



Animal &
Plant Health
Agency

Year End Descriptive Epidemiology Report: Bovine TB in the Edge Area of England 2022 County: Oxfordshire

TB Edge Area - OXFORDSHIRE



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Introduction

The Edge Area was originally 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. 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. The current aim is to obtain OTF status for the Edge Area as soon as possible.

This report describes the frequency and geographical distribution of TB in cattle herds in Oxfordshire, an Edge Area county, in 2022. It examines what factors are likely to be driving TB in this area, and the risks the disease in this county may pose to neighbouring areas.

TB in cattle and other mammals is primarily caused by the bacterium *Mycobacterium bovis* (*M. bovis*), and the disease is subsequently referred to in this report as TB. Although other sources may refer to TB 'breakdowns', this report will use the term 'incidents' throughout.

This report is intended for individuals involved in the control of TB, both locally and nationally. This includes, but it is not limited to, farmers, veterinarians, policy makers and the scientific community.

Details of the data handling methodology used in this report, a glossary of terms, and the TB control measures adopted in the Edge Area, can be found in the [explanatory supplement for the annual reports 2022](#).

Types of TB incident

Unless otherwise specified, this report includes all new TB incidents detected during the reporting period (1 January to 31 December 2022). This includes both 'Officially Tuberculosis-Free Status Withdrawn' (OTF-W) and 'Officially Tuberculosis-Free Status Suspended' (OTF-S) incidents.

OTF-W incidents are those involving at least one skin test reactor positive to the Single Intradermal Comparative Cervical Tuberculin or SICCT test, in addition to either typical lesions of TB identified at post-mortem (PM) meat inspection, or at least one animal with an *M. bovis*-positive culture result from tissue samples collected from carcasses during the PM inspection (or both).

OTF-S incidents are triggered by reactors to the skin test, but without subsequent detection of TB lesions or positive culture results in any of those animals.

TB incidents in [Approved Finishing Units](#) (AFUs) without grazing are not included in the prevalence and incidence calculations in this report due to the limited epidemiological impact of these incidents.

Furthermore, the number of TB incidents and designation of those incidents as OTF-W or OTF-S may differ in this report compared to other official TB statistics due to differences in the information available at the time datasets are accessed.

Cattle industry

Cattle farms in Oxfordshire are predominantly small to medium sized suckler herds, as indicated in Appendix 1. Large herds tend to be dairies in West Oxfordshire and finishing units in the rest of the county. There were 11 AFUs in 2022 compared to 9 in 2021.

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. Thame market was the only livestock market operating in Oxfordshire in 2022. Dedicated sales for TB-restricted cattle in the south-west are the main outlet for calves from TB incident herds.

Oxfordshire was originally divided between 2 TB risk areas. The High Risk Area (HRA) in the east, and the Edge Area in centre and west of the county.

The whole of Oxfordshire was fully incorporated into the Edge Area in January 2018.

Cattle herds routinely undergo 6-monthly (6M) TB surveillance testing in Oxfordshire. However, 26% of cattle herds were regarded as having a lower risk of contracting TB, and thus eligible for annual testing under the [earned recognition scheme](#) in 2022 (25% in 2021).

New TB incidents

In 2022, there were 56 new TB incidents detected in the whole of Oxfordshire, which is one incident less than in 2021. OTF-W incidents have decreased every year since 2017, whilst the annual number of OTF-S incidents has remained stable over this period and unchanged between 2020 and 2022 (25 in all years, as shown in Figure 1).

More than half of the TB incidents in Oxfordshire occurred in herds with a history of TB. First-time TB incidents were widespread, but a few were concentrated in the north-east of the county.

In the original Edge Area of East Oxfordshire OTF-W incidents in 2022 decreased to 21 from 23 in 2021, whereas the number of OTF-S incidents increased to 16 from 12 in 2021.

