stability & relatively low threat to the neighbouring Edge area
4. Descriptive epidemiology of bovine TB in the South East Edge

![All SE Edge Breakdowns 2014 and 2015](image)

**Figure 11**: Number of strongly suspected (OTFS) and fully confirmed (OTFW) breakdowns of bTB in the SE Edge area in 2014 and 2015 (*Totals 2014: 99 [46 OTFW & 53 OTFS] 2015: 95 [47 OTFW & 48 OTFS]*)

The total number of breakdowns in 2015 compared to 2014 has remained about the same although the temporal distribution of breakdowns has changed in 2015 compared to 2014 from the majority being in the first half of the year to a more even distribution throughout the year. The most likely explanation for the 2014 distribution remains as discussed in previous reports that in the first half of 2014, many herds had not been tested within the previous 12 months resulting in a back log of breakdowns to be disclosed. With the removal of this factor from the 2015 testing one might have expected a reduction in breakdowns. However, this has not been seen – something probably explained by the expansion of endemic areas in the SE Edge which has generated more breakdowns.

![Number of suspected (OTFS) and fully confirmed (OTFW) breakdowns in the SE Edge Area counties in 2014 and 2015](image)

**Figure 12**: Number of suspected (OTFS) and fully confirmed (OTFW) breakdowns in the SE Edge Area counties in 2014 and 2015

On a county level comparing 2015 with 2014, Buckinghamshire and Berkshire have remained almost the same. Hampshire has had noticeably fewer breakdowns (13 breakdowns less equivalent to 35%). In
Oxfordshire and East Sussex, the ratio of OTFW to OTFS has changed dramatically from the previous almost equal proportions to almost 2:1 for Oxfordshire and 1:15 for East Sussex.

a. Level of bovine TB

Incidence

Figure 13: County incidence in 2014 and 2015 (total number new herd breakdowns in 2014/2015 divided by the number of OTF cattle herds tested in 2014/2015, x 100, data in Appendix 3). Note that prevalence could not be calculated for this report because of SAM data issues.

Incidence increased in East Sussex and decreased in Hampshire, with the other counties remaining much the same as in 2014. Incidence is lowest in Buckinghamshire where endemic infection in wildlife probably only affects a very small proportion of the county on the western boundary. If enhanced movement controls were in place to have prevented purchased infection in this county, the incidence could have been reduced from the current rate of 1.7% to 0.9%, a level that is approaching OTF status of less than 0.1%. Without better control of exposure to wildlife infection to support cattle movement controls, it is unlikely that the incidence in the other counties will fall to a level consistent with OTF status as defined by EU standards. The level of wildlife infection in the East Sussex Edge area is probably low, and therefore it is likely that other factors are responsible for the current relatively high incidence compared to previous years. However, significant uncertainty remains regarding East Sussex because of lack of genotypes and limited veterinary investigation because of lack of suitable resources.

Figure 14: Incidence per sector by county for all breakdowns (OTFS & OTFW).

* represents part counties. Some approximation was made for the denominator (number of OTF cattle herds tested in 2015 per sector) because this was not available, by multiplying the total for all OTF cattle herds tested by the percentage in the sector calculated from SAM data. Note that the ‘other’ category in the SE Edge totalled zero.
Incidence per county is almost inverse to the herd numbers per county when the industry sectors are compared (compare figures 1 and 14). County incidence by sector shows dairy proportionally affected more than other sectors. For example in Oxfordshire, the probability of a dairy herd becoming infected was 12.5%. This is not the case in Berkshire where all 2015 breakdowns were in beef suckler herds. However, there are ongoing chronic breakdowns in Berkshire in the few dairy farms present in the wildlife endemic area which probably explains the zero incidence in dairy herds in this county. Incidence is consistently lowest in the beef fattening sector, where 65% of the breakdowns were clearly attributed to purchase. Logically, one might expect higher incidence in a sector where purchase from the HRA is almost an occupational hazard because of the general shortage of beef animals to fatten. However, these figures suggest that cattle control measures such as pre-movement testing do considerably mitigate the risk of importation of infection into fattening herds. Infected wildlife seem to have less impact on fattening herds probably because of the relatively transient cattle populations, and tendency to finish in housing. Although wildlife sourced breakdowns were reported in Hampshire in several fattening herds in 2015.

Duration

Figure 17: Mean duration of OTFW breakdowns plotted by county or part county and year (2011-2014) against days. This includes three ongoing breakdowns in Berkshire from 2012 and 2013, one ongoing case in Hampshire...
from 2014 and three in HRA Oxfordshire from 2013 & 2014. Note - too many breakdowns are ongoing to calculate mean durations for 2015. No OTFW breakdowns were recorded for 2013 in the East Sussex edge.

In calculating mean duration, some small data sets were used (n ranges from 1 to 20 for each mean calculation), so any interpretation has to be caveated by this especially where ongoing persistent breakdowns have such an impact on the mean. However, where there is likely to be no or low wildlife endemic infection such as in Buckinghamshire, the majority of breakdowns conclude relatively quickly especially in finishing units where little cattle to cattle spread is observed. This would explain the general lower duration of breakdown observed in Buckinghamshire. Oxfordshire and Berkshire breakdowns tend to last longer. However, the differences between counties are relatively small and therefore, the potential use of duration as a proxy for endemicity is not clear cut - probably because of confounding factors such as heterogeneity of endemic and non-endemic areas with respect to wildlife within Edge counties, uneven distribution of finishing units which have generally much shorter breakdowns, and varying use of IFN-g over the years which can significantly shorten breakdowns in wildlife non-endemic areas but can have, to a very variable extent, the effect of prolonging them in wildlife endemic areas. The only consistent finding year on year on is that mean duration is longer in the Oxfordshire HRA as opposed to the Edge of Oxfordshire.

