Animal &
Plant Health
Agency

Year-end descriptive epidemiology report:

Bovine TB in the Edge Area of England

County: Oxfordshire

Year-end report for: 2019

TB Edge Area - OXFORDSHIRE

OXFORDSHIRE

Contents

Executive summary

Reporting area

Oxfordshire is part of the Edge Area that was established in 2013. The following year, the bovine tuberculosis (TB) surveillance strategy for this area was incorporated into the Government's strategy to achieve Officially Tuberculosis Free (OTF) status for England by 2038. The Edge Area has an overall moderate but recently rising incidence of infected herds with substantial variability from county to county. This end of year report describes bovine TB in Oxfordshire.

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 of cattle 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 TB incidents herds.

New incidents of TB

The annual number of new incidents over the last four years (2016-2019) has remained more or less the same. A slightly lower number of incidents was recorded in 2019, potentially explained by several factors including increased length of incidents, increased frequency of testing and reduced residual infection (recurrent incidents) due to the use of interferon gamma (IFN-γ) testing. The herd prevalence has more or less plateaued over the last four years at 10% of herds under movement restrictions measured at the end of each year.

Suspected sources and risk pathways for TB infection

Infected wildlife is the most common likely source of TB infection for cattle herds reported in Oxfordshire. This has become more evident during the last four years, confirming a cluster of incidents suspected to have a wildlife source, and spreading eastwards from the Oxfordshire border with the HRA. Of particular concern is the increase in the number of incidents with a suspected wildlife source in the eastern corners of the county very close to the Buckinghamshire border. In this county border area, three clusters of incidents have been identified: north-east (Somerton cluster), central east (Chinnor cluster) and south east (Henley cluster). Genotyping, 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 direct and indirect contact with infected wildlife.

Details of the methodology used to calculate the weighted contribution of the different suspected sources of *M. bovis* infection for all new incidents can be found in the main body of the report and in the [Explanatory Supplement to the 2019 bovine TB epidemiology reports](#).

Disclosing tests

Routine surveillance testing of herds accounted for more than half of the new incidents disclosed in 2019, with the rest found during post-incident surveillance tests which in 2019 were completed at the same six month interval as the current routine herd testing in Oxfordshire. Some incidents were detected by pre-movement testing and passive (slaughterhouse) surveillance.

Reactor numbers

In 2017 and 2018, compulsory parallel IFN-γ testing alongside tuberculin skin testing of herds that experienced an Officially Bovine Tuberculosis Free Status Withdrawn (OTF-W) incident, greatly impacted on the number of animals removed per incident. In 2019 this number decreased slightly, possibly due to less spread within herds with increased routine testing and/or lower number of TB incidents.

Risks to the reporting area

Oxfordshire has become as high risk as neighbouring HRA counties. Increased cattle TB controls may reduce the risk to Oxfordshire, but continued spread of infection in wildlife remains a risk.

Risks posed by the reporting area

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 the current regime of radial testing (targeted surveillance of herds located within a 3km radius of a herd with an OTF-W incident) triggered by incidents in Oxfordshire close to the county border. Six monthly surveillance testing could be extended partway into this area.

Forward look

The incidence of bovine TB in Oxfordshire has remained stable since 2016, but the epidemiological picture has become more complex with endemic infection spreading to most of the county. This does not favour the long term objective of achieving OTF status for Oxfordshire by 2038. Eradication of bovine TB in the county may require some form of wildlife intervention as well as tighter control of cattle movements from high risk farms. Early detection of infection through more frequent surveillance testing of herds (six monthly testing started in 2018) and the mandatory use of IFN-γ testing to improve the detection of residual infection in cattle herds with OTF-W incidents might be helping. However, a stronger message about the need to increase on-farm biosecurity measures alongside some form of wildlife control in the county is paramount to stop the spread of bovine TB from the HRA to the LRA through Oxfordshire.

Introduction

This report describes the level of bovine tuberculosis in cattle herds in Oxfordshire in 2019. Bovine TB is caused by the bacterium *Mycobacterium bovis* (*M. bovis*), and will subsequently be referred to as TB. This report explores the frequency and geographical distribution of TB in cattle herds. It examines what is likely to be driving TB in Oxfordshire, and the risks the disease in this county may pose to neighbouring cattle. Although other sources may refer to TB 'breakdown(s)', this report will use the term 'incident(s)' throughout. This report is intended for individuals involved in the control of TB, both in the local area and nationally. This includes, but is not limited to: farmers, veterinarians, policy makers and the scientific community.

In 2014 the Government published its Strategy to achieve Officially TB Free (OTF) status for England by 2038. A key action 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 areas were established (refer to Appendix 1). Oxfordshire forms part of the Edge Area. Overall, the Edge Area has a moderate but recently rising incidence of infected herds with substantial variability from county to county. Control efforts are seeking to slow down and reverse geographic spread, and to reduce the incidence rate. The aim is to obtain OTF status for the Edge Area as soon as possible.

Changes to the Edge Area in 2018

On 1 January 2018 the Edge Area boundary was expanded westwards to absorb the former High Risk Area (HRA) parts of the five previously split counties. Cheshire, Derbyshire, Warwickshire, Oxfordshire and East Sussex all moved fully into the Edge Area. Furthermore, the routine TB testing frequency of herds in the counties in the west of the Edge Area adjoining the HRA (or parts thereof) was increased from annual to six-monthly. The respective descriptive TB epidemiology reports for those five counties of the Edge Area will focus on the whole county and key differences between the old and new parts will be highlighted where relevant.

From January 2018 annual routine herd surveillance testing was replaced by six monthly herd surveillance testing in the whole county of Oxfordshire. At that time Defra also introduced radial skin testing of herds located within a 3km radius of a new OTF-W incident in annual testing parts of the Edge Area to enhance the cattle TB surveillance regime. However since May 2019, cattle herds that meet certain criteria are eligible for annual surveillance testing (earned recognition). These criteria are either: 1) the herd has been in existence for at least six years and has not had a TB incident in that six year period or 2) the herd is registered to a bovine TB health scheme accredited under the Cattle Health Certification Standards (CHeCS) at level one or above.

Cattle industry

Herd types

Almost two thirds of herds in Oxfordshire contain fewer than 100 cattle (Figure 1). They are a mixture of beef suckler, dairy, and beef fattening units. 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 purchase locally from farms and Thame market in Oxfordshire.

Some pedigree cattle breeders are located within Oxfordshire providing pedigree breeding cattle for the whole country. There are also a handful of organic farms, both dairy and beef.
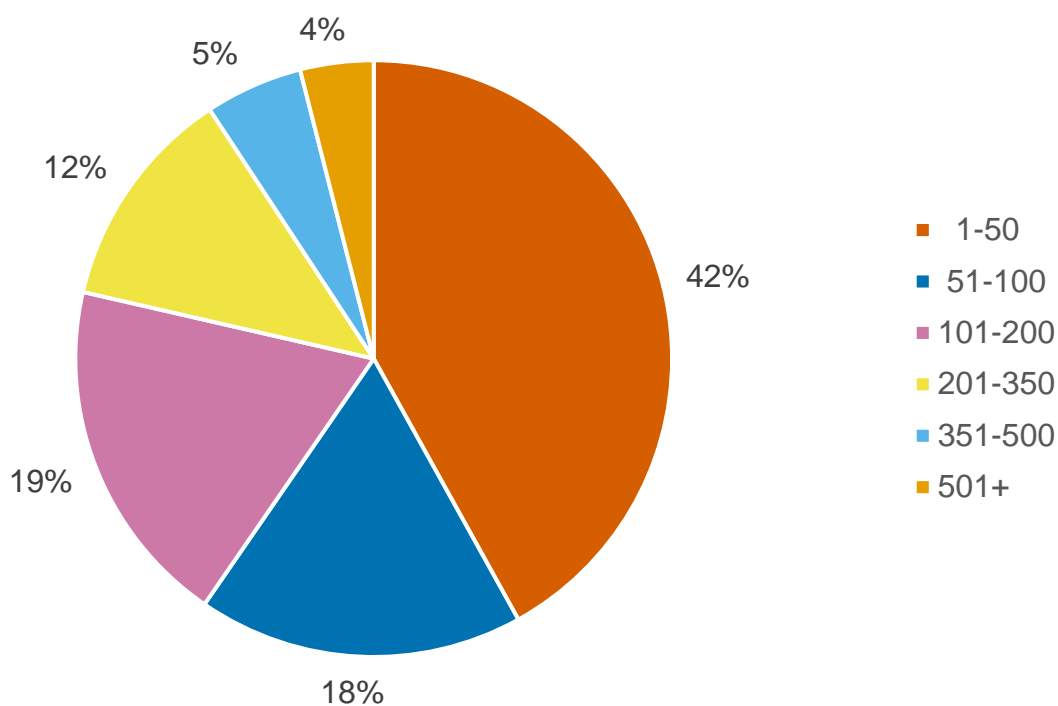

Figure 1: Proportion of cattle holdings by herd size in Oxfordshire in 2019 (n=453 holdings).

The majority of cattle are grass fed whilst outside, with supplementation for dairy cows and young stock. Fattening cattle on large units are often fed with blends of grass, maize silage and food by-products. Use of mineral licks at pasture is variable but are still used, often 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 common in the county (on-farm shoots).

Approved Finishing Units

There are a few large finishing units, some of which have converted to Approved Finishing Units (AFUs) since 2013, providing weekly quotas to abattoirs of cattle finished directly from buildings to fulfil supermarket contracts. One further AFU was approved in 2019 raising the total number in Oxfordshire to nine (four approved in 2017, and four between 2014 and 2016). There has been a growing interest in rearing AFUs mainly to rear surplus calves from the dairy industry but no further applications were received in 2019.

AFUs are not included in the incidence, prevalence or duration of incident figures in Oxfordshire as they are self-contained units with cattle only destined to slaughter. Routine TB testing is not required in AFUs as long as strict biosecurity controls are applied and all the cattle are housed.

Markets

Thame market is the only market in Oxfordshire in 2019. The orange market (dedicated sales for TB-restricted cattle) at Cirencester in the HRA county of Gloucestershire provides a valued outlet for TB-restricted cattle into AFUs across the south.

Common land

The only common land in the county is Port Meadow and Wolvercote Common, 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 risk of introducing infection to local herds grazing the common. The common lies adjacent to the River Thames and floods each year reducing the likelihood of established wildlife infection.

Descriptive epidemiology of TB

Temporal TB trends

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

1. The number of new herd incidents that were disclosed in each year.

2. 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 herd tests that other incidence measures do not (such as new TB incidents per number of herds or tests).

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

All three measures include Officially Tuberculosis Free Status Withdrawn (OTF-W) incidents, and Officially Tuberculosis Free Status Suspended (OTF-S) incidents. OTF-W incidents are those in which at least one animal was identified with typical lesions of TB at post mortem (PM) inspection, and/or positive for *M. bovis* on culture from tissue samples. OTF-S incidents are those with one or more reactors to the Single Intradermal Comparative Cervical Tuberculin (SICCT) skin test, but without full confirmation of *M. bovis* infection by PM inspection or bacterial culture. TB incidents in non-grazing AFUs are not included in the prevalence and incidence calculations in this report due to the limited epidemiological impact of these cases. Furthermore, herds restricted because of an overdue test rather than a TB incident are also excluded from calculations. Measures of incidence and prevalence in this report may be lower than those reported in the official TB statistics.

Prior to 2004, incidents in Oxfordshire were all attributed to infection from purchased cattle, resolved quickly and rarely reoccurred. Thereafter, incidents started to appear in significant numbers in the Faringdon area in south Oxfordshire bordering Gloucestershire (HRA). Initially these incidents involved several genotypes of *M. bovis* including 17:a, 17:b, 17:e, 74:a and 10:a (genotypes prevalent in Wiltshire, Gloucestershire and this area of Oxfordshire). From 2010, incidents have predominantly been genotype 10:a which is probably a reflection of the increasing prevalence of this genotype in wildlife as infection has spread from the neighbouring HRA counties.

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

In 2015 and 2016, a cluster of incidents appeared in the south-east of the county in the Henley-on-Thames area, characterised by 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 homerange 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.

From 2017 to 2019 in addition to endemic infection caused by genotype 10:a, there has been accumulating evidence of new clusters of incidents appearing and becoming established in the east of the county close to the Buckinghamshire border (see section 'Geographical Distribution of TB Cases'). Genotype 10:a is still the predominant genotype affecting the whole county, and is well established in other reported clusters of incidents in the Somerton area (north) and the Henley-on-Thames area (south).

The increasing number of TB incidents in Oxfordshire over the years can still be partially 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. However, there is a possibility that TB infection in local wildlife is now spreading to east Oxfordshire. Both the level of recurrence and the number of persistent incidents

(greater than 18 months duration) show an increased rate of herd re-infection. This is despite the deployment of mandatory IFN-γ testing in OTF-W incident herds in the original Edge Area since 2014 and in the former HRA part of the county since 2018. The number of persistent incidents rose from five in 2017 to ten in 2018 and to twelve in 2019.