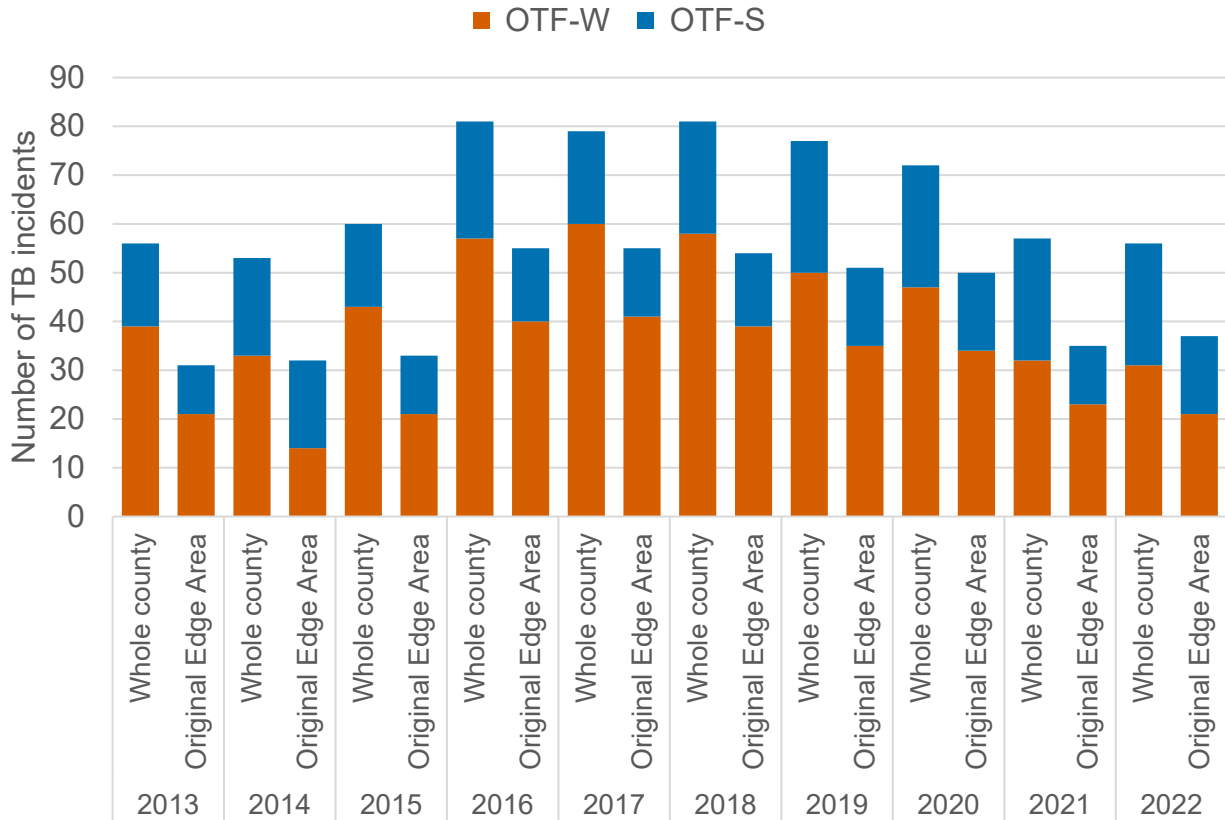


Figure 1: Annual number of new TB incidents in Oxfordshire, from 2013 to 2022.

In 2022, 44% of the total number of new TB incidents occurred in beef suckler herds (55% of all OTF-W and 29% of all OTF-S incidents in Oxfordshire). Beef fattener herds accounted for 35% of all new TB incidents.

Herds of 200 or fewer cattle were responsible for 64% of all new incidents compared to herds with 201 or more (36%).

Disclosing test types

As in previous years, whole-herd (6 or 12-monthly routine surveillance) testing continued to detect the most incidents of TB in Oxfordshire in 2022. This was followed by 6M post-incident surveillance testing, as shown in Figure 2. Trace testing detected 2 incidents in 2022 compared to no incidents in 2021.