Persistence has been a problem with a small number of herds in the SE Edge area particularly in Berkshire. Two dairy herds have been under continuous restrictions for several years – starting in 2012 and 2013 respectively. Over 50 skin reactors and 100 IFN-g reactors during five rounds of IFN-g testing have been removed from the longer duration herd, and 125 skin reactors and 120 IFN-g reactors during eight rounds of IFN-g testing from the other. With exposure of cattle at grazing to infected badgers being the most likely risk pathway for persistence, long term resolution of these breakdowns is very difficult. The value of continued IFN-g testing is questionable in these circumstances. Another persistent case in an Oxfordshire suckler herd resolved in 2015 after 28 months. A sucker herd breakdown which started in 2013 remains persistent in Hampshire.

b. Likelt origin for bTB infection:

Considering the heterogeneity of the SE Edge, not surprisingly, counties differ markedly with respect to source concluded as most likely transmission routes for TB into cattle herds. For some breakdowns, a most likely source is not clear especially for those where a genotype is not available. These have been classified as ‘undetermined’ in Figure 18 below. Purchases have mostly been from the HRA although some have been identified as being from the Edge. For almost all of those attributed to wildlife origin, the specific risk pathway identified as most likely has been exposure to infected badgers at grazing. However, this should be caveated by a possible widespread failure to consider sufficiently other risk pathways involving wildlife such as contamination of feed stores and contact during housing. Such exposures can be reduced with improved biosecurity for which there is substantial advice on the TB Hub which describes the biosecurity five point plan (http://www.tbhub.co.uk/biosecurity/protect-your-herd-from-tb/ ). Further training of case vets is planned to improve investigation capability and raise awareness of this advice.
Oxfordshire and Hampshire have very similar distributions of OTFW origin, most likely because both have probable wildlife endemic and non-endemic areas and similar purchasing patterns (these counties had 10 and 11 OTFS cases respectively that are excluded from this distribution). The main cattle keeping area of Berkshire is in the west of the county where there is now a large probable wildlife endemic area. All OTFW breakdowns in this county have been attributed as most likely associated with badger infection (exposure at grazing), however the possible source of the 5 OTFS cases remains unclear. Buckinghamshire has behaved like the LRA with the majority of OTFW breakdowns being clearly purchased (but with 7 OTFS cases of unclear origin). Three out of the five purchased infections were in finishing units, one an AFU and another later converted into an AFU. The other two purchased breakdowns were in suckler herds: one linked with the purchase of a breeding cow from Wales, and the other with cattle bought in from the HRA to finish. East Sussex only had one OTFW breakdown for which risk pathway analysis has not produced any clear conclusions.

Analysis of OTFS breakdowns (n=48) shows a similar picture to that for OTFW although without a genotype to help link exposure to a particular location, the proportion of obscure origin is much higher. For example, out of the 15 OTFS breakdowns in the East Sussex Edge area, nine were undetermined and the remainder had significant uncertainty associated with the conclusions about source.

The Defra planned survey of badgers in the Edge Area in 2016 for bTB infection may help to decrease the uncertainties associated with some breakdowns where the degree of badger infection is largely unknown.

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**Figure 18: Pie charts for all 47 OTFW incidents by county showing risk pathways distribution** (note there were 48 OTFS cases in the SE Edge where the origin was not assessed, and so are not shown here)
c. Role of other species:

Badgers and other wildlife
There have been no wildlife submissions during 2015, so the picture of wildlife infection remains very incomplete. Referring to figure 19, the genotypes associated with wild deer submissions have mostly matched the local genotypes seen in cattle (10u near Newbury, 17e south-west Oxfordshire, 10a near to the Hampshire-Berkshire border) with the exception of 9d found in a roe deer near Whitchurch, Hampshire in 2010 – see above for more detail on page 9 in the Hampshire discussion. There remains the possibility of a mix up somewhere along the sample submission pathway.

Whatever the explanation, it appears that infection with 9d has not been maintained in the area.

- Generally, most farmers report significant increases in the number of badger setts on their land over the last 20 or so years. Almost all farms report badgers setts either in cattle pasture or nearby. Wild deers, mostly as regular visitors passing through or sometimes resident, are consistent features for most farms although these are generally controlled populations. There is the largest population of wild boar in England in the Weald area of Kent and East Sussex. However, there is no evidence that this is infected.

Figure 19: Wildlife submissions confirmed with M. bovis infection in Edge Area (from 2014 report)
- Historically, badger samples from the East Sussex HRA matched the local cattle breakdowns.
- In 2014, as a prelude to a badger vaccination programme in the Edge area, gamma interferon testing was conducted twice several months apart on a large badger population on the west side of Oxford. Results (from an APHA laboratory) indicated probable recent exposure to M. bovis in some individuals from two setts after giving positive results to the second round of testing. This suggests either spread from infected cattle in neighbouring cattle farms into the wildlife population or more likely spread within the local wildlife population following the advancing infection front eastwards. Evidence for the latter is that source for the two closest breakdowns has been concluded as infected wildlife both having relatively low numbers of reactors during their whole breakdown - six SICCT reactors in a 1,000 head closed dairy herd and 4 SICCT homebred reactors in a 300 head suckler herd.
• Badger Edge Vaccination Scheme (BEVS) funding was allocated to two groups for badger vaccination – one close to Oxford and one near Newbury. Shortages of supply prevented complete vaccination of these groups. However, some vaccination did occur. In the Oxford project, 59 badgers were vaccinated – efforts being targeted at five social groups perceived as being at most risk.

Other domestic species:

![Figure 20: Newbury feline TB cluster 2011 to 2015](image)

Two further *M. bovis* infections in cats were confirmed in 2015 within the previously reported Newbury cluster. These were the same genotype 10:u as previous breakdowns, one being located within the housing estate where seven other breakdowns were confirmed between 2013 and 2014 and up to three more likely but non-confirmed breakdowns all located within a circle of radius 200 metres. All are likely to have been infected from wildlife.
Figure 21: Phylogenetic relationship of the whole genome sequence of a selection of genotype 10:a isolates from cattle and 10:u isolates from cattle and six of the cats in the Newbury area of Berkshire and Hampshire. The close phylogenetic relationship between 10:a and 10:u genotypes is shown (two informative SNPs) as well as the single informative SNPs that identify three clusters within the 10:u strains (arrows). Isolates from cats are marked by red boxes and cattle isolates by blue boxes. If cat-to-cattle transmission is eliminated, the simplest explanation for the two phylogenetic clusters that contain both cat and cattle isolates is that two transmissions from local wildlife or cattle have occurred into Newbury cats (Courtesy Noel Smith). None of the whole genome sequences (WGS) of M.bovis isolated from the cats was identical. However, too little is known currently about variation in whole genome sequence of M.bovis especially when transference occurs between hosts to completely rule out cat-to-cat transmission.

**d. Detection of breakdowns**

![Detection Methods for OTFS & OTFW Breakdowns](image)

Figure 22: Number of breakdowns in 2015 plotted for each county against method of detection for both OTFS breakdowns (n= 48) and OTFW breakdowns (n=47).
For OTFW breakdowns, the data sets for Buckinghamshire, Berkshire, and East Sussex are too small to demonstrate any trends. For example, the three non-routine skin tests for Buckinghamshire comprised of a tracing, pre-movement, and six month check test. Oxfordshire had a higher proportion of non-routine skin testing compared to Hampshire because more of the breakdowns were detected through six and twelve month check testing (4 out of 21). Again, these are small numbers. However, if this trend were sustained, an argument for increased frequency of testing in endemic areas could be made to reduce secondary spread from herds through cattle movements.

