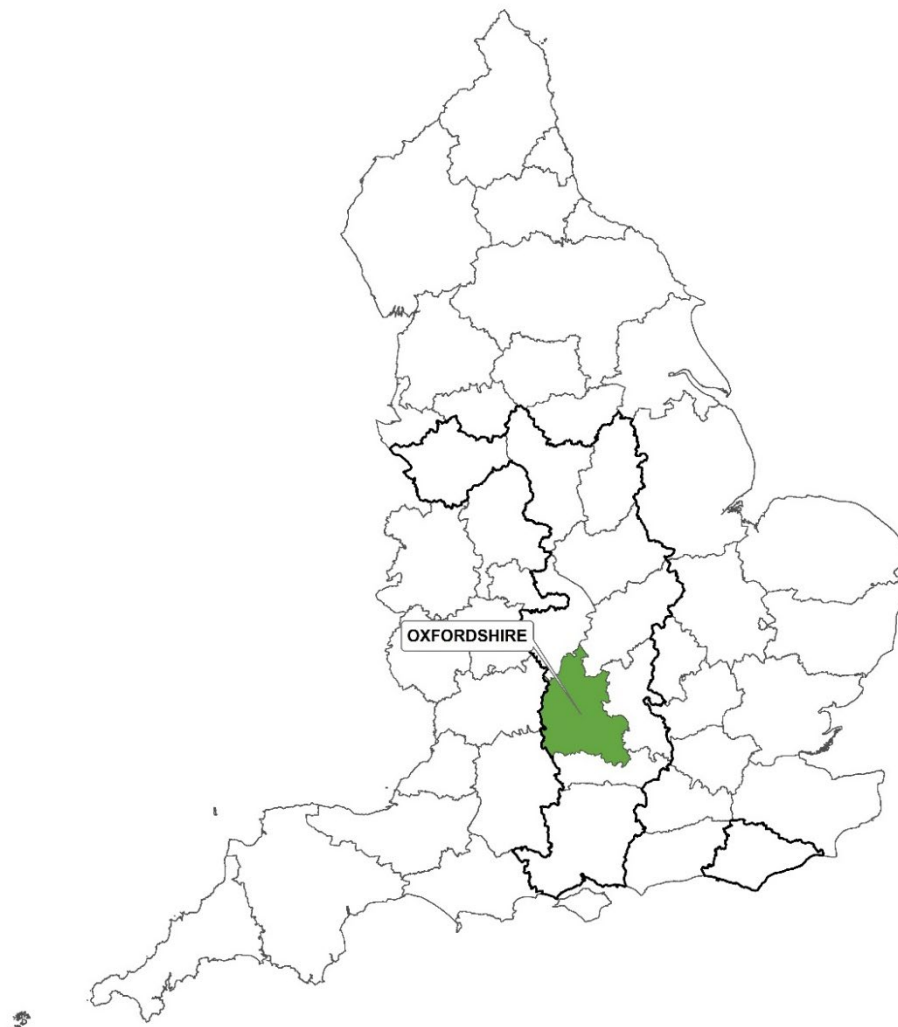




Animal &
Plant Health
Agency

Year-end descriptive epidemiology report: Bovine TB in the Edge Area of England County: Oxfordshire Year-end report for: 2020

TB Edge Area - OXFORDSHIRE



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Executive summary

Reporting area

Oxfordshire is part of the Edge Area that was established in 2013. In 2014, the bovine tuberculosis (TB) surveillance strategy for this area was incorporated into the UK government's strategy to achieve Officially Bovine Tuberculosis Free (OTF) status for England by 2038. This end of year report describes bovine TB in Oxfordshire.

Local cattle industry

Cattle 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.

Smaller farms tend to buy locally within the county. Dedicated sales for TB-restricted cattle in the south-west are the main outlet for calves from TB incident herds.

New TB incidents

The annual number of new TB incidents in Oxfordshire over the last five years (2016-2020) has remained more or less the same. A slightly lower number of incidents was recorded in 2019 (77) and 2020 (72) than in the previous three years.

This is potentially explained by several factors such as increased frequency of herd testing from 2018, reduced residual infection (and associated recurrent incidents) due to the use of interferon gamma (IFN- γ) testing, and modest reductions in TB incidence in some nearby HRA counties decreasing the numbers of purchased cattle with undisclosed infection.

The herd prevalence in Oxfordshire has plateaued over the last four years at 10% of herds under movement restrictions at the end of each year. Additional impacts such as COVID-19 public health restrictions in 2020 are difficult to measure but could have had effects such as restrictions on cattle sales.

Risk pathways for TB infection

Infected wildlife is the most common likely source of TB infection for cattle herds reported in Oxfordshire in 2020. This has become more evident during the last five years, with the appearance of clusters of incidents suspected to have a wildlife source and spread of incidents eastwards from the Oxfordshire border with the HRA.

Of particular concern is the increase in the number of incidents with a suspected wildlife source along the eastern border with Buckinghamshire. In this area, three clusters of

incidents have been identified: north-east (Somerton cluster), central east (Chinnor cluster) and south east (Henley cluster). Other clusters were identified in 2020 in the north, north-west and south-west of the county showing a complex picture of clusters across Oxfordshire.

Genotyping and Whole Genome Sequence (WGS) analysis of *M. bovis* isolates has demonstrated a close degree of genetic relatedness between incidents within these clusters, which can be explained by direct and indirect contact between cattle and infected wildlife in the absence of local cattle movements and contiguous contact between herds.

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 2020 bovine TB epidemiology reports.

Disclosing tests

Routine surveillance testing of herds accounted for more than half of the new incidents disclosed in Oxfordshire in 2020, with the rest found during post-incident tests, which in 2020 were completed at the same six-month interval as the current routine surveillance herd testing. Some incidents were detected by pre-movement testing and 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 increased the number of animals removed per incident. In 2019 and 2020 this number significantly decreased, possibly due to less spread within herds with increased routine testing and/or lower number of TB incidents.

Risks to the reporting area

Increased cattle TB controls may reduce the risk to Oxfordshire but continued spread of infection in wildlife remains a risk. Reduced incidence in some neighbouring counties, possibly associated with wildlife control measures, has mitigated some of the risk of purchasing cattle with undetected infection from these areas.

Risks posed by the reporting area

The continued expansion of the endemic area eastwards is a threat to the LRA, and adjacent Edge Area counties. The neighbouring Edge Area county of Buckinghamshire, which is largely free from endemic infection in wildlife, acts as a buffer zone between Oxfordshire and the LRA.

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 in wildlife 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 will 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 is helping.

Efforts should also be focused on controlling TB near the borders of lower incidence counties (Buckinghamshire and Northamptonshire), 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.

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 2020. Bovine tuberculosis is caused by the organism *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 this area, 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 UK 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. 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

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.

Since May 2019, cattle herds in the six monthly parts of the Edge Area that meet certain criteria are eligible to return to 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

Changes due to COVID-19

During 2020, public health measures adopted by the government to contain the COVID-19 pandemic impacted the ability to carry out some TB testing due to social distancing and self-isolation guidelines, affecting both veterinarians and farmers.

In particular, from 23 March 2020, routine or targeted TB skin tests were not mandatory for cattle under 180 days old where, in the official veterinarian's judgement, the young stock could not be tested safely in line with social distancing guidelines. The temporary amendment allowing calves under 180 days old to be excluded from TB testing did not apply to short interval tests in TB incident herds (required to restore a herds OTF status) or pre- and post-movement testing.

Routine TB skin tests are required within a pre-defined window of time to maintain a herds OTF status. From 23 March 2020, for tests that were allocated until 30 June 2020, the Animal and Plant Health Agency (APHA) permitted an extension to the TB skin testing windows on a case by case basis, where testing had not been completed due to valid reasons associated with COVID-19. The testing window for short interval tests was also extended by up to 30 days, where tests were unable to be completed due to COVID-19.

Furthermore, on-farm epidemiological assessments carried out to establish the route of infection for a TB incident herd were carried out remotely, by telephone, for the majority of 2020.

Cattle industry

Herd types

Almost two thirds of herds in Oxfordshire contain fewer than 100 cattle (Figure 1) and over 69% of all cattle are sired by a beef breed (Table A2.2 in Appendix 2).

Herds are a mixture of beef sucklers predominantly, dairies, and beef fattening units. Many dairy units have dispersed their herds in the last five years and changed production to smaller beef 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 and neighbouring Edge Area counties. Smaller herds tend to purchase locally, either directly from farms or from Thame market in Oxfordshire.

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

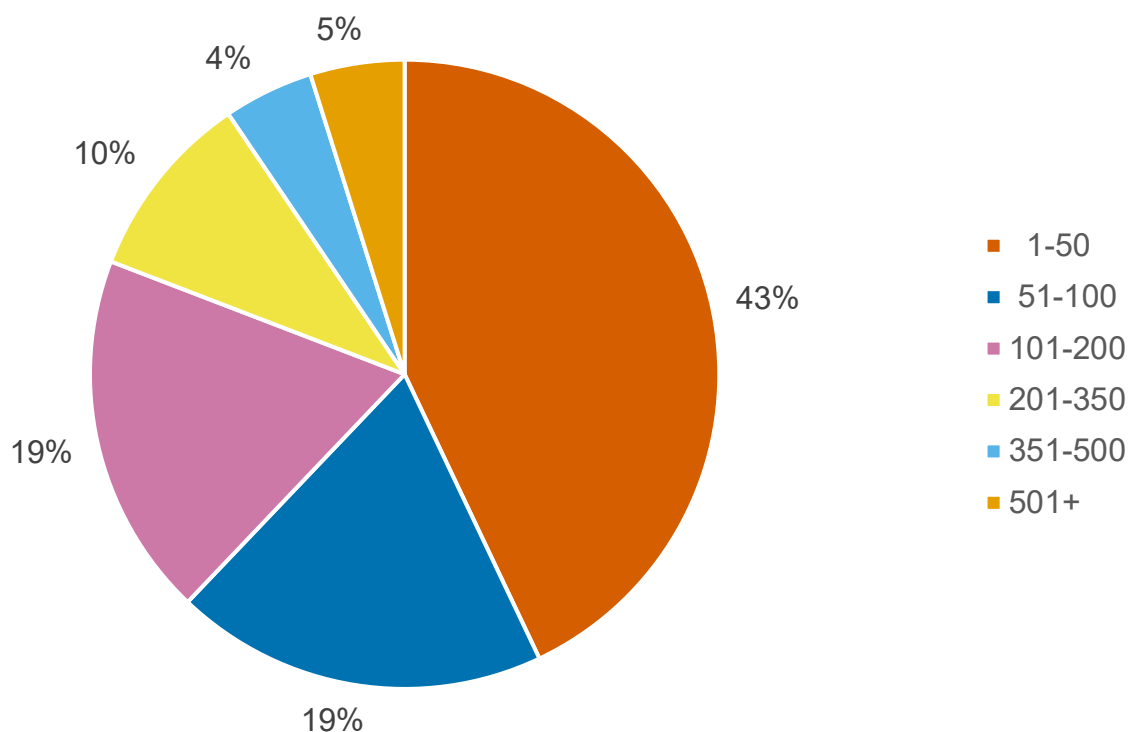


Figure 1: Proportion of cattle holdings in Oxfordshire, by herd size in 2020 (n=454). Note herds with an undetermined size are not shown.

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, to support on-farm shoots.

Markets and abattoirs

Thame market was the only market in Oxfordshire in 2020. The closest dedicated sale for TB-restricted cattle was at Cirencester in the HRA county of Gloucestershire providing a valued outlet for cattle from TB incident herds into AFUs across the south.

Approved Finishing Units

There are a few large finishing units in Oxfordshire, 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.

Dedicated sales for TB-restricted cattle in the south-west are the main outlet for calves from TB incidents herds. Two new AFUs were approved in 2020 raising the total number in Oxfordshire to ten.

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

Common land

In Oxfordshire in 2020 the only common land with cattle grazing together from different owners was the Port Meadow and Wolvercote Common located in the city of Oxford, 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 and protecting the graziers.

Descriptive epidemiology of TB

Temporal TB trends

Three analytical measures are used to describe the level of TB infection in these reports.

1. The number of new herd incidents that were disclosed in each year (Figure 2).
2. The annual herd incidence rate, reported as the number of new incidents per 100 herd-years at risk (100 HYR) (Figure 3). 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 (Figure 4). 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 (excluding Figure 5) 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. Hence measures of incidence and prevalence in this report may be lower than those reported in the official TB statistics.

Prior to 2004, TB 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-west 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 in this area have predominantly been genotype 10:a. This suggests an increasing prevalence of 10:a in wildlife, as infection spread from the neighbouring HRA counties.

Since 2014, 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, with new incidents filling in the 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 cattle 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. Furthermore, the cluster 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.

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).

In 2020, the information provided by WGS has enabled the identification of several clusters in Oxfordshire that were characterised as containing incidents due to closely genetically related *M. bovis* isolates within local geographical areas.

These provide evidence for local spread and where local cattle purchase has not occurred this is most likely caused by infected wildlife. Different genotypes that are probably mutations from the local 10:a and 17:a can now be found affecting specific geographical areas.