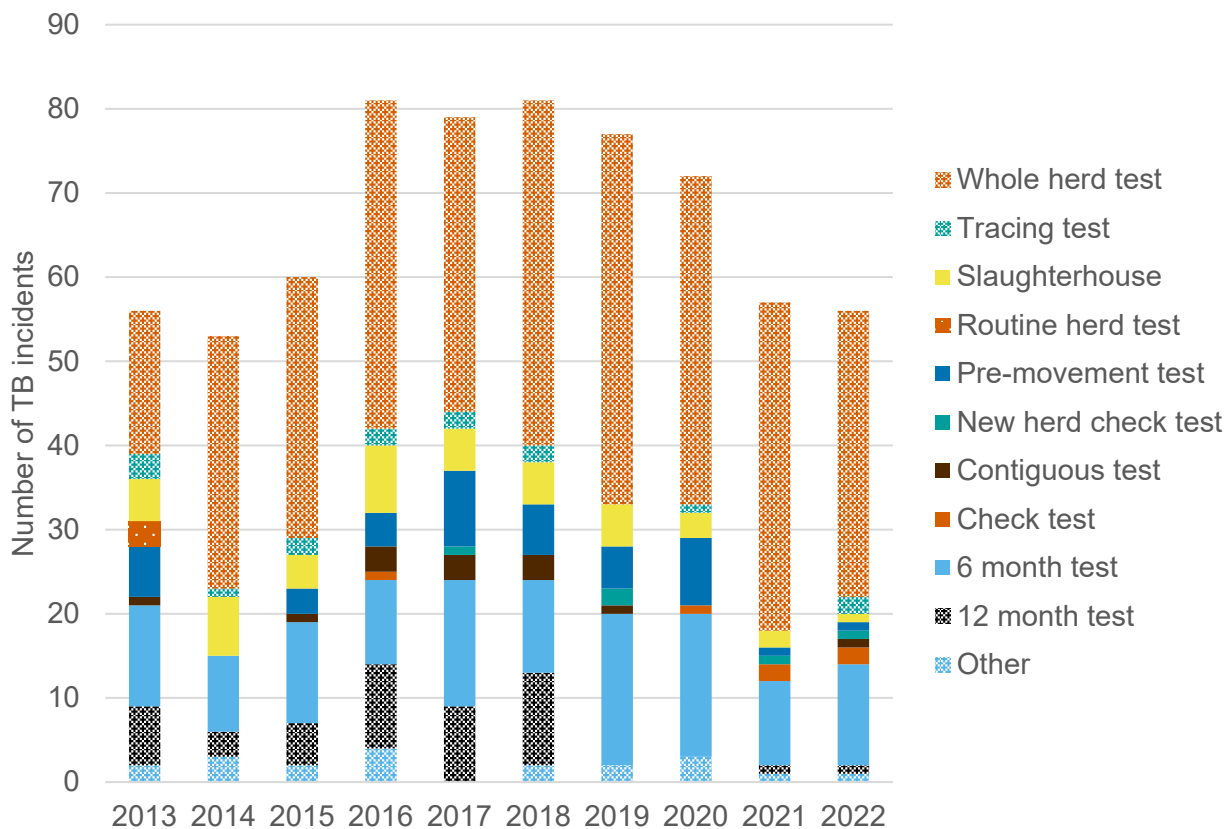


Figure 2: Number of new TB incidents (OTF-W and OTF-S) in Oxfordshire in 2022, according to the surveillance methods that detected them.

Duration of TB incidents

A total of 64 TB incidents were resolved in Oxfordshire during 2022. Of these, 19 were new TB incidents that started in 2022, 34 started in 2021, 8 were from 2020 and 2 started in 2019.

The median duration for OTF-W incidents that ended in 2022 was 310 days (interquartile range (IQR) 197 to 542.5). Eight OTF-W incidents took over 550 days to resolve, but the majority (28 out of 36) were ended in 550 days or less.

Most OTF-S incidents that ended in 2022 (20 out of 28) were resolved within 240 days, however 8 took between 241 and 550 days to resolve, and the median was 180.5 days (IQR 164.5 to 260).

There were 3 TB incidents still open at the end of 2022 that had been open for more than 550 days.

The median duration for all incidents that were ended in 2022 was 230 days (IQR 173.5 to 398.5). This is shorter than the duration of incidents that ended in 2021, which was 243 days (IQR 179 to 346), but the highest median duration of any Edge Area county in 2022.

For the whole Edge Area, the median duration of TB incidents that ended in 2022 was 182 days (IQR 157 to 286).

Changes to the interferon gamma testing policy in England were introduced in July 2021, with a net result of reducing the number of such tests completed in TB incident herds in the 6M testing parts of the Edge Area. This, coupled with the diversion of resource to the highly pathogenic avian influenza (AI) outbreak of 2021 and 2022, is likely to have played a part in prolonging the duration of some incidents in this county compared to annual testing counties. The number of persistent incidents (under movement restrictions for more than 550 days) in 2022 compared to 2021 has also reduced, bringing the overall median duration down.