Slaughterhouse surveillance detected about a quarter (23%) of the OTFW breakdowns and comprised similar proportions across the counties. Again, this provides further support for increased testing frequency to reduce spread.

The majority of breakdowns in Hampshire and East Sussex were detected by routine skin testing considering both OTFW and OTFS breakdowns.

Methods for detection of OTFS breakdowns have been dealt with separately to OTFW because there is a different pattern. Slaughterhouse detection does not appear in the chart because non-confirmed slaughterhouse breakdowns are by definition not breakdowns. Apart from Berkshire, routine tests account for the majority of detections of OTFS breakdowns in the SE Edge. As for the OTFW discussion, the small size of data sets means that a few breakdowns can completely alter the distribution. In Berkshire, four out of five of the OTFS breakdowns have been triggered by a breakdown in one of the Greenham commoners which then triggered breakdowns in the others explaining the high proportion of breakdowns detected by non-routine testing for this county. Oxfordshire had OTFS breakdowns following two 12 month, two 6 month and one CON 12 (second contiguous at 12 months) month check tests, a distribution which reflects the wildlife endemicity of specific areas of the county. For Buckinghamshire, a pre-movement, tracing and 6 month check test detected three out of the seven breakdowns. The four non-routine tests detecting breakdowns in East Sussex were a 6 month, pre-movement, CON 12, and New Herd check test.

Recurrence

![Figure 23: Showing the proportion of all breakdowns (OTFW and OTFS combined) where there has been a previous breakdown in the last 3 years.](image-url)
There were five breakdowns in Oxfordshire which could be considered unrelated separate incidents because of purchasing and/or different genotypes isolated comparing the previous to the 2015 breakdowns (referred to here as ‘secondary’).

The reasons for recurrence during 2015 varied according to the county. The only one in Buckinghamshire was probably due to residual infection in the herd. In Berkshire, Hampshire and Oxfordshire, recurrence was most likely caused by reinfection from wildlife. The absence of recurrence in East Sussex is some evidence for lack of wildlife endemity.

e. Herd Size

Figure 24: Comparison of total OTFW + OTFS herd size distribution compared to normal herd size distribution across SE Edge counties

As in previous reports, breakdowns are predisposed to larger herds. There are county differences. Most notably, East Sussex has a breakdown distribution closer to the population distribution than other counties. Oxfordshire and Hampshire breakdowns clearly show predisposition to larger herds.

Figure 25: Distribution of herds according to size and SE Edge counties.
Figure 26: Distribution of breakdowns according to herd size and county.

f. Burden of bovine TB

Figure 27: Reactor distribution by county
(for actual figures see ‘Animal level statistics’ table in appendix 3)
Referring to Figure 27, Buckinghamshire breakdowns yield far fewer reactors than other SE Edge counties. Factors that increase reactor numbers per breakdown, and related costs, include later detection of disease after incursion, greater herd size and prolonged breakdowns. Presumptively infected wildlife appear to contribute to the latter and may be the most significant of these in the SE Edge, accounting for the main differences between the counties. Such infection enables semi-continuous exposure of cattle to infection that is very difficult to control, and continues after breakdowns have concluded and restrictions have been lifted. Berkshire has two persistently infected dairy herds which have produced many reactors - hence the highest number of reactors per breakdown and per 1000 animal tests for this county. These two herds have made contributed significantly to the cost of control in Berkshire.

**g. Key drivers of the bovine TB epidemic in the SE Edge area.**

Wildlife Endemicity. The high probability of infected wildlife, predominantly badgers, in areas as indicated above is responsible for all of the longer duration and higher reactor number breakdowns and more than half of OTFW breakdowns. Only control of exposure to wildlife mediated infection and high level farm biosecurity will reduce this. In the South East Edge Area, there has been very little evidence for cattle to cattle spread between contiguous herds.

Purchase. Buying cattle from endemic areas (HRA and endemic Edge Area) was most likely responsible for just over 40% of OTFW breakdowns. The majority were bought into finishing units and suckler-finisher combinations. More information about herd TB histories (e.g. through risk-based trading) may inform buyers to enable them to reduce risk, especially significant for breeding animals. However, it is unlikely that the high numbers of cattle required could be met from the lower risk farms alone. The fact that buyers for fattening cattle in the Edge Area have to use mostly HRA markets such as Cirencester to source cattle suggests that the economics and supply and demand still do not favour a more precautionary approach to purchase behaviour. However, a decrease in purchase related breakdowns in Hampshire compared to 2014 may be due to a change in attitude. Defra figures for cattle movements in the period September 2014 to August 2015 suggest that only 18% of cattle movements onto farms in the South East are sourced from outside the South East. For cattle movements off farms in the South East, 37% go to farms outside the region (see figures 28 and 29) suggesting a net export.

Taking the SE Edge Area as a whole, this picture of wildlife endemicity and purchase responsible for driving the TB epidemic, is very similar to that observed in 2014 with almost the same numbers of breakdowns attributed to either route.

![Figure 28: Defra statistics for cattle movements Sept 2014 to Aug 2015 showing where cattle go when leaving farms in the South East](Note that this includes some SE counties that are not Edge)
Figure 29: Defra statistics for cattle movements Sept 2014 to Aug 2015 showing origin of cattle movements onto farms in the South East (Note that this includes some SE counties that are not Edge)

h. County descriptions

**Berkshire:** Wildlife sourced infection and persistence in some dairy herds with continuing infection detected in cattle on Greenham Common made this the county with the highest numbers of reactors per breakdown, longest breakdown duration, and high recurrence rate. To reverse this trend, measures to reduce exposure to wildlife infection are needed.

**Buckinghamshire:** The majority of breakdowns were due to cattle movements from other infected herds. The breakdowns cleared the quickest, yielded fewer reactors and had very low recurrence rates compared to other counties. With the lowest incidence, this is the county most on track to achieve OTF status by 2025. However, unless something is done to reverse the expansion of wildlife endemic areas from Oxfordshire, this will not happen. Purchase of infected animals for breeding also threatens this target.

**Hampshire:** The largest county both in size and cattle numbers was affected by wildlife sourced infections in the north, with a clear predisposition to larger herd size, and produced the highest number of reactors per county in the SE Edge, reflecting the high cattle population. The majority of breakdowns were detected through routine skin tests. Apart from Buckinghamshire, incidence was the lowest in this county probably because a high proportion of the county is still unaffected by wildlife endemicity. Control of wildlife exposure, continued cautious purchasing behaviour and careful management of the New Forest common are needed to reduce overall incidence.