As seen in Figure 2, there have been similar numbers of TB incidents in the last four years since 2016 with a slight reduction in the total number of incidents in 2019 (77). The proportion of OTF-S incidents has increased over the last three years. This may be due to the introduction of six monthly surveillance testing which has detected new infections earlier. The full effect of the increased skin testing and the use of IFN-γ testing is difficult to assess when it varies from year to year. In 2019, some lower risk herds reverted to annual surveillance testing due to satisfying specific earned recognition criteria.
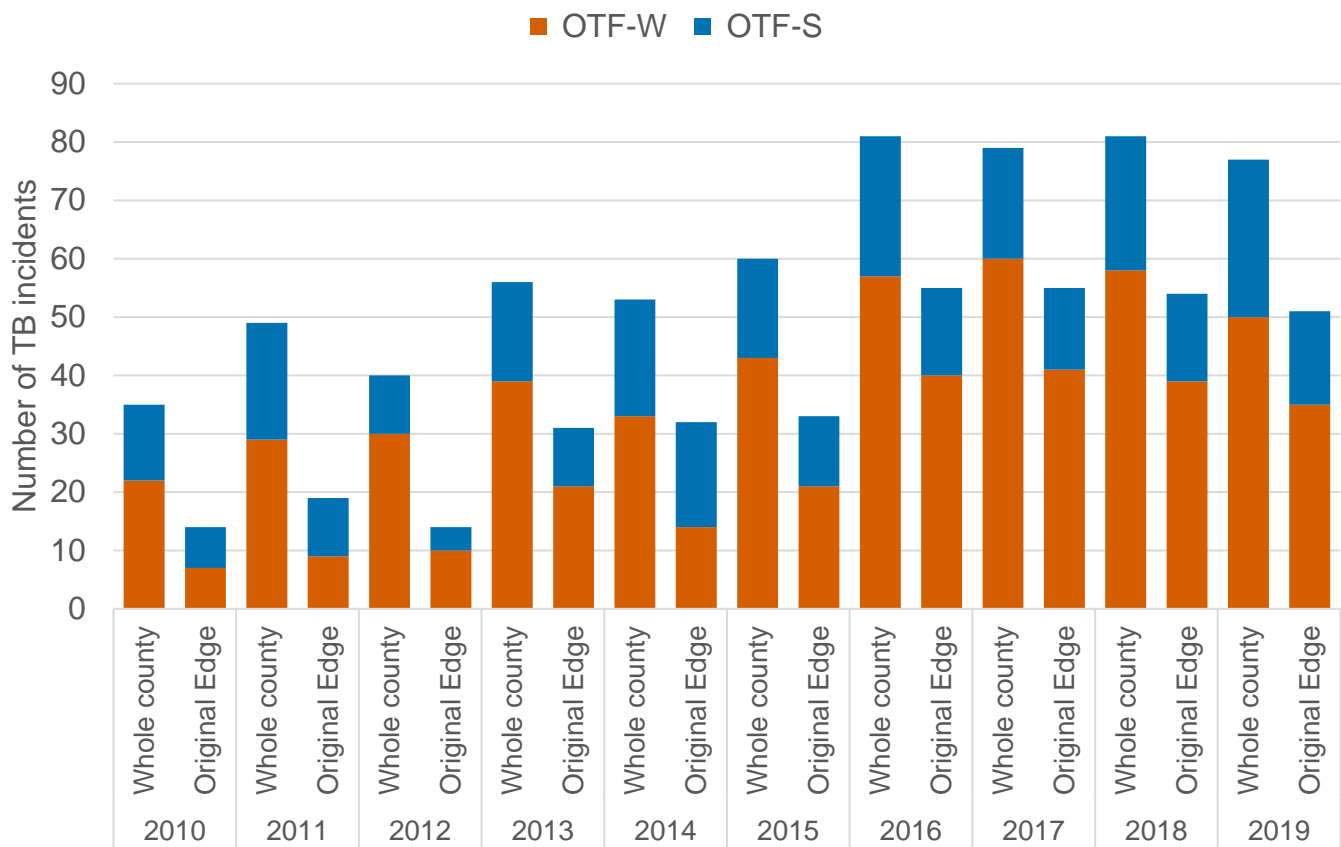

Figure 2: Annual number of new TB incidents in Oxfordshire, 2010 to 2019, showing incidents for the whole county and the original Edge Area.

The trends for all these measures are very similar for the former HRA part and the original Edge Area of Oxfordshire with the difference between the whole county and original Edge over the last four years roughly proportional to the relative geographical size of the former HRA (Figure 2). This indicates that both parts of the county are behaving in the same way. The whole county is now under the same surveillance TB testing regime (six-monthly testing).

The annual herd incidence rate (Figure 3) 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 in 2014 to 18.3 in 2016 (incidents per 100 herd-years at risk). Since then, there has been a decrease in incidence rate in 2018 to 15.8 (even though total number of incidents was highest in 2018 over the last decade), and in 2019 an increase to 23.5 (despite total number of incidents decreasing). This is because, the denominator for this incidence rate measure (herd-years at risk) is sensitive to changes in testing intervals within an area. This should be borne in mind when considering incidence rate trends in some parts of the Edge Area that moved from annual to six-monthly testing in 2018. A detailed description of the methodology used to calculate incidence per 100 HYR is available in the Explanatory Supplement for 2019 (https://www.gov.uk/government/publications/bovine-tb-epidemiology-and-surveillance-in-great-britain-2019). In 2019 this was complicated further by the introduction of earned recognition in the form of annual surveillance testing for lower risk herds. To allow incidence comparison in the last three years, the incidence risk per 100 unrestricted herds is included (Figure 3). This measure shows that incidence has levelled off since 2016 (16.7 in 2016 to 17.1 in 2019).
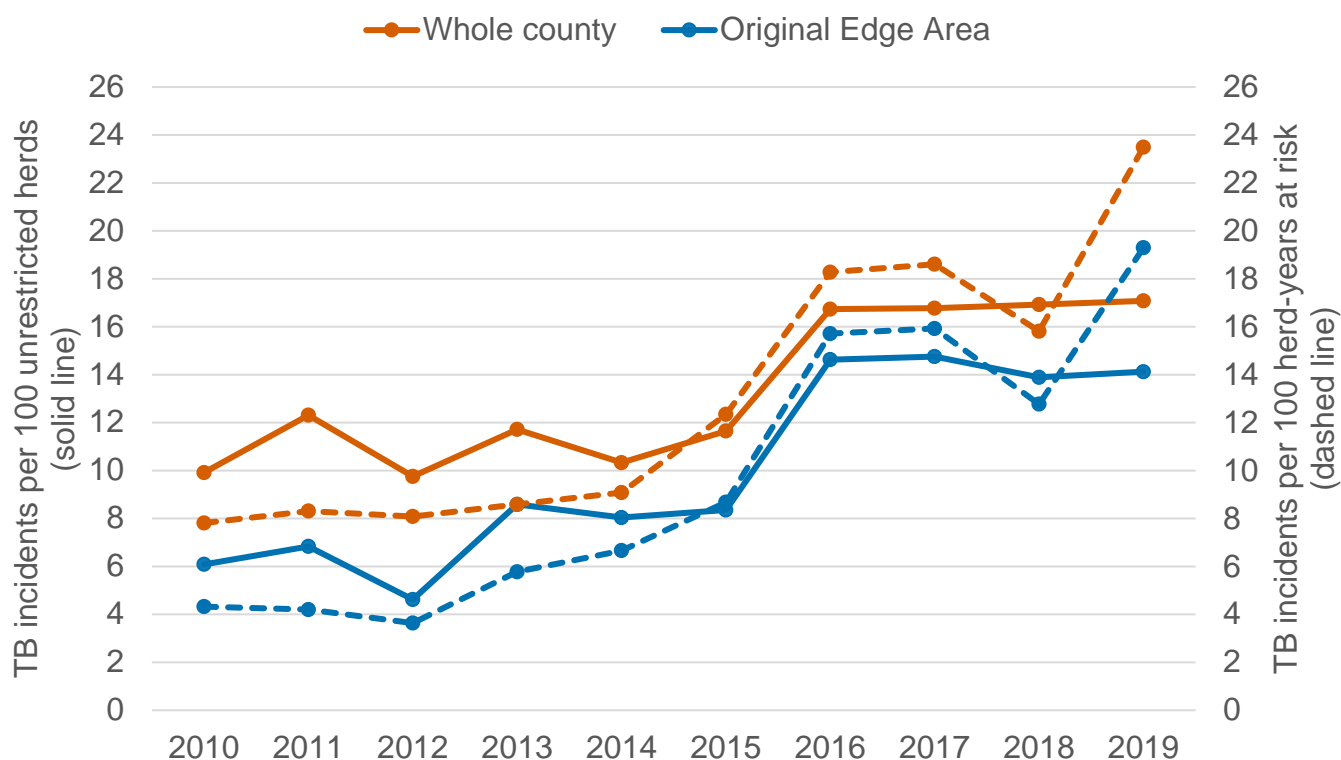

Figure 3: Annual herd incidence rate (per 100 herd-years at risk and per 100 unrestricted herds) for all new incidents (OTF-W and OTF-S) in Oxfordshire, 2010 to 2019, showing data for the whole county and for the original Edge Area

Figure 4 shows the prevalence of herds under movement restrictions at the end of each year. The continued increasing trend is explained by more herds remaining under restriction for longer periods of time including incidents that started in previous years. In comparison with 2018 (13.35%), fewer herds were under restrictions by the end of 2019 (11.75%). This is explained by fewer incidents and

earlier detection of infection through more frequent testing supported by IFN-γ testing which can identify infected animals at an earlier stage of infection and more effectively than skin testing alone.
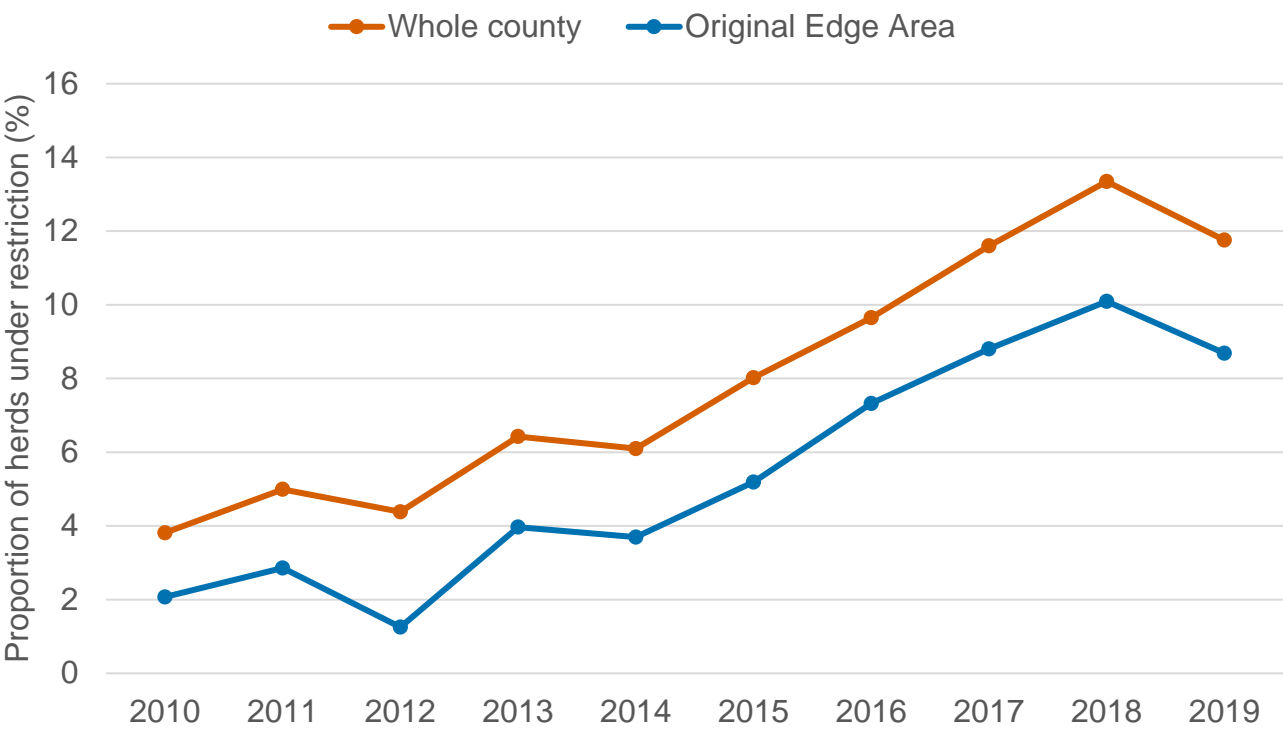

Figure 4: Annual end of year TB herd prevalence in Oxfordshire, 2010 to 2019, showing data for the whole county and for the original Edge Area.