Unusual TB incidents

There were no individual TB incident investigations in Oxfordshire in 2022 to explore unusual TB incidents.

TB in other species

There is no statutory routine TB surveillance of non-bovine species, apart from post-mortem examination (PME) of animals slaughtered for human consumption. Targeted TB testing takes place in non-bovine herds with laboratory confirmed *M. bovis* infection, and in specific herds of camelids, goats and captive deer at an elevated risk of infection.

In Oxfordshire, TB was reported in one wild fallow deer in 2022 found near Henley-on-Thames. Whole Genome Sequence (WGS) can be used to examine the relationship between cattle incidents in the area and wild deer populations. The WGS of this *M. bovis* deer isolate was closely related to a large cluster of TB in an area to the west of Henley, which has been apparent since 2016. This may suggest a part for deer in the transmission of infection between cattle and wildlife.

A persistent TB incident on a large breeding alpaca farm operating in the south of the county was initially detected in 2019 and continued into 2022. Clade B6-85 of *M. bovis* was identified in 2022, which is different to the original local clade B6-62 that had been isolated on this farm previously. This new clade has been identified recently in a local cluster of cattle incidents. There were no identifiable links via movements of animals between the alpaca and cluster of cattle incidents, nor were these premises contiguous to each other. Therefore, this points towards another local source in this area.

This incident was also part of a large investigation by UKHSA on the zoonotic spread of *M. bovis* to humans after it was linked by comparing WGS to a cluster of human incidents in the south-west of England. The human cluster also included a domestic cat with isolates closely related to this B6-85 cluster in south Oxfordshire. Abattoir workers with close

contact with infected cattle, shared habitat with infected wildlife in Berkshire/Oxfordshire or contact with infected alpacas are all possible pathways still under investigation.

APHA, in collaboration with the University of Nottingham, conducted a project to detect the presence and location of TB infection in badgers in Buckinghamshire, Oxfordshire, Berkshire, Hampshire and East Sussex - collectively known as the 'Southern Edge Area'. Volunteers were recruited in each county to help with the safe and timely retrieval of badger carcasses. They were delivered to the University of Nottingham, where they underwent PME and testing for the presence of TB infection by culture. Those that tested positive were sent for further whole genome sequencing and clade identification (genetic strain). The project aimed to collect 100 carcasses of badgers found dead per county, most likely those killed in road traffic accidents (RTAs). Once 100 carcasses of a sufficient quality were examined per county, collection ceased in that county. Once county targets were achieved, all stakeholders were informed. The survey ended in April 2023 and its results will be communicated to all stakeholders once all the bacteriological cultures and WGS analysis have been completed. Its results will help develop a picture of the disease situation in the Southern Edge Area.

Incidence of TB

Oxfordshire had the highest incidence of TB per 100-herd years at risk out of the 11 Edge Area counties (15.1). The incidence in Oxfordshire was also higher than 5 High Risk Area counties and the HRA overall (14.4). However, the incidence rate decreased in 2022 for the third year running in Oxfordshire (Figure 3).