**Oxfordshire:** With probably the largest area of wildlife endemicity, Oxfordshire has the highest recurrence rate with a higher proportion of breakdowns detected through non-routine tests especially 6M and 12M. Over half of the breakdowns were probably wildlife sourced – specifically exposure to wildlife infection at pasture. Breakdowns have long durations and are predisposed to larger herd sizes. As a county it produced almost the same large number of reactors as Hampshire, reflecting the predominance of breakdowns in larger herds and the comparatively high incidence rate for an Edge county. Without control of exposure to wildlife sources (probably mostly badgers), cattle measures alone are very unlikely to reverse these trends.

**East Sussex:** Although this county had a zero recurrence rate, and the source of infection remains undetermined for the majority of breakdowns, it did not behave like a largely non-endemic county such as Buckinghamshire. It had a relatively high incidence rate, longer duration, and higher reactor numbers per breakdown compared to Buckinghamshire. 15 out of 16 breakdowns were OTFS compared to the usual
50:50 seen across the rest of the Edge and the predisposition to larger herd size was not seen as marked as in the other counties. This suggests that the TB dynamics in East Sussex are somewhat different compared to the rest of the SE Edge and may reflect something unique to the county. Although, the incidence of OTFW breakdowns was very low, the unexplained relatively high numbers of OTFS breakdowns are a concern and do not project well for the future regarding OTF status by 2025.

5. Summary of risks for spread of bovine TB in the South East Edge Area

● During the two years of reporting (2014 and 2015), expansion of endemically infected areas in the Edge has continued. Using the techniques for mapping illustrated in figures 6, 7, and 8, variable spread has occurred: in Oxfordshire at the most northern tip, this has been about 4km, north of Oxford, 8km, and south of Wantage, 10km. In Berkshire, noticeable expansion has occurred in an north-easterly direction about 15km with the development of a new cluster of 10a. In Hampshire, the area has grown about 8km eastwards and 9km southwards. This may seem only marginal on the face of it, but the timescales for TB eradication make this rate of creep very significant. It was only about 12 years ago, that the first signs of wildlife endemicity started to appear on the Oxfordshire-Gloucestershire border. In that time it has traversed the entire county and is now at the border with Buckinghamshire and probably has already crossed over.

● Compared to the situation of expanding areas of infected wildlife in Oxfordshire, Berkshire and Hampshire, such obvious expansion has not been seen in the East Sussex area either into the adjacent LRA or the Edge. However although East Sussex has the unique characteristic of having HRA adjacent to LRA it is only at one point which corresponds more or less with the city of Brighton, so disease spread is very unlikely this way.

● Where cattle are acting as sentinels of wildlife infection, breakdowns may be happening months or potentially years after infection has spread into local wildlife, so the true location of the infection front comprised of infected wildlife may be closer to the LRA than the current thinking of 22 to 27km (closest at Bicester Bucks border to Bedfordshire, and Tadley in Hampshire to Surrey border – see Figure 30). At the current rate of detected spread, the known infected area could spread into the LRA within 5 years. Previous thinking about the effectiveness of the river Thames slowing down spread still stands, but this can only affect a relatively narrow corridor as the river meanders south of Oxford until it joins the Berkshire border at Reading and then heads due east. Infection fronts have been creeping north and south of this area in an easterly direction.

Figure 30 – minimal distances to LRA from endemic areas.

● In the north of Buckinghamshire, cattle densities are the highest in the region (figure 4) providing a more certain sentinel for endemic infection should it be present than for example, south Buckinghamshire, and east Berkshire where cattle densities are low. The level of uncertainty about the area around Aylesbury in Buckinghamshire reported previously has continued to reduce with time as no more potentially linked breakdowns or similar clusters arise there. Strategically, this area is very close to the LRA – 0 to 10 km from the border.
● Thame market, located on the Oxfordshire-Buckinghamshire border in the Edge, forms a hub where HRA, Edge and LRA cattle are all traded together. This could facilitate flow of HRA and Edge area cattle into the LRA, so risk based trading could make a significant positive difference to TB control.

● West Sussex is in the unusual position of being in the LRA with both adjacent HRA and Edge of East Sussex. In 2015, several incursions of TB from East Sussex occurred, which could be traced back over the course of several years as originating from the east side of the HRA involving genotype 13:a. This happened through a series of steps involving non-bovines, their carcases and cattle movements. Some farming enterprises span both counties, and Hailsham market acts as a conduit for cattle movement between these different risk areas. This continues to pose a threat to West Sussex and other nearby LRA counties.

Summary of the risk to the Edge Area from the HRA

● Purchase/importation of cattle from the HRA has been the probable cause of 18% (17/95) of all breakdowns in the SE Edge. Two of these were moves into AFUs. However, as a proportion of the total, this is reduced compared to 2014 and may reflect changing attitudes of farmers when purchasing cattle.

● There is now sufficient wildlife endemic area within the Edge Area on the western side of Oxfordshire and Berkshire that the Oxfordshire, Gloucestershire and north Wiltshire HRAs pose less of a risk with respect to wildlife migrations because of the growing distances between HRAs and clean (non-wildlife endemic country). However, the further migrations of wildlife from these areas potentially threaten the clear genotype distributions of 10:a and 10:u (figures 6 & 8). For example, the small pockets of 9:d and 17:a in the Oxfordshire HRA could confuse future epidemiological assessments of breakdowns in the Edge Area and complicate consequent control measures and advice given to farmers.

● Spreading wildlife infection from the direction of the HRA still remains the most significant risk to the Edge Area in the SE – especially those areas not already infected such as Hampshire from Dorset and Wiltshire, and East Sussex from the South Downs HRA. However, there was little evidence that this happened during 2015. What might possibly explain the appearance of some new clusters is fallow deer ranging. However, deer are not thought to be an important maintenance wildlife host, though fallow deer do cover large distances sometimes in a semi-migratory form.

● The risk from movements of cattle within large farm enterprises that straddle these areas has been mitigated by increased requirement for pre-movement testing between policy risk zones and further development of 10 mile radius limits for size of CPH premises. However, farmers not aware of these rules might regularly move infected cattle into the Edge from the HRA. The incomplete sensitivity of the skin test means that for example, the several businesses that rear their heifers in the HRA run a continued risk of importing infection unknowingly.

● Low cattle density areas (figure 4) may mask moving wildlife infection fronts because of the absence of cattle sentinels obscuring what is wildlife endemic area and what is not. Some areas of the HRA in Oxfordshire appear to have little TB but also happen to have low cattle densities.

● Common grazing poses a significant risk of spreading infection both into and out of the commons because of cattle imported from the HRA. The policy on pre-movement testing should mitigate this risk for the majority of commons in the South East although it could be stronger. For example the New Forest TB control plan offers a different and more rigorous approach. This is a two stage strategy. Firstly whole herd testing was completed for all commoners during the 2014-15 winter period (15 October to 31st January) when cattle are off the common to establish general herd status. The second stage is to defend this disease status by reducing the risk from purchased cattle. Any purchased cattle must be isolated for 60 days and then post-movement tested (additional to compulsory pre-movement testing on herd of origin). Cattle that are exempted from the pre-movement testing requirement must not be mixed with, nor have contact on the home premises with other cattle with a lower or unknown disease status.