The increasing number of TB incidents in Oxfordshire over the years can still be partially attributed to the purchase of undetected infected cattle from HRA and Edge Area counties, from herds with a history of TB in the previous three years.

However, increasingly there is evidence that TB infection in local wildlife has now spread throughout the whole county. Both the level of recurrence and the number of persistent incidents (greater than 18 months duration) show an increased rate of herd re-infection not linked to purchase of cattle.

This was 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 15 in 2020.

Figure 2 shows that the number of new TB incidents peaked at around 80, from 2016 until 2018, and then reduced modestly over the last two years: 77 in 2019 and 72 in 2020.

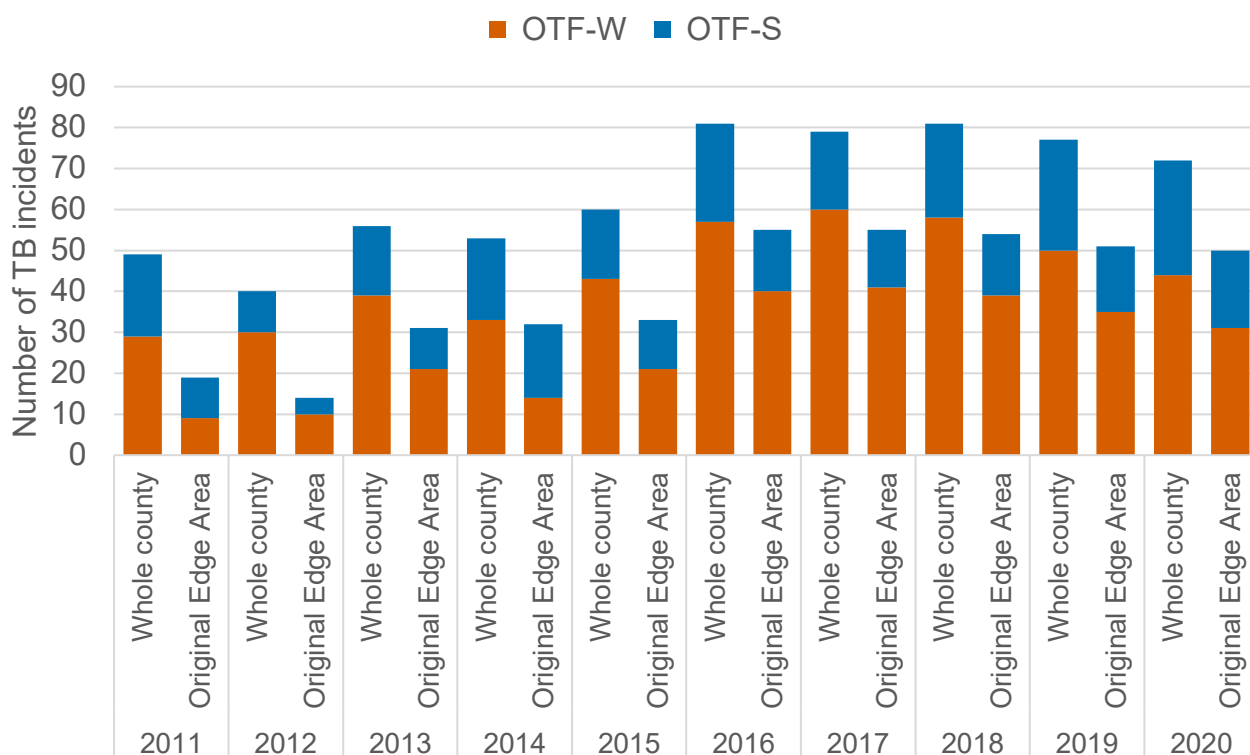


Figure 2: Annual number of new TB incidents in Oxfordshire, from 2011 to 2020, showing incidents for the whole county and the original Edge Area.

The number of OTF-S incidents has increased over the last three years, while the number of OTF-W incidents has decreased. This trend was most pronounced in the original Edge Area of the county. This may be due to the introduction of six-monthly surveillance testing (introduced in 2018) which has detected infections earlier leaving less time for lesion development following infection.

Increased used of IFN- γ testing (in the whole county since 2018) has reduced the level of residual infection left within herds at the end of incidents and the likelihood of consequent recurrence. The full effect of the increased surveillance testing frequency and the use of IFN- γ testing in TB incident herds is difficult to assess.

From May 2019, herds have the option to revert to annual surveillance testing (earned recognition) if they had no history of TB in the previous six years or are registered to a bovine health scheme accredited by CHECS (Cattle Health Certification Standards) at level 1 or above.

In addition to this, COVID-19 public health restrictions in 2020 may have caused a slight reduction in the total number of TB herd tests and the total number of cattle tested in 2020. Only four herds due for routine herd testing in 2020 were not tested in that year, none of which cited COVID-19 as the reason for the delay.

Compared to 2019, there was a 7% reduction in both whole herd skin tests (892 to 831) and numbers of cattle tested (149,950 to 140,052, see table A3.2 in Appendix 3). This can mostly be explained by herds reverting to annual surveillance testing and the lower number of TB incidents. Overall, the effects of COVID-19 public health restrictions appear to be of low influence.

Figure 3 shows the annual herd incidence rate in Oxfordshire from 2011-2020 (dashed lines). This has been increasing since 2009 but levelled off after 2016. The largest rate of increase occurred in the period between 2014 and 2016 when incidence doubled from 9.1 incidents per 100 herd-years at risk in 2014 to 18.3 in 2016.

The incidence rate decreased in 2018 to 15.8, even though the total number of incidents was the highest, and in 2019 increased to 23.5, despite the total number of incidents decreasing. In 2020 a slight decrease to 19.4 occurred, despite the number of incidents being the lowest since 2016.

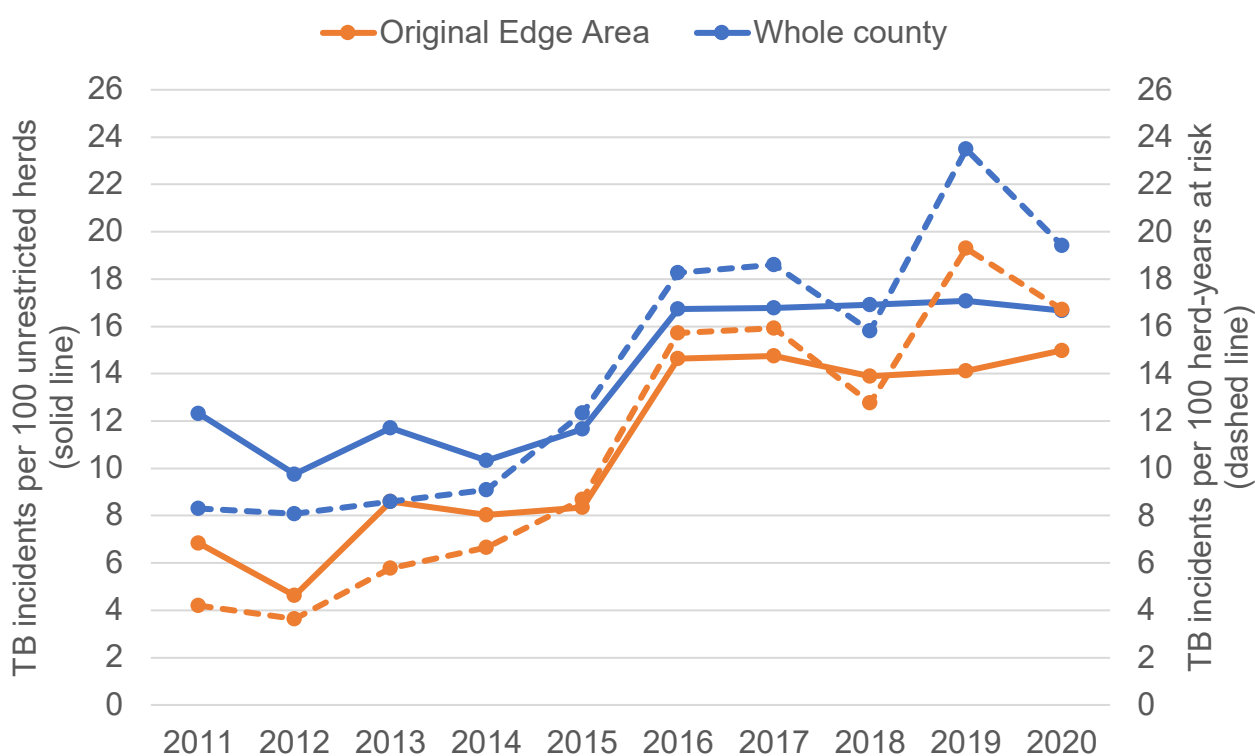


Figure 3: Annual incidence rate (per 100 herd-years at risk and per 100 unrestricted herds) for all new incidents (OTF-W and OTF-S) in Oxfordshire, from 2011 to 2020, showing incidence for the whole county and the original Edge Area.

This unusual oscillation of the incidence rate over the last three years is related to changes in surveillance testing intervals on the denominator for the incidence rate (herd-years at risk).

This should be borne in mind when considering incidence rate trends in parts of the Edge Area that moved from annual to six-monthly surveillance testing in 2018. Some herds also reverted to annual testing following introduction of earned recognition in 2019.

A detailed description of the methodology used to calculate incidence per 100 HYR is available in the [Explanatory Supplement](#) for 2020.

To adjust for the changing denominator, incidence risk per 100 unrestricted herds tested has also been calculated (Figure 3, solid lines). This measure shows that incidence has levelled off since 2016, remaining between 16.7 and 17.1 incidents per 100 unrestricted herds tested.

Figure 4 shows the herd prevalence in Oxfordshire from 2011 to 2020 (proportion of herds under movement restrictions at the end of each year). The increasing trend from 2014 to 2018 is explained by more herds remaining under movement restrictions for longer periods of time, including incidents that started in previous years.

In comparison with 2018 (13.4%), fewer herds were under restrictions by the end of 2019 (11.8%), and 2020 (12.1%). This may be explained by fewer TB incidents, but earlier detection and resolution of infection through more frequent surveillance testing and IFN- γ testing of TB incident herds may also have an effect.

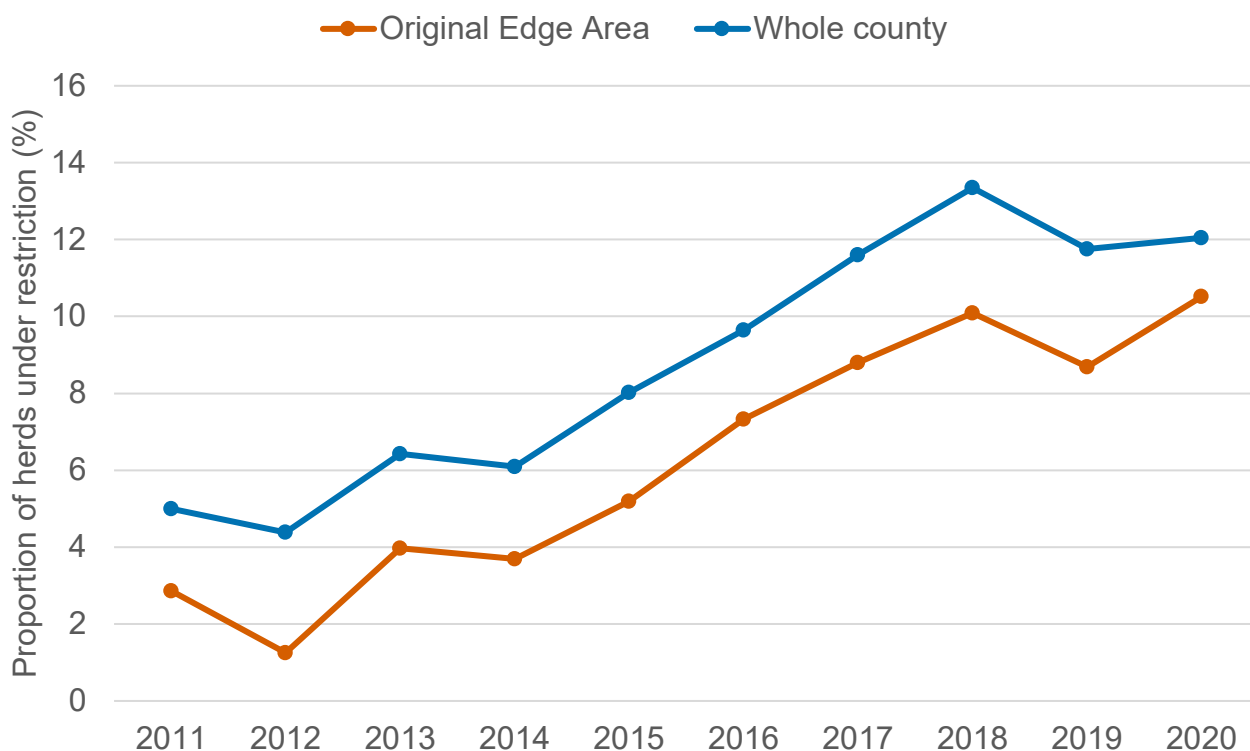


Figure 4: Annual end of year prevalence in Oxfordshire, from 2011 to 2020, showing incidents for the whole county and the original Edge Area.