Geographical distribution of TB incidents

As shown in Figure 5, Oxfordshire has the highest incidence of all the Edge Area counties (23.8 incidents per 100 herd-years at risk). This is considerably higher than the average incidence of the Edge Area (9.9), and is also higher than the average incidence for the HRA (16.9).
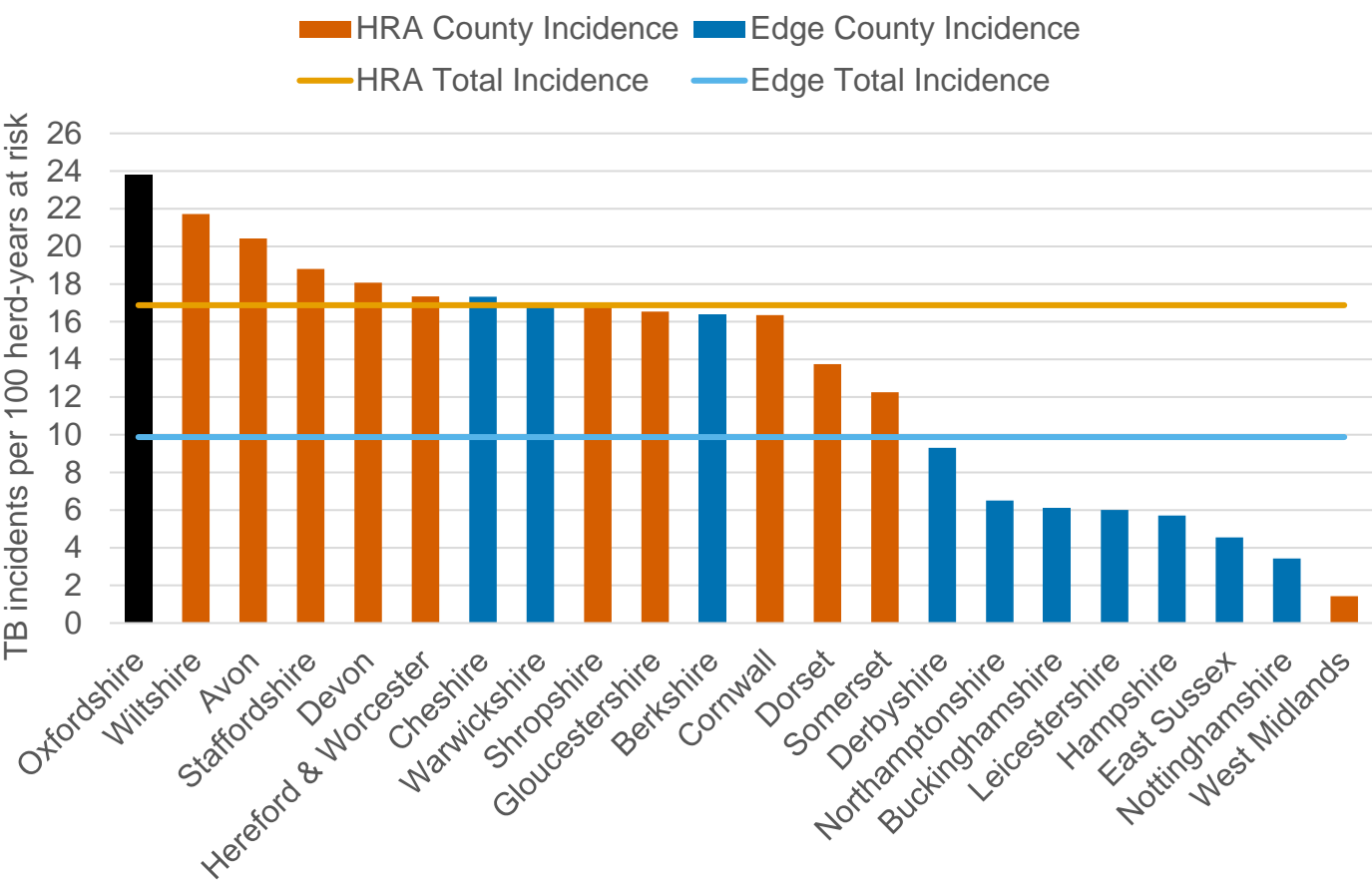

Figure 5: Incidence rate (per 100 herd-years at risk) for all new incidents (OTF-W and OTF-S) in 2019, by HRA and Edge Area County.

Continuing the trend of previous years, the distribution of incidents in Oxfordshire has continued to advance eastwards. Figure 6 shows the locations of incidents overlaid on a cattle population density map. Figure 6 is additionally annotated with the three main clusters of incidents (shown by red, blue and green circles) with presumptive wildlife source. These have expanded in addition to the established clusters near the HRA border (represented by a black rectangle).
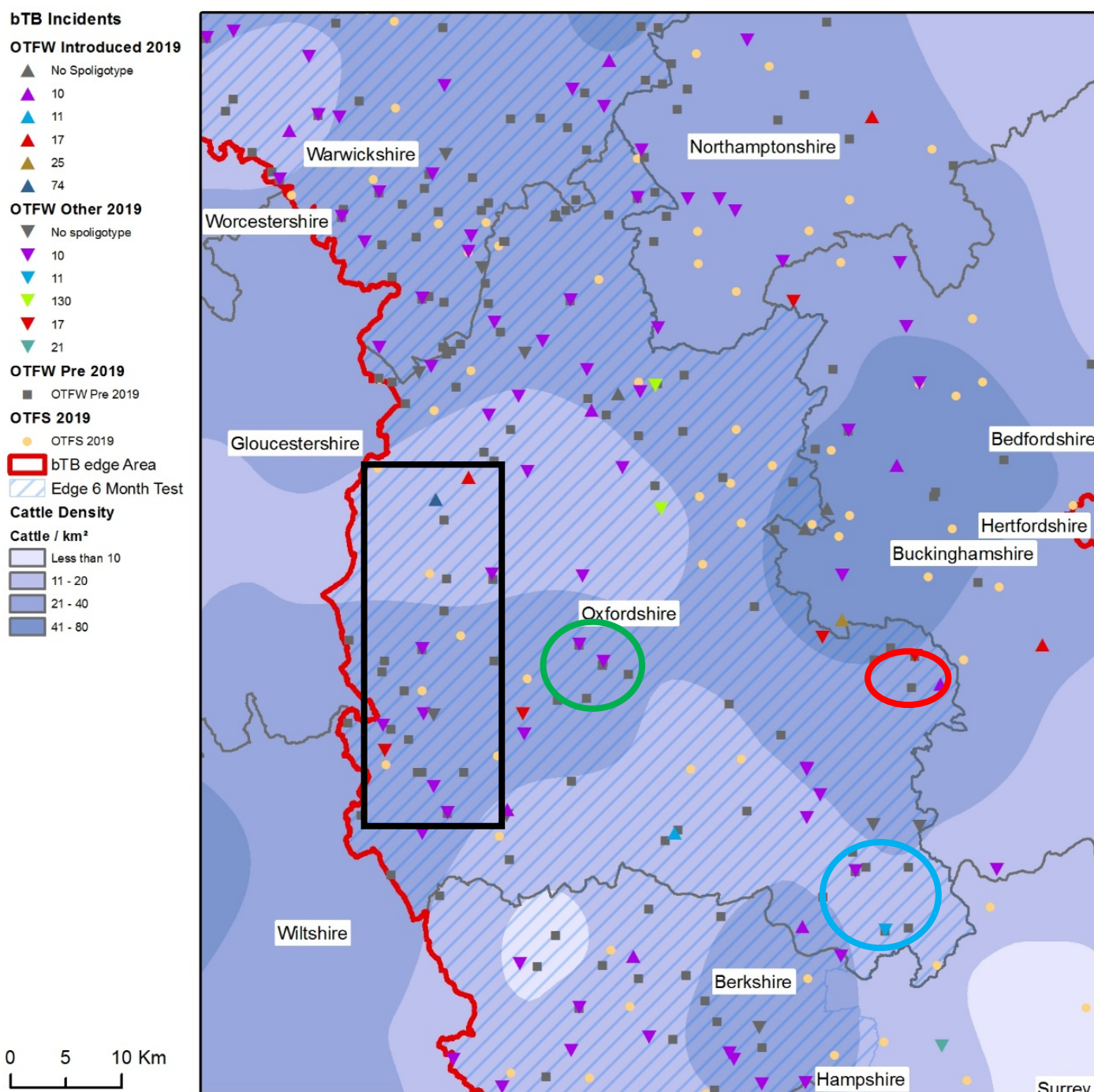
Figure 6: Location of cattle holdings in Oxfordshire with new TB incidents (OTF-W and OTF-S) in 2019 and cattle holdings with pre-2019 OTF-W incidents that are still ongoing at the beginning of 2019, overlaid on a cattle density map and annotated with the three main clusters of incidents (shown by red, blue and green circles) with presumptive wildlife source and established clusters near the HRA border (represented by a black rectangle). To note, 'OTF-W Introduced 2019' refers to OTF-W incidents in which introduction of infection through cattle movements was the most likely source identified.

These developing clusters of incidents located in the east of the county are:

- Somerton area (Figure 6, green circle) in the north-east of the county.

  The most common genotype in 2019, and previous years is the local genotype 10:a. This appears to have mutated in this local area.

  Two incidents in 2019 were attributed to a recently identified spoligotype: 130, which appears unique to this area (two spoligotype 130 incidents were detected in 2018 and two in 2017). WGS analyses of four spoligotype 130 isolates and three nearby incidents attributed to genotypes 10:h and 10:a indicate a close genetic relationship between these genotypes, differing by a single SNP (single nucleotide polymorphism). This strongly suggests that this local cluster of at least seven incidents in the last two years (one a closed herd for 20 years) had been exposed to a common source of infection. This is considered most likely to be wildlife as there was no contiguous inter-herd contact, no cattle movements between the herds nor cattle movements from the same source.

- Henley-on-Thames (Figure 6, blue circle) in the south-east of the county.

  Genotype 10:a is the most commonly found *M. bovis* genotype in this area including a confirmed case in wild deer in 2018 and a confirmed case in a large alpaca breeding farm in 2019.

  For the time period 2015 to 2019, WGS analyses identified a cluster of 18 incidents attributed to almost identical isolates (0 to 1 SNP difference) within a 400 square kilometre area adjacent to Henley. The isolate of *M. bovis* is the same as that identified from a nationwide *M. bovis* outbreak in cats. The cluster started with four cattle incidents in 2015-2016 in the geographical centre, attributed to identical isolates. This spread concentrically outwards in the following years. Local cattle movements are possible transmission pathways for three incidents although this is uncertain. By elimination of other transmission pathways, infected wildlife was concluded as the most likely source of the majority of the incidents. Wild fallow deer could have been a source in the centre of the cluster where they are abundant, and co-graze with cattle.

  From 2017, incidents of genotype 11:a (homerange in the south west of England) started to appear in this area close to the Berkshire border: two in 2019, two in 2018 and two in 2017. They were first thought to all be linked to purchases of cattle but the two most recent incidents, including an incident in a closed herd, suggests that this may not be the case and there could be a potential wildlife source.

- Chinnor-Thame (Figure 6, red circle) in the most eastern corner of the county, bordering Buckinghamshire.

  In 2017, a new *M. bovis* genotype NT:7-5-5-4*-3-3.1, (considered a mutation of genotype 10:a), was first identified in three incidents (one a closed herd for 10 years) situated very close to one another. An absence of epidemiological links between them suggested wildlife as the most likely common source. In 2018, this genotype was classified as genotype 17:g and three more incidents were identified within 3km in this cluster. In 2019, two additional incidents

closely related to 17:g were also disclosed in the cluster area. WGS analyses indicated genetic relatedness (zero to two SNPs difference).

Radial testing in Buckinghamshire was triggered by these 2018 and 2019 OTF-W incidents in the Chinnor-Thame cluster. Two incidents (one OTF-S incident and one OTF-W incident of a different genotype) were detected and were both attributed to purchased cattle. Therefore, spread appears to be limited to within Oxfordshire.

The established areas of endemic TB infection since the mid-2000s are located in the west of the county (Figure 6, black rectangle) 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, characterised by predominantly wildlife attributed genotype 10:a infection, high rate of recurrence and persistent incidents. The purchase of cattle to replace those lost during TB incidents has also increased the risk of purchased infection.

Figure 7 represents *M. bovis* genotypes detected in Oxfordshire (plus Hampshire and Berkshire), from OTF-W incidents where a wildlife source was considered most likely compared to other transmission pathways. The approach was different to that of the algorithm used for Figure 13. Data from previous reports were updated with data from 2019. Each DRF was assessed individually to determine the incidents where badger risk pathways were scored with the highest certainty. Where residual infection from a previous incident attributed to a badger source was scored at the same level as badger sources, these were still included as badger source because it is not possible to distinguish between the two for recurrent incidents. However, where purchase or other sources and badgers were scored with equal likelihood, these were not included in this map.

Genotype 10:a continues to be the predominant genotype in Oxfordshire. This mirrors the presumptive wildlife endemic area illustrated by the grey 3km circles in Figure 7, attributed to wildlife. These historically mainly cover the western side of the county bordering the HRA, with more recent spread to the east of the county accounting for portions of the Henley cluster and the Somerton cluster in the east of the county.

