

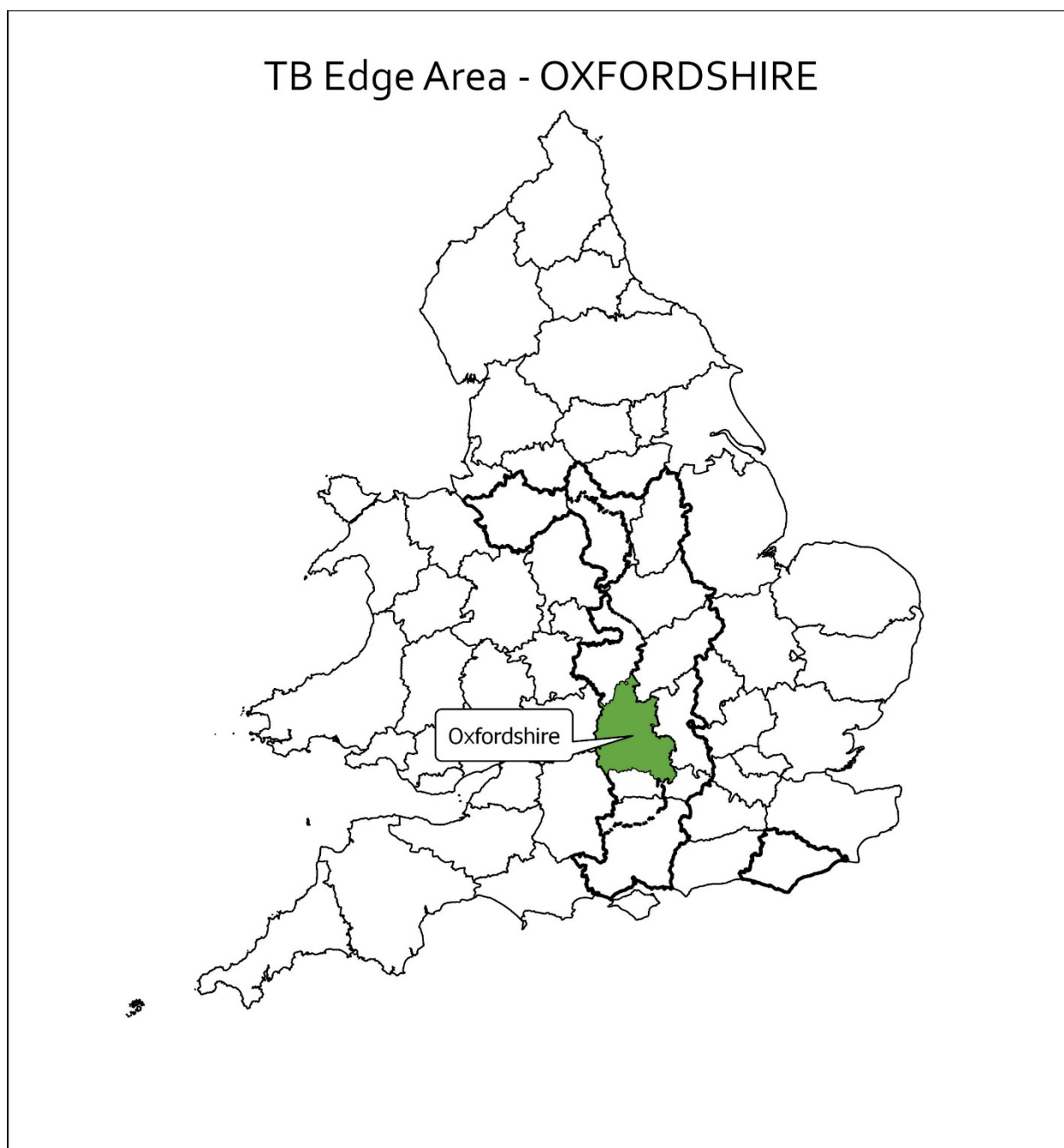


Year End Descriptive Epidemiology Report: Bovine TB Epidemic in the England Edge Area

Delivery Area: Southern

Name of County: Oxfordshire

Year-end report for: 2018



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Executive Summary

1. The Edge Area has a low but recently rising incidence of infected herds. **Oxfordshire** is part of the Edge Area that was established in 2013 as part of the Government's strategy to achieve Officially Bovine Tuberculosis Free (OTF) status for England by 2038. Originally, only the northern, eastern and southern parts of the county were included in the Edge Area established in 2013. The rest of the county was part of the High Risk Area (HRA) until 1st January 2018, when the HRA portion of Oxfordshire was incorporated into the Edge Area. This end of year report describes the bovine tuberculosis (TB) epidemic in the whole county of Oxfordshire in 2018.
2. **Local cattle industry.** Farms in Oxfordshire are predominantly medium sized suckler herds. Large herds tend to be dairies in west Oxfordshire and finishing units in the rest of the county, including several Approved Finishing Units (AFUs). Purchases are mainly from the High Risk Area (HRA) and neighbouring Edge Area counties. Dedicated Sales for TB Restricted Cattle (Orange markets) in the south west are the main outlet for calves from restricted herds. Last year was an unusually dry summer increasing the use of supplementary feed during grazing which may be contributing to an increased risk of wildlife contact.
3. **New breakdowns of TB.** The number of breakdowns in the last three years has remained more or less the same with a lower incidence this year possibly due to breakdowns in Oxfordshire becoming persistent. The prevalence has plateaued at 10% of herds under restrictions at any given time during the last three consecutive years.
4. **Risk pathways for TB infection.** Wildlife is the most commonly reported likely source of infection in Oxfordshire. This has been more evident during the last three years confirming a pattern of breakdowns, suspected to have a wildlife source, moving eastwards from the Oxfordshire border with the HRA.
5. **Eastern clusters.** Of particular concern is the increase in the number of breakdowns with a suspected wildlife source in the eastern corners of the county near the Buckinghamshire border. Three clusters were identified here: north-east (Somerton cluster), central east (Chinnor cluster) and south east (Henley cluster). Genotype, Disease Report Form (DRF) assessment and Whole Genome Sequence (WGS) analysis of *M. bovis* isolates has demonstrated a close genetic link between cases within these clusters, which can be explained by wildlife contact and spread.
6. **Role of other species.** Very little information received in 2018. Only one case reported in wild deer with confirmed local genotype in the Henley cluster. No suspected cases in domestic species.
7. **Disclosing tests.** Routine surveillance testing of herds accounted for half of the new breakdowns disclosed in 2018, whilst the other half were found during post-breakdown surveillance tests (6 and 12 month tests) as recurrence. In addition, some were detected by pre-movement testing (PRMT).
8. **Impact of TB breakdowns and reactor numbers.** In 2018 compulsory parallel interferon gamma testing for herds which experienced an Officially Bovine Tuberculosis Free Status Withdrawn (OTFW) breakdown was extended from the original Edge Area portion of the county to include the former HRA of the county also. Impact was particularly felt by farmers who suffered recurrent breakdowns with high reactor numbers.
9. **Risks to the Low Risk Area (LRA).** The continued expansion of the endemic front eastwards is a threat to the LRA. The neighbouring Edge Area county of Buckinghamshire acts as a buffer zone between Oxfordshire and the LRA. It is the only county largely free from endemic TB before

reaching the LRA. Efforts should be focused on controlling TB near its borders such as by increased radial testing.

10. **Risks from the High Risk Area (HRA) and/or other adjacent Edge Area counties.** Oxfordshire has become as high risk as neighbouring HRA counties. Increased cattle TB controls might reduce the risk to Oxfordshire, but continued spread of infected wildlife from the HRA seems inevitable without wildlife interventions. There is some evidence of movement of the endemic front from the Edge Area county of Warwickshire into the north of Oxfordshire.
11. **Forward look.** The incidence of bovine TB has remained the same since 2016, but the epidemiological picture has become more complex with endemic infection spreading to more of the county. This does not favour the long term objective of achieving OTF status in Oxfordshire for 2025. Eradication of bovine TB will require some form of wildlife intervention as well as tighter control of cattle movements from farms in the HRA into the Edge Area. Early detection of infection through more frequent surveillance testing of herds (six monthly testing started in 2018) and the mandatory use of interferon gamma testing to improve the detection of residual infection in cattle herds with OTFW breakdowns will help. However, a stronger message about the need to increase biosecurity alongside some form of wildlife controls in the county is paramount to stop the spread of bovine TB from HRA to LRA through this Edge Area county.

Introduction

A key action in the implementation of the Government's objective to achieve Officially Bovine Tuberculosis Free (OTF) status for England by 2038 was to recognise the different levels of TB in different parts of the country and to vary the approach to control accordingly. To this end three management regions or zones have been established. Overall, the Edge Area has a low but recently rising incidence of infected farms and control efforts are seeking to slow down and reverse geographic spread, and reduce the incidence rate, with the aim of obtaining OTF status for this area as soon as possible. This report describes the epidemiology of bovine TB in Oxfordshire, which forms part of the Edge Area since its establishment in 2013 (see Appendix 1).

Changes to the Edge Area in 2018

On 1st January 2018 the Edge Area boundary was expanded westwards to absorb fully into the Edge Area the former HRA parts of the five previously split counties of Cheshire, Derbyshire, Warwickshire, Oxfordshire and East Sussex. The reports for those five counties will focus on incidents of bovine TB in the whole county, but noting key differences between the old and new parts where relevant.

From January 2018 annual routine herd surveillance testing was replaced by six monthly herd surveillance testing in the whole county of Oxfordshire.

Cattle industry in Oxfordshire

Almost two thirds of herds contain fewer than 100 cattle (Figure 1). There is a mixture of beef suckler, dairy, and fattening units in Oxfordshire (Figure 2). Many dairy units have dispersed their herds and changed production to smaller beef suckler herds. However, relatively high concentrations of large dairy farms still exist in south west Oxfordshire. The majority of fattening units in Oxfordshire source cattle from the HRA, particularly the south west of England, through markets or directly from farms. A smaller number purchased locally from farms and Thame market (Oxfordshire).

There are a few large finishing units, some of which have converted to AFUs since 2013, providing weekly quotas to abattoirs of cattle finished directly from buildings to fulfil supermarket contracts. Fewer applications for AFUs were received in 2018 compared to previous years, raising the total number of AFUs in Oxfordshire by just one to nine in 2018 (eight in 2017, just four in 2016).

The Orange Market at Cirencester in the HRA county of Gloucestershire has provided a valued outlet for TB restricted cattle into AFUs across the south. Some pedigree cattle breeders are located within the county providing pedigree breeding cattle for the whole country. There are also a handful of organic farms, both dairy and beef.

The majority of cattle are grass fed whilst outside, with supplementation for dairy cows and young stock. This was especially evident in 2018 at the end of summer after an unusually long dry season which caused severe grass shortage and subsequent extra supplementary feeding at pasture may have increased cattle-wildlife interactions. Fattening cattle on large units are often fed with blends of grass and maize silage and food by-products. Use of mineral licks at pasture is variable but where used, almost always are molasses based and accessible to badgers.

There is a trend towards a reduced dependence on maize silage as conserved winter forage compared to recent years but maize used as pheasant cover by farmers is increasingly common in the county (own farm shoots).

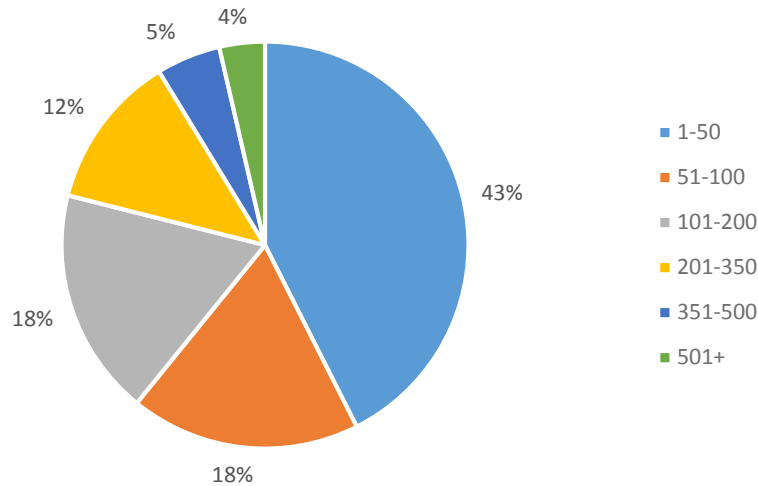


Figure 1: Proportion of cattle holdings by herd size in Oxfordshire in 2018 (n=471)

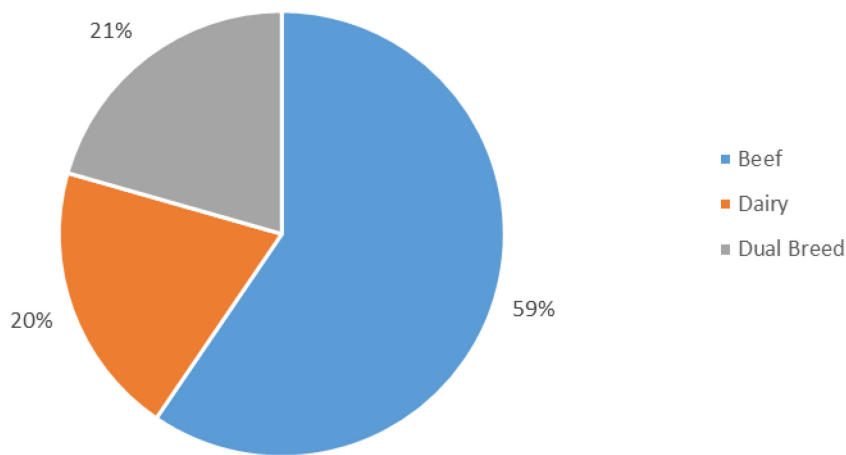


Figure 2: Proportion of cattle holdings by breed purpose in Oxfordshire in 2018 (n=720)

(Note: the total number of holdings in Figure 1 varies from the total number of holdings in Figure 2 because holdings were counted more than once when cattle with different breed purposes are present.)