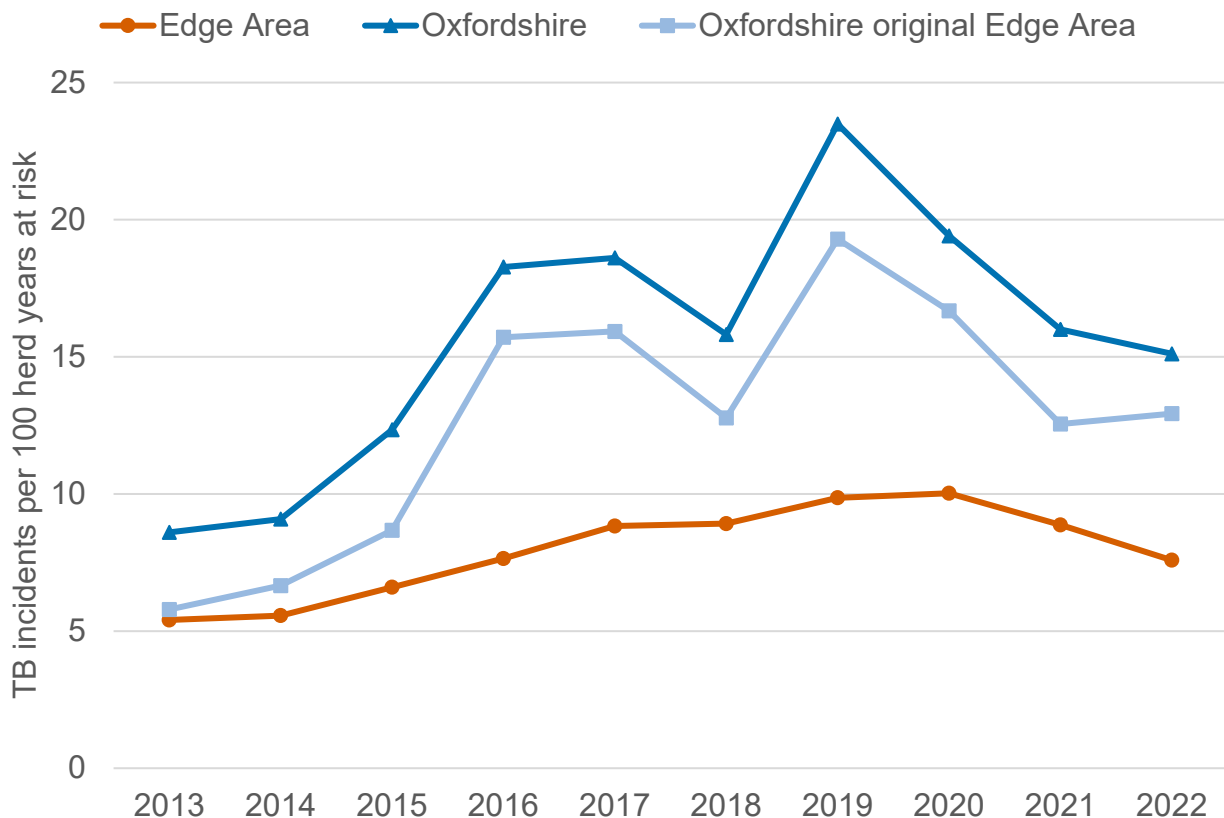


Figure 3: Annual incidence rate per 100 herd-years at risk for all new incidents (OTF-W and OTF-S) in Oxfordshire, from 2013 to 2022.

The incidence in the original Edge Area portion of Oxfordshire increased to 12.9 in 2022 from 12.6 in 2021. In the whole county in 2022, the incidence decreased to 15.1 from 16.0 in 2021.

The marginal decrease in incidence is potentially explained by several factors that have been driving the decrease in incidence over the last 3 years:

- A reduction of residual infection by using interferon gamma blood testing in cattle herds affected by OTF-W TB incidents, leading to fewer re-occurrent incidents. The new interferon gamma testing policy introduced in July 2021 prioritises test use in re-occurrent and chronic incidents.
- Earlier detection of incidents (due to increased frequency of surveillance herd testing since 2018) also reducing spread and residual infection within the herd causing re-occurrent.
- Licensed intensive badger culling operations started in the west side of Oxfordshire in 2019. Additional areas were licensed in 2022 covering the east of the county, which had an increasing incidence of TB in 2022. This additional intervention has

probably started to have a positive impact in western areas of the county where incidence has reduced.

In 2021 and 2022, many eligible herds reverted to annual routine surveillance testing (approximately one quarter of all the cattle herds) through the '[Earned Recognition](#)' scheme. Whole-herd interferon gamma blood testing decreased due to changes in policy and the diversion of APHA staff to controlling the H5N1 AI outbreak. This might have slowed down a further decrease in incidence this year.

Reduction of TB incidence and prevalence in nearby HRA counties has also helped to reduce infection pressure in general for other parts of the England, by decreasing the numbers of purchased cattle from the HRA with undisclosed infection.

Figure 3a shows the incidence calculated as the number of new TB incidents per 100 unrestricted herds tested. This additional measure was introduced to account for the effects of changing testing frequency between 2018 (when 6-monthly testing was introduced) and 2019 (when earned recognition allowed for some herds to return to annual testing). The county incidence per 100 unrestricted herds tested plateaued from 2016 to 2020 and then decreased in the 2 following years.