Other genotypes attributed to wildlife referred to in Figures 7 and well established in 2019 are genotype 17:g in the Chinnor area represented by the light blue 3km circles, spoligotype 130 in the Somerton area represented by orange 3km circles and genotype 11:a in the Henley area which could represent movement of infected cattle and/or wildlife into the area from the HRA and consequent local spread (not shown in Figure 7 because of high uncertainty).
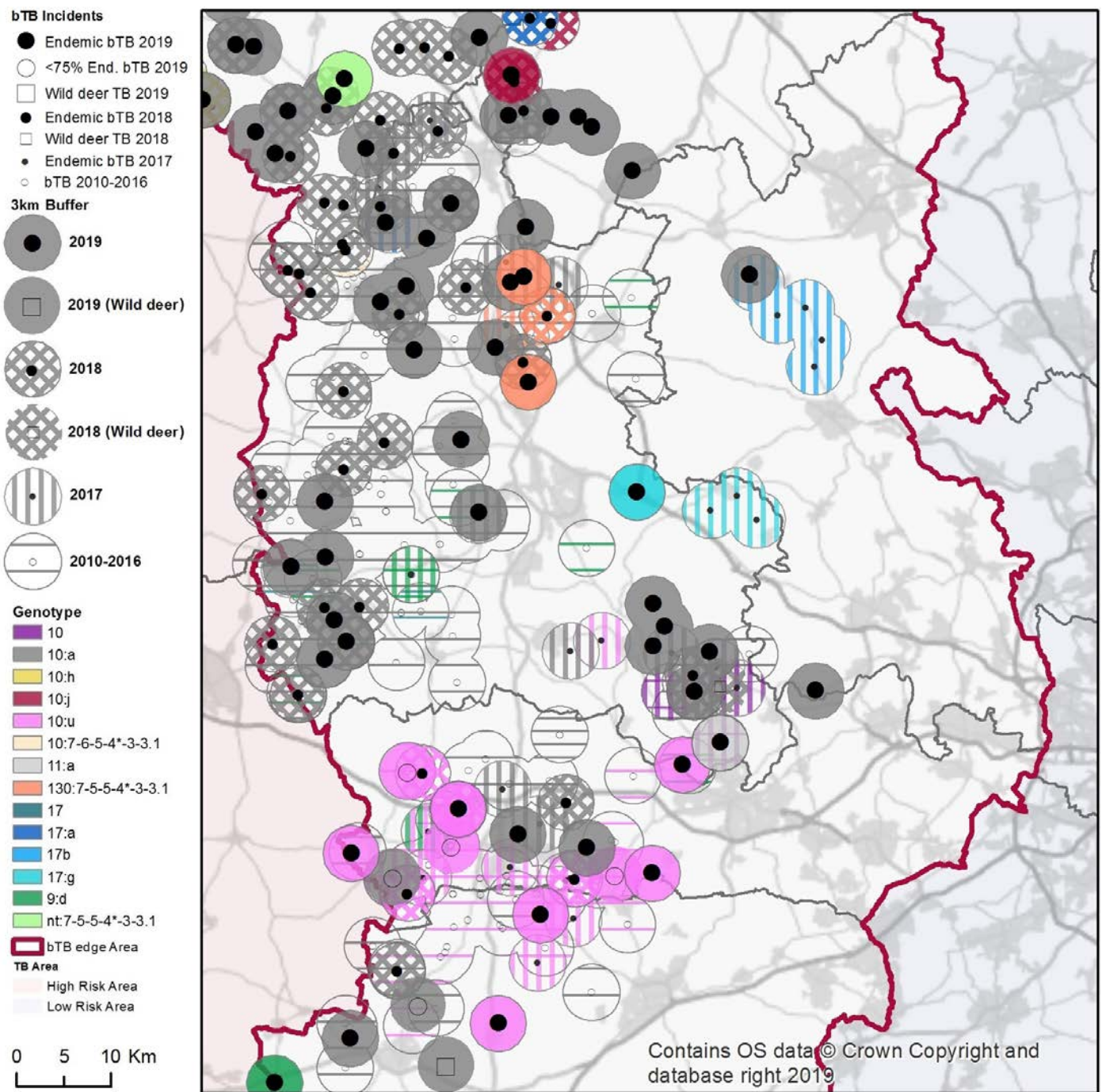
Figure 7: Genotypes of *M. bovis* detected in Oxfordshire in 2018 and 2019, where a wildlife source was attributed with a 75% certainty or above, as an indication of endemic infection within local wildlife populations (OTF-W incidents only). To note five additional incidents where a wildlife source was attributed with less than 75% certainty have been included in the map.

Historically there has been a narrow band running from west to east also attributed to wildlife infection involving spoligotype 17 (genotypes 17:a,17:b and more recently 17:e) and spoligotype 9 (9:d mainly and one 9:b first ever isolated). No incidents of spoligotype 9 were found in 2019. Two incidents with genotype 17:a were thought to be wildlife related; an ongoing and now persistent 2018 incident located in north-west Oxfordshire, and one in 2019 in south-west Oxfordshire.

Two isolated incidents of genotype 17:e in 2018 and 2019 in south Oxfordshire represent local spread. The only previous case of 17:e in this area was in 2011 in Uffington (near the county border with Wiltshire and Gloucestershire) where there is a genotype 17:e homerange.

Some incidents may represent wildlife movements across the county border into Oxfordshire. Several cases of genotype 10:a and 74:a and previous year 10:a mutations have been detected near the border with Warwickshire with similar cases occurring on the other side of the border. Although cattle movements (purchases) cannot be ruled out, the distribution of incidents suggests some wildlife involvement.

Historically incidents west of Oxfordshire were mostly attributed to transmission from a badger source, whereas those in the east of Oxfordshire were less likely to be attributed to wildlife due to the paucity of evidence for local genotypes and homeranges established in this area. However, this has changed in the last two years in the face of mounting genetic evidence within clusters of incidents that points towards wildlife sources. OTF-S incidents are more likely to be given a purchased source or undetermined (Figure 8).
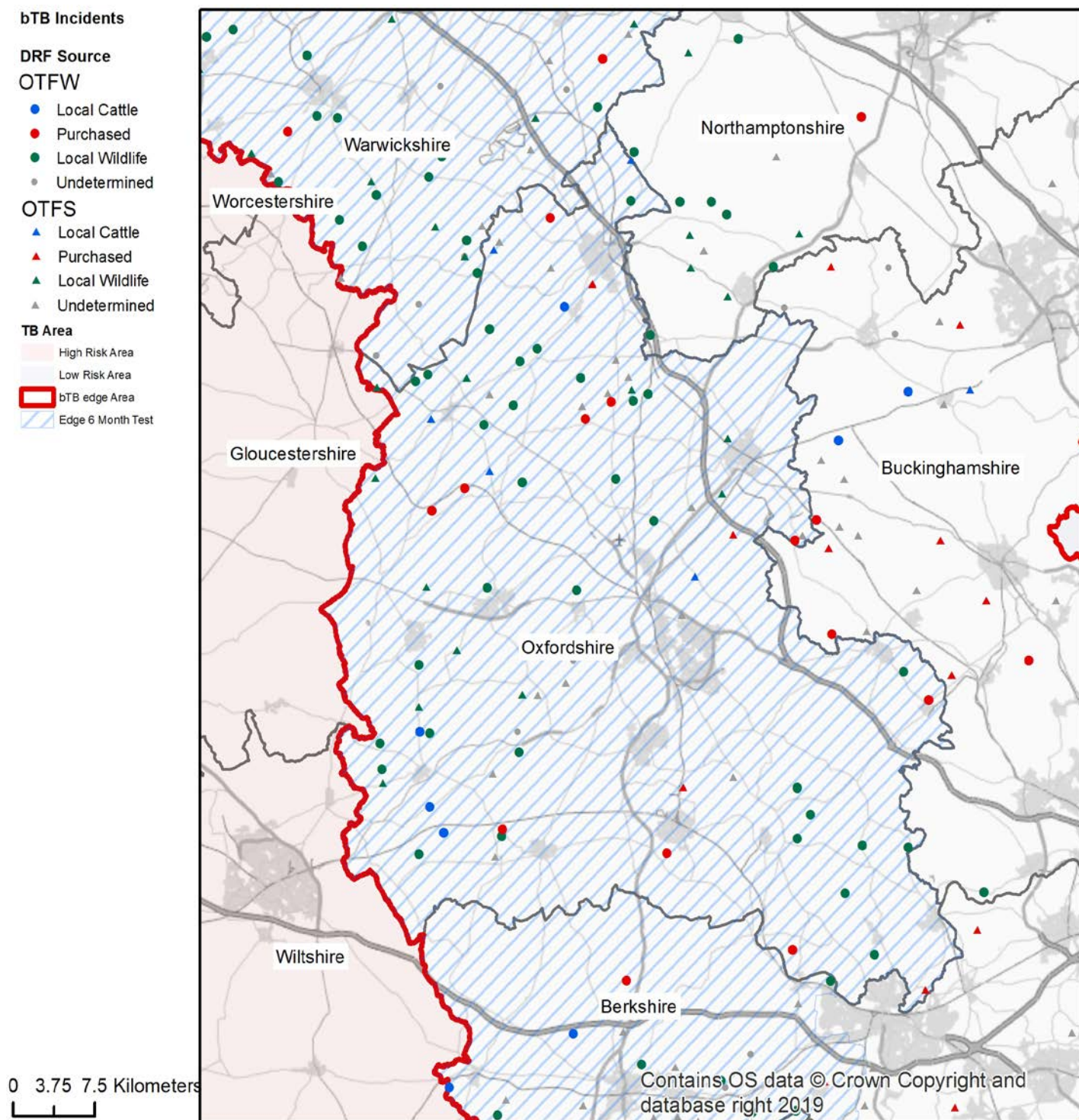
Figure 8: Map of the source of infection pathway recorded with the highest level of certainty for all TB incidents (OTF-W and OTF-S) in Oxfordshire, and its adjoining Edge Area counties, which started in 2019.

Other characteristics of TB incidents

Incidents by herd types

Most incidents occur in herds of 200 cattle or less (Figure 9). However, as with previous years, when Figure 1 (proportion of herds per size category) is considered, new incidents showed a predilection for medium/large herd size (over 100 cattle). The majority of herds affected were in the beef sector but this is also the most common production sector in Oxfordshire.
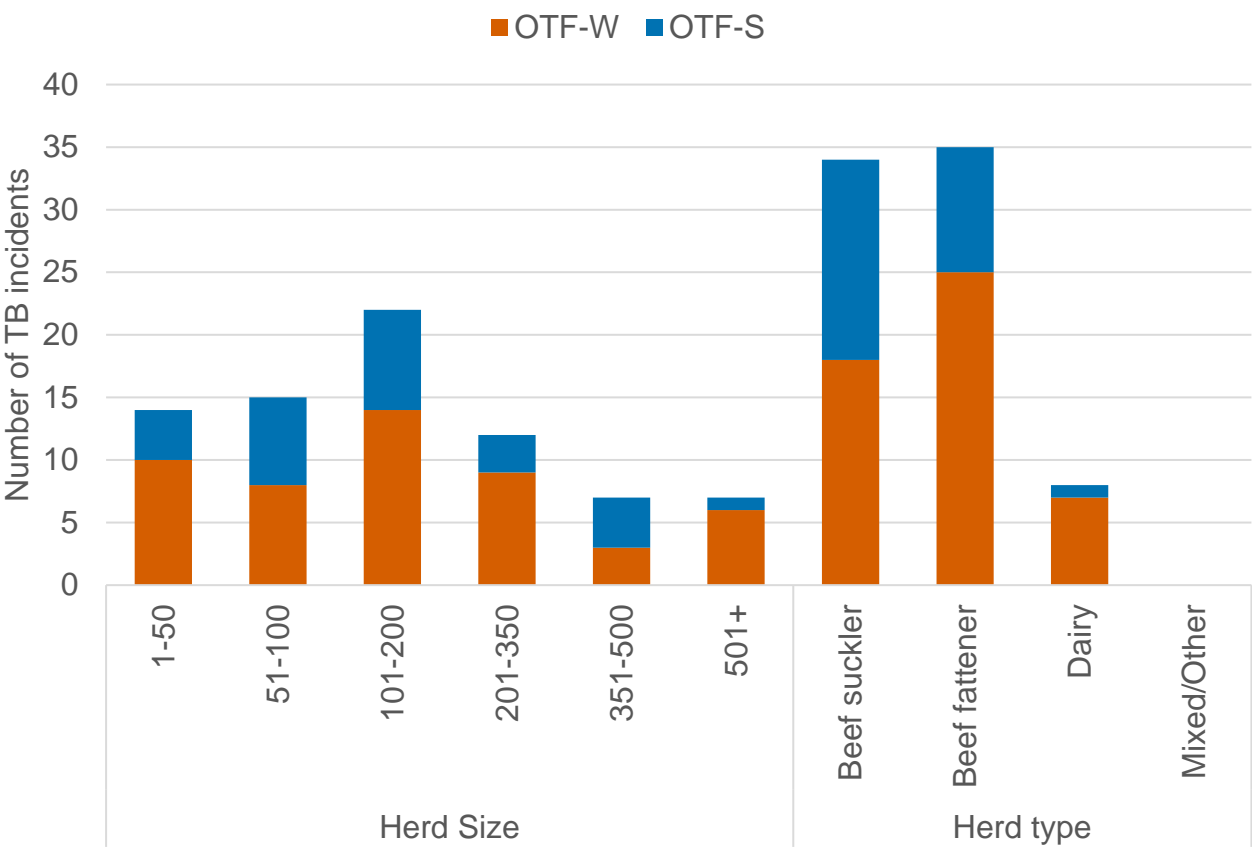

Figure 9: Number of new TB incidents (OTF-W and OTF-S) in Oxfordshire in 2019, by cattle herd size and type.