Overview of bovine TB epidemic in Oxfordshire

History of bovine TB in Oxfordshire

Three measures are used to assess the level of bovine TB in this report.

Firstly, the number of new herd breakdowns that were disclosed in each year.

Secondly, the annual herd incidence rate, reported as the number of new incidents per 100 herd-years at risk (100 HYR). This is the number of new TB incidents detected in the year, divided by the time those herds were at risk of contracting TB. The 100 HYR incidence rate is used in this report as it accounts for different intervals between tests in herds that other incidence measures do not¹, such as new TB incidents per number of herds or tests.

¹The 100 HYR incidence rate measure is described further in 'Bovine tuberculosis in Great Britain in 2018: Explanatory Supplement to the annual reports' <https://www.gov.uk/government/publications/bovine-tb-epidemiology-and-surveillance-in-great-britain-2018>

Thirdly, the annual end of year prevalence. This is the number of herds under restriction due to a TB incident at the end of the reporting year, divided by the number of active herds at that same point in time, and provides a snap shot of the burden of TB on the local cattle industry.

For all three measures, both breakdowns where lesions at post-mortem or *M. bovis* in tissue samples have been identified (officially tuberculosis free status withdrawn, OTFW) and breakdowns where lesions at post-mortem or *M. bovis* in tissue samples have not been identified (officially tuberculosis free status suspended, OTFS) are included. However, TB incidents in non-grazing approved finishing units (AFUs) are not included in the prevalence and incidence calculations in the Edge Area reports due to the limited epidemiological impact of these cases. Furthermore, herds restricted due to an overdue test rather than a TB incident are also excluded from calculations.

Prior to 2004, breakdowns in Oxfordshire were all attributed to infection from purchased cattle, which cleared quickly and rarely reoccurred. Thereafter, breakdowns started to appear in significant numbers in the Faringdon area just west of the Edge Area in south Oxfordshire bordering Gloucestershire – a high incidence area. Initially these breakdowns were of several genotypes including 17:a, 17:b, 17:e, 74:a and 10:a (genotypes prevalent in Wiltshire, Gloucestershire and this area of Oxfordshire). From 2010, breakdowns have mostly changed genotype to 10:a – probably a reflection of the increasing prevalence of this genotype in wildlife as infection has spread from the neighbouring HRA counties.

Since 2014, when reports were started for the Edge Area, new areas of probable wildlife source infections for genotype 10:a appeared north, east and south-east of the Faringdon area. The infection initially appeared as isolated clusters but later joined up with the endemic Faringdon area, situated to the west of Oxford, as new breakdowns have occurred and filled in these gaps.

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

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

In 2017 and 2018 new clusters appeared to be now established in the east of the county close to the Buckinghamshire border. A specific genotype previously unknown (17:g) was isolated in three breakdowns in 2017 and another three in 2018 in the Thame-Chinnor area within 5km radius of each other (one of them a completely closed herd with no contact with neighbouring herds). This strongly suggested that a new genotype (perhaps mutated from a local one or purchased originally) was now established in wildlife in this area very close to Buckinghamshire.

Other new genotypes (perhaps mutations of local ones) have been isolated in breakdowns close to each other, also pointing to local wildlife spread. These are genotype 17:a in north west Oxfordshire, spoligotype 130 in north central Oxfordshire, genotype 11:a in south east Oxfordshire, genotype 74:a in south west Oxfordshire, isolated incursions of genotype 17:b and genotype 9:d, and one isolated case of genotype 9:b (with no evidence of purchase and never previously isolated in Oxfordshire).

Genotype 10:a is still the predominant genotype affecting the whole county, and is well established in other reported clusters in the Somerton area (north) and the Henley on Thames area (south) moving from west to east.

The increasing number of TB breakdowns in Oxfordshire over the years (Figure 3) can still be attributed to the purchase of infected cattle from HRA and Edge Area counties (from herds with a history of TB in the previous three years). More recently there is increasing evidence of infection in local badgers having now spread to east Oxfordshire. Both the level of recurrence and the number of persistent breakdowns (greater than 18 months duration) show an increased re-infection rate of herds. This is despite the deployment of interferon gamma testing in OTFW breakdown herds in the original Edge Area since 2014 and in the former HRA part of the county in 2018. The number of persistent cases rose from five in 2017 to ten in 2018.

As seen in Figures 3a and 3b there have been similar numbers of TB breakdowns in the last three years since 2016.

The annual incidence rate (Figures 4a and 4b) has been increasing since 2009, but levelled off after 2016. The largest rate of increase occurred in the period between 2014 and 2016 where incidence doubled from 9.1 to 18.1. There was a decrease in incidence in 2018 compared to 2017 and 2016 even though the total number of breakdowns in 2018 (Figure 3) was the highest of the last decade. This is because the denominator of the incidence calculation, number of 100 herd years at risk, rose to 470 in 2018 (from 419 in 2017). In the years prior to 2018 the denominator had been steadily decreasing over the years as more herds were taken out of the calculation due to the rising number of breakdowns especially of long duration (mostly seen in the former HRA portion of the county). It is unclear what has caused the reversal of the downward trend in 2018 but it will be interesting to see what happens in 2019 and whether this becomes an established pattern or just a one off.

Figures 5a and 5b show the prevalence of herds under TB2 restrictions at the end of each year. The continued increasing trend is explained by more herds remaining under restriction for long periods of time including breakdowns which started in previous years.

The trends for all these measures are very similar for the former HRA part and the original Edge Area of Oxfordshire. This shows that both parts of the county behave in the same way, the original Edge Area being larger than the former HRA, and now with the whole county under the same TB eradication rules.

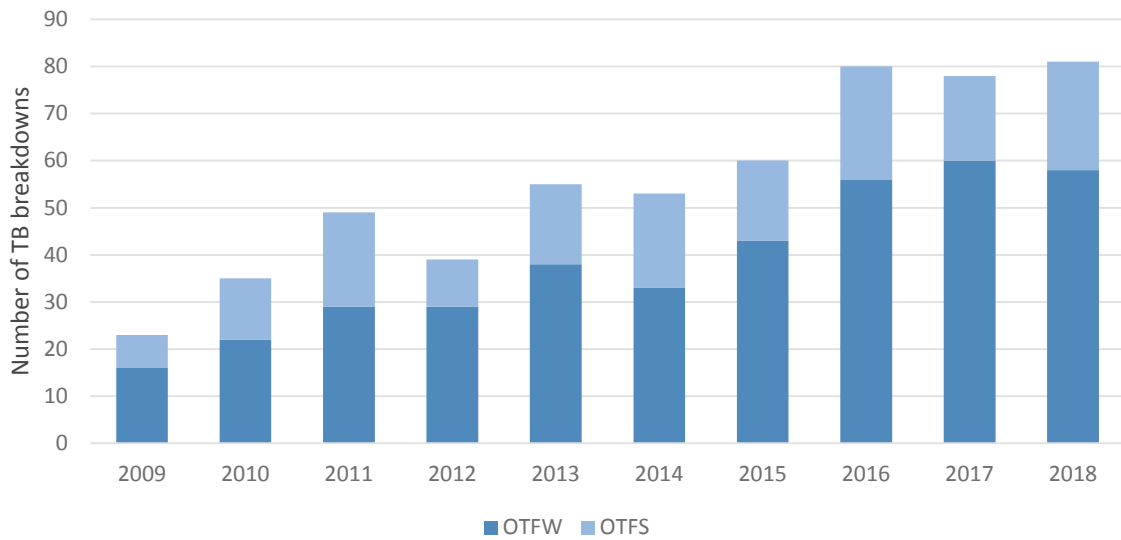


Figure 3a: Annual number of new TB breakdowns in Oxfordshire, 2009-2018

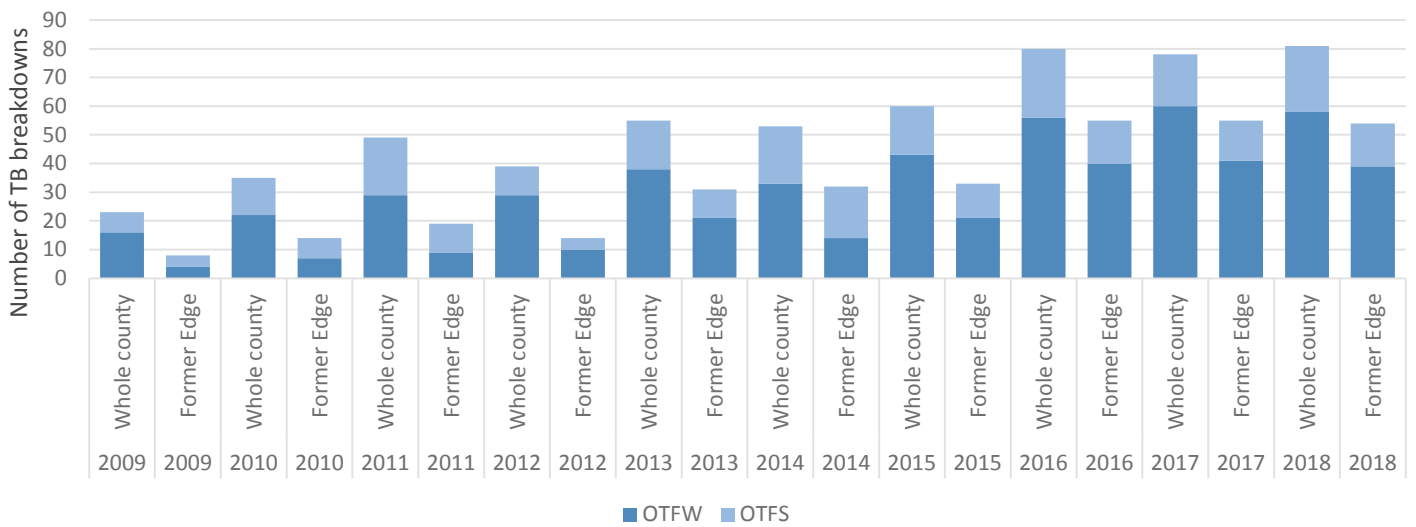


Figure 3b: Annual number of new TB breakdowns in Oxfordshire, 2009-2018 for previously split county

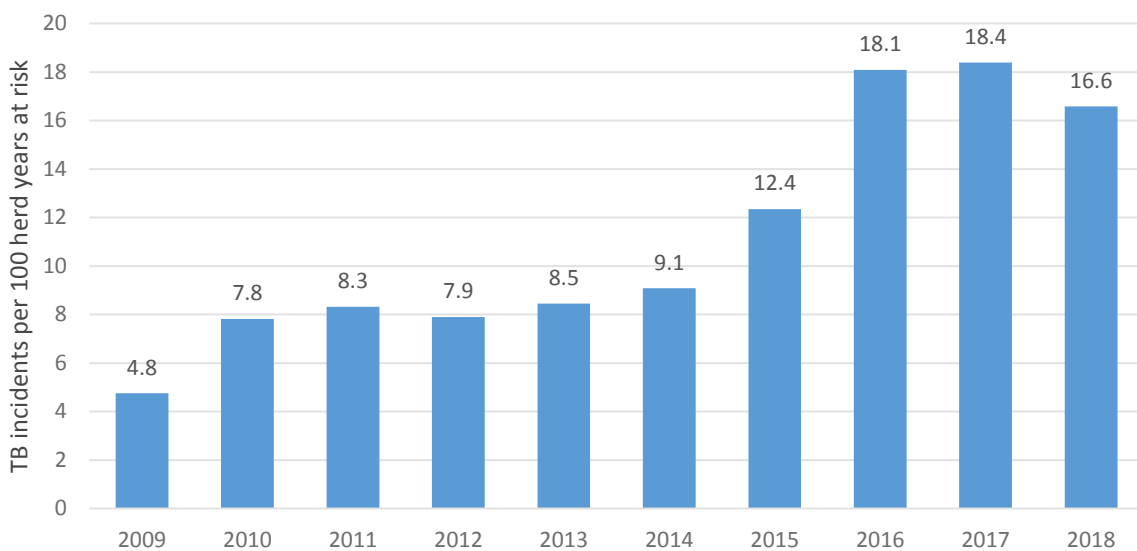


Figure 4a: Annual incidence rate (per 100 herd-years at risk) for all new breakdowns (OTFW and OTFS) in Oxfordshire 2009-2018

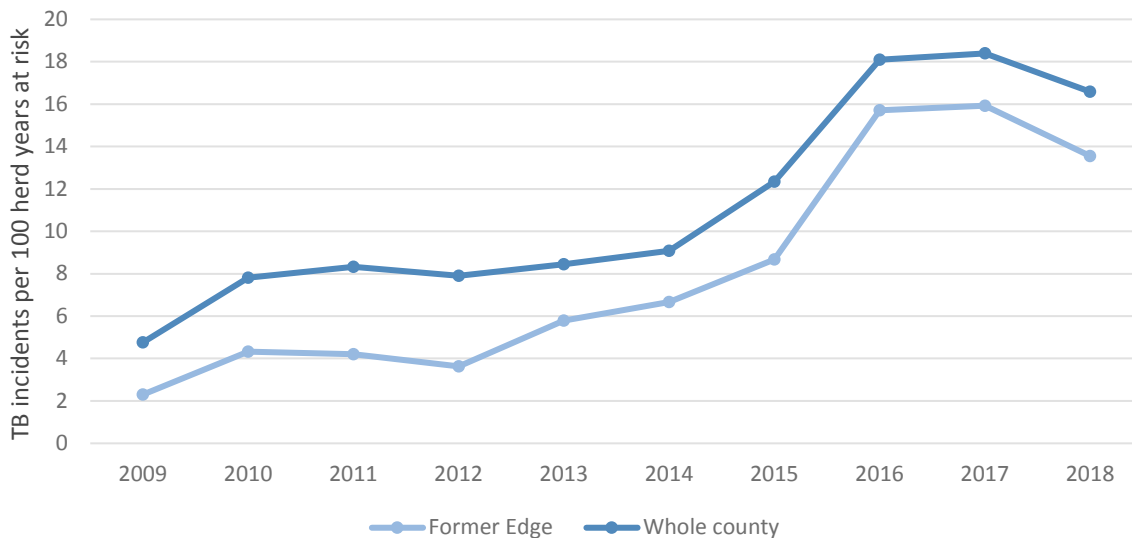


Figure 4b: Annual incidence rate (per 100 herd-years at risk) for all new breakdowns (OTFW and OTFS) in Oxfordshire 2009-2018 for previously split county.