Geographical distribution of TB incidents

As shown in Figure 5, Oxfordshire still has the highest incidence of all the Edge Area counties when including AFU TB incidents (19.7 incidents per 100 herd-years at risk).

This is considerably higher than the average incidence of the Edge Area (10.1) and is also higher than the average incidence for the current HRA (16.3) although these comparisons are caveated by the effect of changes in testing intervals on the calculation as explained above.

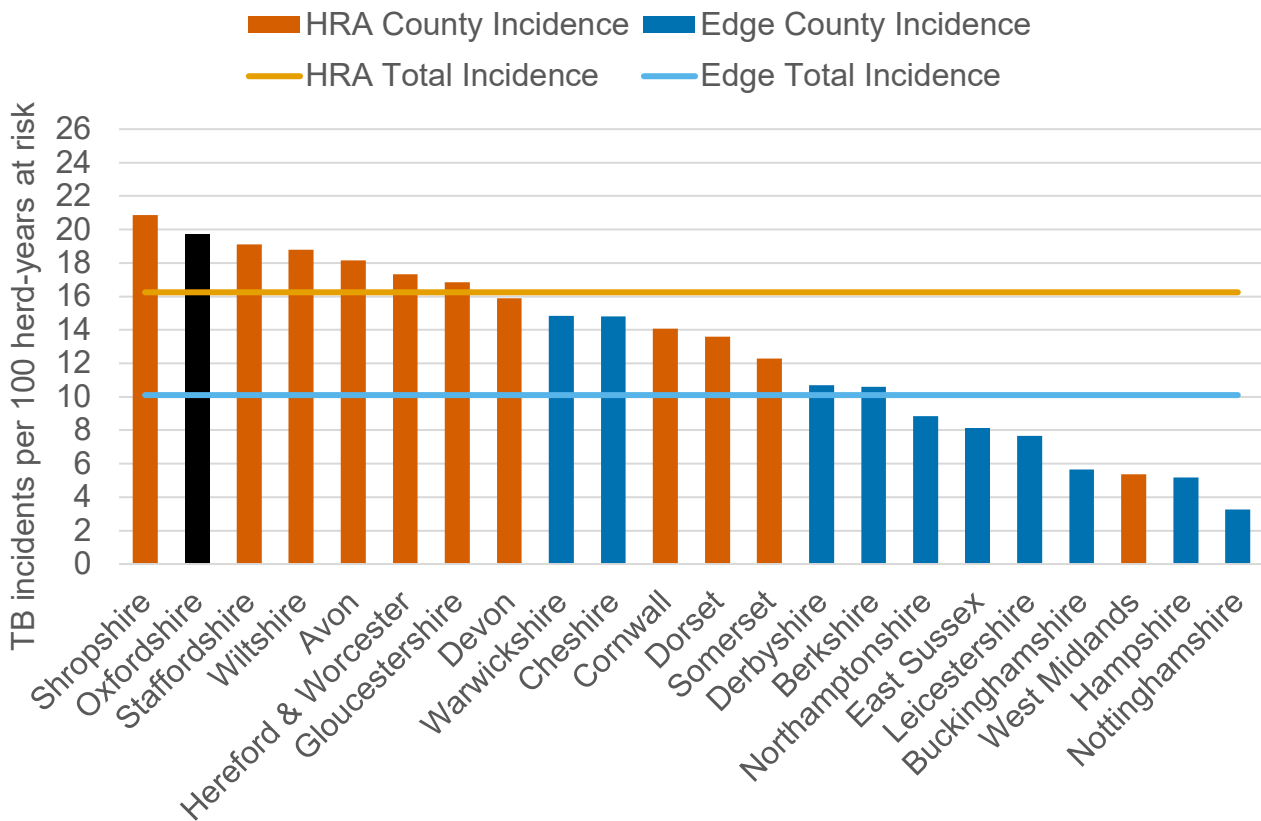
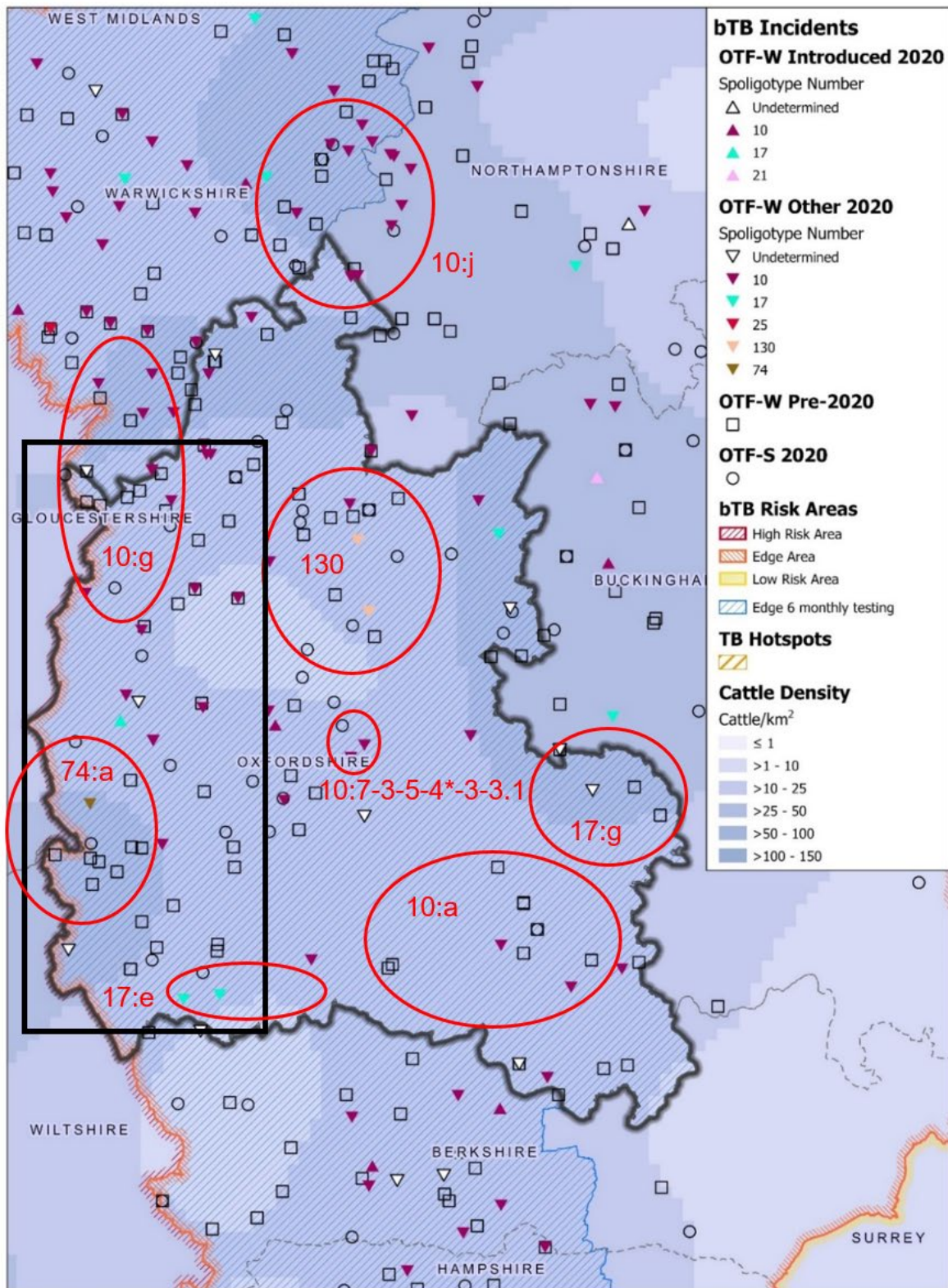


Figure 5: Incidence rate (per 100 herd-years at risk) for all new incidents (OTF-W and OTF-S including finishing units) in 2020, by HRA and Edge Area County, highlighting the county of Oxfordshire.

Over the past decade, the distribution of incidents in Oxfordshire has continued to advance eastwards covering the whole county, as described in the temporal trends section of this report.

Figure 6 shows the locations of incidents overlaid on a cattle population density map and is additionally annotated with identified clusters of incidents (shown by red circles with most common *M. bovis* genotype) with a presumptive wildlife source.

These have expanded in addition to the previously established area of known clusters near the HRA border (represented by a black rectangle). The area represented by the black rectangle is in the former HRA part of Oxfordshire, where most persistent, recurrent and/or chronic incidents usually concentrate.



Creator: GIS Team
 Source: Sam
 OTFW data as at 15th of April 2021
 Ref: 20210701
 Date: 01/07/2021

TB Cattle Density - Oxfordshire

0 3.75 7.5 15 Kilometers

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 Ordnance Survey 100051110



The new and developing clusters of incidents presented in Figure 6 are:

- Somerton-Deddington cluster (red circle with 130 spoligotype)
- Henley-on-Thames cluster (red circle with 10:a genotype)
- Chinnor-Thame cluster (red circle with 17:g genotype)
- Banbury-Northants cluster (red circle with 10:j genotype)
- Shipston-on-Stour-Chastleton-Fifield (red circle with 10:g)
- Other smaller clusters with unique genotypes in Oxfordshire: Wantage cluster (red circle with 17:e) and Oxford cluster (red circle 10:7-3-5-4*-3-3.1).

Somerton-Deddington cluster

Shown in Figure 6 (red circle with 130 spoligotype) in the north-east of the county.

Historically, the most common *M. bovis* genotype in this area has been the local genotype to Oxfordshire, 10:a. This appears to have mutated in recent years in this locality to a different spoligotype, 130.

Two incidents in 2019 and two in 2020 were attributed to this newly identified spoligotype which appears unique to this area. Two spoligotype 130 incidents were also detected in 2018 and two more in 2017.

WGS analyses of these *M. bovis* isolates found 13 incidents genetically related varying between zero and two single nucleotide polymorphisms (SNPs) apart in the same geographical area.

These included isolates of genotype 10:h and 10:a as well as the spoligotype 130 isolates. This strongly suggests a local cluster of incidents which has become apparent over the period of 2017 to 2020.

Herds with these incidents were probably exposed to a common source of infection, and this is considered most likely to be infected wildlife. There was no contiguous inter-herd contact, no cattle movements between the herds nor cattle movements from the same source.

In fact, cattle purchases into several of these herds has been minimal or not at all. One herd has been closed for over 20 years, another over 10 years is now persistently infected, and others closed for the last five years.

If other *M. bovis* isolates with a few more SNP differences are also considered, this Somerton-Deddington cluster of incidents appears to be part of an infection front moving from west to east in the county.

Henley-on-Thames cluster

Shown in Figure 6 (red circle with 10:a genotype) in the south-east of the county.

Genotype 10:a has been the most commonly found genotype in this area, including two culture confirmed infected wild deer in 2018 and an incident in an alpaca farm in 2019 that has continued into 2020.

For the time period 2015 to 2019, WGS analyses identified a cluster of 18 incidents attributed to almost identical *M. bovis* isolates within a 400 km² area adjacent to Henley. 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 were possible transmission pathways for three incidents although this was 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 were abundant. Isolates from a number of *M. bovis* cases in cats distributed nationwide were closely related genetically to this cluster.

From 2017, incidents with genotype 11:a (homerange in the south-west of England) started to appear in this area, close to the Berkshire border. Two of the 11:a incidents were detected 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 (one in a closed herd) suggests that this may not be the case, and there could be a potential wildlife source. No cases on genotype 11:a were detected in 2020.

Chinnor-Thame cluster

Shown in Figure 6 (red circle with 17:g genotype) in the most eastern part of the county, bordering Buckinghamshire.

In 2017 in this area, 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 other epidemiological links between the incidents suggested infected wildlife was the most likely common source.

In 2018 and 2019 genotype 17:g, a very closely related genotype, was identified in five more incidents within six km of this cluster, including one recurrent incident.

In 2020, another recurrent incident occurred on one of these farms, and the isolate was identified as genotype NT:7-5-5-4*-3-3.1 again. WGS analyses indicated very close genetic relatedness between all isolates. A total of seven farms were involved, all close to the border with Buckinghamshire.

Radial testing in Buckinghamshire was triggered in 2019 by these OTF-W incidents in the Chinnor-Thame cluster to investigate lateral spread into this county.

Banbury-Northants cluster

Shown in Figure 6 (red circle with 10:j genotype) in the most northern corner of the county, bordering Warwickshire, and Northamptonshire.

In 2020 (and previously in 2018) a new *M. bovis* genotype to Oxfordshire, 10:j was isolated. Historically, 10:j has been found mostly in Warwickshire and Northamptonshire.

Introduction from neighbouring counties sharing the same genotype could not be explained by cattle movements and the Oxfordshire 10:j was probably a mutation of the local genotype 10:a.

WGS was used to identify a cluster of closely related incidents across the borders with these counties. A total of four incidents were found closely related genetically to the incident in Oxfordshire, all within a three km radius – three km from Warwickshire and one km from Northamptonshire.