● Badger relocations from HRA into the Edge Area could seed new infection into naïve local wildlife populations. Whether this has occurred recently is unknown, but relocations have happened in the past.
6. **Assessment of effectiveness of controls and forward look**

- The rate of spread of wildlife endemic areas especially in an eastwards direction with respect to Oxfordshire, Berkshire and Hampshire and the apparent ineffectiveness of cattle measures to slow this over the last two years of the Edge Area strategy is a concern. If they have been correctly implemented, this suggests that the most effective current measures focussed on cattle (which are also the easiest to implement) may not, in themselves, be effective in reducing the incidence of cattle TB in the Edge Area.

- Current repeated and automatic usage of the IFN-g test in OTFW breakdowns identified in endemic areas of the Edge where there are further confirmed or standard reactors at short interval tests, does not resolve some of the persistent breakdowns but decimates the herd. It is not clear whether, if due to reinfection rather than residual infection, this can be reduced through improved biosecurity, however additional analysis of risk pathways intended for 2016 will help to determine this. This policy was modified in May 2016 in order to limit the number of parallel blood tests where exposure to endemic wildlife infection is suspected as a the reason for breakdown persistence.

- Wildlife surveillance is required to assess the extent of the wildlife endemic areas. The Defra-funded TB prevalence survey of badgers in the Edge area in 2016-17 is a step towards achieving this.

- To reduce the rate of spread and reverse the TB epidemic in the Edge Area, effective reduction in exposure to wildlife infection must be implemented at the same time as the current cattle control measures.

- The BEVS badger vaccination scheme for the Edge Area had poor take up and at most would have only had some local effects, which probably would not have impacted the larger scale picture. The withdrawal of vaccine for the scheme during 2015 and for the foreseeable future because of a worldwide BCG shortage has stopped even this low significance wildlife measure for the time being.

- Uncertainty about whether applications for badger culling licences will be forthcoming for the Edge area, and to what coverage will be achieved may end up with a similar disappointing result to uptake of the Badger Vaccination scheme.

- Buckinghamshire could achieve OTF county status in a few years. However, the current picture at the western border of nearing wildlife infection and possible pockets of endemic infection in wildlife already established in the county seriously threatens this.

- SE TB Eradication Board activities – planning to hold a regional TB conference for veterinary practitioners to enable more effective advice to their clients with regards to bovine TB.
APPENDICES

Appendix 1: Overview of risk and surveillance areas of England and Edge Area objectives and controls

Figure A1: Bovine TB risk and surveillance areas of England (in effect from January 2013, as set out in the strategy for achieving Officially Bovine Tuberculosis Free status for England)

1.1 Policy objectives for the Edge Area:
Short to medium term:
- Slow down geographic spread
- Maintain crude herd incidence of OTFW breakdowns <2% overall by 2019
- Begin to reduce the incidence rate

Longer term:
- Reduce geographic spread of bTB and push the Edge Area boundaries westward
- Reduce OTFW herd incidence to <1% by 2025
- 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 Derbyshire (radial testing), with 6 month follow-up
c. 6 monthly whole herd testing in Cheshire from January 2015
d. Survey of badgers found dead in the Edge area (starting Spring 2016)

Management of cases (‘breakdowns’)
a. Increased sensitivity of breakdown herd testing:
   • OTFS breakdowns to pass 2 short interval tests at severe interpretation to regain OTF status
   • Mandatory IFN-g parallel testing in OTFW
b. Enhanced epidemiological investigation & data analysis

Preventive measures
a. Compulsory pre-movement TB testing
b. Remove CTS links between HRA and Edge areas
c. Approved Finishing Units (AFUs) with grazing not permitted
d. Promote risk based trading of cattle
e. Badger (Edge) vaccination scheme (currently suspended due to vaccine supply issues)
f. bTB biosecurity review project (underway)
g. Local bTB awareness events and Eradication Boards
h. Information sharing – location of breakdown herds published
Appendix 2: Cattle industry in the Edge Area of the region

There is a mixture of beef suckler, dairy, and fattening units with geographical concentrations. As with other areas of the country, many dairy units have disappeared reverting to beef especially in Oxfordshire. However, relatively high concentrations of large dairy farms still exist in areas such as south-west Oxfordshire (partially in the Edge area). The majority of the fattening units in Oxfordshire, Berkshire and Hampshire source cattle from the South-West through markets or directly from farms with a smaller number purchased locally from farms and local markets such as Thame in Oxfordshire. With store prices buoyant, trade in almost finished cattle from the region’s Edge area has been high mostly through Thame market, Ashford and Hailsham markets in Kent and Cirencester in Gloucestershire. There are several very large finishing units in the Edge area providing weekly quotas to abattoirs of cattle finished from buildings to fulfil supermarket contracts. The orange market at Cirencester has provided a valued outlet for TB restricted cattle in the Edge area. Many pedigree cattle breeders are located within the region providing pedigree breeding cattle for the whole country. There are a handful of organic farms, both dairy and beef and just two water buffalo farms. 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 wildlife. There is a trend towards lesser dependence on maize silage as conserved winter forage compared to recent years. Some producers with out-lying rented land on long term lets are turning to sheep due to pre-movement testing rules with a predicted reduction of cattle farmed within the Edge area over the next few years.

Number of cattle premises by size band in the Edge Area of the region at 1 January 2015

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<td>58</td>
<td>25</td>
<td>20</td>
<td>520</td>
<td>122</td>
<td>59</td>
</tr>
<tr>
<td>East Sussex</td>
<td>10</td>
<td>372</td>
<td>94</td>
<td>73</td>
<td>32</td>
<td>9</td>
<td>11</td>
<td>601</td>
<td>75</td>
<td>32</td>
</tr>
<tr>
<td>TOTAL</td>
<td>37</td>
<td>921</td>
<td>354</td>
<td>343</td>
<td>183</td>
<td>94</td>
<td>94</td>
<td>2051</td>
<td>201</td>
<td>101</td>
</tr>
</tbody>
</table>

Number of Approved Finishing Units (AFUs) registered:
Buckinghamshire – 4, Oxfordshire – 3, Berkshire – 2, East Sussex - 1 (Total of 10 – all without grazing)

Number of Exempt Finishing Units (EFUs) registered:
Hampshire – 2, East Sussex – 1 (Total of 3)