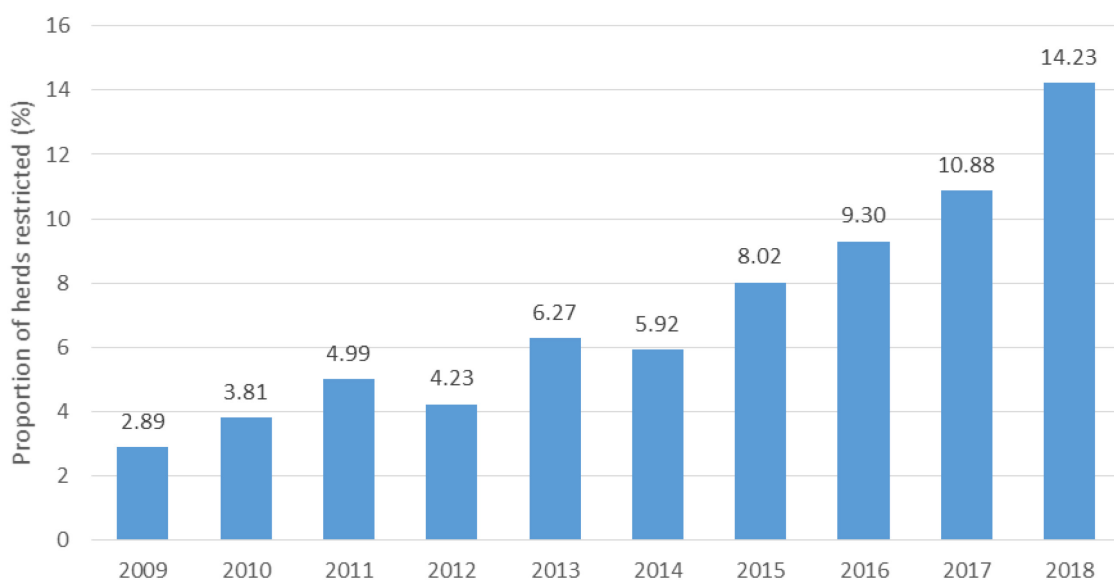


Figure 5a: Annual end of year prevalence of restricted herds in Oxfordshire, 2009-2018

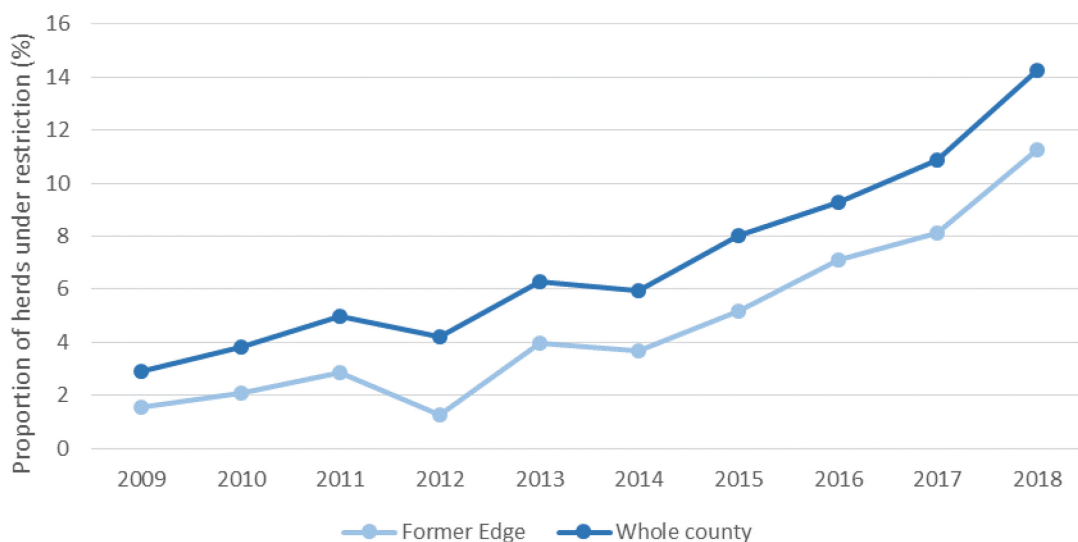


Figure 5b: Annual end of year prevalence of restricted herds in Oxfordshire, 2009-2018, for previously split county

Geographical distribution of bovine TB cases (new and ongoing) in Oxfordshire

Continuing the trend of previous years, the distribution of breakdowns has continued to advance eastwards. As shown in Figure 6, three main clusters (shown with elliptical shapes) with presumptive wildlife source are expanding in addition to the established clusters near the HRA border (shown with a black rectangle).

These developing clusters appearing in the east of the county are:

a) Deddington-Somerton area (green circle) in the north east of the county.

The most common genotype found in this area and confirmed in previous years is the local genotype 10:a. This appears to have mutated over the years in the local area.

Two new breakdowns in 2018 were identified with spoligotype 130 (in addition to two spoligotype 130 breakdowns detected in 2017) which seemed to be unique to this area. Information from whole genome sequencing (WGS) of the two spoligotype 130 isolates and two more isolates from nearby breakdowns (6 to 10 km away) with genotypes 10:h and 10:a (all from 2018) showed close genetic relationship with only one SNP (single nucleotide polymorphism) difference between them. This strongly suggests that this cluster of four cases in total this year has been exposed to a common source of infection. This is most likely to have been wildlife as there was no contiguous inter-herd contact, no cattle movements between the herds nor cattle movements from the same source. The APHA WGS database currently contains isolates cultured mostly from June 2017 onwards and so only shows a partial picture of the geographical areas which may be affected.

b) Henley-on-Thames (blue circle) in the south east corner of the county.

Genotype 10:a is the most commonly found genotype in this area including a confirmed case in wild deer reported in 2018 which was found very close to the Buckinghamshire border.

In 2017 and 2018, cases of genotype 11:a (homerange in the south west of England) started to appear in this area: two this in 2018 and two in 2017. They were first thought to be linked to purchases but recent cases shed doubt on this, suggesting a potential wildlife source too. Historically, genotype 11:a has been found in five of thirteen OTFW cases in the south east of the county.

c) Chinnor (orange circle) in the most eastern corner of the county, very close to Buckinghamshire.

In 2017 a new genotype NT:7-5-5-4*-3-3.1, probably a mutation of genotype 10:a, was found in three breakdowns situated very close to one another but with no links between them (one was a completely closed herd). This suggests infected wildlife in the area as the most likely common source. In 2018 this new genotype was reclassified as genotype 17:g. At the beginning of 2018 three more cases (less than 3km apart) had this same genotype, confirming this new cluster. WGS has shown that they are all closely related genetically (zero to two SNPs difference).

Radial testing generated by OTFW cases near the border which started in 2018 have not found any farms affected in Buckinghamshire with the same genotype and therefore the spread may still be limited.

The established areas of TB in the west of the county (black rectangle) remain the same in the highest cattle density areas - in the north of the county near Banbury and Epwell and in the south west of the county - where there is a concentration of large dairy herds. In 2018, the whole county became Edge Area joining the western strip of former HRA with the rest of the Edge Area in Oxfordshire. The epidemiology of both areas has been very similar: predominantly wildlife source of infection with genotype 10:a, high rate of recurrence and an increased number of persistent breakdowns.

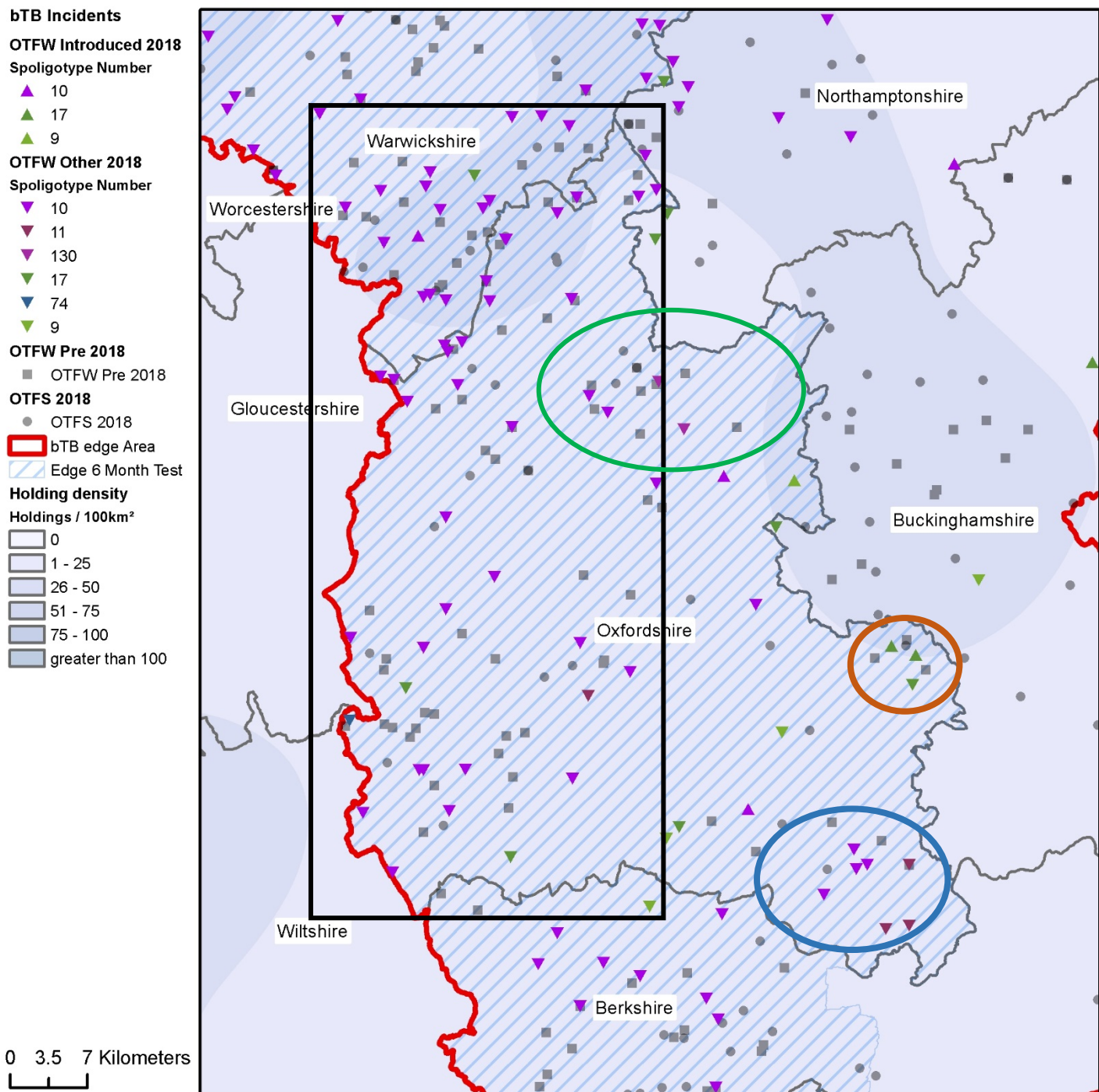


Figure 6: Geographical distribution of all new TB breakdowns (OTFW and OTFS) in 2018 and pre 2018 OTFW breakdowns still ongoing at the end of the report period overlaid on a cattle holding density map, with a cattle density map for the area inset

Main genotype 10:a – the predominant genotype of *M. bovis* continues to be genotype 10:a in Oxfordshire. This mirrors the presumptive wildlife endemic area illustrated by the grey 3km circles in Figures 7a and 7b attributed to wildlife. The green triangles and pentagons with hatched radial zones represent new cases in 2018 (including wild deer) and green without hatched radial zones represent cases new in 2017. These mainly cover the western side of the county bordering the HRA. Also attributed to wildlife with genotype 10:a is a portion of the Henley cluster and the Somerton cluster in the east of the county.