Evidence gathered from investigation of these incidents ruled out cattle movements (one herd had been closed for at least 20 years), suggesting a wildlife source of infection.

This 10:j genotype has also been found in an alpaca TB incident in south-west Oxfordshire which had recently purchased alpacas from a breeder in north Buckinghamshire. This incident was first suspected in November 2020 and later confirmed in February 2021. In 2020, 10:j was also isolated from incidents in two farms neighbouring this alpaca breeder in Buckinghamshire.

WGS of the alpaca isolate identified it as closely related to the nearby 10:j cluster of incidents described above. It is likely that both neighbouring incidents are also linked to this cluster and to the alpaca incident.

This points towards a wildlife source affecting bovines and non-bovines in a much larger area covering parts of Oxfordshire, Warwickshire, Northamptonshire, and Buckinghamshire.

Shipston-on-Stour-Chastleton-Fifield

Shown in Figure 6 (red circle with 10:g) in the north-west former HRA portion of the county, bordering Gloucestershire, and Warwickshire.

One 2020 *M. bovis* isolate of 10:g in Oxfordshire was closely related genetically to six incidents from 2017 to 2020. The six related incidents were all genotype 10:a located within a six km radius: three in Oxfordshire, three in Warwickshire and one in Gloucestershire.

After ruling out purchased cattle and contiguous contact with neighbouring cattle herds, the most likely source of infection was attributed to wildlife, probably moving from the neighbouring HRA into Oxfordshire.

North Faringdon cluster

Shown in Figure 6 (red circle with 74:a) in the south-west former HRA portion of the county, bordering Gloucestershire, and Wiltshire.

Six genetically related incidents dating from 2017 to 2020 were clustered in this area within a four kilometre radius, including one incident in Gloucestershire. Five were genotype 74:a, which is mostly found in neighbouring counties close to the Oxfordshire border, and one was genotype 17:a.

After ruling out purchased cattle and contiguous contact with neighbouring herds, the most likely source of infection for some of these incidents was attributed to wildlife.

Other clusters might exist in the south Faringdon area, affecting several persistent and recurrent incidents. Due to a lack of *M. bovis* isolates in historic and ongoing incidents however, this area is difficult to assess.

In areas, where TB has been endemic for a long time it is likely that several sources can be attributed to each incident. Several overlapping clusters are appearing over time. Systematic WGS analysis might be able to identify more clusters of incidents in future.

Other smaller clusters

Unique *M. bovis* genotypes in Oxfordshire include the Wantage cluster (Figure 6, red circle with 17:e) and the Oxford cluster (Figure 6, red circle 10:7-3-5-4*-3-3.1).

A recurrent incident in 2020 with 17:e genotype (previous incident in 2018) was identified in the same area as a 2019 incident of the same genotype in a herd grazing fields near Wantage. The isolates from these two incidents were very closely related genetically with only one SNP difference.

No cattle movements or contacts were shared between the farms leaving exposure to a common wildlife source of infection as the most likely risk pathway.

A rare genotype, 10:7-3-5-4*-3-3.1, was identified in 2020 near Oxford. Another incident with the same genotype was identified in 2014 in the same area, and on the opposite side of a wooded area containing a large and well-studied badger population.

No cattle movements or other contacts have been identified to link the two incidents, apart from common exposure to infected wildlife populations.

From the mid-2000s, areas of endemic TB infection have been located in the high cattle density areas to the west of the county (Figure 6, black rectangle). These areas include parts of the north of the county, near Banbury and Epwell, and the south of the county near Faringdon, where there was a concentration of large dairy herds.

In 2018, the whole county became part of the Edge Area, joining the western strip of the former HRA portion with the rest of the Edge Area in Oxfordshire.

The epidemiology of both areas has been very similar since, 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 in those areas complicating the picture even further.

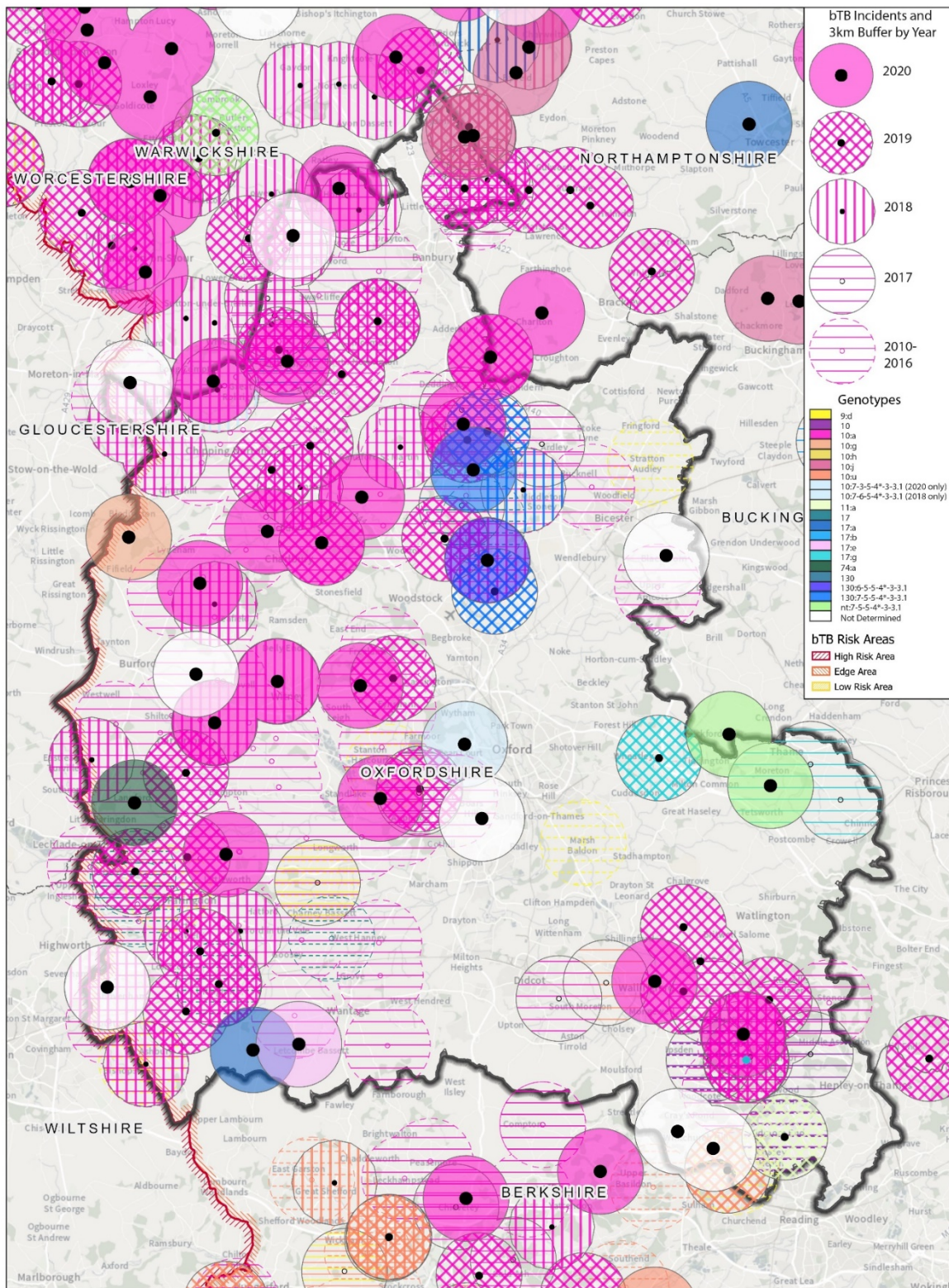
Genotypes of *M. bovis* attributed to wildlife

Figure 7 represents *M. bovis* genotypes detected in Oxfordshire in 2020 from OTF-W incidents where a wildlife source was considered most likely compared to other transmission pathways. Data from previous reports were updated with data from 2020.

The disease report form (DRF) for each TB incident was assessed individually to determine the incidents where wildlife and/or residual risk pathways were scored with the highest certainty. Genotype 10:a continues to be the predominant genotype in Oxfordshire.

This mirrors the presumptive wildlife endemic area illustrated by the pink 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 the Henley cluster and the Somerton cluster.

Other *M. bovis* genotypes attributed to wildlife in Figure 7 include: genotype 17:g in the Chinnor area represented by the light blue circles, spoligotype 130 in the Somerton area represented by orange circles and genotype 74:a in the Faringdon area.



Creator: GIS Team
 Source: Sam
 OTFW data as at 15th of April 2021
 Ref: 20210929
 Date: 29/09/2021

Oxfordshire Endemic bTB Incidents

0 3 6 12 Kilometers

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 Ordnance Survey 100051110



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 identified in 2020.

Three incidents with genotype 17:a were disclosed in 2020, one with a definite purchased source, another one most likely attributed to badgers (first 17:a incident in Oxfordshire with no cattle purchase link), and a third one uncertain (cattle purchase and wildlife sources equally likely).

Other characteristics of TB incidents

Incidents by herd type

Most TB incidents in Oxfordshire in 2020 occurred in herds of 200 cattle or less (Figure 8). However, as with previous years, when Figure 1 (proportion of herds per size category) is considered, new incidents showed a predilection for medium or large herd size (over 100 cattle). The majority of herds affected were in the beef sector which is the most common production sector in Oxfordshire.

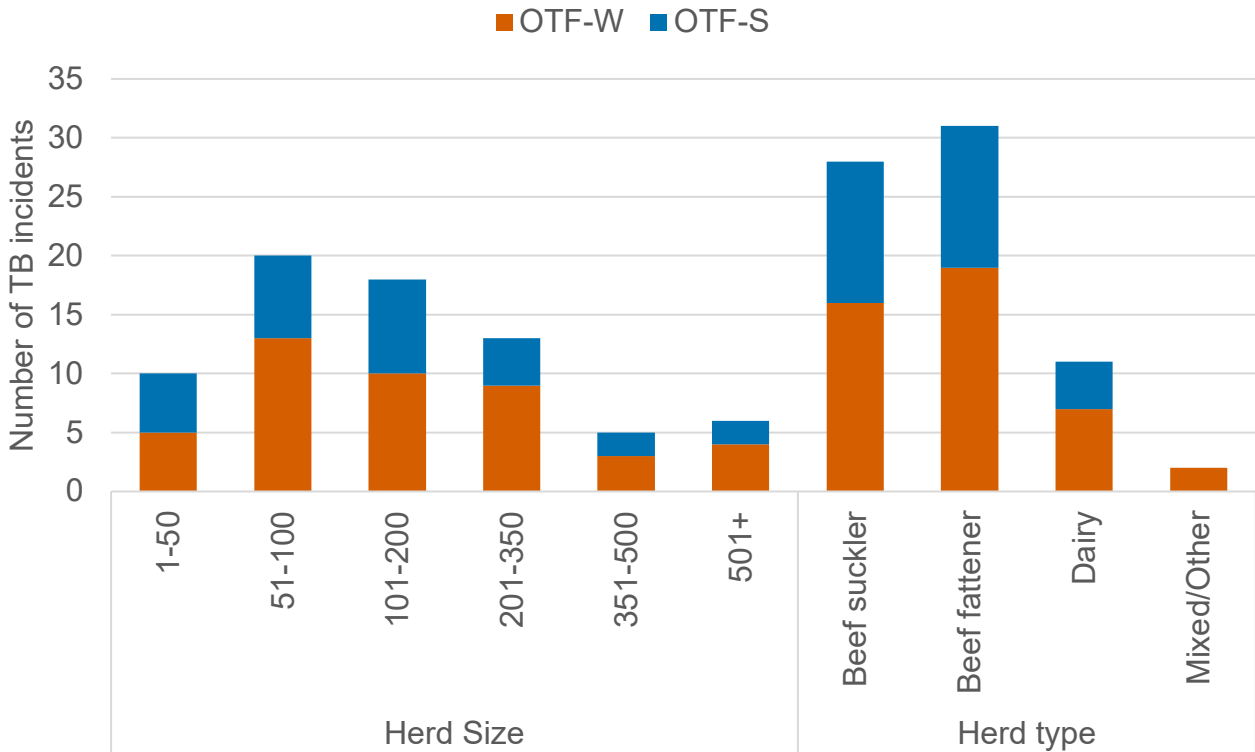


Figure 8: Number of TB incidents (OTF-W and OTF-S) in Oxfordshire in 2020, by cattle herd size and type.

Incidents by month of disclosure

The majority of TB skin testing is usually 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 right after grazing.

There was a good correlation between the number of incidents disclosed per month (Figure 9) and the number of skin tests carried out (Figure 10) with the two peaks in October and March matching both data sets.