Common land:

a) Hampshire – New Forest National Park: This common is used all year round for some 140 different cattle holdings, with many cattle moving between the common and the home holding on a daily basis. The purchase pattern of some cattle graziers represents a significant risk of introduction of infection into the common. However the implementation of the New Forest TB plan mitigates this by ensuring isolation and post-movement testing after 60 days of all cattle imported from outside the ‘Forest Herd’. All annual testing has to be completed by 31st January. This is all rigorously monitored by the verderers and agisters, and the very few non-compliances found are reported to APHA with verderers ensuring that corrective action is taken. APHA are regularly consulted by commoners for advice about the plan especially regarding conditions for isolation. Plans are in place to update and rewrite the plan to clarify some of the points that have caused confusion. Historically wildlife have been found infected with _M. bovis_ (see section 4 b. C. Hampshire) although no associated cattle infection has been conclusively recorded.

b) 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 Bovine TB significance. However, it is likely that the infection front for genotype 10a is now very close. The Thames may be a significant barrier to wildlife, but people have reported badgers swimming the river at this point which is some 30 metres across. Compliance issues regarding pre-movement testing are being investigated by the local authority and APHA.

c) Berkshire – Greenham Common: 4km in length, this common historically had three graziers. However, a fourth new grazier added cattle to the common in 2014, and two more have more recently joined totalling six. One of the latter formed a herd from cattle pre-existing on the common belonging to another commoner. Infection was found at relatively low levels in 2013, following testing triggered by feline cases in the nearby housing estate. Breakdowns have continued through 2014 into 2015. However, the current breakdown which started at the end of 2014 remains OTFS. From a spatial viewpoint, it is the cattle herd which mostly graze the western aspect that has had most reactors over 2015. This is the closest area of the common to where the ongoing cat cluster in the Greenham housing estate is. Unlike the New Forest, there is no TB control plan in place. Commoners have pre-movement tested cattle on and off the common.

-Hungerford Common: This is another small common comprised of three separate land areas – effectively three populations of cattle that do not mix. The main common has three active graziers. The current management is that a third party purchases cattle for these graziers mostly from the HRA and often buys them back to finish.

Cattle/herd purpose:

<table>
<thead>
<tr>
<th>County</th>
<th>Beef Number</th>
<th>Beef %</th>
<th>Dairy Number</th>
<th>Dairy %</th>
<th>Dual purpose Number</th>
<th>Dual purpose %</th>
<th>Unknown Number</th>
<th>Unknown %</th>
<th>Total Number</th>
</tr>
</thead>
<tbody>
<tr>
<td>Berkshire</td>
<td>14164</td>
<td>70.0%</td>
<td>5436</td>
<td>26.9%</td>
<td>632</td>
<td>3.1%</td>
<td>4</td>
<td>0.0%</td>
<td>20236</td>
</tr>
<tr>
<td>Buckinghamshire</td>
<td>42975</td>
<td>70.9%</td>
<td>16109</td>
<td>26.6%</td>
<td>1547</td>
<td>2.6%</td>
<td>11</td>
<td>0.0%</td>
<td>60642</td>
</tr>
<tr>
<td>Hampshire</td>
<td>38013</td>
<td>54.4%</td>
<td>28372</td>
<td>40.6%</td>
<td>3419</td>
<td>4.9%</td>
<td>18</td>
<td>0.0%</td>
<td>69822</td>
</tr>
<tr>
<td>Oxfordshire</td>
<td>41945</td>
<td>66.4%</td>
<td>18534</td>
<td>29.3%</td>
<td>2731</td>
<td>4.3%</td>
<td>5</td>
<td>0.0%</td>
<td>63215</td>
</tr>
<tr>
<td>East Sussex</td>
<td>28883</td>
<td>64.1%</td>
<td>14746</td>
<td>32.8%</td>
<td>1363</td>
<td>3.0%</td>
<td>33</td>
<td>0.1%</td>
<td>45025</td>
</tr>
</tbody>
</table>
Appendix 3: Summary of the Edge Area regional headline cattle TB statistics

Herd Level Statistics

In this report bTB incidents which are strongly suspected ('OTFS') and fully confirmed ('OTFW') are presented separately in recognition of the Edge characteristic of spanning the High and Low risk areas (HRA and LRA) in which the predictive value of positive tests differ. In general cattle that react positively to any of the bTB tests are likely to be infected, however in the LRA where disease is much less common, there is more chance that a positive test could occur in an animal that was not infected with bTB. The situation is less clear cut in the Edge, particularly in view of the hypothesis that infected animals tested early in the progress of infection are likely to give a positive result to the live animal tests that cannot be confirmed by post mortem tests. The increased controls in the Edge Area are expected to find disease earlier, so the proportion of OTFS classified breakdowns will increase if this hypothesis is valid, but the probability that they are infected will remain higher than similar breakdowns in the LRA due to the higher incidence of disease. Analysis of the Edge Area data provides the opportunity to explore this as shown in this report.

Herd-level statistics

<table>
<thead>
<tr>
<th></th>
<th>Berkshire</th>
<th>Buckinghamshire</th>
<th>Hampshire</th>
<th>Oxfordshire</th>
<th>East Sussex</th>
<th>Total SE Edge Area</th>
<th>Total SE Edge Jan-Dec</th>
</tr>
</thead>
<tbody>
<tr>
<td>a. Total number of cattle herds live on Sam at the end of the reporting period</td>
<td>241</td>
<td>561</td>
<td>907</td>
<td>431</td>
<td>498</td>
<td>2638</td>
<td>2668</td>
</tr>
<tr>
<td>b. Total number of herd tests carried out in the period</td>
<td>377</td>
<td>764</td>
<td>1198</td>
<td>757</td>
<td>535</td>
<td>3449</td>
<td>3724</td>
</tr>
<tr>
<td>c. Total number of OTF cattle herds TB tested during the period for any reason</td>
<td>329</td>
<td>745</td>
<td>1113</td>
<td>670</td>
<td>503</td>
<td>3360</td>
<td>3401</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>224</td>
<td>546</td>
<td>889</td>
<td>407</td>
<td>486</td>
<td>2552</td>
<td>2582</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>227</td>
<td>552</td>
<td>902</td>
<td>417</td>
<td>492</td>
<td>2590</td>
<td>2636</td>
</tr>
<tr>
<td>f. Total number of new TB breakdowns detected in cattle herds during the report period</td>
<td>11</td>
<td>13</td>
<td>24</td>
<td>31</td>
<td>16</td>
<td>95</td>
<td>101</td>
</tr>
<tr>
<td>• OTF status suspended (OTF-S)</td>
<td>5</td>
<td>7</td>
<td>11</td>
<td>10</td>
<td>15</td>
<td>48</td>
<td>53</td>
</tr>
<tr>
<td>• OTF status withdrawn (OTF-W)</td>
<td>6</td>
<td>6</td>
<td>13</td>
<td>21</td>
<td>1</td>
<td>47</td>
<td>48</td>
</tr>
<tr>
<td>g. Of the OTF-W herd breakdowns:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></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>0</td>
<td>5</td>
<td>4</td>
<td>7</td>
<td>0</td>
<td>16</td>
<td>10</td>
</tr>
<tr>
<td>• New OTF-W breakdowns triggered by skin test reactors or 2xIRs at routine herd tests</td>
<td>3</td>
<td>1</td>
<td>8</td>
<td>12</td>
<td>0</td>
<td>24</td>
<td>31</td>
</tr>
<tr>
<td>• New OTF-W breakdowns triggered by skin test reactors or 2xIRs at other TB test types (forward)</td>
<td>1</td>
<td>3</td>
<td>2</td>
<td>6</td>
<td>0</td>
<td>12</td>
<td>11</td>
</tr>
</tbody>
</table>
and back-tracings, contiguous, check tests, etc.)