Other genotypes attributed to wildlife referred to in Figures 7a and 7b and well established in 2018 are: genotype 17:g represented by dark green triangles and blue hatched radial zones in the Chinnor area, spoligotype 130 in the Somerton area (including related cases of genotypes 10:h and 10:a

marked with stripes across) and genotype 11:a in the Henley area. The latter, genotype 11:a could represent movement into the area from the HRA and consequent local spread (WGS information is pending). The three former new genotypes started appearing in 2017 probably as a result of mutations of local genotype 10:a.

Historically there has been a narrow band running from west to east also attributed to wildlife infection involving spoligotype 17 (genotypes 17:a and 17:b) and genotype 9:d but no cases in this area were found in 2018. There was a persistent breakdown ongoing with genotype 17:a in 2018, located in north west Oxfordshire, and most likely attributed to a wildlife source.

An isolated case of genotype 17:e in south Oxfordshire may represent spread of the genotype 17:e endemic area. The only previous case in this area with this genotype was in 2011 in Uffington (near the county border with Wiltshire and Gloucestershire) where there is a genotype 17:e homerange.

Some breakdowns may represent wildlife movements across the county border into Oxfordshire. Several cases of genotype 10:a, one case of genotype 10:7-6-5-4*-3-3.1 and genotype 10:j have been detected near the border with Warwickshire and similar cases have occurred on the other side of the border. Although cattle movements (purchases) cannot be ruled out, the pattern of breakdowns suggests wildlife involvement. A case of genotype 74:a in 2018 near the border with the HRA where the same genotype has occurred in the adjoining counties of Gloucestershire and Wiltshire suggests a common wildlife source because other transmission pathways have been ruled out.

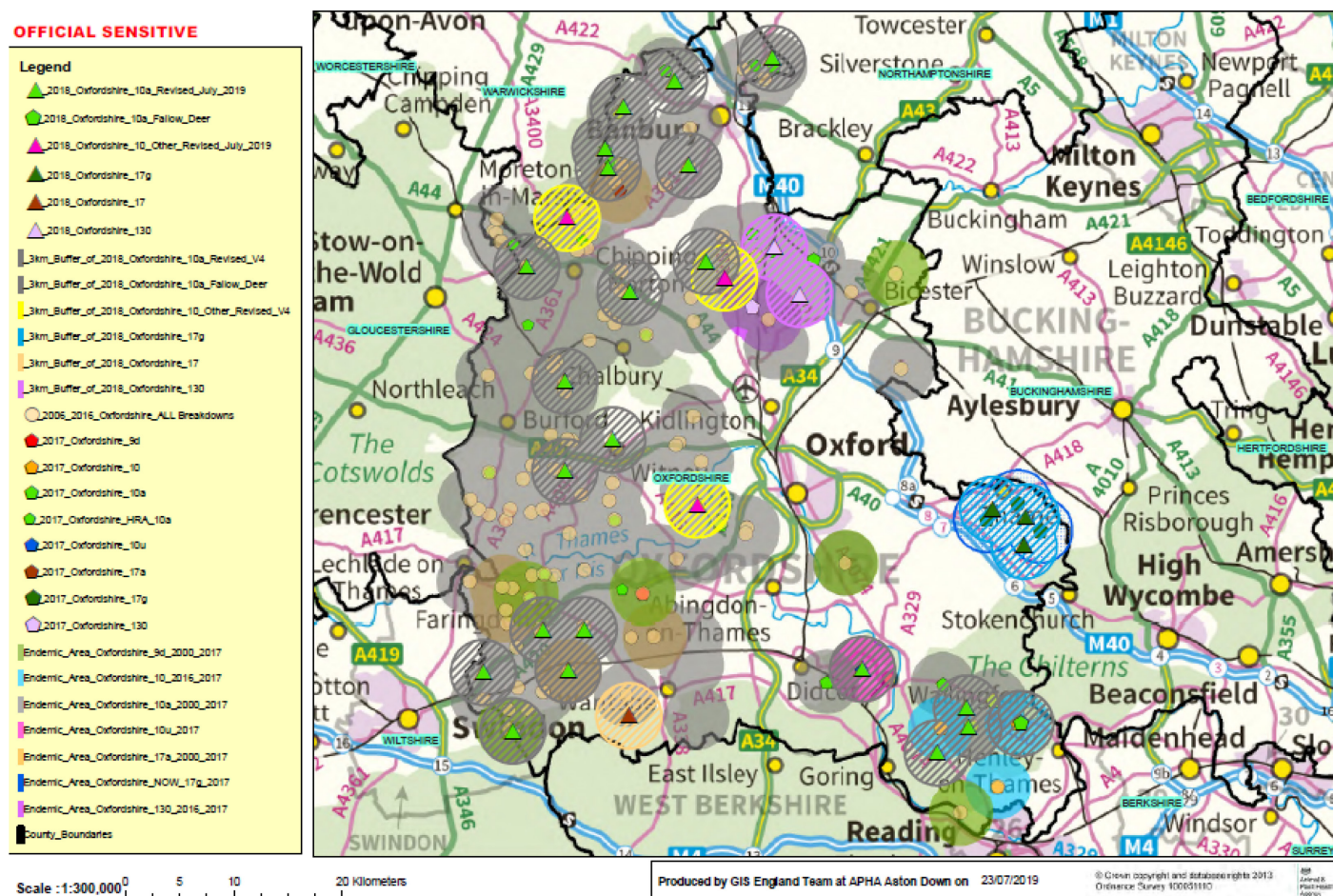


Figure 7a: Genotypes detected in Oxfordshire, where a wildlife source was attributed as most likely, providing an indication of endemicity within local wildlife populations (OTFW breakdowns only)

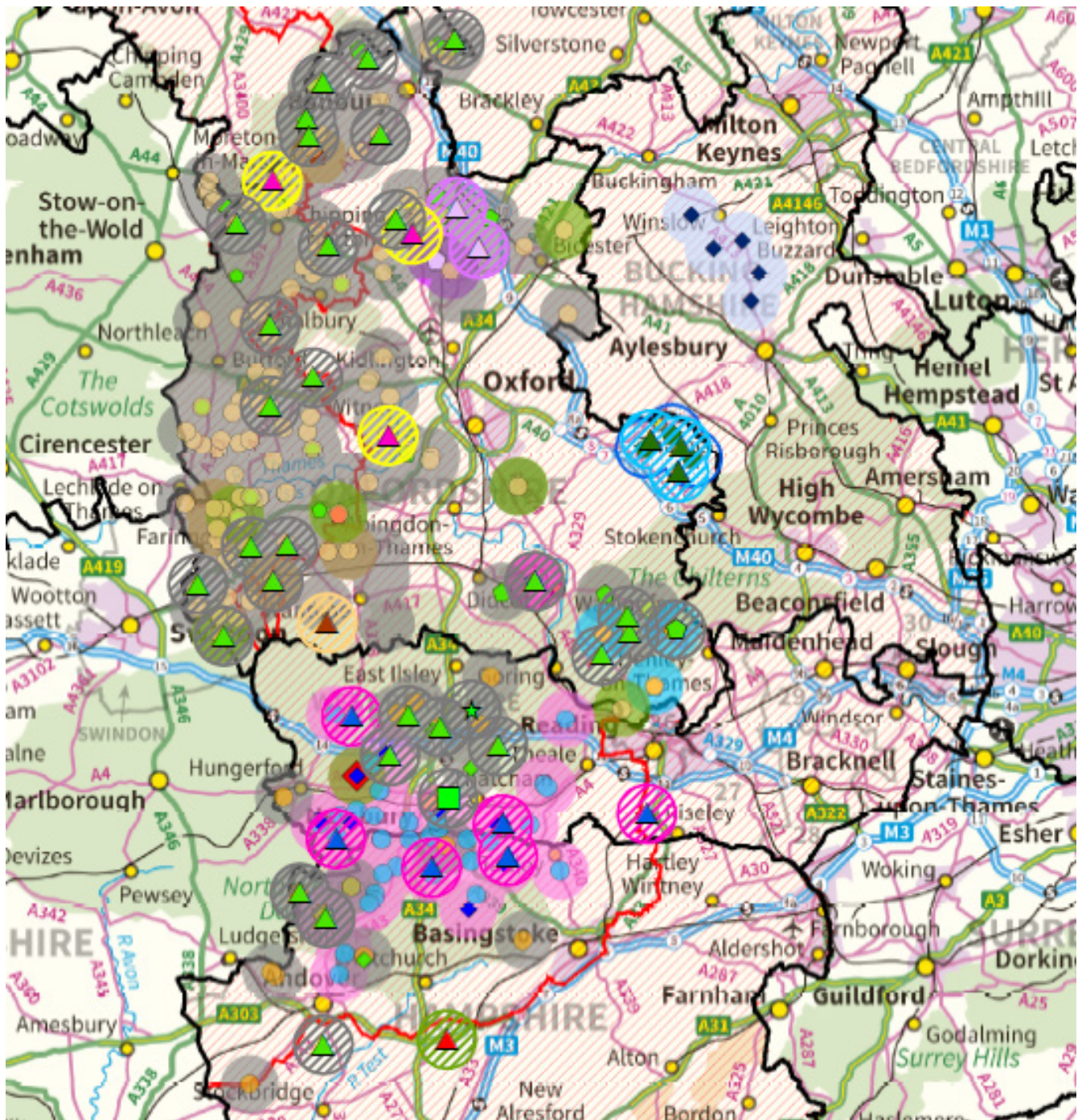
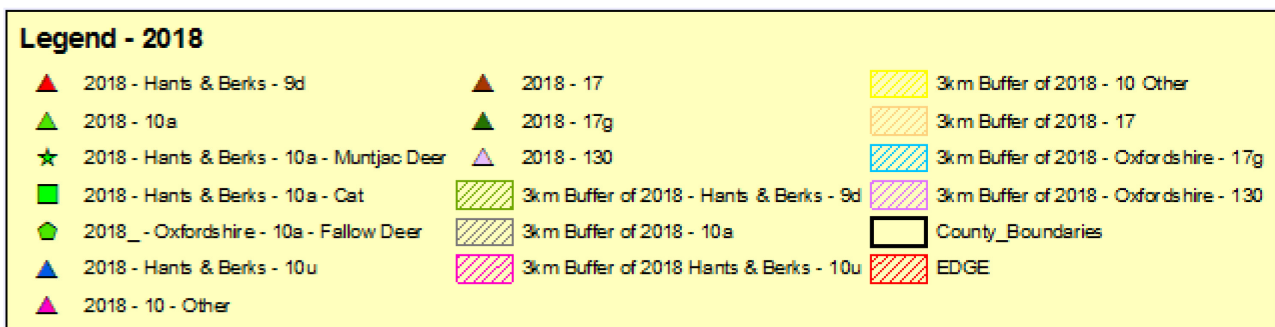


Figure 7b (legend below): Overview of Oxfordshire, Berkshire, Hampshire and Warwickshire genotypes attributed to wildlife source breakdowns (OTFW breakdowns only). Note for main genotypes - grey circles (including those hatched for 2018 cases) represent 10:a, pink - 10:u, light blue - 17:g, yellow – genotypes related to 10:a.



Legend - 2000-2017

 Bucks 2017 - 17b	 Oxfordshire 2017 - 17g	 3km Buffer - Oxon, Hants & Berks 2000-2017 - 9d
 Oxfordshire 2006-2016 - ALL Breakdowns	 Oxfordshire 2017 - 130	 3km Buffer - Oxfordshire 2016-2017 - 10
 Oxfordshire 2017 - 9d	 Hants & Berks 2006-2016 - 10a	 3km Buffer - Oxon, Hants & Berks 2000-2017 - 10a
 Oxfordshire 2017 - 10	 Hants & Berks 2006-2016 - 10u	 3km Buffer - Oxon, Hants & Berks 2000-2017 - 10u
 Oxfordshire 2017 - 10a	 Hants & Berks 2017 - 10a	 3km Buffer - Oxfordshire 2000-2017 - 17a
 Oxfordshire HRA 2017 - 10a	 Hants & Berks 2017 - 10u	 3km Buffer - Oxfordshire 2017 - NOW 17g
 Oxfordshire 2017 - 10u	 Hants & Berks 2017 - 9d	 3km Buffer - Oxfordshire 2016-2017 - 130
 Oxfordshire 2017 - 17a	 3km Buffer - Bucks 2017 - 17b	 County_Boundaries

Cases west of Oxfordshire were mostly attributed to transmission from a badger source (Figure 8). Cases in the east of Oxfordshire were less likely to be attributed to wildlife due to the lack of evidence of local genotypes and homeranges established in this area, and therefore historical cattle movements (purchases) usually were weighted more in the risk pathway assessments.