Incidents by month of disclosure

The majority of TB testing in 2019 was carried out before and after the summer grazing months when cattle are housed. Six-monthly routine herd testing has spaced out surveillance before and after grazing and provided more information as to whether infection is disclosed within a herd after housing or after grazing. The highest number of incidents was disclosed in November when the cattle are housed after summer grazing, suggesting that risk of infection is highest during the grazing period (Figure 10).
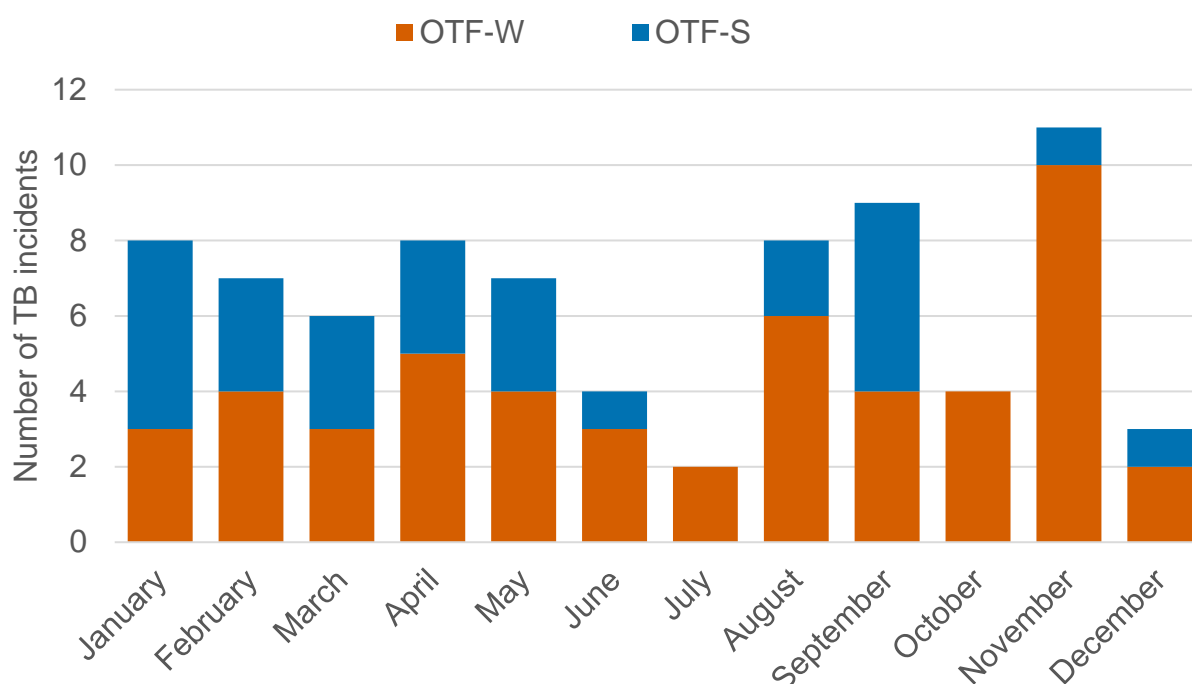
Figure 10: Number of new TB incidents (OTF-W and OTF-S) in Oxfordshire in 2019, by month of disclosure.

Genotypes of *M. bovis* isolated

As shown in Figure 11, the predominant *M. bovis* genotype in Oxfordshire is 10:a. The second most common genotypes found in 2019 were 11:a, 130:7-5-5-4*-3-3.1 and 17:g, with the two latter ones being specific to Oxfordshire (likely mutations) and only found in their specific geographical areas (Henley, Somerton and Chinnor cluster). Genotype 74:a and 17:e are rarely found in Oxfordshire but they are common in the neighbouring HRA county of Wiltshire so it is likely to be moving into this area. Genotype 17:a has been in Oxfordshire for some time often affecting the same farms and most likely caused by residual infection or re-infection from local wildlife.

The genotype 10:a homerange is large, including neighbouring counties to Oxfordshire, and therefore provides less information as to whether infection is contracted 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 wildlife to neighbouring farms. The use of WGS has provided further useful epidemiological information for assigning the most likely source of infection to these incidents.
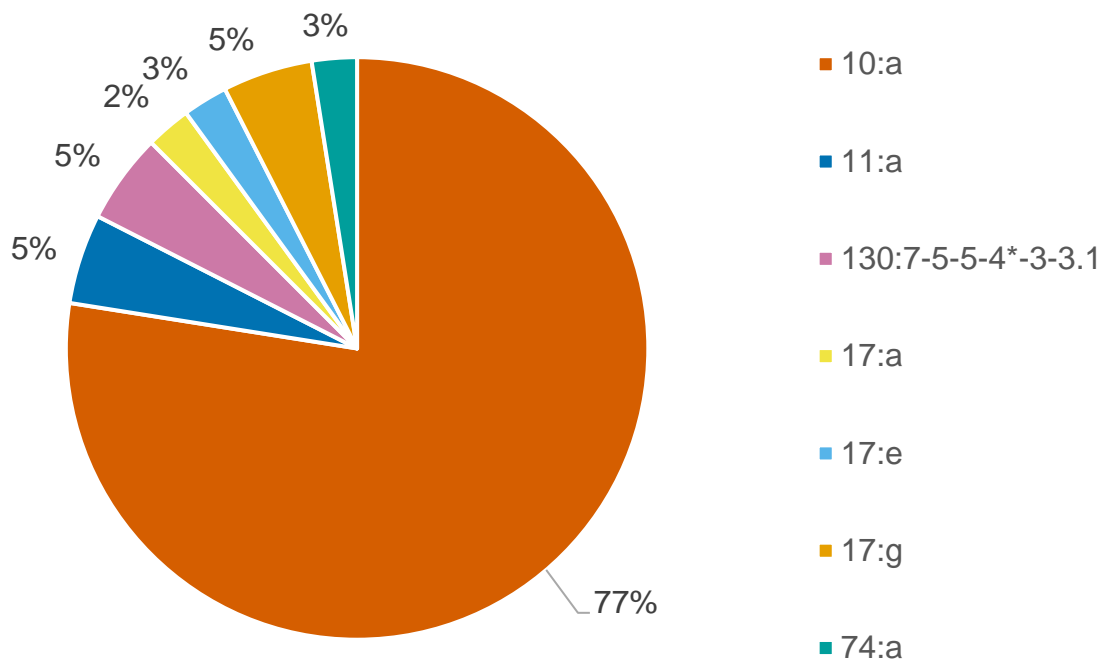
Figure 11: Genotypes of *M. bovis* identified in herds with OTF-W incidents in Oxfordshire in 2019 (n=40).

Duration of incidents

The duration of incidents tended to increase in recent years in most OTF-W cases, explained by increasing infection pressure from within herds and from infected wildlife, with IFN-γ detecting residual infection (undetected by skin testing) at stages when skin testing alone would have resolved incidents. In 2019 this trend appeared to be reversing and most incidents averaged between 150-240 days compared to 240-550 in 2018 (Figure 12). This might be explained by more frequent testing, which detects infection earlier before it can become fully established in the herd, and reduction of residual infection from previous incidents following the use of IFN-γ testing. The number of persistent incidents (lasting over 550 days) remained high in 2019 at fifteen (calculated as the total of the last two bars in Figure 12).
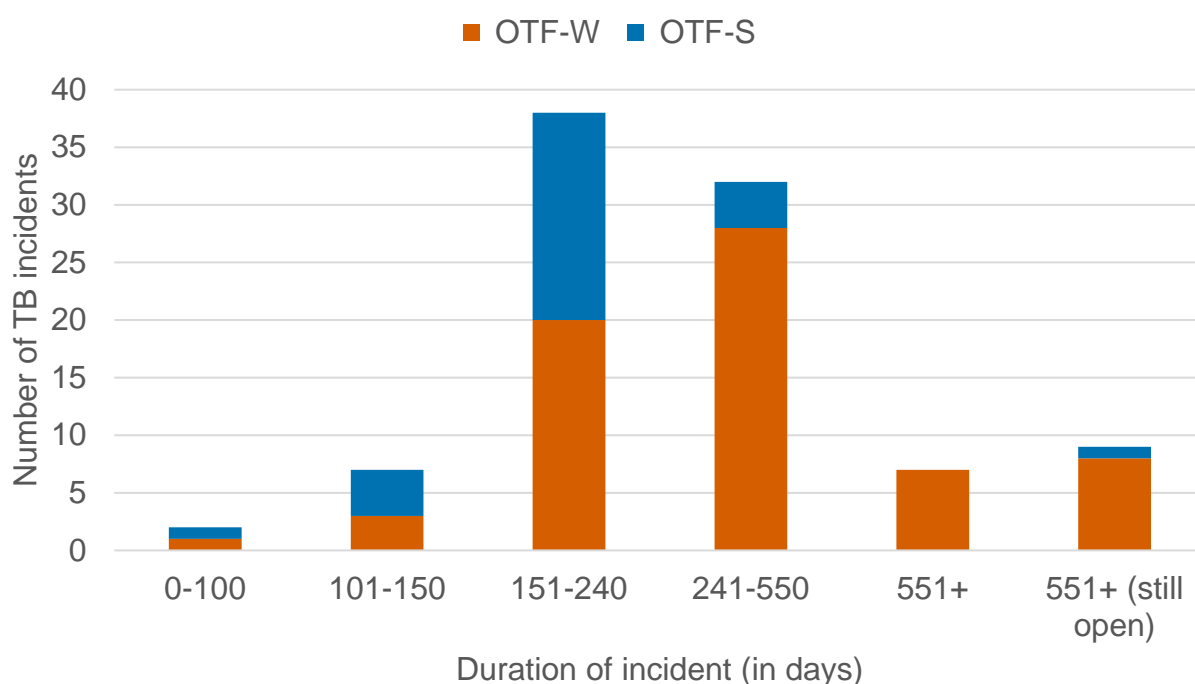
Figure 12: Duration of all TB incidents (OTF-W and OTF-S) that ended in 2019, and the number of persistent TB incidents (551+ days) that were unresolved at the end of 2019 in Oxfordshire. Note that Approved Finishing Units (AFUs) have been excluded.

Suspected sources, risk pathways and key drivers for TB infection

It can be challenging to retrospectively establish the route of infection for a TB incident herd. The Animal and Plant Health Agency (APHA) aims to complete an epidemiological assessment for all TB incidents in the Edge Area (both OTF-W and OTF-S). This includes a thorough on-farm investigation and scrutiny of routinely collected data; such as cattle movement records, and the results of molecular analyses where available.

During the assessment up to three risk pathways of infection are selected for each herd. Each risk pathway is given a score that reflects the likelihood of that pathway bringing TB into the herd. The score assigned has been updated this year to reflect developing understanding of how likelihood is being assessed in practice. It is recorded as either definite (score 8), most likely (score 6), likely (score 4) or possible (score 1). The source(s) for each incident are weighted by the certainty ascribed. Any combination of definite, most likely, likely or possible sources can contribute towards the overall picture for possible routes of introduction in to a herd. If the overall score for a herd is less than six, then the score is made up to six using the 'Other/Unknown Source' option. Buffering up to six in this way helps to reflect the uncertainty in assessments where only 'likely' or 'possible' sources are identified.

The weight of infection outputs in Appendix 4 are produced by combining the data from multiple herds and providing the proportion of pathways in which each source was identified, weighted by certainty that each source caused the introduction of TB. The outputs do not show the proportion of

herds where each pathway was identified (this is skewed by the certainty calculation). Genotyping of *M. bovis* isolates can be a powerful tool in identifying a likely source of infection, however genotypes are not determined for OTF-S herds. The inclusion of OTF-S herds in these calculations increase the uncertainty in the outputs. As a result, the relative proportions of each risk pathway is very approximate and only broad generalisations should be made from these data. A more detailed description of this methodology is provided in the Explanatory Supplement for 2019 (https://www.gov.uk/government/publications/bovine-tb-epidemiology-and-surveillance-in-great-britain-2019).

Key drivers of infection

The key drivers of the TB epidemic within Oxfordshire are as follows:
- Infected wildlife
- Cattle movement/purchase
- Residual infection

Sources of infection and risk pathways

Figures 13a and 13b show wildlife as the highest weighted source pathway for TB infection in incidents in Oxfordshire. The weighted source pathways of infection for all new incidents in 2019 is described in Appendix 4. Cattle movement, 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 four years where there has been an increase in the proportion of badger source incidents compared to purchased cattle source.

Approximately 55% of the weighted source pathways recorded for incidents in 2019 were attributed to wildlife source compared to 50% in 2018. However, due to the updated approach to the analysis of DRF risk pathways in 2019, it is difficult to directly compare these figures. The gradual spread of incidents over the last 14 years has been in an eastwards direction from the Gloucester and Wiltshire border thought to be caused by a moving front of infected wildlife. Possibly unrelated to this front, new endemic areas have appeared in the east side of the county, which was formerly considered free from endemic wildlife infection.