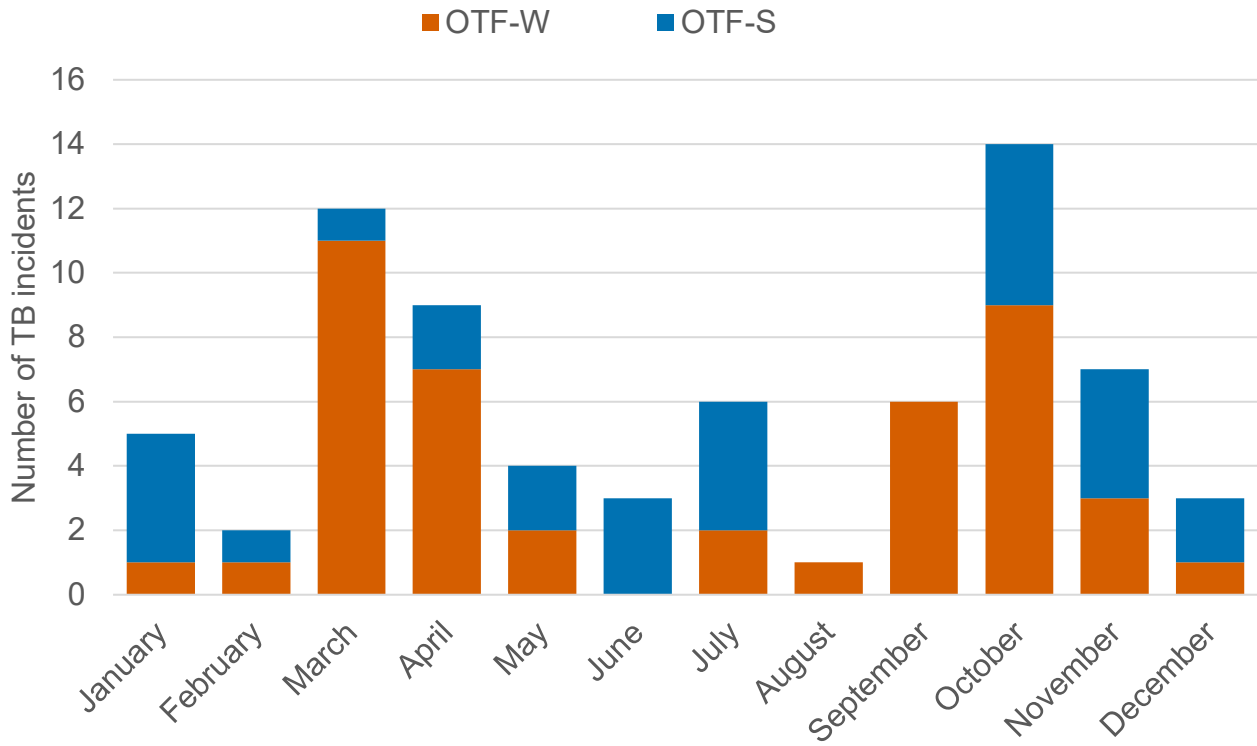


Figure 9: Number of TB incidents (OTF-W and OTF-S) in Oxfordshire in 2020, by month of disclosure.

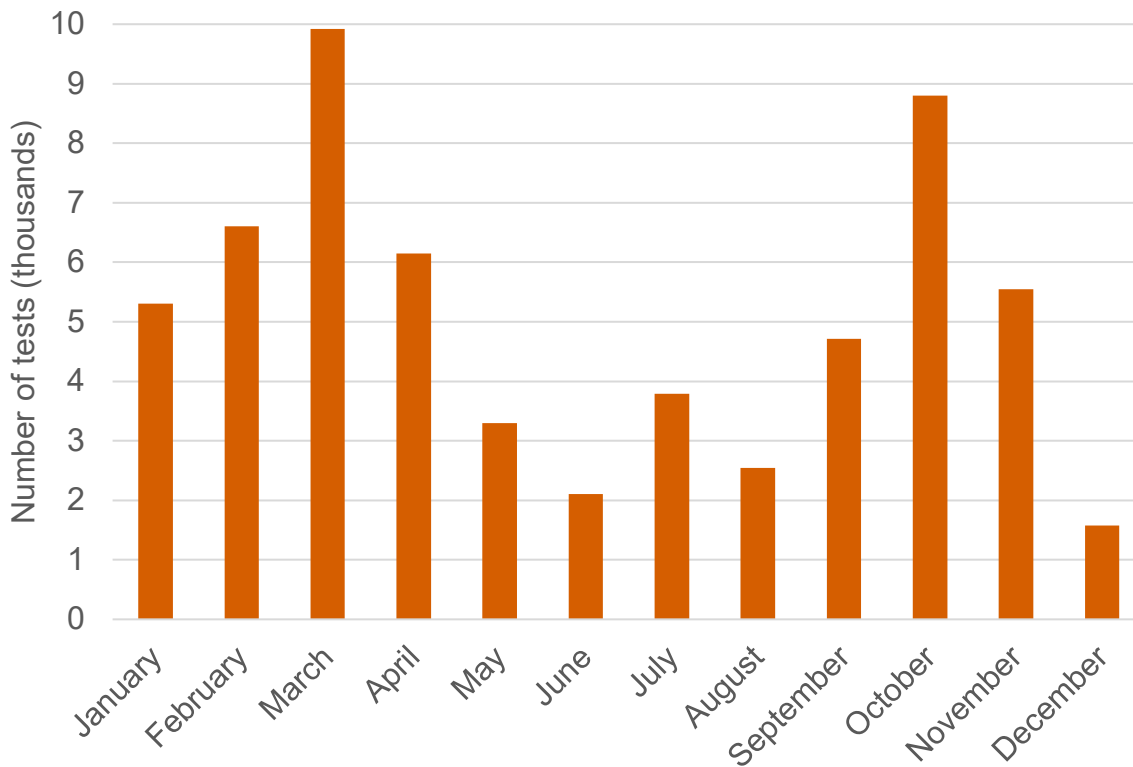


Figure 10: Number of tests undertaken in OTF herds in Oxfordshire in 2020, by month.

Duration of incidents

The duration of OTF-W incidents tended to increase up to 2018. Reasons for this include, increasing infection pressure from within herds, re-infection from wildlife and IFN- γ testing detecting residual infection (undetected by skin testing) at stages when skin testing alone would have resolved incidents.

In 2019 and 2020, this trend appeared to be reversing and most incidents averaged between 150 to 240 days compared to 240 to 550 in 2018 (Figure 11). This might be explained by more frequent surveillance testing, which detects infection earlier before it can become fully established in the herd.

Additionally, reduction of residual infection from previous incidents following the use of supplementary IFN- γ testing during TB incidents may reduce duration.

The number of persistent incidents (lasting over 550 days) remained high in 2019 (15 incidents, nine still unresolved by the end of 2019) and in 2020 (15 incidents, with seven still unresolved by the end of 2020).

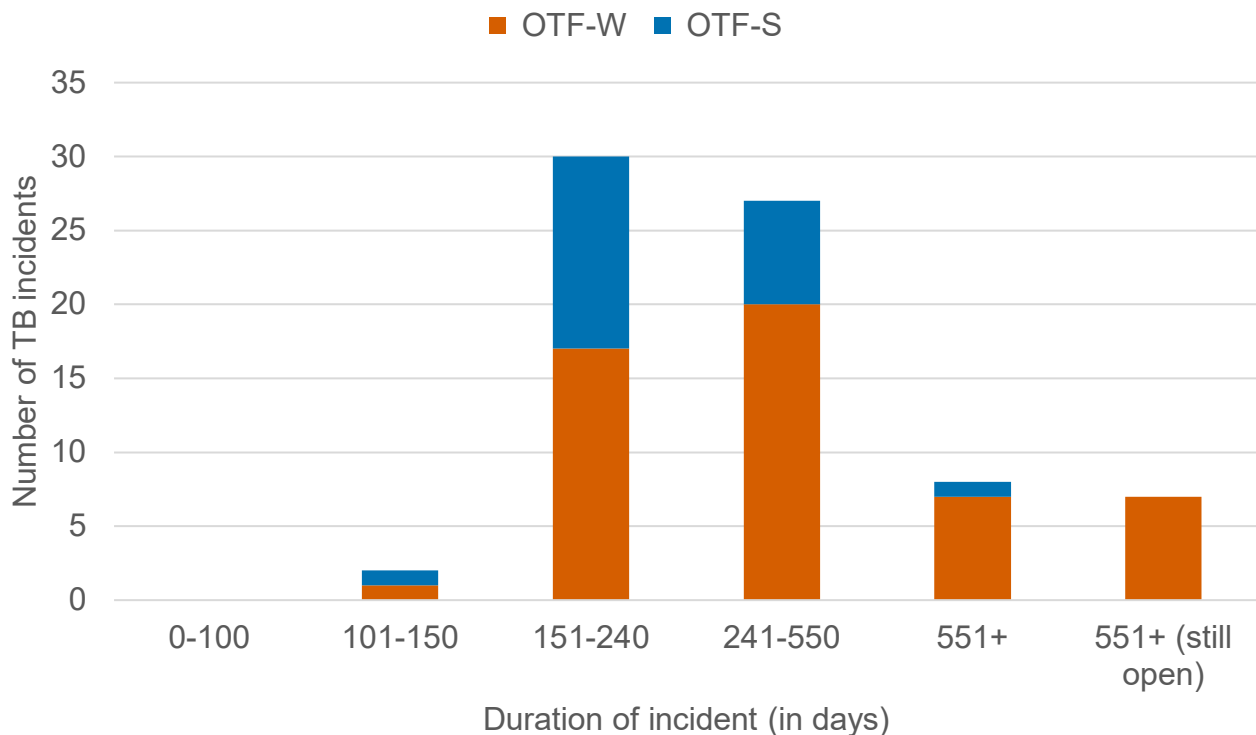


Figure 11: Duration of all TB incidents (OTF-W and OTF-S) that ended in 2020, and the number of persistent TB incidents (551+ days) that were unresolved at the end of 2020 in Oxfordshire. Note that Approved Finishing Units (AFUs) have been excluded.

Genotypes associated with TB incidents

Genotyping of *M. bovis* isolates has been used to trace the origin of TB infection. It is particularly useful in identifying where spread has occurred through cattle movements. Stable genotype clusters tend to be found in areas where there is a persistent local reservoir of infection.

APHA implemented whole genome sequencing (WGS) in place of genotyping from April 2021. During 2020 however, genotyping was still performed on *M. bovis* samples isolated from all OTF-W herds in the Edge Area.

As shown in Figure 12, the predominant *M. bovis* genotype in Oxfordshire in 2020 was 10:a, followed by 17:a, which has also been in Oxfordshire for some time. Other genotypes found in Oxfordshire were likely mutations of 10 and 17, and only found in specific geographical areas.

These were: 10:d, 10:g, 10:j, 130, 17:e, 74:a, NT:7-5-5-4*-3-3.1 or 17:g (one derived from the other) and 10:7-3-5-4*-3-3.1. This variety of genotypes provides more information on developing clusters, although some of the genotypes are so closely related genetically to each other that WGS analysis is necessary to provide more granularity.

Compared to 2019 when 10:a comprised 77% of the *M. bovis* genotypes identified, in 2020 this decreased to 65% because of the increasing number of other genotypes and different mutations appearing in specific cluster areas.

The homerange of genotype 10:a is large and includes neighbouring counties to Oxfordshire. Therefore, genotype data provides limited information as to whether infection is contracted locally or moved from these neighbouring counties via cattle movements, compared to new genotypes with much smaller homeranges.

New mutations of genotype 10:a have provided more information regarding local establishment and spread of infection 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.

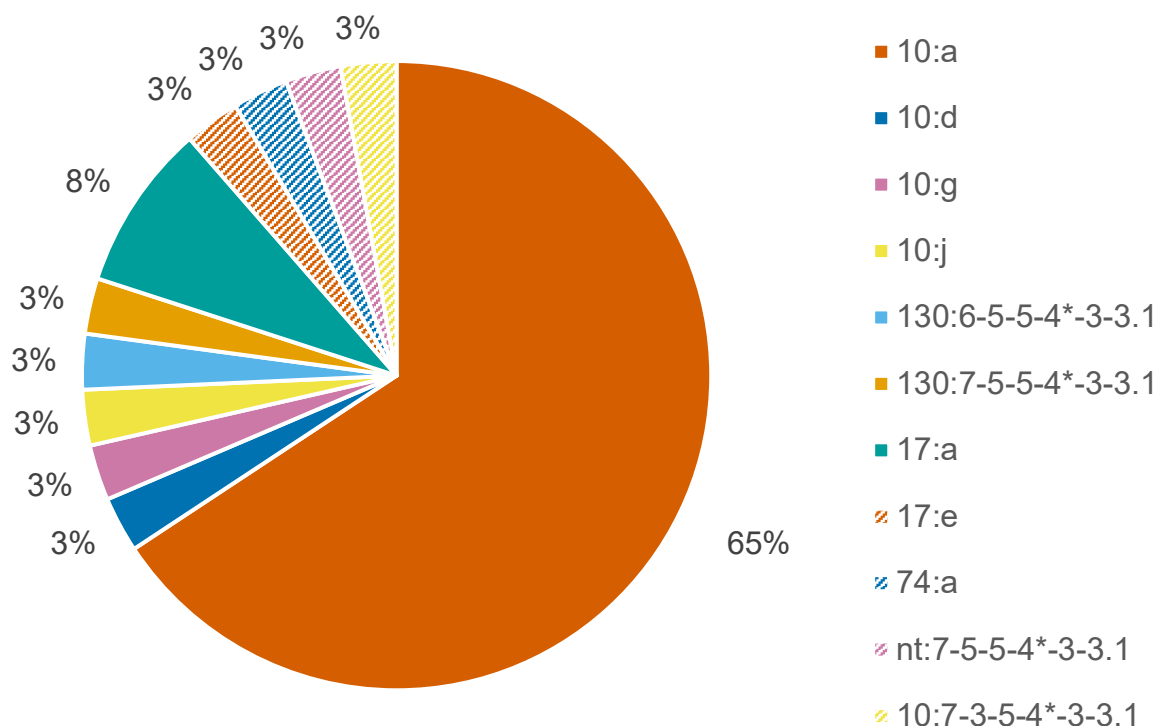


Figure 12: Genotypes of *M. bovis* identified in herds with OTF-W incidents in Oxfordshire that began in 2020 (n=35).