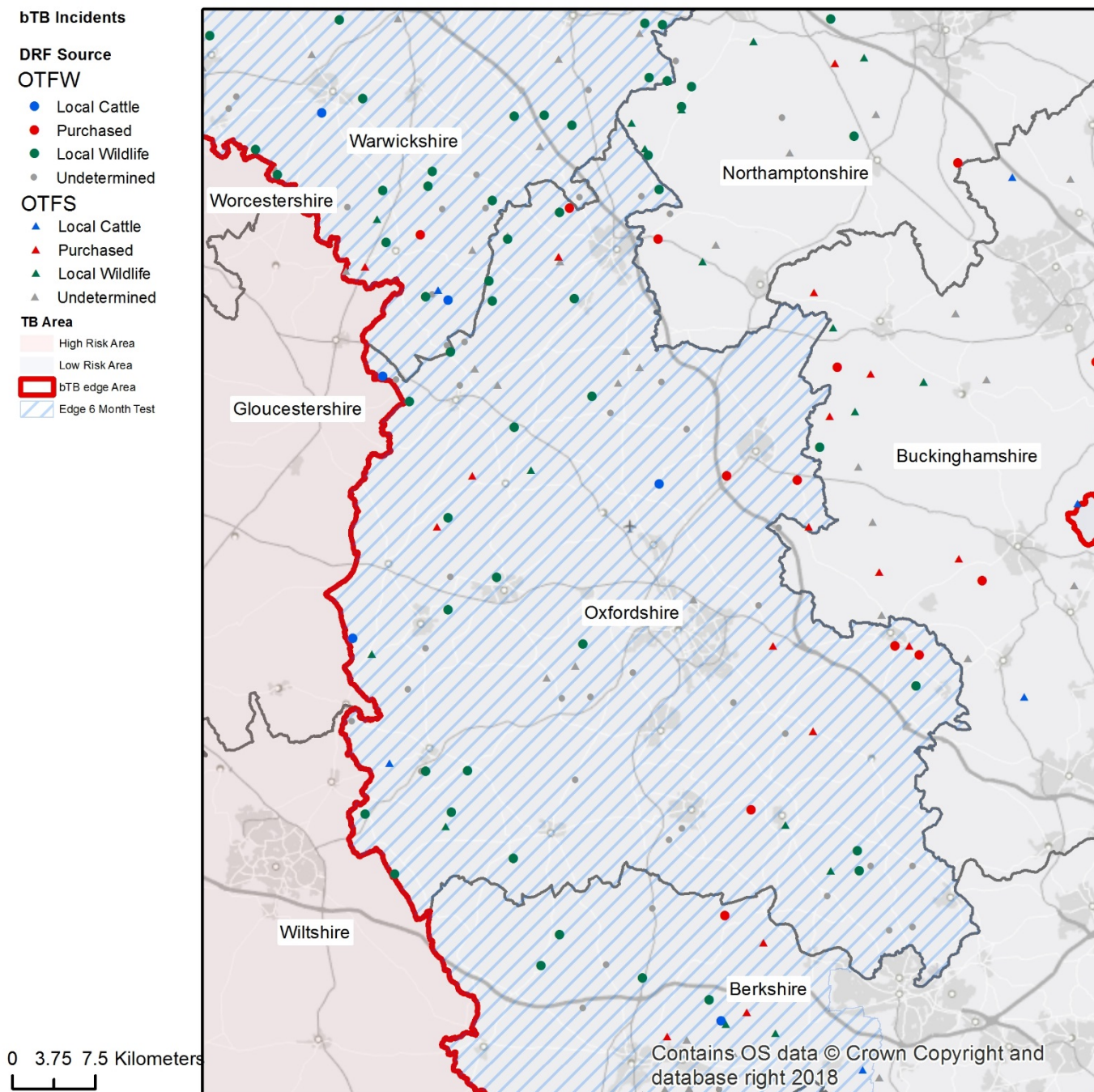


Figure 8: The most likely source of infection recorded, for all TB breakdowns (OTFW and OTFS) that started in 2018

Descriptive epidemiology of bovine TB in Oxfordshire

Characteristics of bovine TB in Oxfordshire:

As for previous years, breakdowns showed a predilection for medium/large herd size (100 to 300 cattle). Figure 9 shows that breakdowns were almost evenly distributed across the herd size categories compared to the overall frequency of distribution of herds according to herd size (Figure 1). The majority of herds affected were in the beef sector but this is also the most common sector in Oxfordshire.

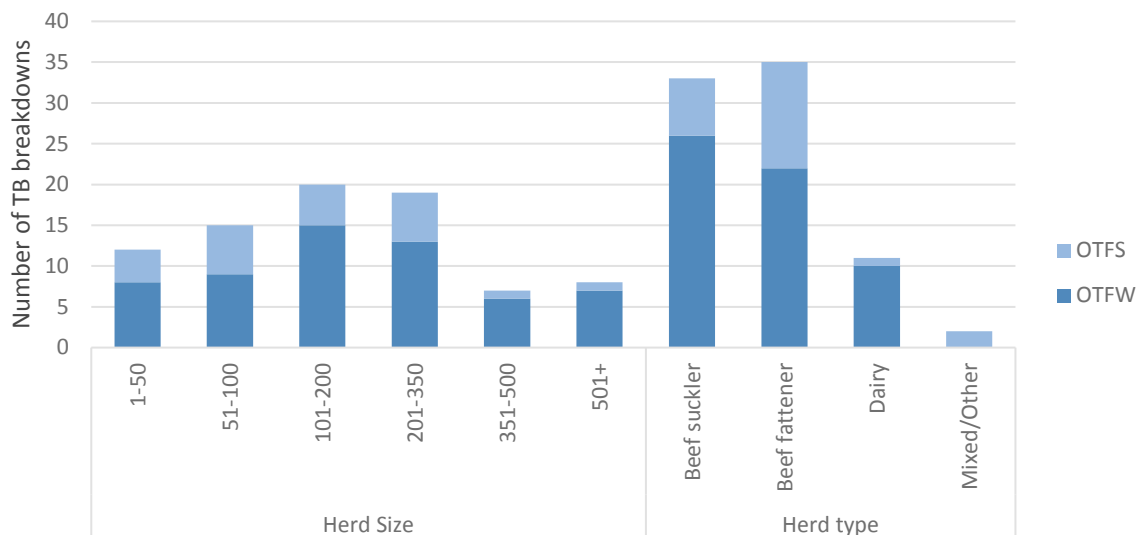


Figure 9: Number of new TB breakdowns (OTFW and OTFS) in Oxfordshire by cattle herd size and type.

The majority of TB testing is carried out in the winter months when the cattle are housed. This coincides with the end of summer grazing and is when wildlife infection appears to be more likely to be disclosed as shown in Figure 10 (more cases disclosed in October and November).

Six monthly routine herd testing should space out surveillance before and after grazing and provide more information as to whether infection is disclosed after housing or after grazing.

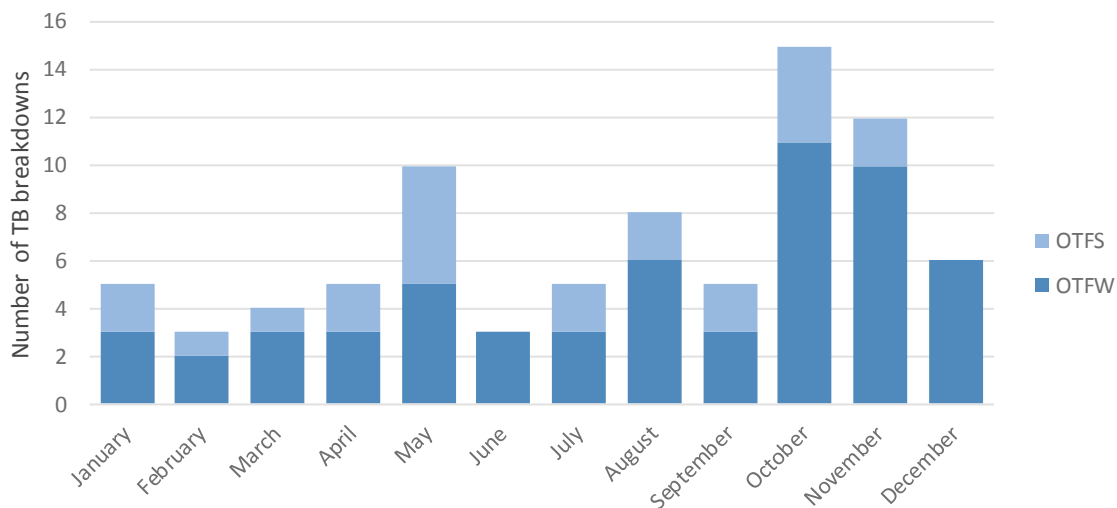


Figure 10: Number of new TB breakdowns (OTFW and OTFS) in Oxfordshire, by month of disclosure.

As shown in Figure 11, the predominant genotype in Oxfordshire is 10:a. The second most common genotype is 17:g but only found in a specific geographical area (Chinnor-Thame cluster). Genotype 11:a is also common near the border with Berkshire. Genotype 9:d and many other variations of spoligotype 10 are likely to be mutations from or precursors to genotype 10:a.

The genotype 10:a homerange is large, including neighbouring counties to Oxfordshire, and therefore provides less information as to whether infection is picked up locally or moved from these neighbouring counties via cattle movements compared to genotypes with much smaller homeranges. New mutations of genotype 10:a provide more information regarding local establishment and spread via local wildlife

to neighbouring farms. Future use of WGS should provide further useful epidemiological information for these cases.

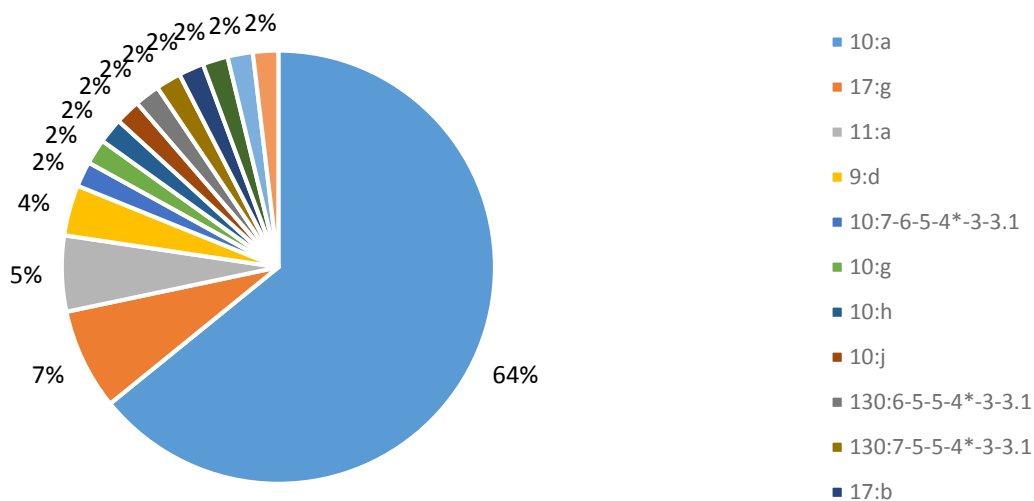


Figure 11: Genotypes of *M. bovis* (OTFW only) identified in Oxfordshire in 2018 (n=53).

The duration of breakdowns has increased in recent years in most OTFW cases (Figure 12). Multiple sources of infection and residual infection being picked up by more interferon gamma testing (necessitating further testing) might explain this trend. The number of persistent breakdowns (lasting over 550 days) increased in 2018 to ten cases compared to five in 2017. Note that Figure 12 refers only to breakdowns which closed in 2018 and therefore does not include the ongoing persistent breakdowns.

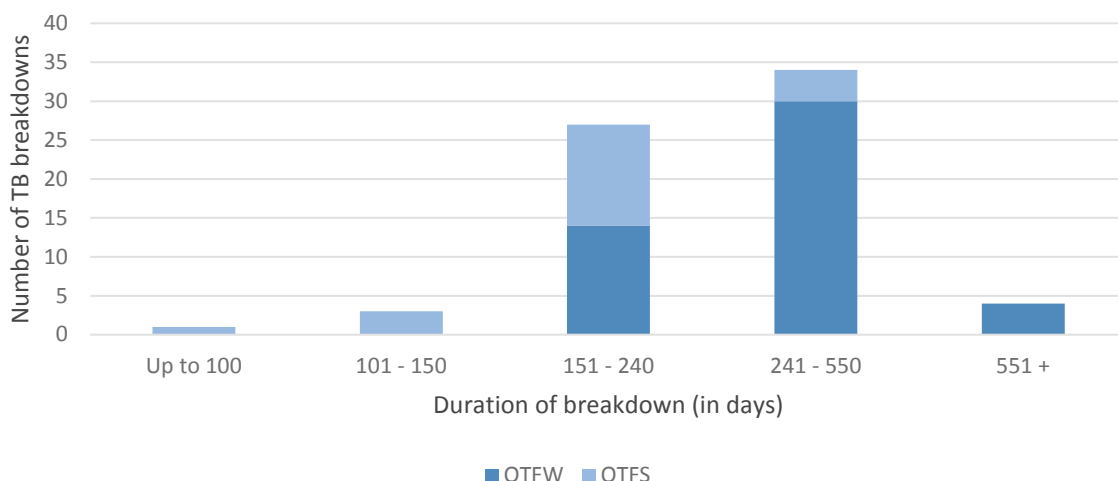


Figure 12: Duration of TB breakdowns (OTFW and OTFS) closed in Oxfordshire in 2018.