Approximately 21% of the weighted source pathways recorded for incidents in 2019 were attributed to the purchase of cattle with undetected infection from the HRA and Edge Area compared to almost 30% last year, although as noted above direct comparison between years is difficult due to an updated approach to the analysis. This source affected mostly fatteners including AFUs. TB incidents in AFUs were the only incidents with a definitive source identified (same genotype as origin, and no wildlife source) because of the presence of robust biosecurity measures preventing exposure of cattle in the units to infected wildlife. Source attribution for other incidents was less certain, especially when no genotype was available (OTF-S incidents), with assessment leaning towards a purchased source if cattle were bought in during the previous five years.
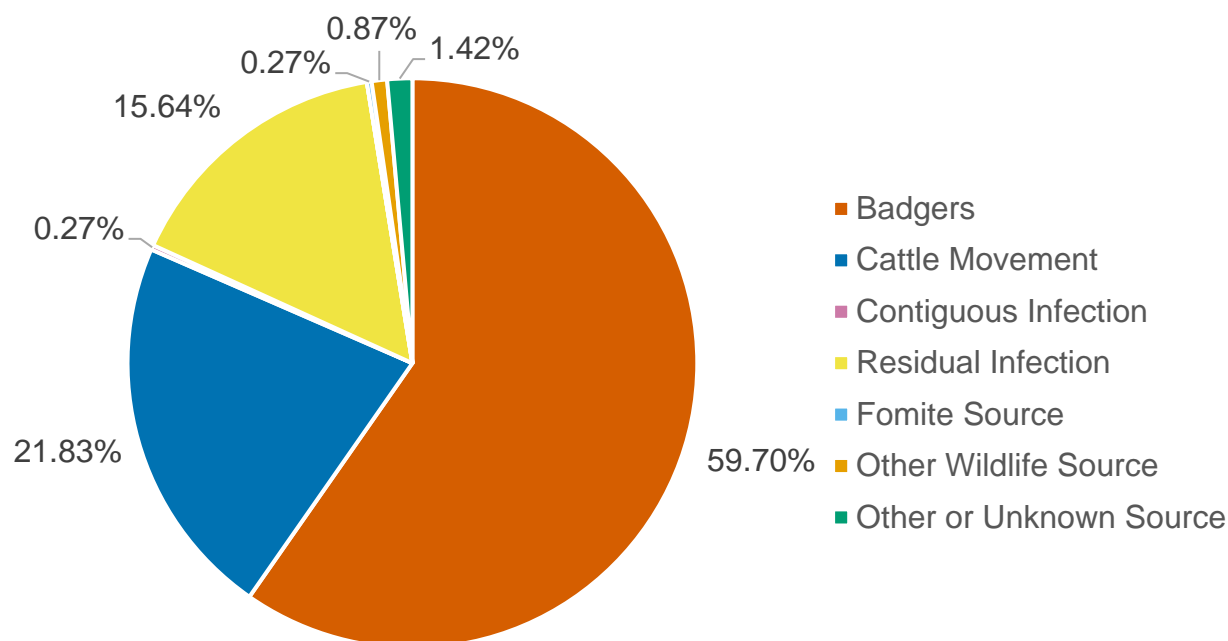
Figure 13a: Summary of the weighted source of infection pathways attributed for all OTF-W incidents in Oxfordshire that started in 2019, that had a completed DRF (47).
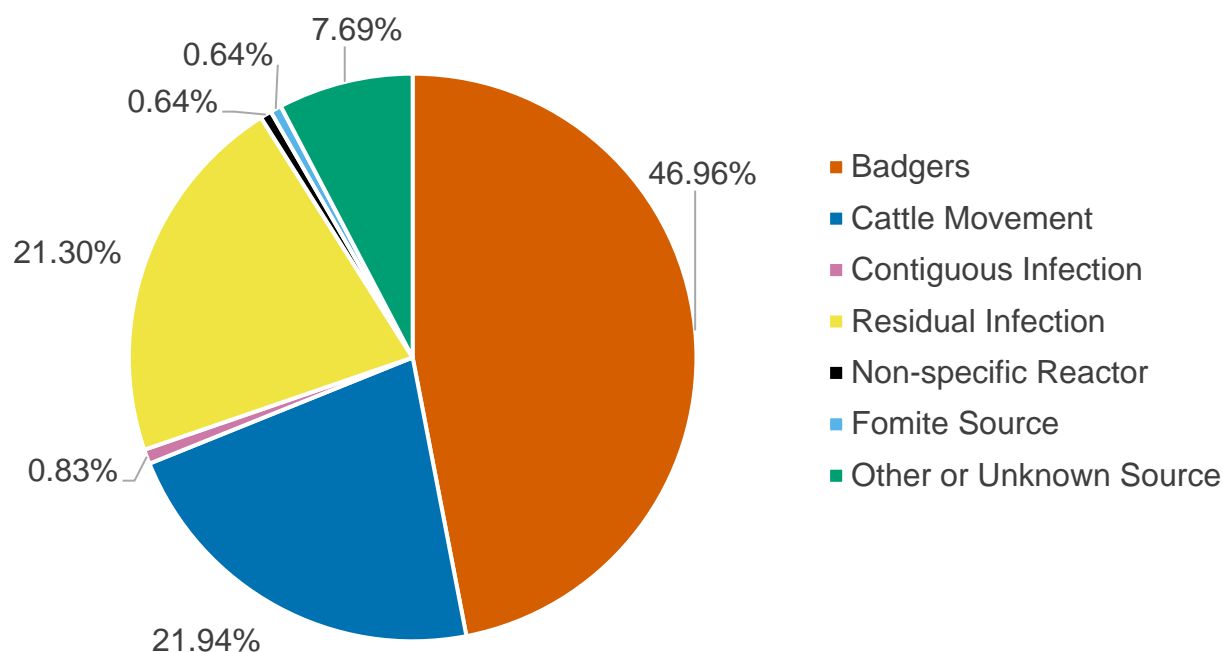

Figure 13b: Summary of the weighted source of infection pathways attributed for all OTF-S incidents in Oxfordshire that started in 2019, that had a completed DRF (26).

An increased proportion of weighted source pathways recorded for incidents were attributed to residual cattle infection from a previous TB incident. A high proportion of all incidents have had a history of TB. Considering any previous history, 63 out of 77 incidents in 2019, of which 52 had a history of TB in the last three years compared to 39 in 2018. This is much more evident in the former HRA part of Oxfordshire where, prior to 2018, IFN-γ testing was not routinely deployed in incident herds. This resulted in a higher likelihood of leaving infection undetected by skin testing alone. It is very difficult to distinguish between badger source infection and residual infection.

Very few incidents 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 incidents 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. Potential fomite sources such as contaminated shared machinery and manure or slurry spread near livestock farms are very difficult transmission pathways to assess.

Figure 14 illustrates the most likely source of infection according to the herd type. Beef sucklers, possibly due to more 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, were reported with a higher proportion of infection caused by purchase of cattle with undetected infection, although some incidents were still linked to wildlife. Whereas contact with wildlife was considered to be the most common explanation for OTF-W incidents, OTF-S incidents were mostly attributed to purchase of cattle with undetected infection, but with a lack of genotype evidence it is harder to attribute sources of infection. Dairy herds, due to larger herd sizes and lifespan of breeding stock exposed to wildlife and their policy of minimal purchase of replacements in order to maintain their high health status, were more likely to have incidents exclusively attributed to local wildlife and residual infection rather than to cattle movements.
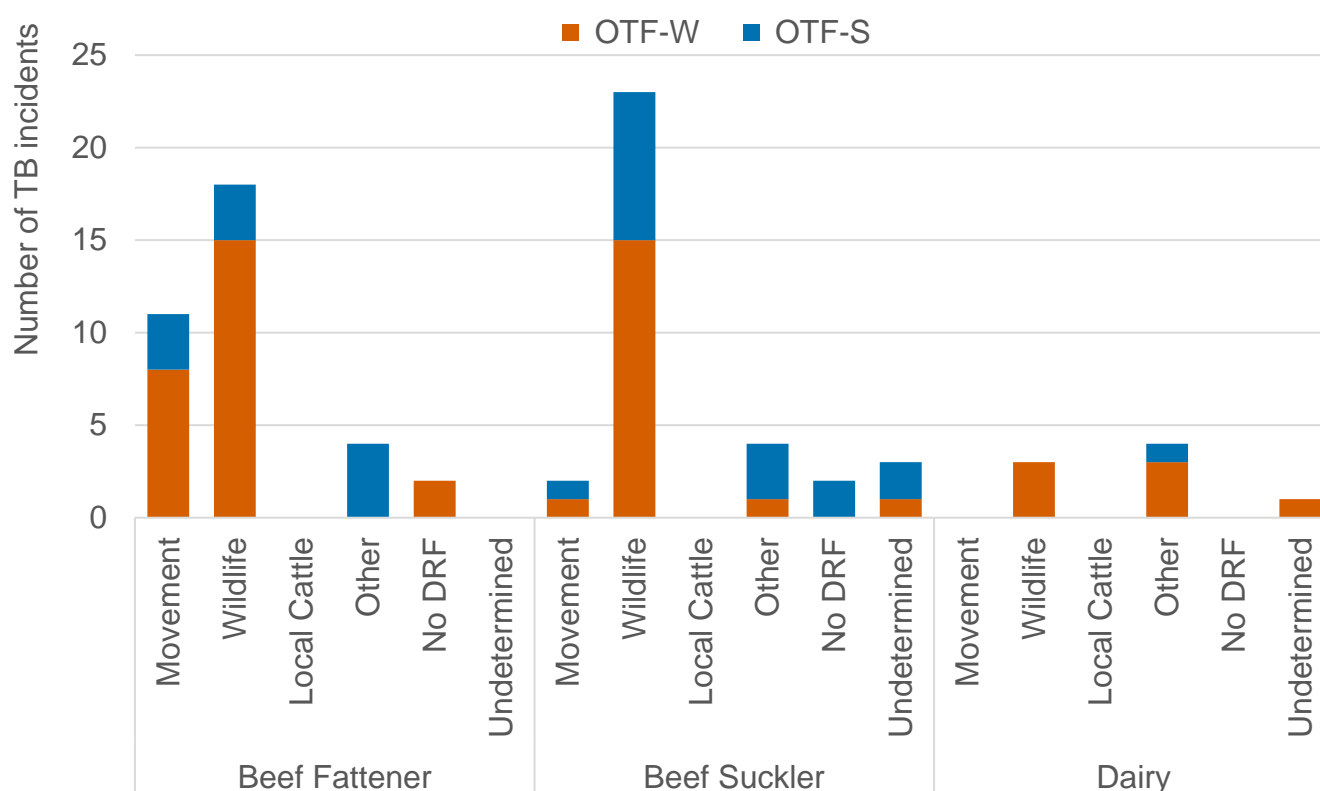
Figure 14: Source of infection recorded with the highest level of certainty for all TB incidents (both OTF-W and OTF-S) in Oxfordshire in 2019, by herd type. Note that the categories 'movement', 'wildlife', and 'local cattle' are comprised of incidents where these were the most likely single source of infection recorded. Incidents where the most likely single source was stated as 'unknown' were assigned to the category 'undetermined'. 'Other' includes incidents where there was equal weighting between the most likely sources of infection as well as other pathways not categorised elsewhere.

TB in other species

There is no statutory routine TB surveillance of non-bovine species, apart from post mortem examination (PME) of suspected clinical cases reported to APHA and post mortem meat inspection of animals (e.g. sheep, goats, pigs) slaughtered for human consumption.

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

One confirmed case of *M. bovis* (genotype 10:a) in wild deer was reported in 2018 in the Henley-on-Thames cluster. This genotype and WGS matched isolates from cattle in this area.

Clinical cases were confirmed with genotype 10:a in 2019 in a large breeding herd of alpacas. WGS supported initial introduction of *M. bovis* from wildlife in the absence of cattle contacts.

A clinical case was confirmed with *M. bovis* genotype 10:a in north Oxfordshire in 2019 in a domestic cat, unrelated by phylogeny to any TB clusters currently investigated, but likely infected locally within the 10:a homerange.

Detection of incidents

The majority of incidents were detected by routine herd surveillance tests which were by default, six-monthly in 2019, as shown in Figure 15a. This is similar to previous years (Figure 15b).
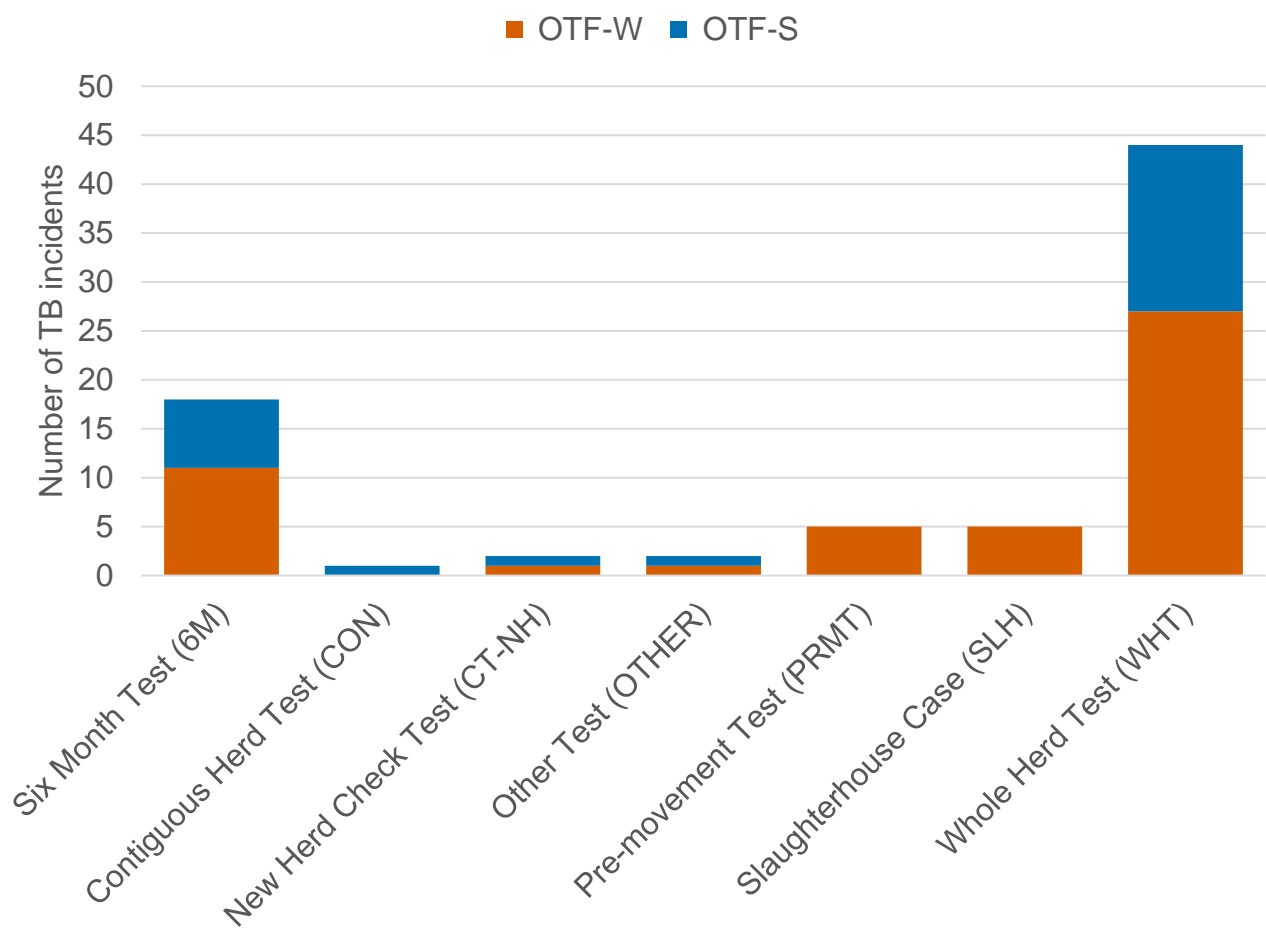