Unusual TB incidents

None described in Oxfordshire in 2020.

Suspected sources, risk pathways and key drivers for TB infection

Key drivers of infection

The key drivers of the TB epidemic in Oxfordshire during 2020 were as follows:

- Infected wildlife
- Movements of undetected infected cattle
- Residual infection

Sources of infection and risk pathways

It can be challenging to retrospectively establish the route of infection for a TB incident herd. 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. This information is captured on the Disease Report Form (DRF).

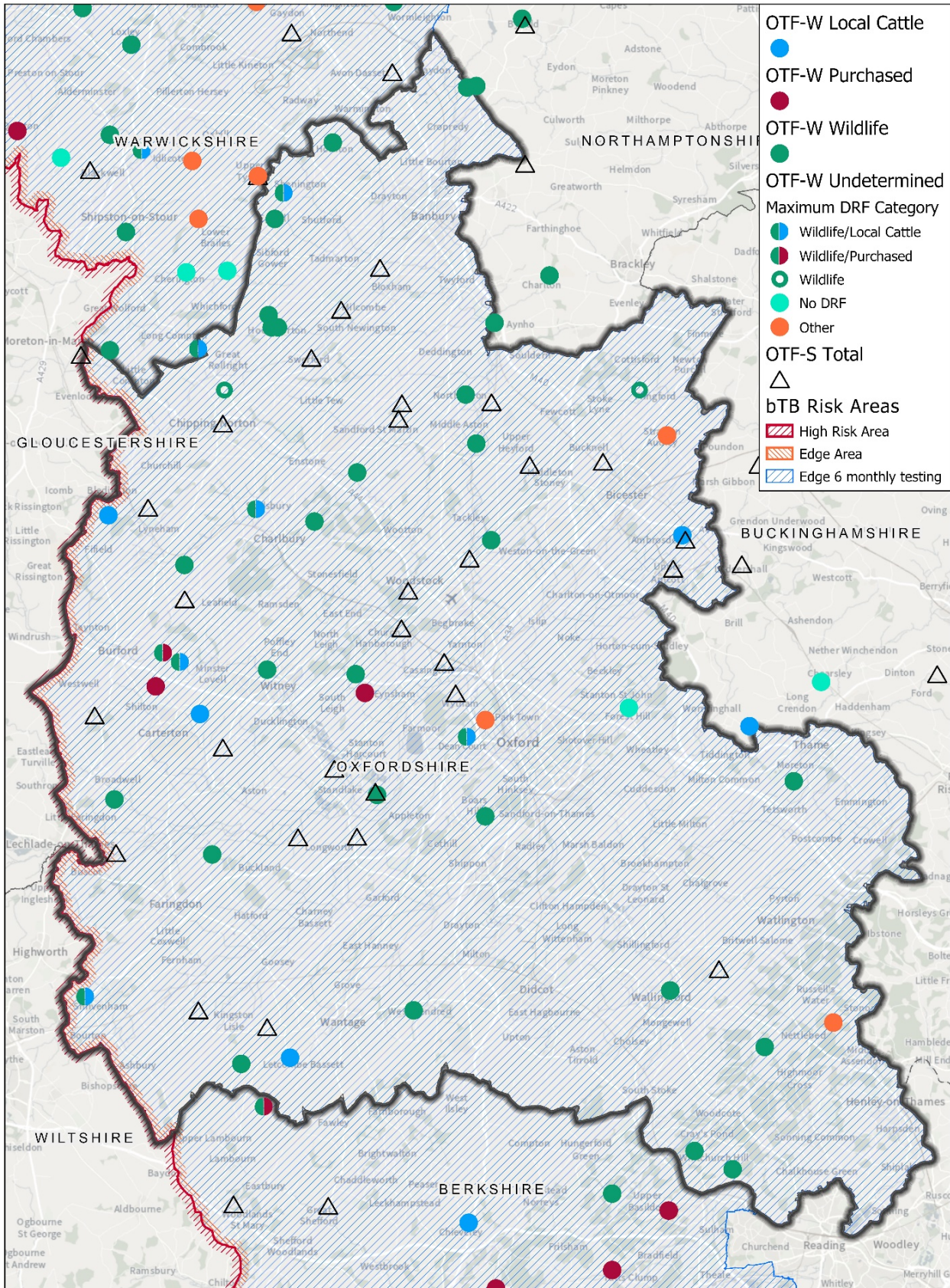
During the assessment up to three risk pathways of infection are selected for each herd. Each risk pathway is given a score that reflects the likelihood of that pathway bringing TB into the herd.

The score is recorded as either definite (score 8), most likely (score 6), likely (score 4) or possible (score 1). Risk pathway data are explored both at the herd and county level.

The most likely source of infection in individual TB incidents

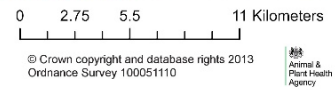
The most likely source identified by the APHA veterinary assessment is explored spatially for individual TB incidents. The most likely source of infection for individual TB incidents discounts additional risk pathways identified with a lower level of certainty.

Where two sources were ranked equally as the most likely source for an incident, both sources are reported for the incident using a split symbol in the map.



Creator: GIS Team
 Source: Sam
 OTFW data as at 15th of April 2021
 Ref: 20210604
 Date: 04/06/2021

DRF Source - Oxfordshire



The weighted source of infection at county level

To consider the contribution of all sources of infection within an area, the sources 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. This presents the overall proportion of pathways in which each source was identified, weighted by the level of certainty 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](#).

Figures 14a and 14b show wildlife as the highest weighted source pathway for TB infection in incidents in Oxfordshire in 2020. The calculation of weighted source pathways of infection for all new incidents in 2020 is described in Appendix 4. Cattle movements, although still significant, are less likely to contribute to the relatively high incidence of TB in Oxfordshire.

Approximately 55% of the total weighted source pathways recorded for all new incidents in 2020 (OTF-W and OTF-S) were attributed to a wildlife source compared to 50% in 2018, and 56% in 2019. Residual infection has remained relatively high (18% in 2019 and 20% in 2020) and reflects the tendency of incidents in Oxfordshire towards being more chronic and recurrent. However, calculations of weighted source attributions have been modified over the years and therefore it is difficult to directly compare previous years' figures.

Although caveated by this, there has been a reduction in the relative contribution of attribution to the purchase of cattle with undetected infection from the HRA and Edge Area: 21% in 2020 compared to 22% in 2019 and 30% in 2018. This source affected mostly beef fattener herds.

TB incidents in AFUs were the only incidents with a definitive source identified in 2020. The presence of robust biosecurity measures reduced 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). Assessment of OTF-S incidents leaned towards a purchased source where cattle were bought into the herd during the previous five years from high

incidence areas. Hence, the weighted risk pathways for OTF-S incidents had a high proportion attributed to purchased cattle sources (26%) compared to OTF-W incidents (18%), where information on genotypes was available to investigate sources more accurately.

Distinguishing source attribution between badgers and residual infection in recurrent incidents is difficult and likely to be a combination of both.

Very few incidents were attributed to contiguous cattle-to-cattle spread from neighbouring premises, 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, and there remains high uncertainty as to their role in transmitting TB to cattle. Potential fomite sources such as contaminated shared machinery and manure or slurry spread near livestock farms are very difficult transmission pathways to assess.

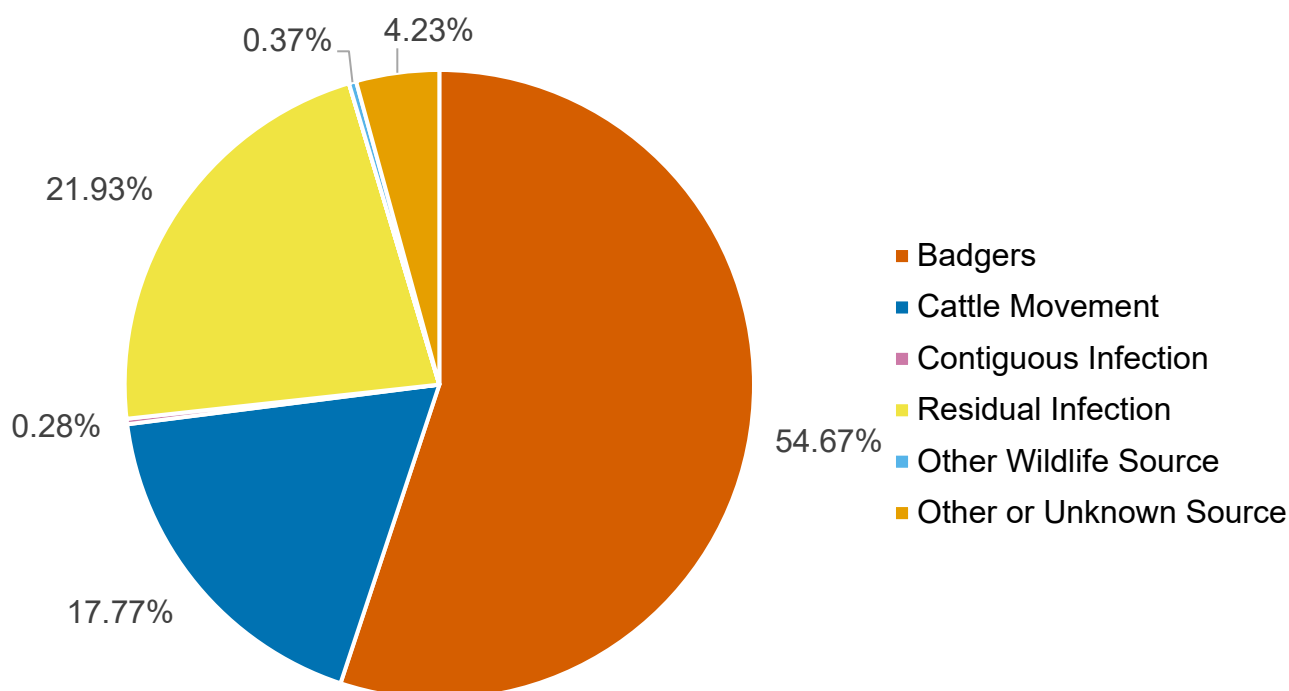


Figure 14a: Summary of the weighted source of infection pathways attributed for OTF-W TB incidents that started in 2020 in Oxfordshire, that had a completed DRF (n=43).

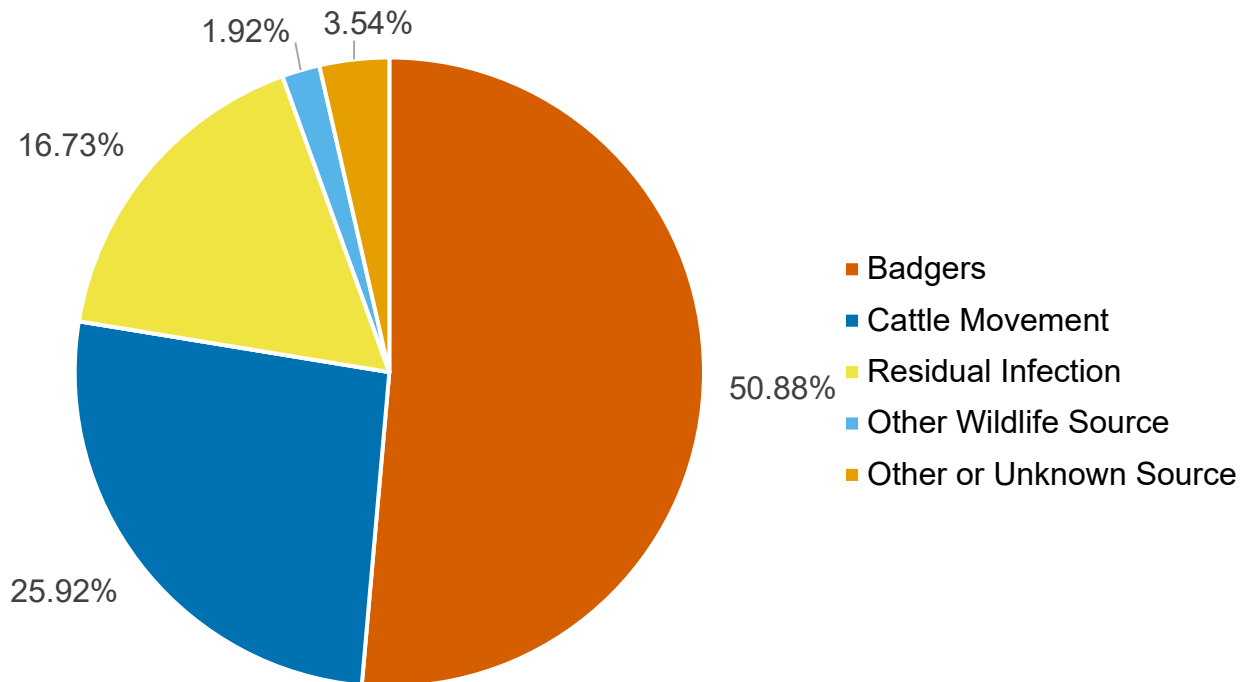


Figure 14b: Summary of the weighted source of infection pathways attributed for OTF-S TB incidents that started in 2020 in Oxfordshire, that had a completed DRF (n=26).