Risk pathways for TB infection in Oxfordshire

Establishing the route of entry of infection into a herd experiencing a new TB incident can be challenging. The Animal and Plant Health Agency (APHA) aims to complete an epidemiological assessment of all TB incidents in the Edge Area (both OTFW and OTFS), including a thorough on-farm

investigation. However where resource constraints exist, as many new incidents as possible are randomly selected or triaged for an investigation visit. Scrutiny of routinely collected data such as cattle movements and *M. bovis* genotypes (available for OTFW incidents only), combined with data from the on-farm investigation and knowledge of the local area epidemiological situation provides information which enables APHA case vets to assess and then rank the possible disease pathways.

A mathematical algorithm based on risk pathway data was used for the 2018 period to determine the relative contribution of different sources for each breakdown herd. However, this methodology also included those incidents where certainty about risk pathways was lower because of gaps in the epidemiological evidence. The effect of uncertainty has been increased by the inclusion of OTFS herds, where by definition, no genotype was determined. Therefore the relative proportions of each risk pathway are very approximate, and broad generalisations only can be made from these data.

A more detailed description of this methodology is provided in the Explanatory Supplement.

Figure 13 shows wildlife as the most likely source of TB in Oxfordshire. Cattle movement (mostly the purchase of cattle with undetected infection) although still significant is less likely to contribute to the relatively high incidence of TB in Oxfordshire. This has been the case in the last three years where there has been an increase in the proportion of badger source breakdowns compared to purchased cattle source.

An increased number of breakdowns are now attributed to residual cattle infection from a previous TB breakdown. A high proportion of all breakdowns have had a history of TB (62 out of 81 breakdowns, of which 39 had a history of TB in the last three years). This is much more evident in the former HRA of Oxfordshire where, prior to 2018, interferon gamma testing was not routinely deployed to clear herds of TB infection. This resulted in a higher chance of leaving infection undetected by skin testing alone. It is very difficult to distinguish between badger source infection and residual infection.

Very few breakdowns were attributed to contiguous cattle-to-cattle spread and never as a primary source. This was considered as a low likelihood source in a few cases when neighbouring farms had a history of cattle straying or hypothetical contact with neighbouring cattle with similar TB history.

Other sources are more difficult to ascertain such as wild deer because there is very little available surveillance information. In the same way fomites such as contaminated shared machinery and manure or slurry spread near livestock farms are very difficult transmission pathways to assess.

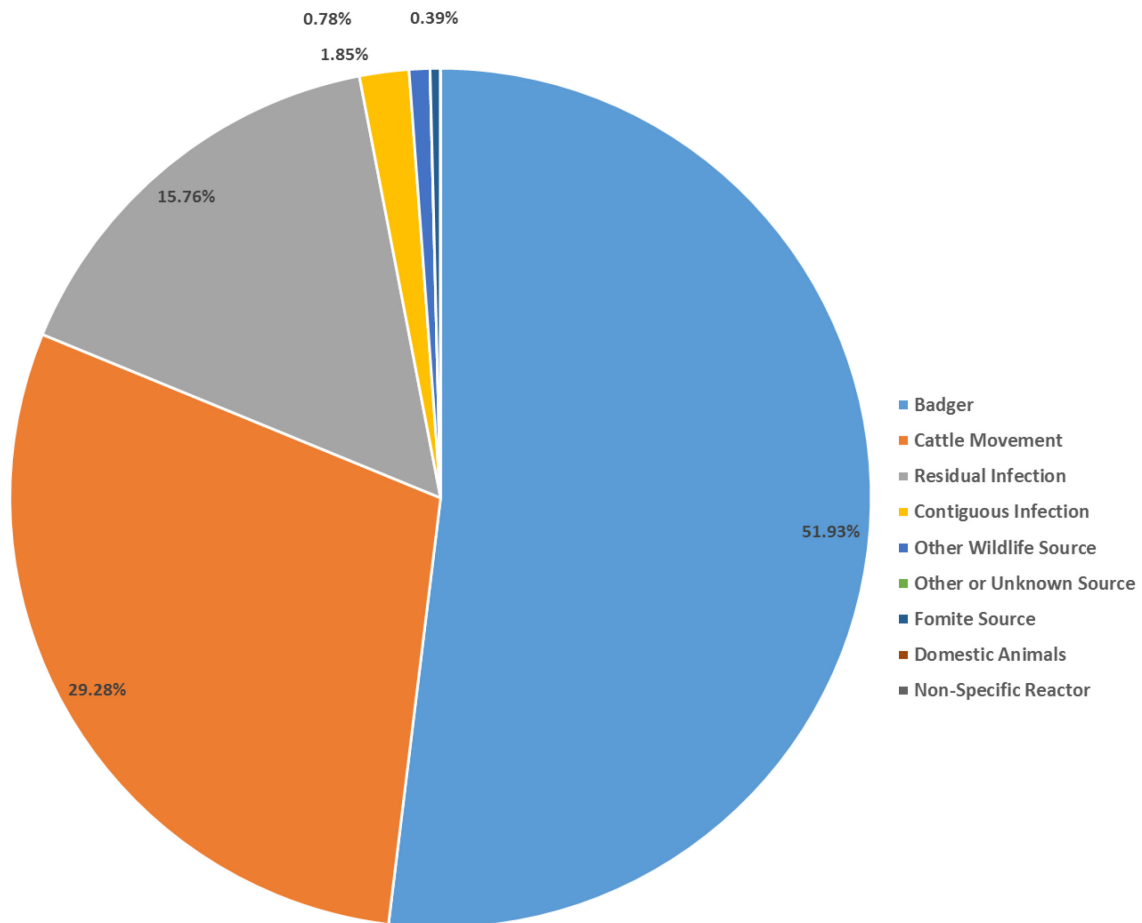


Figure 13: Summary of the weighted source of infection attributed for all incidents (both OTFW and OTFS) in Oxfordshire that started in 2018

Figure 14 illustrates the most likely source of infection according to the herd type. Beef sucklers, possibly due to extensive grazing, were associated with wildlife as the most likely source. In comparison, beef fatteners which rely on constant purchase of cattle kept for shorter periods of time, although still much linked to wildlife, were reported with a higher proportion of infection caused by purchase of cattle with undetected infection. Contact with wildlife is considered to be significant in OTFW breakdowns. OTFS breakdowns are usually attributed to purchase of cattle with undetected infection when there is a lack of evidence of local genotypes infecting purchased cattle. Dairy herds, due to the numbers and lifespan of breeding stock exposed to wildlife, and their policy of minimal purchases in order to maintain their high health status, were more likely to have breakdowns exclusively attributed to local wildlife rather than to cattle movements.

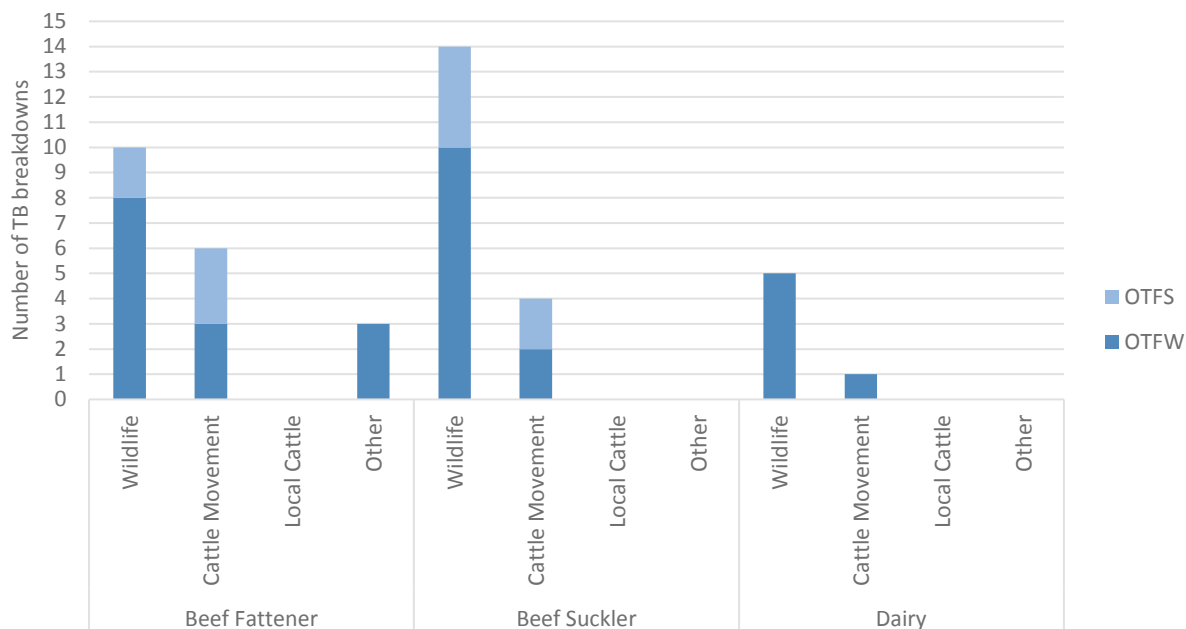


Figure 14: Source of infection recorded with the highest level of certainty for all TB breakdowns (both OTFW and OTFS) in Oxfordshire, by herd type.

Role of other species in Oxfordshire

Badgers and other wildlife

A lack of data for *M. bovis* infection in wildlife from the county continues to add uncertainty to any conclusions for wildlife being the source for cattle infection, which are made largely by a process of elimination of other source pathways, but also from analysis of geographical clusters plus whole genome sequence information.

One confirmed case of TB (genotype 10:a) in wild deer was reported in March 2018 in an estate in the Henley-on-Thames cluster. This genotype and whole genome sequence matched isolates from cattle breakdowns in the same cluster, but occurred in cattle in a different year (genotype 11:a in 2018 but genotype 10:a in 2017).

The Defra-funded Found Dead Badger Survey was undertaken in Oxfordshire and other counties of the Edge Area in 2016 and 2017 by the University of Surrey. Results have not yet been published.

Other domestic species

A suspected case of TB in alpacas was investigated with preliminary negative results. Investigations continue after disclosure of positive results following a blood test (awaiting culture confirmation).

Detection of cases in Oxfordshire

The majority of cases were detected by routine annual herd surveillance tests (which became six monthly in 2018), as shown in Figure 15a. This is equivalent to previous years (Figure 15b). The number of cases disclosed at routine annual tests (41) is the same as the number of cases found adding together all the other tests (40) which include post-breakdown tests at 6 and 12 months after breakdowns concluded (demonstrating a high level of recurrence). Other useful disclosing tests are pre-movement tests (PRMT). Slaughterhouse cases (SLH) cases were mainly found in AFUs. This might suggest that the testing regime of skin test and parallel gamma interferon test for OTFW breakdowns in non-AFU herds is detecting infected animals before they are slaughtered.

Comparing OTFW and OTFS breakdowns new in 2018 (Figure 15a), as in previous years, OTFW breakdowns are more likely to be disclosed at the 6M check test than 12M check test as they usually have the highest level of recurrence.

Changing the testing regime from routine yearly tests to six monthly tests should detect infection earlier at routine testing increasing the proportion of breakdowns detected by routine herd testing and hence decreasing the dependency on passive surveillance such as slaughterhouse detection. However, it is too early to judge the impact of six monthly testing.

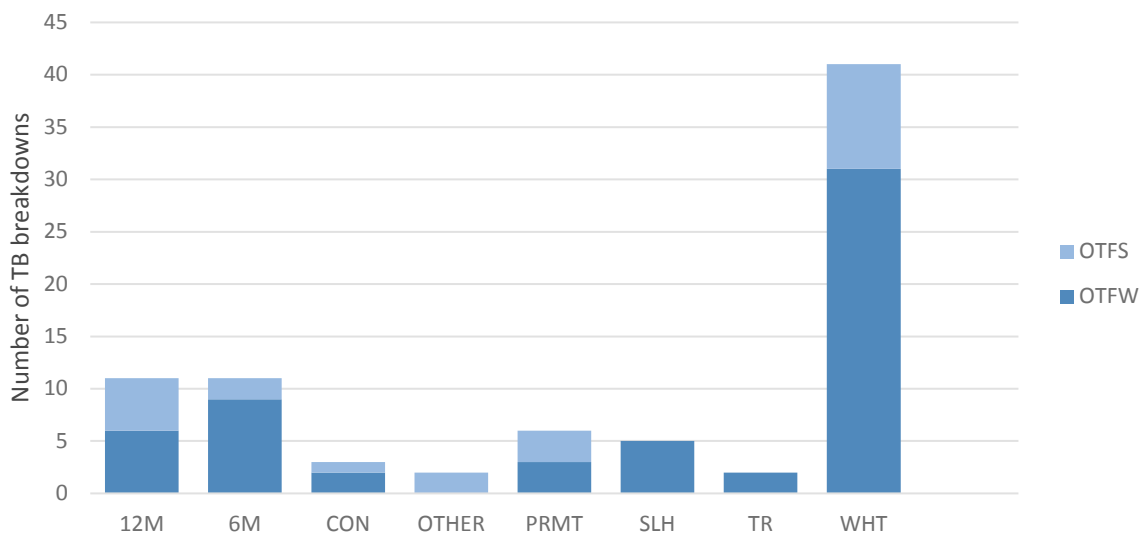


Figure 15a: Number of TB breakdowns (OTFW and OTFS) in Oxfordshire in 2018, disclosed by different surveillance methods (surveillance method types are further described in the Explanatory Supplement¹).