Figure 15a: Number of TB incidents (OTF-W and OTF-S) in Oxfordshire in 2019, disclosed by different surveillance methods.
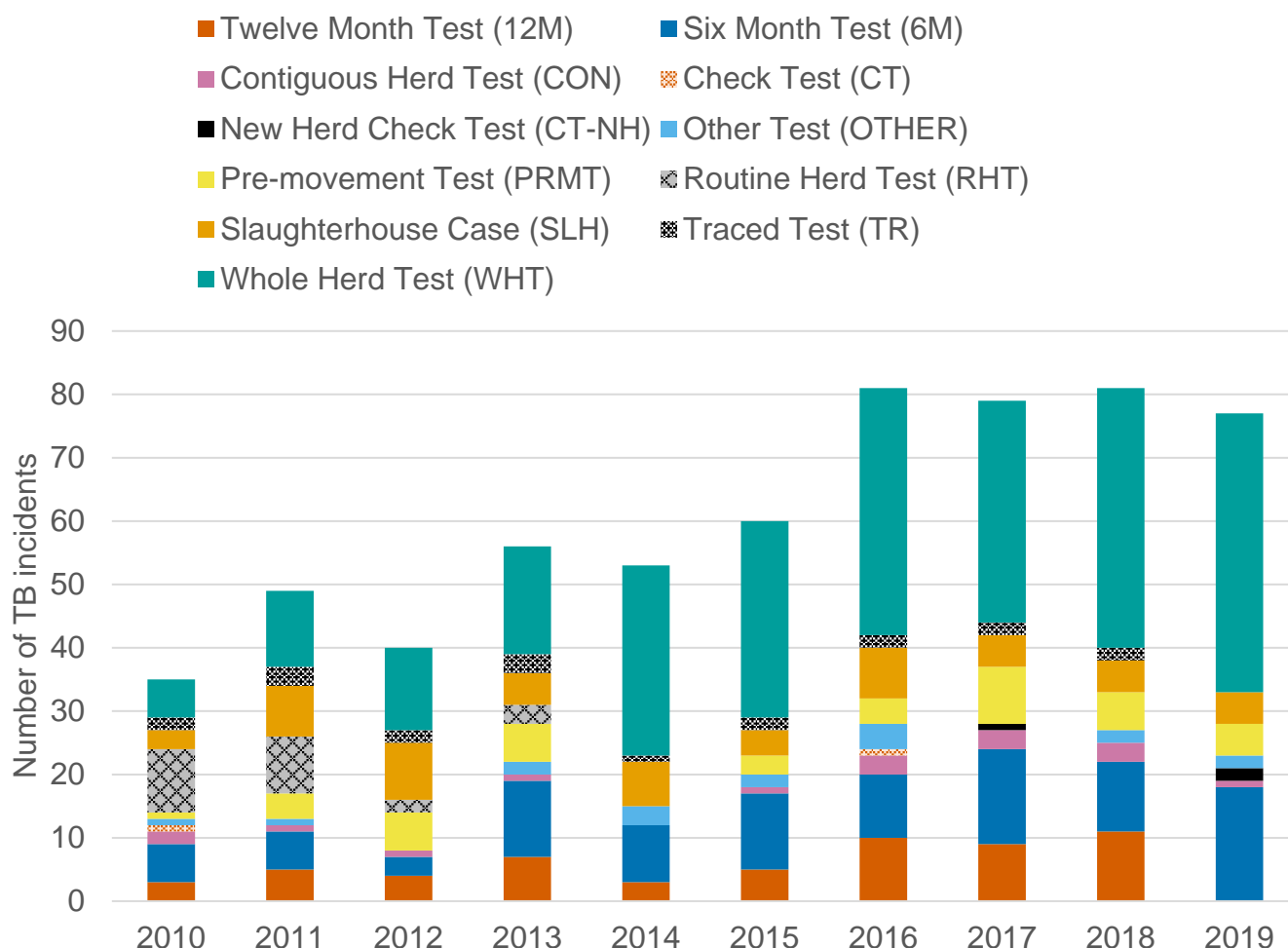
Figure 15b: Number of TB incidents (OTF-W and OTF-S) in Oxfordshire, 2010 to 2019, disclosed by different surveillance methods by year.

Increasing the frequency of surveillance testing from annual to six-monthly is detecting infection earlier, increasing the proportion of incidents detected by routine herd testing with or without a previous history of TB where six-monthly testing was carried out after incidents. This has also decreased the reliance on passive slaughterhouse surveillance (SLH) and pre-movement testing (PRMT). However, these still remain important to detect possible anergic cows undetected by skin testing, and infected stock earlier before moving to another herd.

As shown in Figure 16, more than half of incident herds had a history of TB in the previous three years with this proportion slightly higher for OTF-W herds (59% OTF-W and 54% OTF-S). The number of OTF-W incidents compared to OTF-S has not changed considerably since 2016 with OTF-W incidents still representing approximately double the number of OTF-S incidents in Oxfordshire (see Figure 2a). This likely reflects widespread endemic TB infection in the county compared to the neighbouring county of Buckinghamshire where OTF-S incidents predominate.
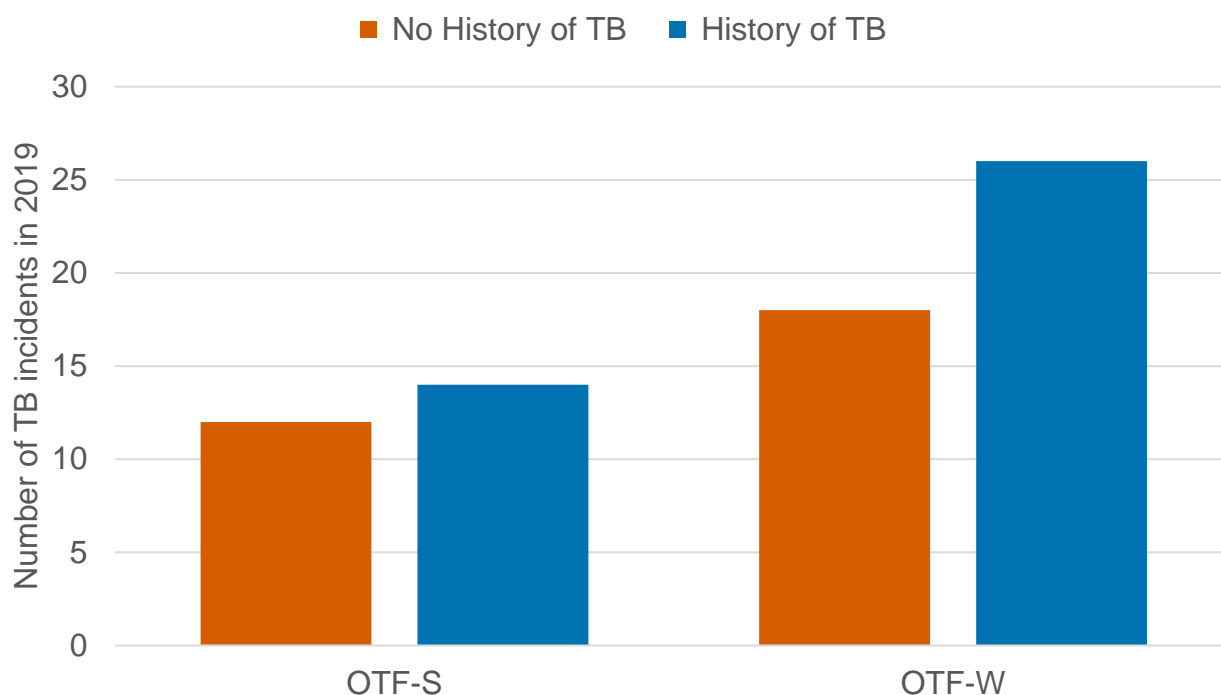
Figure 16: Number of TB incidents (OTF-W and OTF-S) in Oxfordshire in 2019 on holdings that have suffered an OTF-W incident in the previous three years, and holdings with no history of TB in the previous three years.

Skin test reactors and interferon gamma test positive animals removed

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 IFN-γ positive animals). This more than doubled in 2017 and 2018 with 1347 in 2017 (813 IFN-γ positives), and 1410 in 2018 (750 IFN-γ positives). In 2019 the number of reactors removed decreased slightly to 1159 (603 IFN-γ positives).

The sudden increase in reactors removed since 2016 was most likely due to increased mandatory use of IFN-γ testing, longer incident duration in 2017 and incorporation of the former HRA part of the county into the Edge Area in 2018. In 2019 more frequent surveillance testing might have reduced the number of reactors disclosed per test due to infection having less time to spread within the herd. The number of herd skin tests carried out in the last consecutive four years increased from 686 in 2016 to 703 in 2017, to 875 in 2018 and 892 in 2019 even though the total number of incidents was lower (Appendix 3).
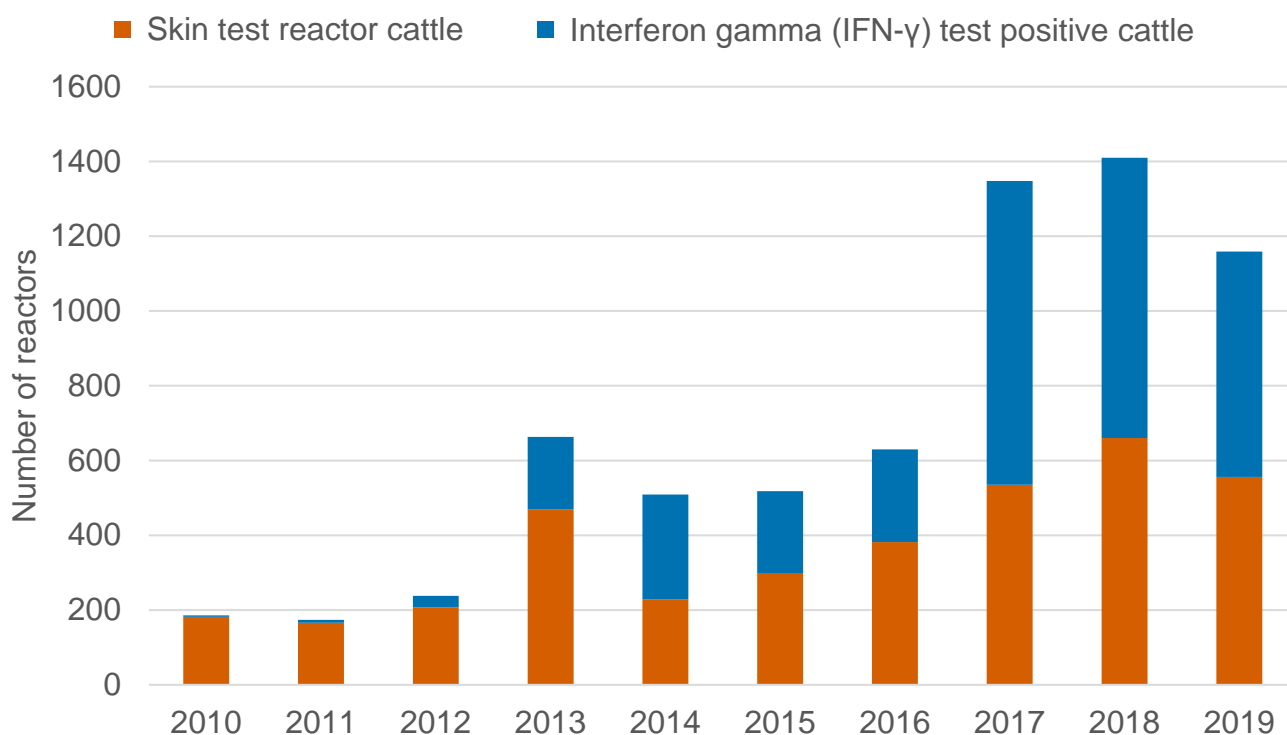
Figure 17: Number of skin test reactors and interferon gamma (IFN-γ) test positive cattle removed by APHA for TB control reasons, in Oxfordshire, 2010 to 2019.

Summary of risks to Oxfordshire

Presumptive spread of TB-infected wildlife is now evident in the whole county, increasing the likely areas of endemicity. The number of *M. bovis* genotypes involved has risen, making the spatial distribution 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.

Most incidents attributed to purchase of cattle involved movements of cattle from the HRA and Edge Area. The increasing number of AFUs in Oxfordshire since 2016 mitigates this risk by channelling these cattle into a biosecure environment, with moves exclusively to slaughter. Only AFUs without grazing are permitted in the Edge Area. Unannounced inspections by APHA should ensure that high standards of biosecurity are maintained and they do not cause spill over 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.

Summary of risks from Oxfordshire to surrounding areas

The number of incidents in the last four years has remained more or less stable, with herd incidence rate variations more affected by changes to surveillance testing frequency (six-monthly testing introduced in Oxfordshire in 2018) and persistence than numbers of incidents. The herd prevalence has plateaued at 10% of herds under movement restrictions at the end of each year during the last four consecutive years.