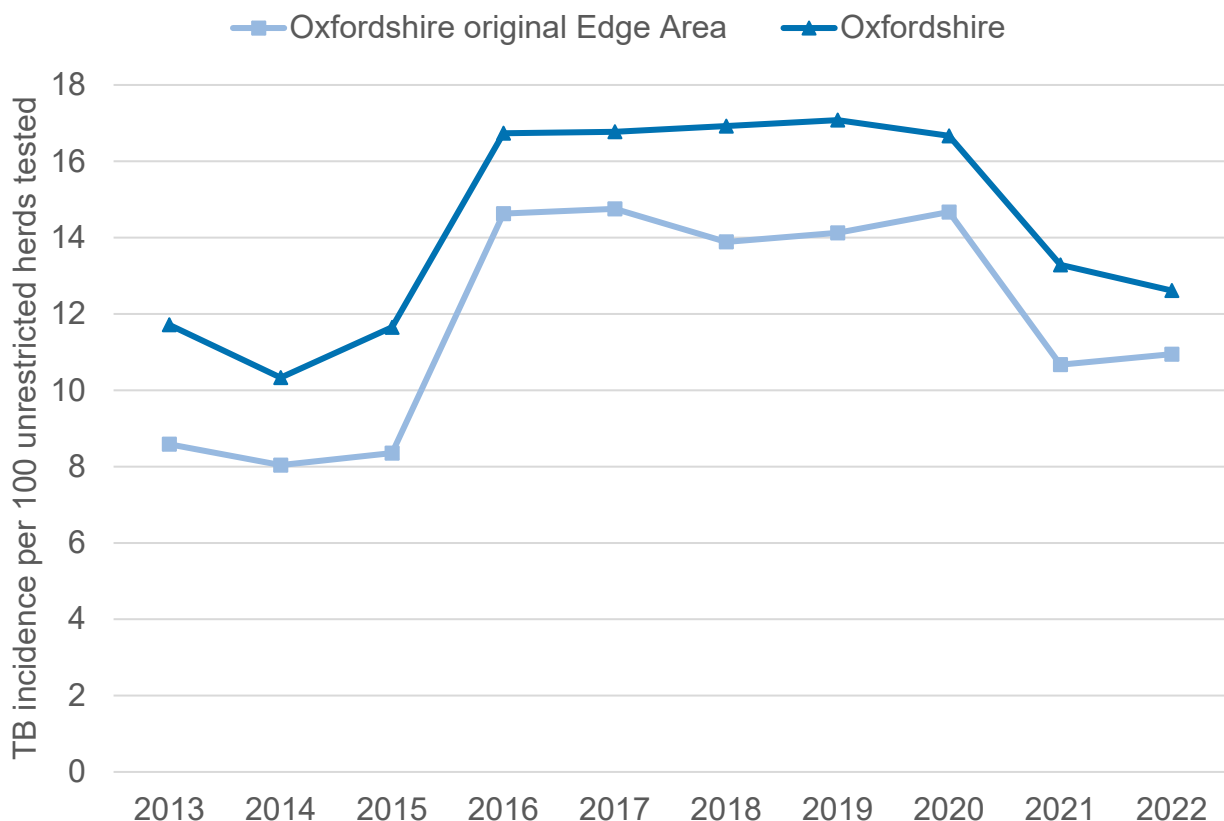


Figure 3a: Annual incidence rate per 100 unrestricted herds tested for all new incidents (OTF-W and OTF-S) in Oxfordshire, from 2013 to 2022.

Prevalence of TB

The herd prevalence for both the whole of Oxfordshire and the original Edge Area decreased in 2022 (8.3% and 6.7%) compared to 2021 (9.6% and 7.9% respectively, see Figure 4).

The herd prevalence in Oxfordshire had plateaued in the last 5 years at just over 10% of herds under movement restrictions (due to a TB incident) at the end of each year. A reason for the decline in 2021 and 2022 was the reduction in the number of new TB incidents.