- New OTF-W breakdowns first detected through routine slaughterhouse TB surveillance

|       | 2 | 2 | 3 | 3 | 1 | 11 | 6 |

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)

- OTF-S N/A N/A N/A N/A N/A N/A

- OTF-W N/A N/A N/A N/A N/A N/A

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)

|       | 8 | 6 | 10 | 12 | 0 | 36 | 31 |

j. New confirmed (positive *M. bovis* culture) incidents in non-bovine species detected during the report period (indicate host species involved)

|       | 2 (cats) | 0 | 0 | 0 | 0 | 2 | 3 (2 farmed deer, 1 cat) |

### Animal-level statistics (cattle)

<table>
<thead>
<tr>
<th>Animal-level statistics (cattle)</th>
<th>Berkshire</th>
<th>Buckinghamshire</th>
<th>Hampshire</th>
<th>Oxfordshire</th>
<th>East Sussex</th>
<th>Total SE Edge Area</th>
<th>Total SE Edge 2014 Jan-Dec</th>
</tr>
</thead>
<tbody>
<tr>
<td>a. Total number of cattle tested in the period (animal tests)</td>
<td>27398</td>
<td>64054</td>
<td>85969</td>
<td>66624</td>
<td>33274</td>
<td>277319</td>
<td>287644</td>
</tr>
<tr>
<td>b. Reactors detected:</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>• tuberculin skin test</td>
<td>92</td>
<td>18</td>
<td>91</td>
<td>74</td>
<td>37</td>
<td>312</td>
<td>357</td>
</tr>
<tr>
<td>• additional IFN-gamma blood test reactors (skin-test negative or IR animals)</td>
<td>126</td>
<td>23</td>
<td>182</td>
<td>192</td>
<td>76</td>
<td>599</td>
<td>504</td>
</tr>
<tr>
<td>c. Reactors per breakdown</td>
<td>19.82</td>
<td>3.15</td>
<td>11.38</td>
<td>8.58</td>
<td>7.06</td>
<td>9.60</td>
<td>8.43</td>
</tr>
<tr>
<td>d. Reactors per 1000 animal tests</td>
<td>7.96</td>
<td>0.64</td>
<td>3.18</td>
<td>3.99</td>
<td>3.40</td>
<td>3.28</td>
<td>2.96</td>
</tr>
<tr>
<td>e. Additional animals identified for slaughter for TB control reasons (DCs, including any first-time IRs)</td>
<td>8</td>
<td>0</td>
<td>2</td>
<td>5</td>
<td>1</td>
<td>16</td>
<td>40</td>
</tr>
<tr>
<td>f. SLH breakdowns (tuberculous carcasses) reported by FSA</td>
<td>2</td>
<td>6</td>
<td>9</td>
<td>7</td>
<td>2</td>
<td>26</td>
<td>40</td>
</tr>
<tr>
<td>g. SLH breakdowns confirmed by culture of <em>M. bovis</em></td>
<td>2</td>
<td>2</td>
<td>4</td>
<td>4</td>
<td>1</td>
<td>13</td>
<td>14</td>
</tr>
</tbody>
</table>
Appendix 4: Suspected sources of *M. bovis* infection for all the new OTF-W breakdowns identified in the report period, n = 47
(Note that Final conclusions are made following disclosure of genotype information which then usually provides evidence to either maintain the provisional conclusion or alter it to another risk pathway highlighted during the initial investigation. Occasionally, further evidence also comes to light such as clustering of a particular genotype which suggests a common source, usually wildlife.)

<table>
<thead>
<tr>
<th>Most likely origin</th>
<th>Berkshire</th>
<th>Buckinghamshire</th>
<th>Hampshire</th>
<th>Oxfordshire</th>
<th>East Sussex</th>
</tr>
</thead>
<tbody>
<tr>
<td>Introduction (e.g. purchase) of infected animal(s)</td>
<td>- -</td>
<td>5</td>
<td>4</td>
<td>6</td>
<td>- -</td>
</tr>
<tr>
<td>Local - lateral spread from neighbouring holdings</td>
<td>- -</td>
<td>- -</td>
<td>- -</td>
<td>- -</td>
<td>- -</td>
</tr>
<tr>
<td>• exposure to infected wildlife</td>
<td>- 6</td>
<td>- -</td>
<td>- 7</td>
<td>13</td>
<td>- -</td>
</tr>
<tr>
<td>• other farmed species</td>
<td>- -</td>
<td>- -</td>
<td>- -</td>
<td>- -</td>
<td>- -</td>
</tr>
<tr>
<td>• recrudescence of residual infection from a previous TB breakdown</td>
<td>- -</td>
<td>- -</td>
<td>1</td>
<td>- -</td>
<td>- -</td>
</tr>
<tr>
<td>• infected human source</td>
<td>- -</td>
<td>- -</td>
<td>- -</td>
<td>- -</td>
<td>- -</td>
</tr>
<tr>
<td>Undetermined/obscure</td>
<td>- -</td>
<td>- -</td>
<td>2</td>
<td>2 - 1</td>
<td>- -</td>
</tr>
<tr>
<td>Other (explain)</td>
<td>- -</td>
<td>- -</td>
<td>- -</td>
<td>- -</td>
<td>- -</td>
</tr>
</tbody>
</table>

Categorisation of all new OTFW TB breakdowns identified in SE Edge region according to (a) the probability of being the result of introduced infection (inward cattle movements) and (b) the strength of evidence that this is an isolated incident without further propagation from the primary farm to neighbouring herds (or vice versa). (Greyed-in boxes show introduced breakdowns with no evidence of local spread)