TB in other species

There is no statutory routine TB surveillance of live non-bovine species. Post mortem examination (PME) is performed on suspected clinical cases reported to APHA. Furthermore, post mortem meat inspection is carried out on all captive animals (for example, sheep, goats, pigs or deer) slaughtered for human consumption.

Wildlife

A lack of data for *M. bovis* infection in wildlife in Oxfordshire in 2020 continues to add uncertainty to any conclusions for wildlife being the source of TB incidents in cattle. These assessments are made largely by a process of elimination of other source pathways, but also from analysis of geographical clusters and WGS information.

Alpacas

More clinical cases with *M. bovis* genotype 10:a occurred in a large breeding herd of alpacas in Oxfordshire in 2020 that had undergone several rounds of TB skin and antibody parallel testing, in an incident that had started in early 2019.

WGS analyses supported initial introduction of *M. bovis* from local wildlife in the absence of cattle contacts, and very close genetic relationship with other TB incidents in cattle herds in the local area.

Pigs

A clinical case was confirmed with *M. bovis* genotype 21:a in a large indoor batch-rearing pig finishing unit. WGS analyses supported a purchased origin from one of several outdoor pig breeding units located in the south-west of England supplying the farm with piglets.

Goats

A clinical case was confirmed with *M. bovis* genotype 10:a in a recently established goat dairy farm. After set-up, this has been operated as an indoor closed herd. WGS investigation found poor genetic relationship to local cattle isolates, which makes it unlikely that local wildlife was the source.

The closest genetically related isolates were from cattle herds in other counties, which are currently under investigation. One of these herds is contiguous to several goat holdings.

Detection of TB incidents

The majority of incidents (54%) in Oxfordshire in 2020 were detected by routine herd surveillance tests (Figure 15), which have been six-monthly by default since 2018, or reverting to annual testing from 2019 (earned recognition). The next most common detection method (24%) was six-month post-incident tests when recurrence has occurred due to re-infection or residual infection in cattle.

A small proportion of incidents (11%) were detected by pre-movement tests (PRMT), highlighting their importance in detecting infection before potentially spreading infection to other herds.

The number of incidents detected after a slaughterhouse case was low (4%). This may be partially associated with the higher frequency of surveillance testing in Oxfordshire, which detected infection earlier and reduced spread of infection within herds.

Although six-monthly surveillance testing has decreased the reliance on passive slaughterhouse surveillance (SLH) and pre-movement testing (PRMT), these still remain important to identify infected animals undetected by skin testing, and infected stock before being moved to other herds.

Figure 16 shows the number of new OTF-W and OTF-S incidents in 2020, that had experienced an OTF-W incident in the previous three years. It excludes new incidents that were also on restrictions in the first four or more months of 2020 due to an incident that started before 2020. The [Explanatory Supplement](#) (see section 4.3) provides more details on the reporting of recurrent TB incidents.

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 incidents (59% OTF-W and 54% OTF-S).

TB incidents in the former HRA part of Oxfordshire were more likely to have had a TB incident in the past three years, as prior to 2018 IFN- γ testing was not routinely deployed in TB incident herds. This resulted in a higher likelihood of leaving infection undetected by skin testing alone.

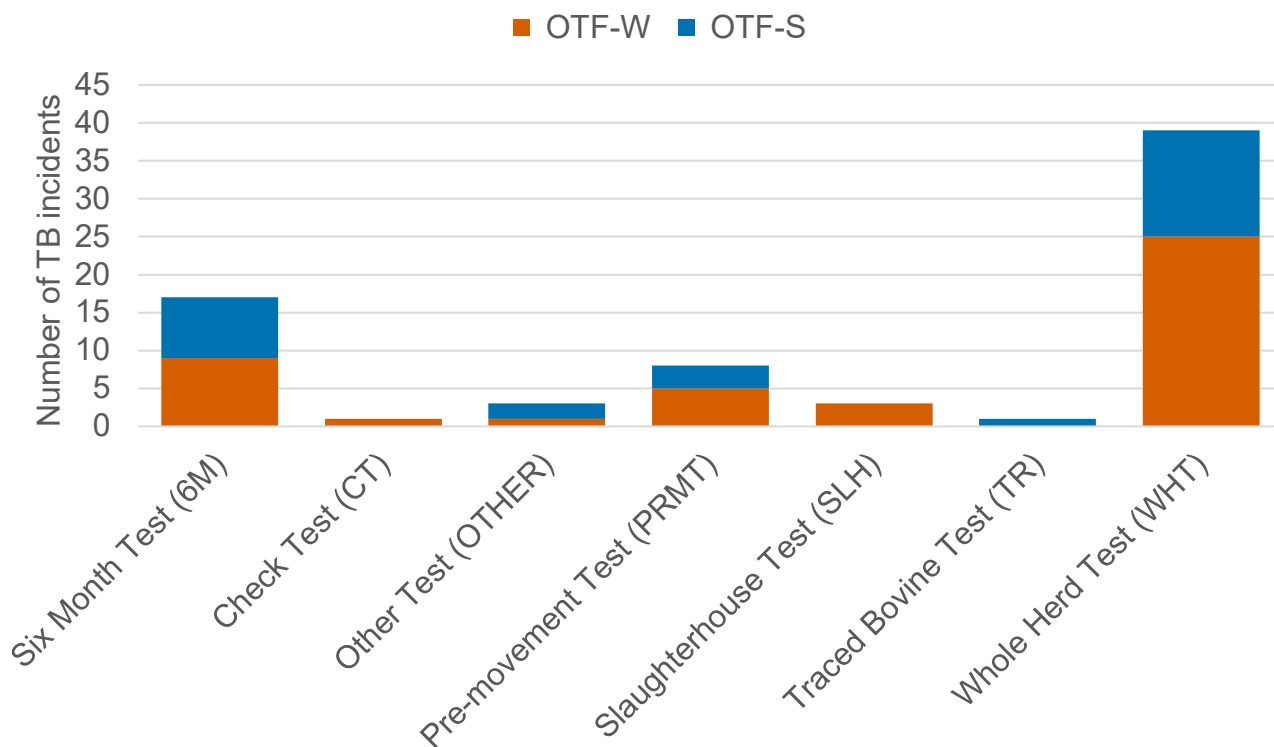


Figure 15: Number of TB incidents (OTF-W and OTF-S) in Oxfordshire in 2020, disclosed by different surveillance methods.

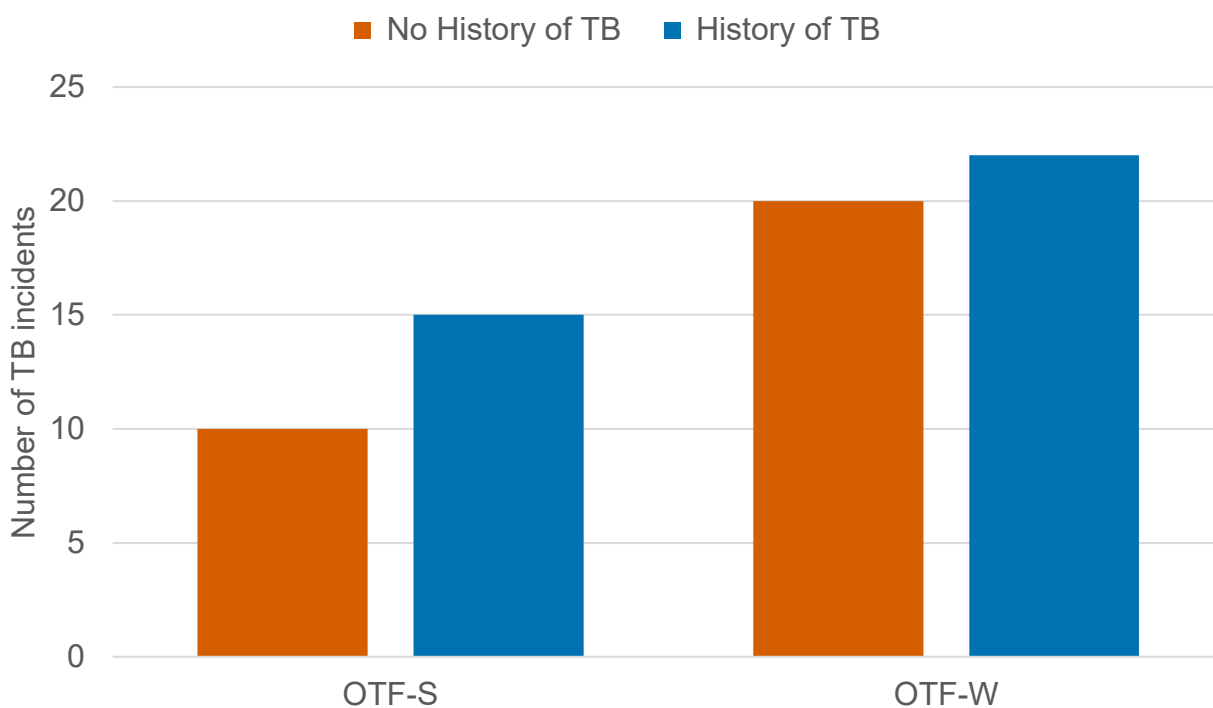


Figure 16: Number of herds with a TB incident (OTF-W and OTF-S) in Oxfordshire in 2020, with a history of TB (herds that experienced an OTF-W incident in the previous three years), and holdings without a history of TB in the previous three years.

Skin test reactors and interferon gamma test positive animals removed

Reactor numbers can be used as a proxy measure of the financial burden of TB in Oxfordshire (Figure 17). In 2016 there were 629 reactors (248 were IFN- γ test-positive animals). This more than doubled in 2017 and 2018 with 1,347 in 2017 (813 IFN- γ test-positives), and 1,410 in 2018 (750 IFN- γ test-positives).

In 2019, the number of reactors removed decreased slightly to 1,159 (603 IFN- γ test-positives). This has been more evident in 2020 where the number of reactors removed has noticeably decreased to 792 (390 IFN- γ test-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 and 2020, more frequent surveillance testing might have reduced the number of reactors disclosed per incident due to infection having less time to spread within the herd. The number of herd skin tests carried out in Oxfordshire in the last consecutive four years increased from 686 in 2016 to 703 in 2017, 875 in 2018 and 892 in 2019 even though the total number of incidents was lower (Appendix 3).

In 2020, the number of tests was much reduced at 831 which can be explained by a lower number of incidents, shorter incidents, herds reverting to annual surveillance testing through earned recognition and some delay in testing due to COVID-19 public health restrictions. The number of reactors per incident has continued to decrease from 17.4 in 2018 and 15.1 in 2019 to 11.0 in 2020 suggesting a reduced infection rate within herds.

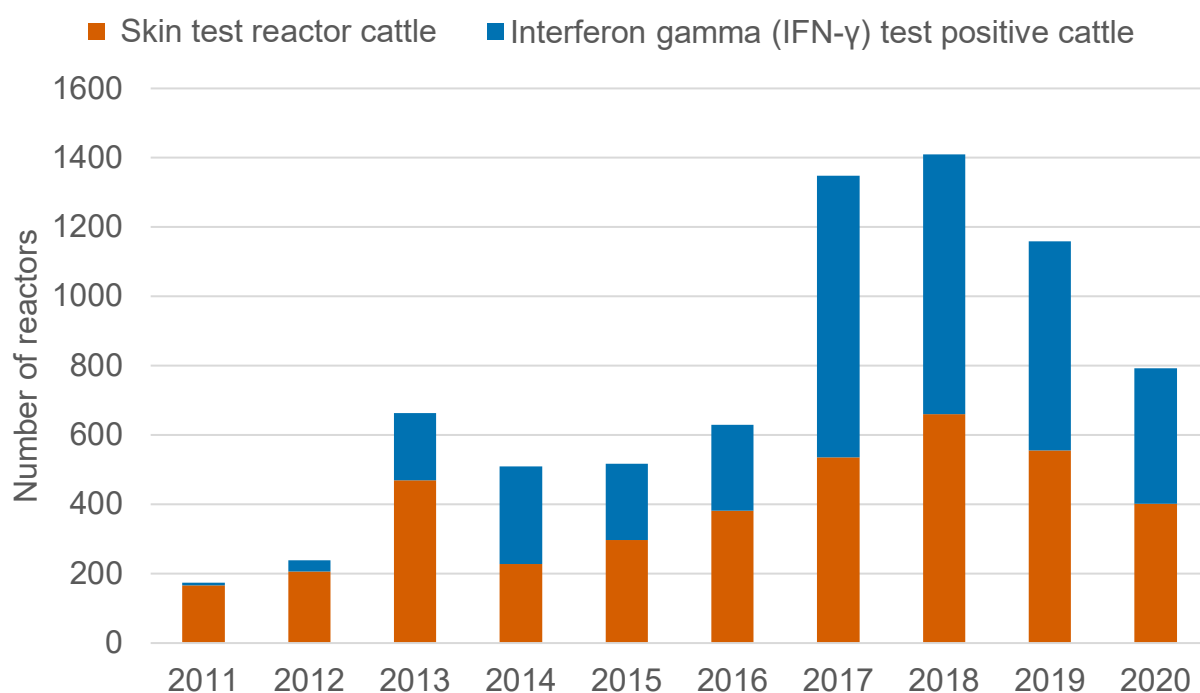


Figure 17: Number of skin test reactors and interferon gamma (IFN- γ) test positive cattle removed by APHA for TB control reasons in Oxfordshire, 2011 to 2020.