Despite the number of herd incidents of TB remaining more or less the same since 2016, the epidemiological picture has become more complex with endemic infection spreading to other parts of the county.

Spread of the presumptive wildlife infected area eastwards into Buckinghamshire (Edge Area) and beyond that towards the LRA counties is the most serious long term risk to achieving OTF status for 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 2019, 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 incidents continues. 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 cattle movements into the LRA from higher incidence areas. The introduction of Licensed Finishing Units (LFUs) in the LRA has also provide a barrier to introduction of infection into the wildlife and contiguous herds for animals which have not been pre-movement tested.

Assessment of effectiveness of controls and forward look

The number of herd incidents of TB in Oxfordshire has remained the same since 2016, but the epidemiological picture has become more complex. This does not favour the long term objective of reducing OTF-W incidence to <1% for Oxfordshire by 2025. The whole of Oxfordshire became part of the Edge Area in 2018 when the evidence for endemic TB was strong across the whole county.

Eradication of TB may require some form of wildlife intervention as well as tighter control of cattle movements from farms in the HRA into the Edge Area, as well as between endemic counties like Oxfordshire and non-endemic ones like Buckinghamshire.

Early detection of infection through more frequent surveillance testing of herds will help (such as six-monthly routine herd surveillance testing which started in 2018), alongside the use of mandatory IFN-γ testing for OTF-W incidents, particularly for those that recur due to residual herd infection. A

stronger message regarding improving on-farm biosecurity and informed purchasing, and some form of wildlife control in the county is paramount to stop the spread of TB from wildlife both within Oxfordshire and into the LRA.

Appendices

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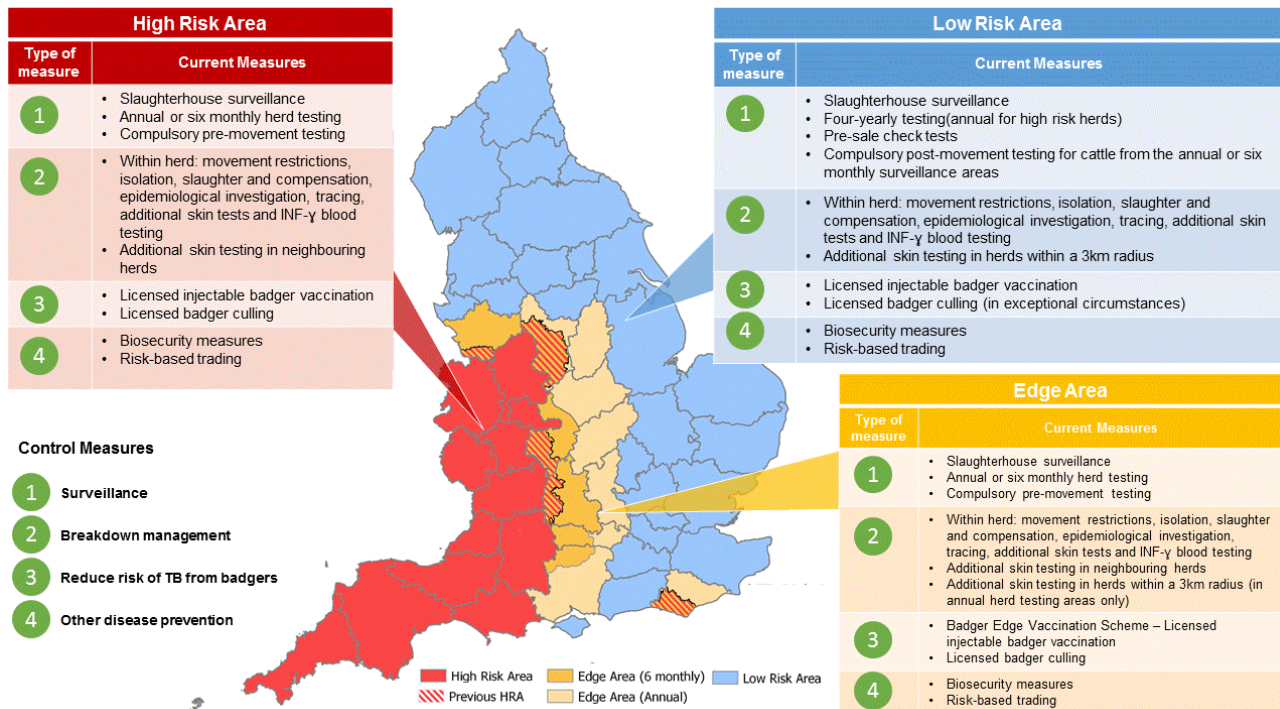

Figure A1: TB risk and surveillance areas of England effective since January 2018, as set out in the Government's Strategy for Achieving Officially Bovine Tuberculosis Free status for England. Map based on information published on www.tbhub.co.uk.

Policy objectives for the Edge Area

Short to medium term:

- slow down geographic spread
- maintain crude herd incidence of OTF-W incidents <2% overall by 2019
- begin to reduce the incidence rate

Longer term:

- reduce geographic spread of TB and push the Edge Area boundaries westward
- reduce OTF-W herd incidence to <1% by 2025
- attain OTF status (crude incidence of indigenous OTF-W herd incidents <0.1%) for the lowest incidence counties in the Edge Area

For more information about the governments approach to controlling TB, visit the strategy for achieving Officially Bovine Tuberculosis Free status for England, published in 2014 and independently reviewed in 2018, see:

https://www.gov.uk/government/publications/a-strategy-for-achieving-officially-bovine-tuberculosis-free-status-for-england

https://www.gov.uk/government/news/government-sets-out-next-phase-of-strategy-to-combat-bovine-tuberculosis

Key control measures

Surveillance:
- six monthly or annual routine herd testing
- additional targeted surveillance of cattle herds located within a 3km radius of new OTF-W incidents in annual testing sections of the Edge Area (radial testing)
- slaughterhouse (SLH) surveillance

Management of cases ('incidents'):
- increased sensitivity of incident herd testing:
- all incident herds must pass two consecutive short interval skin tests at severe interpretation to regain OTF status, irrespective of PM and bacteriological findings
- mandatory IFN-γ parallel testing of herds with OTF-W incidents
- enhanced management of herds with persistent incidents
- enhanced epidemiological investigation and data analysis
- information sharing - location of incident herds publicly available (using ibTB online (www.ibtb.co.uk) interactive mapping tool)
- restriction for life of all inconclusive reactors (IRs) that give a negative result on a re-test was introduced in November 2017. The only permitted movements of these animals are to slaughter or an Approved Finishing Unit

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 incidents

Summary of enhanced TB control measures in Oxfordshire

Edge Area testing policy:
- The Edge Area was established in January 2013 as part of the government's strategy to achieve officially TB free status for England
- In January 2018 six-monthly routine surveillance herd testing (in place of annual testing) was introduced across the whole county of Oxfordshire and fully established in 2019
- In May 2019 earned recognition allowed annual surveillance TB testing for lower risk herds in the Edge Area of England. These herds had to meet either of the following criteria: the herd had not had a TB incident in the last six years, or was registered to a TB health scheme accredited under the Cattle Herd Certification Standards (CHeCS)
- Compulsory IFN-γ testing became applicable for all new OTF-W incidents in the county in 2018. IFN-γ 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 IFN-γ testing were applied to some beef fattening herds, or large dairies with clearly differentiated epidemiological groups
- Enhanced case management measures were applied to some persistent incidents in the Edge Area of Oxfordshire. Historically, persistent incidents were only in the former HRA area of Oxfordshire but newly persistent incidents appeared in the original Edge Area (still in the western part) in 2018 and 2019

Other testing measures:
- Overdue TB testing has been reduced to a very low level by working with the county's local authority on the enforcement of TB testing as well as automatic referral of TB testing breaches to the Rural Payments Agency.
- Radial testing introduced in 2018 in Buckinghamshire has occasionally been generated from incidents in Oxfordshire near the eastern border to monitor any spread of TB into Buckinghamshire.

Other control measures:
- Provision of free biosecurity advice by the TB Advisory Service (TBAS, www.tbas.org.uk/)
- 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 veterinary surgeons are key to TB control.
- Natural England did not issue any badger culling licenses in Oxfordshire in 2019. Two sites in Oxfordshire were licensed by Natural England to vaccinate badgers in 2018, and in 2019 a total of 23 badgers were vaccinated in 7.6km^2.

Appendix 2: cattle industry in Oxfordshire

Table A2.1: Number of cattle premises by size band in Oxfordshire at 1 January 2019. (RADAR data)

Size of Herds	Un*	1-50	51-100	101-200	201-350	351-500	501+	Total Number of Herds	Mean Herd Size	Median Herd Size
Number of Herds in Oxfordshire	2	190	80	86	55	24	18	455	135	71

*The number of herds with an undetermined size.

Table A2.2: Number of animals by breed purpose in Oxfordshire at 1 January 2019.

Breed purpose	Beef	Dairy	Dual purpose	Unknown	Total
Number of Cattle in Oxfordshire	42,798 (69%)	15,499 (25%)	2995 (4%)	0	61,292

Appendix 3: summary of headline cattle TB statistics

Table A3.1: Herd-level summary statistics for TB in cattle in Oxfordshire between 2017 and 2019.

Herd-level statistics	2017	2018	2019
(a) Total number of cattle herds live on Sam at the end of the reporting period	576	554	561
(b) Total number of whole herd skin tests carried out at any time in the period	703	875	892
(c) Total number of OTF cattle herds having TB whole herd tests during the period for any reason	421	421	418
(d) Total number of OTF cattle herds at the end of the report period (i.e. herds not under any type of Notice Prohibiting the Movement of Bovine Animals (TB02) restrictions)	494	462	477
(e) Total number of cattle herds that were not under restrictions due to an ongoing TB incident at the end of the report period	510	476	491
(f) Total number of new TB incidents detected in cattle herds during the report period, (including all FUs)	79	81	77
• OTF-S	19	23	27
• OTF-W	60	58	50
(g) Of the OTF-W herd incidents:			
• How many can be considered the result of movement, purchase or contact from/with an existing incident based on current evidence?	13	7 (4 AFU)	6 (1 AFU)
• New OTF-W incidents triggered by skin test Reactors or 2xIRs at routine herd tests	37 (including 12M test)	37 (including 12M test)	36 (including 6M test)

Herd-level statistics	2017	2018	2019
• New OTF-W incidents triggered by skin test Reactors or 2xIRs at other TB test types (forward and back-tracings, contiguous, check tests, etc.)	16	16	8
• New OTF-W incidents first detected through routine slaughterhouse TB surveillance	4	5 (4 AFU)	6 (1 AFU)
(h) Number of new incidents revealed by enhanced TB surveillance (radial testing) conducted around those OTF-W herds	n/a	n/a	n/a
• OTF-S	n/a	n/a	n/a
• OTF-W	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 incidents that began in a previous reporting period, but not including non-grazing Approved Finishing Units)	55	61	53
(j) New confirmed (positive *M. bovis* culture) incidents in non-bovine species detected during the report period (indicate host species involved)	0	1	2
(k) Number and type of finishing units active at end of the period:			
• Approved Finishing Units: Grazing	0	0	0
• Approved Finishing Units: Non Grazing	7	7	8
• Exempt Finishing Units: Grazing	0	0	0
• Exempt Finishing Units: Non Grazing	0	0	0

Table A3.2: Animal-level summary statistics for TB in cattle between 2017 and 2019.

Animal-level statistics (cattle)	2017	2018	2019
(a) Total number of cattle tested in the period (animal tests)	139,336	148,857	149,951
(b) Reactors detected in tests during the year:			
• Tuberculin skin test	535	660	556
• Additional IFN-γ blood test reactors (skin-test negative or IR animals)	813	750	603
(c) Reactors detected during year per incidents disclosed during year *	17.1	17.4	15.1
(d) Reactors per 1000 animal tests	9.7	9.5	7.7
(e) Additional animals slaughtered during the year for TB control reasons:			
• DCs, including any first-time IRs	20	49	15
• Private slaughters	6	9	7
(f) SLH cases (tuberculous carcases) reported by Food Standards Agency (FSA)	12	9	18
(g) SLH cases confirmed by culture of *M. bovis* **	10	5	9

* Note: reactors may be from incidents disclosed in earlier years, as any found through testing during the report year count here.
** Note: not all cases reported are submitted for culture analysis. All cases reported are from any period prior to or during restrictions.

Appendix 4: suspected sources of *M. bovis* infection for all of the new OTF-W and OTF-S incidents identified in the report period

Table A4.1: Suspected sources of *M. bovis* infection for all of the new OTF-W and OTF-S incidents identified in Oxfordshire, in 2019.

Source of infection	Possible (1)	Likely (4)	Most likely (6)	Definite (8)	Weighted contribution
Badgers	14	23	35	1	55.2%
Cattle Movements	27	8	9	1	21.9%
Contiguous	3	0	0	0	0.5%
Residual Infection	17	12	9	0	17.7%
Domestic Animals	0	0	0	0	0.0%
Non-specific Reactor	1	0	0	0	0.2%
Fomites	2	0	0	0	0.4%
Other Wildlife	3	0	0	0	0.6%
Other or Unknown Source	0	0	0	0	3.7%

Please note that each TB incident could have up to three potential pathways so totals may not equate to the number of actual incidents that have occurred. Details of the methodology used to calculate the weighted contribution of the different suspected sources of *M. bovis* infection for all new incidents can be found in the main body of the report and in the Explanatory Supplement for England 2019 (https://www.gov.uk/government/publications/bovine-tb-epidemiology-and-surveillance-in-great-britain-2019).