**Berkshire**

<table>
<thead>
<tr>
<th>Probability of introduced <em>M. bovis</em> infection</th>
<th>Probability of isolated, sporadic ('one-off') breakdown, without secondary cattle to cattle spread</th>
</tr>
</thead>
<tbody>
<tr>
<td>Definite</td>
<td>Likely (no secondary breakdowns detected)</td>
</tr>
<tr>
<td>Likely</td>
<td>Possible (no secondary breakdowns detected, but dataset incomplete)</td>
</tr>
<tr>
<td>Possible</td>
<td>Not likely (secondary spread has occurred)</td>
</tr>
<tr>
<td>Not likely (indigenous infection in the locality)</td>
<td>7</td>
</tr>
</tbody>
</table>
### Buckinghamshire

<table>
<thead>
<tr>
<th>Probability of introduced <em>M. bovis</em> infection</th>
<th>Probability of isolated, sporadic (‘one-off’) breakdown, without secondary cattle to cattle spread</th>
</tr>
</thead>
<tbody>
<tr>
<td>Definite</td>
<td>Likely (no secondary breakdowns detected)</td>
</tr>
<tr>
<td></td>
<td>Possible (no secondary breakdowns detected, but dataset incomplete)</td>
</tr>
<tr>
<td></td>
<td>Not likely (secondary spread has occurred)</td>
</tr>
<tr>
<td>Likely</td>
<td>5</td>
</tr>
<tr>
<td>Possible</td>
<td>1</td>
</tr>
<tr>
<td>Not likely (indigenous infection in the locality)</td>
<td></td>
</tr>
</tbody>
</table>

### Hampshire

<table>
<thead>
<tr>
<th>Probability of introduced <em>M. bovis</em> infection</th>
<th>Probability of isolated, sporadic (‘one-off’) breakdown, without secondary cattle to cattle spread</th>
</tr>
</thead>
<tbody>
<tr>
<td>Definite</td>
<td>Likely (no secondary breakdowns detected)</td>
</tr>
<tr>
<td></td>
<td>Possible (no secondary breakdowns detected, but dataset incomplete)</td>
</tr>
<tr>
<td></td>
<td>Not likely (secondary spread has occurred)</td>
</tr>
<tr>
<td>Likely</td>
<td>3</td>
</tr>
<tr>
<td>Possible</td>
<td>1</td>
</tr>
<tr>
<td>Not likely (indigenous infection in the locality)</td>
<td>7</td>
</tr>
</tbody>
</table>
### Oxfordshire

<table>
<thead>
<tr>
<th>Probability of introduced <em>M. bovis</em> infection</th>
<th>Probability of isolated, sporadic ('one-off') breakdown, without secondary cattle to cattle spread</th>
</tr>
</thead>
<tbody>
<tr>
<td>Definite</td>
<td>Likely (no secondary breakdowns detected)</td>
</tr>
<tr>
<td>Likely</td>
<td>7</td>
</tr>
<tr>
<td>Possible</td>
<td>1</td>
</tr>
<tr>
<td>Not likely (indigenous infection in the locality)</td>
<td>11</td>
</tr>
</tbody>
</table>

### East Sussex

<table>
<thead>
<tr>
<th>Probability of introduced <em>M. bovis</em> infection</th>
<th>Probability of isolated, sporadic ('one-off') breakdown, without secondary cattle to cattle spread</th>
</tr>
</thead>
<tbody>
<tr>
<td>Definite</td>
<td>Likely (no secondary breakdowns detected)</td>
</tr>
<tr>
<td>Likely</td>
<td></td>
</tr>
<tr>
<td>Possible</td>
<td>1</td>
</tr>
<tr>
<td>Not likely (indigenous infection in the locality)</td>
<td></td>
</tr>
</tbody>
</table>
Appendix 5: Overview of the bTB Control Programme in this Region of the Edge Area

5.1 Edge Testing Policy specific for the SE Edge

- Discretionary IFN-g testing was carried out on Greenham common whilst OTFS because of the perceived risk of disseminating infection amongst the five commoner herds with dispersal to home herds.
- Discretionary removal of inconclusive reactors whilst still OTFS has continued but to a much lesser extent than in 2014.
- Slaughter of IRs in OTFW herds has continued where there has been farmer co-operation.
- One exemption to whole herd IFN-g testing was granted to a beef finisher for groups of housed cattle that were scheduled for slaughter before turnout. The rest of the cattle on the farm were included in IFN-g blood tests.
- Where wildlife appear to be a continued source of infection to herds in the endemic area, the cost-benefit advantages of the IFN-g after two or three whole herd tests becomes questionable. The lower specificity with high reactor removal rate, and relatively high test cost makes the policy very expensive for both farmer and tax payer in persistently infected herds as discussed.
- For persistent herds, looking to provide more information about wildlife biosecurity but farmers have difficulty in investing large sums of money without seeing a farm where it has been put into practice and worked – concept of ‘model farm’. Demonstarion events are planned from 2016.

5.2 Unusual bTB breakdowns

- In the northern HRA of Oxfordshire, 4.5km from the Edge, towards the end of 2015 two unusual breakdowns occurred centred around pasture grazing in two adjoining fields. On one of the farms, a beef fattener, high reactor numbers occurred in two groups of yearlings: 59 out of 106 animals, 43 having visible lesions at post-mortem. Of the 400 plus animals on the farm, the difference in management of these two groups were that they were fed supplementary food at pasture consisting of a home mix containing molasses whereas none was given to any other groups. Two badgers had also been seen walking around the area in the middle of the day during the summer, a behaviour possibly associated with TB infection. Three months later, the neighbouring suckler herd broke down with infection focused in a group of cows and calves grazed in the adjacent fields: 23 reactors with 16 visibly lesioned. None of the other cattle on the farm were affected. Supplementary feeding at grazing was also practised. The most likely transmission route was concluded to have been close contact with potentially sick infected badgers probably encouraged by the supplementary feeding at pasture.

5.3 Other Testing Measures

- Discretionary exemptions to fatteners are only given to those with complete annual turnover, permanently housed, no births and all are finished and go direct to slaughter.
- No hotspots were established in the Edge during 2015.
- Overdue tests are rare having been managed intensively by the SE TB delivery team.

5.4 Other Control Measures

- Regional meetings held with farmers and OVs as requested and co-ordinated by the regional NFU representative.
- Continued meetings of representatives of TB delivery team with enforcement bodies.
- The SE TB Eradication Board has been looking at raising money for surveying road traffic accident badger carcases for TB. Consequent to the Defra initiative to do this in the Edge area, this focus is now shifting to the LRA particularly the area close to the HRA and Edge in West Sussex. Plans are underway to hold a TB conference in early summer 2016 to educate vets in practice about TB with a regional slant, recognising that there is a hunger for more information in this sector. If successful, this may be repeated at another location in the South East later on in the year.

The Animal and Plant Health Agency is an Executive Agency of the Department for Environment, Food and Rural Affairs working to safeguard animal and plant health for the benefit of people, the environment and the economy.