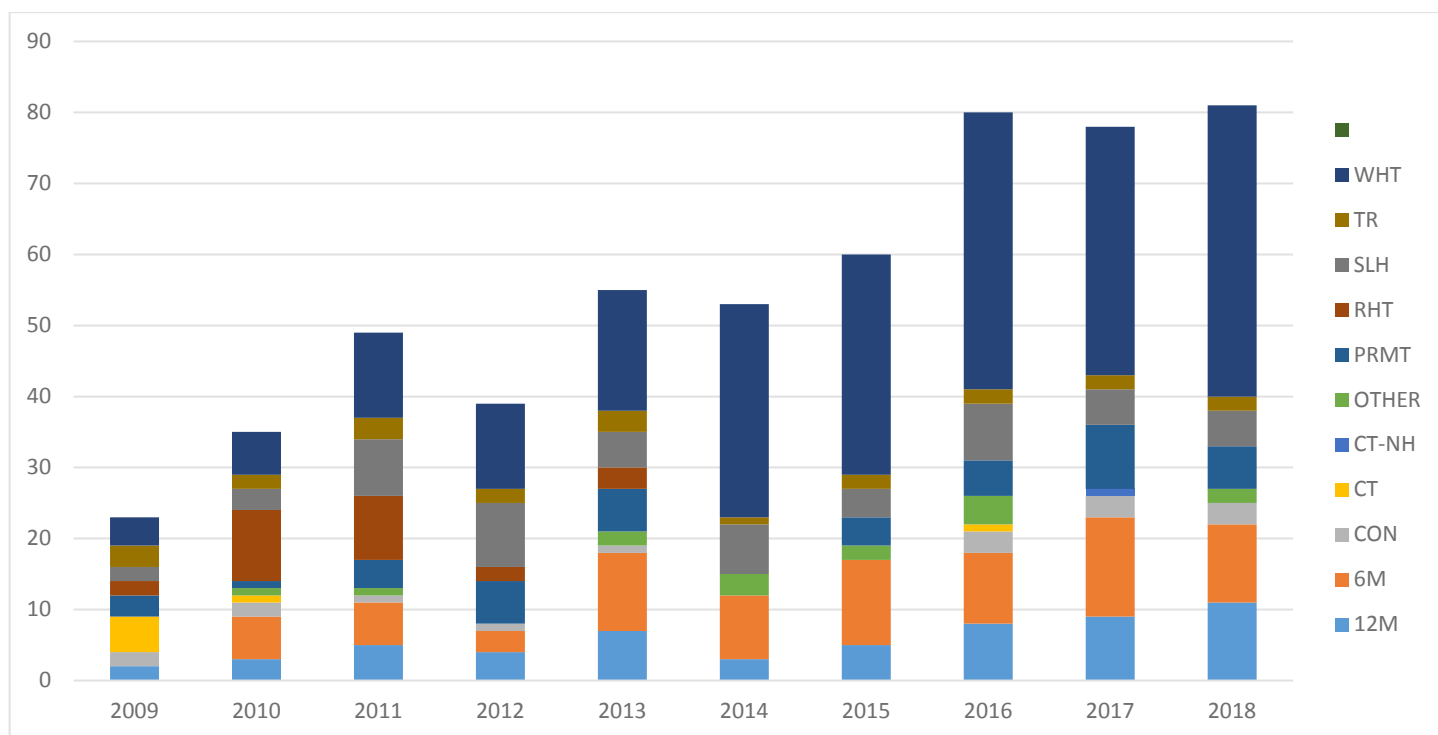


Figure 15b: Number of TB breakdowns (OTFW and OTFS combined) in Oxfordshire disclosed by different surveillance methods from 2009 to 2018 (surveillance method types are further described in the Explanatory Supplement¹).

As shown in Figure 16, more than half of OTFW herds had a history of TB in the previous three years whilst the converse was true for OTFS herds. The number of OTFW breakdowns compared to OTFS

has not changed since 2016 with OTFW breakdowns representing more than double the number of OTFS breakdowns in Oxfordshire.

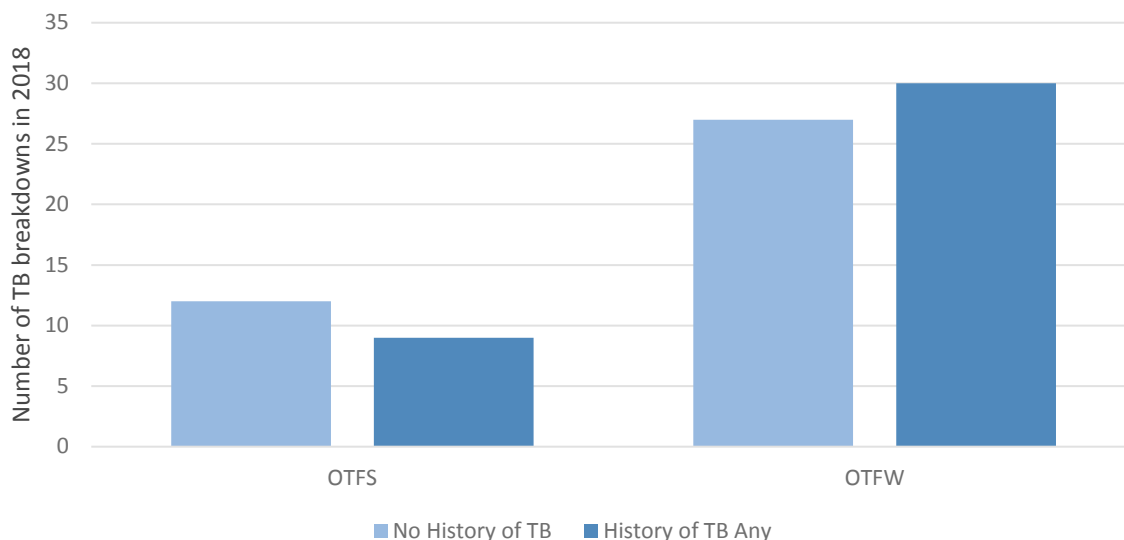


Figure 16: Number of TB breakdowns (OTFW and OTFS) in Oxfordshire which experienced a breakdown in the previous 3 years.

Burden of bovine TB

Reactor numbers can be used as a proxy measure of the burden of TB in Oxfordshire (Figure 17). In 2016 there were 629 reactors (248 were interferon gamma reactors). This more than doubled in 2017 and 2018 with 1347 in 2017 (814 interferon gamma reactors), and 1410 in 2018 (750 interferon gamma reactors).

On an individual breakdown level, the average number of reactors removed per breakdown has increased from 8 in 2016 to 17 in 2017 and 2018. Since there is no significant change in the number of breakdowns from 2016 (80) to 2017 (78) and 2018 (81), and the numerator of the calculation includes reactors taken from breakdowns ongoing from previous years, this increase reflects a number of characteristics such as longer breakdown duration, more reactors per breakdown, possibly larger herds affected, and a higher number of herd tests carried out in the year (from 686 in 2016 to 700 in 2017, increased to 872 in 2018).

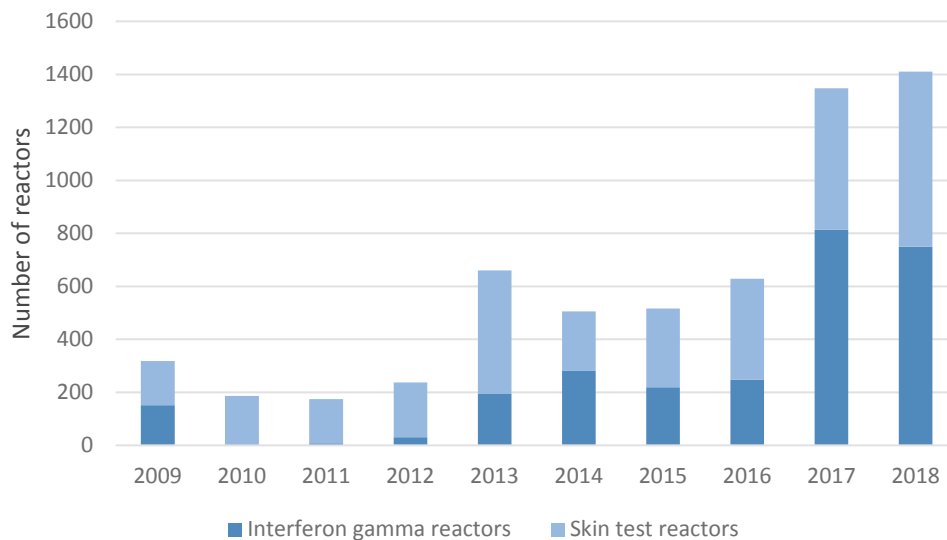


Figure 17: Number of reactors detected by interferon gamma and skin tests in Oxfordshire, 2014 to 2018

Key drivers of the bovine TB epidemic

Cattle Movements

Approximately 30% of breakdowns in 2018 were attributed to the purchase of cattle with undetected infection from the HRA and Edge Area as a higher ranked source pathway. This source affected mostly fatteners including AFUs. AFU cases were the only breakdowns with a definitive source identified (same genotype as origin, and no wildlife source). Source attribution for other breakdowns was more uncertain, especially when no genotype was available, with assessment tending towards a cattle source if cattle were bought in during the last five years.

Residual Infection

Approximately 15% of breakdowns were attributed to residual infection, the third most important source in Oxfordshire. The number of reactors per breakdown has increased in the last two years reflecting an increased level of infection within herds and the proportion of new breakdowns of OTFW status compared to OTFS also seems to be increasing. Residual infection in herds with repeated breakdowns is suspected to be caused by undetected infected cattle remaining in the herd, with cattle to cattle spread, as well as continued exposure to wildlife sources.

Infected Wildlife

Excluding those breakdowns associated with purchase of cattle with undetected infection, the gradual spread of breakdowns over the last 14 years in an eastwards direction from the Gloucestershire border has been reported previously and is thought to be caused by infected wildlife. In addition to this moving front, new areas have appeared in the south east of the county, formerly considered clear of endemic wildlife infection. New genotypes are being detected in presumptive wildlife sourced cases around the county complicating the picture of endemicity.

Monitoring of wildlife (badgers and deer) may provide more certainty.

County summary

The number of breakdowns in the last three years has remained more or less stable, with a lower herd incidence rate in 2018 (possibly due to breakdowns in Oxfordshire becoming persistent.) The herd

prevalence has plateaued at 10% of herds under restrictions at any given time during the last three consecutive years.

Despite the incidence of bovine TB remaining the same since 2016, the epidemiological picture has become more complex with endemic infection spreading to more of the county. This does not favour the long term objective of achieving OTF status in Oxfordshire for 2025. Eradication of bovine TB will require some form of wildlife intervention as well as tighter control of cattle movements from farms in the HRA into the Edge Area. Early detection of infection through more frequent surveillance testing of herds (six monthly testing started in 2018) and the mandatory use of interferon gamma testing to improve the detection of residual infection in cattle herds with OTFW breakdowns will support progress towards this goal.

Summary of the risk to the Low Risk Area (LRA) and any mitigating factors

Spread of the presumptive wildlife infected area eastwards into Buckinghamshire (Edge Area) towards the LRA counties is the most serious long term risk to the future possible OTF status of the LRA. The Henley and Chinnor clusters illustrate this risk. Evidence for these clusters being generated by wildlife infection from genotype and WGS analysis has increased in 2018, and implies that the infection front is approaching the LRA over a much larger area than in previous years.

Movement of cattle from Oxfordshire to the LRA mainly through local markets will become more risky as TB endemicity spreads undetected along the county border with Buckinghamshire, and the trend of increasing numbers of recurrent breakdowns continues rather than those just limited to purchased animals with undetected infection. Breeding cattle are likely to pose most risk to receiving herds because of their longevity and wider contact with other cattle groups at destination farms. Compulsory post-movement testing now provides extra mitigation for all cattle movements into the LRA. The introduction of Licensed Finishing Units (LFUs) in the LRA will also provide an extra barrier to introduction of infection into the wildlife and contiguous herds.

Summary of the risk to the Edge Area from the HRA

Most breakdowns attributed to purchase of cattle involved movements of cattle from the HRA. The increasing number of AFUs in Oxfordshire in 2017 and 2018 mitigates this risk by channelling these cattle into a biosecure environment. Only AFUs without grazing are permitted in the Edge Area. Unannounced inspections should ensure that the standards are maintained and they do not cause a spillover of new genotypes into the local wildlife. The number of slaughterhouse cases found in AFUs was low - averaging one per AFU a year or less.

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

Summary of the risk to Oxfordshire from the adjacent Edge Area counties

The enlargement of the apparent endemic area in Oxfordshire from the HRA on the western county border, has mostly been in a direction out of the county with regards to other Edge Area counties, spreading into Berkshire and probably Buckinghamshire. However, some breakdowns in the north of the county could represent spread from Warwickshire.