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 in TB incidents in Oxfordshire 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.

Incidents attributed to purchase mostly involved movements of cattle from the HRA and Edge Area, but there was some uncertainty recorded because investigations concluded this as the most likely source for only a few incidents.

The increasing number of AFUs in Oxfordshire since 2016 mitigates the risk of cattle movements by channelling these cattle into a biosecure environment, with moves exclusively to slaughter. Only AFUs without grazing are permitted in the Edge Area. 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

Despite the number of TB incidents remaining more or less the same since 2016, the epidemiological picture in Oxfordshire 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 a serious long term risk to achieving OTF status for the LRA. The Henley and Chinnor clusters illustrate this risk, as well as clusters close to the Northamptonshire and Warwickshire border.

Evidence for these clusters being generated by wildlife infection from genotype and WGS analyses has increased in 2020. This implies that the infection front is approaching the LRA over a much larger area than in previous years.

Movement of undetected infected cattle from Oxfordshire to the LRA, mainly through local markets, will become more likely as TB endemicity spreads undetected along the county border with Buckinghamshire and Northamptonshire.

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 provided a barrier to introduction of infection into the wildlife and contiguous herds for animals which have not been post-movement tested.

Assessment of effectiveness of controls and forward look

Effectiveness of controls

The number of herd incidents of TB per year in Oxfordshire has remained similar since 2016, but the epidemiological picture has become more complex. This does not favour the long term objective of reducing OTF-W incidence to less than 1% for Oxfordshire by 2025.

The OTF-W crude incidence in 2020 reached 7.8, which compared to 2019 at 8.9 shows a downward trend despite still being the highest in all counties in the Edge Area.

Early detection of infection through more frequent surveillance testing of cattle herds, alongside the use of mandatory IFN- γ testing for OTF-W incidents, has helped to reduce the spread of TB within herds.

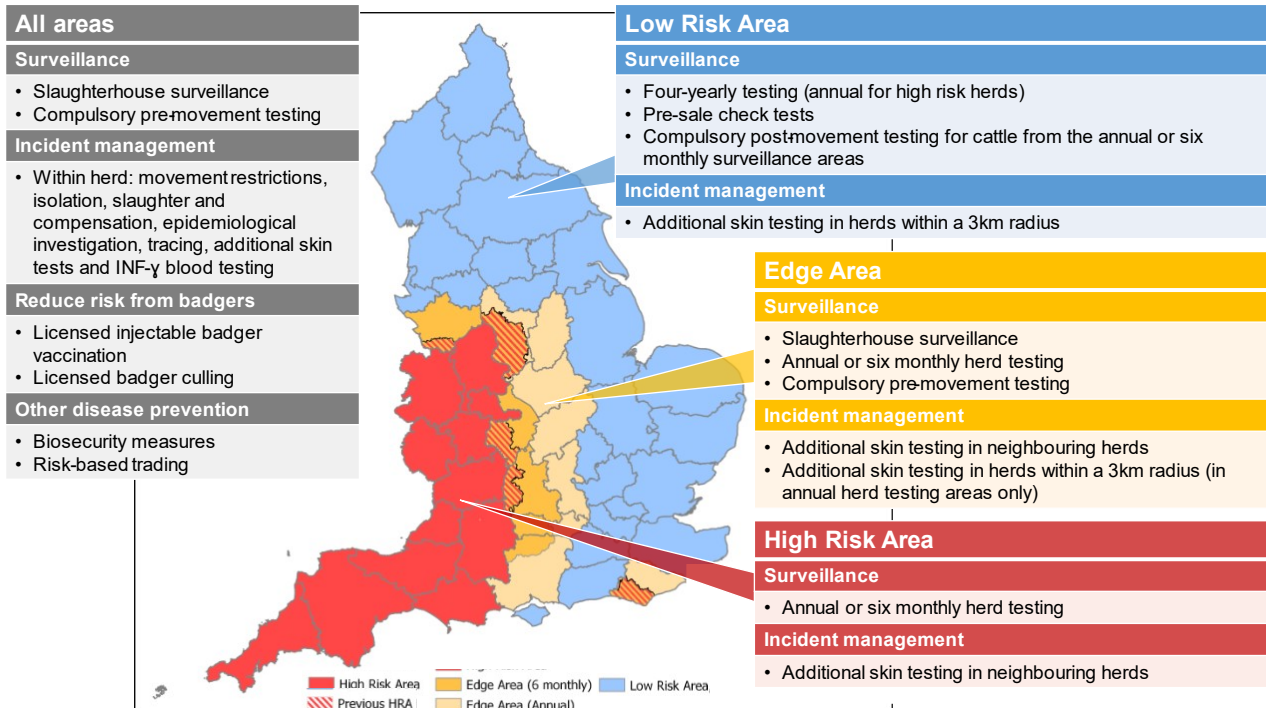
This is particularly the case for herds with recurring TB incidents due to residual herd infection. Stronger messaging regarding improving on-farm biosecurity, informed purchasing of cattle, and wildlife control is paramount to stop the spread of TB within Oxfordshire and into the LRA.

Forward look

Eradication of TB will require some form of wildlife intervention as well as tighter control of cattle movements from farms in the HRA and Edge Areas.

Appendices

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



[Explanatory Supplement for England](#)

[2020.](#)

Policy objectives for the Edge Area

Short to medium term:

- slow down geographic spread of endemic infection
- maintain crude herd incidence of OTF-W incidents less than 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 less than 1% by 2025
- attain OTF status (crude incidence of indigenous OTF-W herd incidents less than 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:

- [A strategy for achieving officially bovine tuberculosis free status for England](#)
- [Government sets out next phase of strategy to combat bovine tuberculosis](#)

Key Control Measures

Surveillance:

- six monthly or annual routine whole 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 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 ('resolved IRs' policy). The only permitted movements of these animals are to slaughter or an Approved Finishing Unit, or after being subjected to a private IFN- γ test with negative results

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

- 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) at level 1 or above
- Compulsory IFN- γ testing became applicable for all new OTF-W incidents in the whole 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 part of Oxfordshire, but newly persistent incidents appeared in the original Edge Area, in 2018, 2019 and 2020, although still in the western half of the county.

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 OTF-W incidents in Oxfordshire near the eastern border to monitor any spread of TB into Buckinghamshire. Contiguous testing is only carried out in limited scenarios since the introduction of six-monthly testing.
- Laboratory confirmed cases of *M. bovis* in non-bovine species have increased in Oxfordshire which has increased testing of non-bovine species. These incidents were linked to local wildlife or movements of non-bovines, and none of them were linked directly to cattle.

Other control measures

- Provision of free biosecurity advice by the [TB Advisory Service \(TBAS\)](#)
- No meetings of the local TB eradication group for Oxfordshire occurred because of COVID-19 restrictions.
- Some badger control activities took place in Oxfordshire during 2020. However, this covered only a small proportion of the western half of the county extending from the border with the HRA.

Appendix 2: Cattle industry in Oxfordshire

**Table A2.1: Number of cattle premises by size band in Oxfordshire at 1 January 2020.
(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	4	195	87	85	44	21	22	458	130	66

*The number of herds with an undetermined size.

Table A2.2: Number of animals by breed purpose in Oxfordshire at 1 January 2020.

Breed purpose	Beef	Dairy	Dual purpose	Unknown	Total
Number of cattle	41,511 (69%)	14,612 (24%)	3,191 (5%)	2 (less than 0.01%)	59,316

Appendix 3: Summary of headline cattle TB statistics

Table A3.1: Herd-level summary statistics for TB in cattle in Oxfordshire between 2018 and 2020.

Herd-level statistics	2018	2019	2020
(a) Total number of cattle herds live on Sam at the end of the reporting period	554	561	564
(b) Total number of whole herd skin tests carried out at any time in the period	875	892	831
(c) Total number of OTF cattle herds having TB whole herd tests during the period for any reason	421	418	406
(d) Total number of OTF cattle herds at the end of the report period (herds not under any type of Notice Prohibiting the Movement of Bovine Animals (TB02) restrictions)	462	477	467
(e) Total number of cattle herds that were not under restrictions due to an ongoing TB incident at the end of the report period	476	491	491
(f) Total number of new TB incidents detected in cattle herds during the report period, (including all FUs)	81	77	72
• OTF-S	23	27	28
• OTF-W	58	50	44
(g) Of the OTF-W herd incidents:			
• How many can be considered the result of movement, purchase or contact from or with an existing incident based on current evidence?	7 (4 AFU)	6 (1 AFU)	4 (1 AFU)

Herd-level statistics	2018	2019	2020
<ul style="list-style-type: none"> New OTF-W incidents triggered by skin test Reactors or 2xIRs at routine herd tests 	37	27	24
<ul style="list-style-type: none"> New OTF-W incidents triggered by skin test Reactors or 2xIRs at other TB test types (such as ,forward and back-tracings, contiguous or check tests) 	16	17	17
<ul style="list-style-type: none"> New OTF-W incidents first detected through routine slaughterhouse TB surveillance 	5 (4 AFU)	6 (1 AFU)	3 (1 AFU)
(h) Number of new incidents revealed by enhanced TB surveillance (radial testing) conducted around those OTF-W herds			
<ul style="list-style-type: none"> OTF-S 	0	0	0
<ul style="list-style-type: none"> OTF-W 	0	0	0
(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)	61	53	49
(j) New confirmed (positive <i>M. bovis</i> culture) incidents in non-bovine species detected during the report period (indicate host species involved)	1	2	3
(k) Number and type of finishing units active at end of the period:			
<ul style="list-style-type: none"> Approved Finishing Units: Grazing 	0	0	0
<ul style="list-style-type: none"> Approved Finishing Units: Non Grazing 	7	8	10
<ul style="list-style-type: none"> Exempt Finishing Units: Grazing 	0	0	0
<ul style="list-style-type: none"> Exempt Finishing Units: Non Grazing 	0	0	0

Table A3.2: Animal-level summary statistics for TB in cattle in Oxfordshire between 2018 and 2020.

Animal-level statistics (cattle)	2018	2019	2020
(a) Total number of cattle tested in the period (animal tests)	148,857	149,950	140,052
(b) Reactors detected in tests during the year:			
• Tuberculin skin test	660	556	402
• Additional IFN- γ blood test reactors (skin-test negative or IR animals)	750	603	390
(c) Reactors detected during year per incidents disclosed during year	17.4	15.1	11.0
(d) Reactors per 1,000 animal tests	9.5	7.7	5.7
(e) Additional animals slaughtered during the year for TB control reasons:			
• DCs, including any first-time IRs	49	15	21
• Private slaughters	9	7	2
(f) SLH cases (tuberculous carcasses) reported by Food Standards Agency (FSA)	9	18	7
(g) SLH cases confirmed by culture of <i>M. bovis</i>	5	9	4

Note: (c) Reactors detected during year per incidents disclosed during year, reactors may be from incidents disclosed in earlier years, as any found through testing during the report year count here.

Note: (g) SLH cases confirmed by culture of *M. bovis*, 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 the new OTF-W and OTF-S incidents identified in the report period

Table A4: Suspected sources of *M. bovis* infection for all the new OTF-W and OTF-S incidents identified in Oxfordshire , in 2020.

Source of infection	Possible (1)	Likely (4)	Most likely (6)	Definite (8)	Weighted contribution
Badgers	13	14	41	0	53.6%
Cattle movements	28	14	4	1	21.1%
Contiguous	1	0	0	0	0.2%
Residual infection	12	17	9	0	20.1%
Domestic animals	0	0	0	0	0.0%
Non-specific reactor	0	0	0	0	0.0%
Fomites	0	0	0	0	0.0%
Other wildlife	1	1	0	0	1.0%
Other or unknown source	1	0	0	0	4.0%

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](#).



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