Assessment of effectiveness of controls and forward look

The incidence of TB has remained the same since 2016, but the epidemiological picture has become more complex. This does not favour the long term objective of OTF status in Oxfordshire for 2025. The whole of Oxfordshire became part of the Edge Area in 2018 when the evidence for endemic TB was strongest across the whole county.

Eradication of TB will require wildlife controls as well as tighter control of cattle movements from farms in the HRA into the Edge Area. Early detection of infection through more frequent surveillance testing of herds will help (such as the six monthly routine herd surveillance testing started in 2018), alongside the use of interferon gamma testing for OTFW breakdowns (particularly for breakdowns which recur due to residual herd infection). A stronger message regarding biosecurity and some form of wildlife controls in the county is paramount to stop the spread of TB from wildlife both in this county and into the LRA.

APPENDICES

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

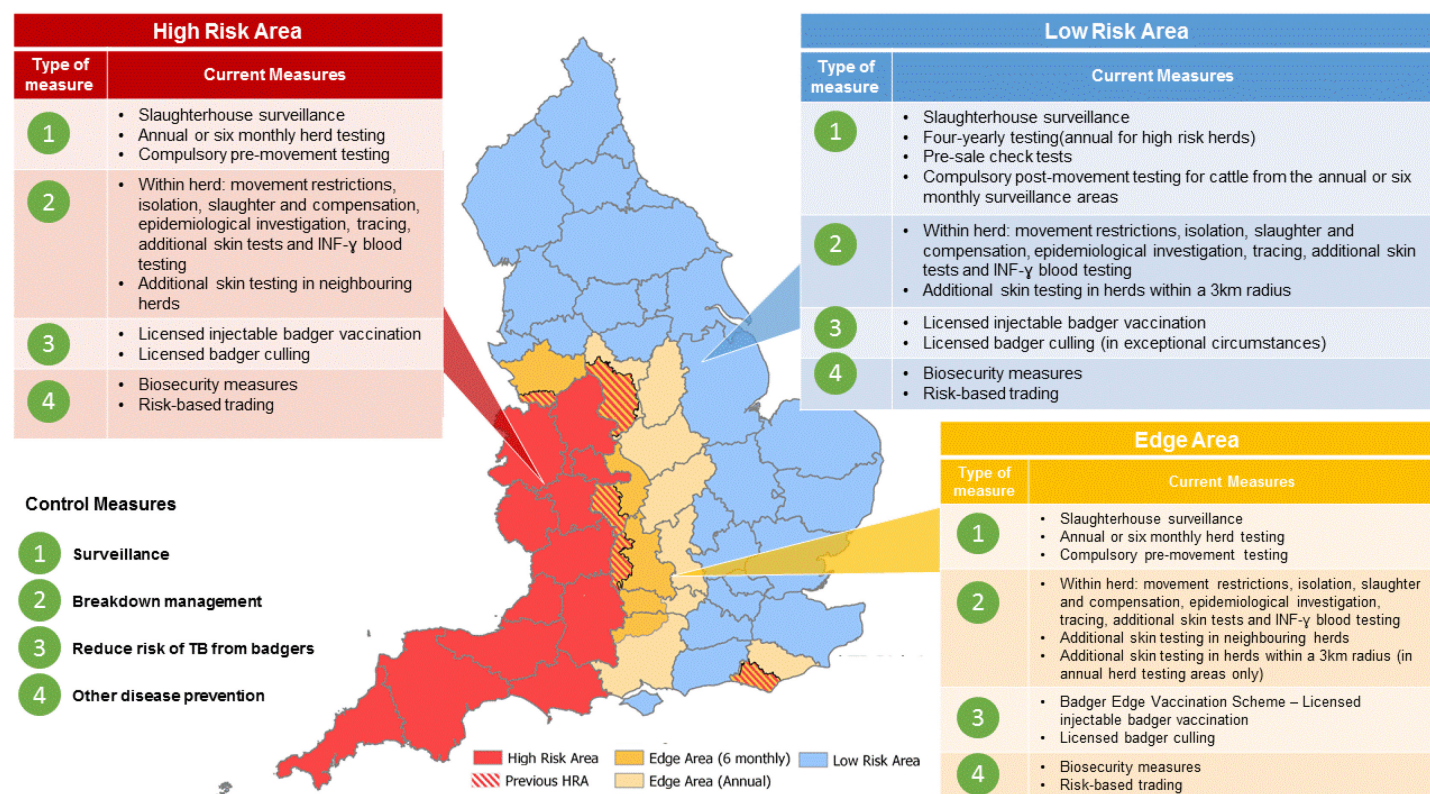


Figure A1: Bovine TB risk and surveillance areas of England effective since January 2018, as set out in the Government's Strategy for Achieving Officially Tuberculosis-Free Status for England².

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 (crude incidence of indigenous OTFW herd breakdowns <0.1%) for the lowest incidence counties in the Edge Area.

1.2 Key Control Measures

Surveillance:

- six monthly or annual routine herd testing
- additional targeted surveillance of cattle herds located within a 3km radius of new OTFW breakdowns in annual testing sections of the Edge Area (radial testing)

² <http://www.tbhub.co.uk/wp-content/uploads/2017/09/infographic-TB-measures.pdf>

- slaughterhouse surveillance

Management of cases ('breakdowns'):

- increased sensitivity of breakdown herd testing:
 - all breakdown herds must pass two consecutive short interval skin tests at severe interpretation to regain OTF status, irrespective of post-mortem and bacteriological findings
 - mandatory IFN-gamma parallel testing of herds with OTFW breakdowns
 - enhanced management of herds with persistent breakdowns
- enhanced epidemiological investigation and data analysis
- information sharing - location of breakdown herds publicly available (via ibTB interactive mapping tool)³

TB controls in the wildlife reservoir (badgers):

- licensed badger culling in high incidence sections of the Edge Area
- Government grants for licensed voluntary badger vaccination projects using injectable badger BCG (Badger Edge Vaccination Scheme - BEVS)

Other measures:

- compulsory pre-movement skin testing of cattle moved between herds
- promotion of herd biosecurity measures to reduce the risk of new breakdowns

³ ibTB interactive mapping tool - <https://ibtb.co.uk/>

Appendix 2: Cattle industry in the Edge Area of the region

Number of cattle premises by size band in the Edge Area of the region at 1 January 2018

(RADAR data)

Cattle per premises	1-50	51-100	101-200	201-350	351-500	501+	All	Mean	Median
Number of premises	200	86	85	58	24	17	471	129.9851	66

Finishing units registered in Oxfordshire:

	Grazing	Non-grazing
Number of Approved Finishing Units (AFUs)	9	0
Number of Pre-movement Testing Exempt Finishing Units (EFUs)	0	0

There are nine AFUs in total, up from eight in 2017. Although interest is increasing in setting up these units there were not many new applications received in 2018 in Oxfordshire compared to the previous year.

Common land in the county: Port Meadow and Wolvercote Common 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 TB significance.

Cattle/herd purpose: (Note that for the row entitled "Holdings", this is the number of holdings where breeds of that type are present as recorded on CTS and does not represent, for example, the number of dairy farms).

	Beef		Dairy		Dual purpose		Unknown		Total
	Number	%	Number	%	Number	%	Number	%	Number
Cattle	42057	68.7	16138	26.4	3026	4.9	2	0.0	61223
Holdings	428		143		148		1		

Appendix 3: Summary of the Oxfordshire headline cattle TB statistics

Herd-level statistics	2016	2017	2018
Total number of cattle herds live on Sam at the end of the reporting period	573	576	554
Total number of herd tests carried out in the period	686	700	872
Total number of OTF cattle herds TB tested during the period for any reason	450	420	420
Total number of OTF cattle herds at the end of the report period (i.e. herds not under any type of TB02 restrictions)	503	494	462
Total number of cattle herds that were not under restrictions due to an ongoing TB breakdown at the end of the report period.	519	510	476
Total number of new TB breakdowns detected in cattle herds during the report period	80	78	81
OTF status suspended (OTFS)	24	18	23
OTF status withdrawn (OTFW)	56	60	58
Of the OTFW herd breakdowns:			
How many can be considered the result of movement, purchase or contact from/with an existing breakdown based on current evidence?	20	13	7 (4 AFU)
New OTFW breakdowns triggered by skin test reactors or 2xIRs at routine herd tests	19 (Edge only)	54 (whole county)	41
New OTFW breakdowns triggered by skin test reactors or 2xIRs at other TB test types (forward and back-tracings, contiguous, check tests, etc.)	12 (Edge only)	24 (whole county)	40
New OTFW breakdowns first detected through routine slaughterhouse TB surveillance	7 (Edge only)	7 (whole county)	5 (4 AFU, 1 fattener)
Number of new breakdowns revealed by enhanced TB surveillance (radial testing) conducted around those OTFW herds (may not be applicable to every county in the Edge Area)			
OTFS	n/a	n/a	n/a
OTFW	n/a	n/a	n/a
Number of OTFW herds still open at the end of the period (including any ongoing OTFW breakdowns that began in a previous quarter)	44	55	62
New confirmed (positive <i>M. bovis</i> culture) incidents in non-bovine species detected during the report period (indicate host species involved)	0	0	1

Animal-level statistics (cattle)	2016	2017	2018
Total number of cattle tested in the period (animal tests)	120564	138906	148421
Reactors detected:			
tuberculin skin test	381	533	660
additional IFN-gamma blood test reactors (skin-test negative or IR animals)	248	814	750
Reactors per breakdown	7.9	17.3	17.4
Reactors per 1000 animal tests	5.2	9.7	9.5
Additional animals identified for slaughter for TB control reasons (DCs, including any first-time IRs)	20	20	49
SLH cases (tuberculous carcasses) reported by FSA	10	12	9
SLH cases confirmed by culture of <i>M. bovis</i>	8	10	5

Appendix 4: Suspected sources of *M. bovis* infection for all the new OTFW and OTFS breakdowns identified in the report period

Source of infection	Possible	Likely	Most likely	Definite	Weighted contribution
Badgers	25	26	20	0	51.9%
Cattle Movements	30	19	3	0	29.3%
Contiguous	4	1	0	0	1.9%
Residual infection	19	7	4	0	15.8%
Domestic Animals	0	0	0	0	0.0%
Non-specific Reactors	0	0	0	0	0.0%
Fomites	1	0	0	0	0.4%
Other Wildlife	2	0	0	0	0.8%
Other	0	0	0	0	0.0%
Unknown source	0	0	0	0	0.0%

Appendix 5: Overview of the bovine TB Control Programme in Oxfordshire

Summary of TB control measures specific to Oxfordshire:

5.1 Edge Testing Policy

- In January 2018 six monthly routine surveillance herd testing (instead of twelve monthly) was introduced across the whole county.
- Compulsory interferon gamma testing became applicable for all OTFW breakdowns in the county i.e. including former HRA herds.
- Compulsory interferon gamma testing has been applied to all OTFW cases apart from those in the former HRA which were first detected prior to 2018 and so considered not eligible. For that reason several breakdowns were excluded from gamma interferon testing until they reached 18 months under restrictions (and became eligible for interferon gamma testing because of their persistent status). Interferon gamma testing increases the detection of infected cattle but may not reduce persistence in those cases where the risk of re-infection from wildlife remains high.
- Limited exemptions from interferon gamma testing have been applied to some beef fattening herds, or large dairies with clearly differentiated epidemiological groups.
- No enhanced case management measures were applied to persistent breakdowns in the original Edge Area of Oxfordshire. Historically, persistent breakdowns were only in the former HRA area of Oxfordshire: five persistent breakdowns since 2013 of which two were subject to enhanced measures in 2018. New cases appeared in the original Edge Area (in the western part) in 2018. There were a total of ten persistent breakdowns in the whole of Oxfordshire by the end of 2018.

5.2 Unusual TB breakdowns

- One explosive breakdown occurred at the end of 2017 in a large dairy herd of 1000 cattle with 200 skin reactors, 100 of those visibly lesioned at slaughter. This was in an endemic area close to Faringdon (west Oxfordshire) where several dairy herds have suffered recurrent breakdowns in the last five years.
- In 2018 there was an increase in the number of reactors and explosive breakdowns in relatively small herds or groups of cattle grazing fields in west Oxfordshire. A particularly dry summer with extra feeding at grazing may have contributed to higher exposure to infected wildlife whilst grazing. This was illustrated by affected groups in the four following breakdowns: 17 reactors out of 21 animals in one field, 23 reactors out of a herd of 58, 12 reactors out of a 29 cattle herd, and 23 reactors in the young stock group of a dairy herd.

5.3 Other Testing Measures

- Overdue testing has been brought down to a very low level by working with the county's local authority on the enforcement of TB testing.
- Radial testing introduced in 2018 in Buckinghamshire sometimes generated from cases near the eastern border of Oxfordshire will monitor any spread of TB into Buckinghamshire.

5.4 Other Control Measures

- The South East TB Eradication Board has continued to meet and discuss initiatives such as holding a veterinary practitioner conference to increase knowledge about the local TB situation, recognising that the private vet is key to TB control.
- In 2017 with the National Farmers' Union (NFU), APHA established a new TB Eradication Group for Buckinghamshire, Berkshire and Oxfordshire with the first meeting held in March 2018.
- Two sites in Oxfordshire were licensed by Natural England to vaccinate badgers in 2018.

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