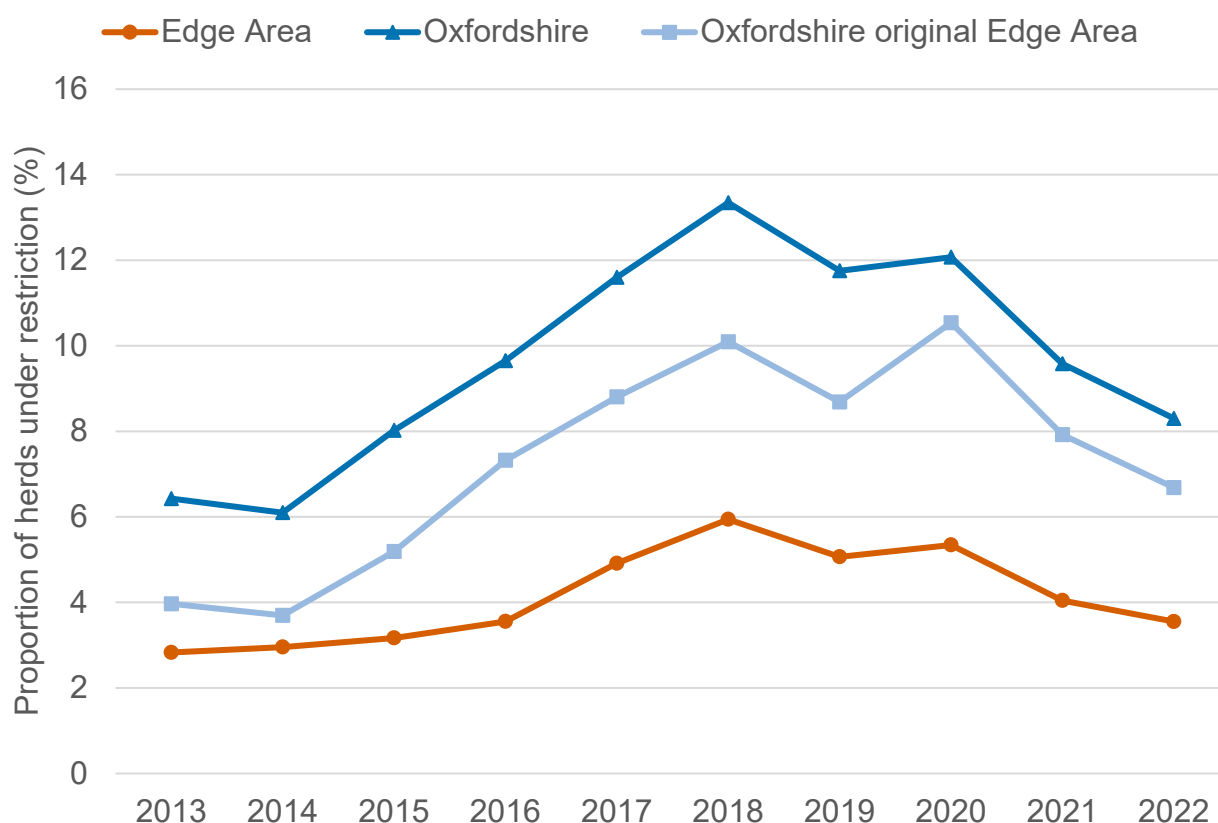


Figure 4: Annual end of year prevalence in Oxfordshire, from 2013 to 2022.

Re-occurring TB incidents

In Oxfordshire, there was a total of 25 herds with new TB incidents in 2022 that had not had a TB incident in the previous 3 years. Of these, 15 were OTF-S and 10 OTF-W (Figure 5). Incidents re-occurred in 31 herds in 2022, with OTF-S incidents in 10 herds and OTF-W incidents in 21 herds with a history of TB. The proportion of herds in Oxfordshire with a re-occurring TB incident was 55%, which was slightly higher than the overall Edge area (50%).

Re-occurrence of an incident in the same herd is a problem in Oxfordshire. Residual cattle infection remaining in the herd from a previous incident and reinfection from other sources, especially wildlife, likely explain most of the re-occurrent incidences which are OTF-W.

Interferon gamma testing is routinely deployed in Oxfordshire when an incident becomes re-occurrent (defined by the interferon gamma policy as a herd which was OTF-W less than 18 months before becoming OTF-W again). This is very common in endemic counties like Oxfordshire.

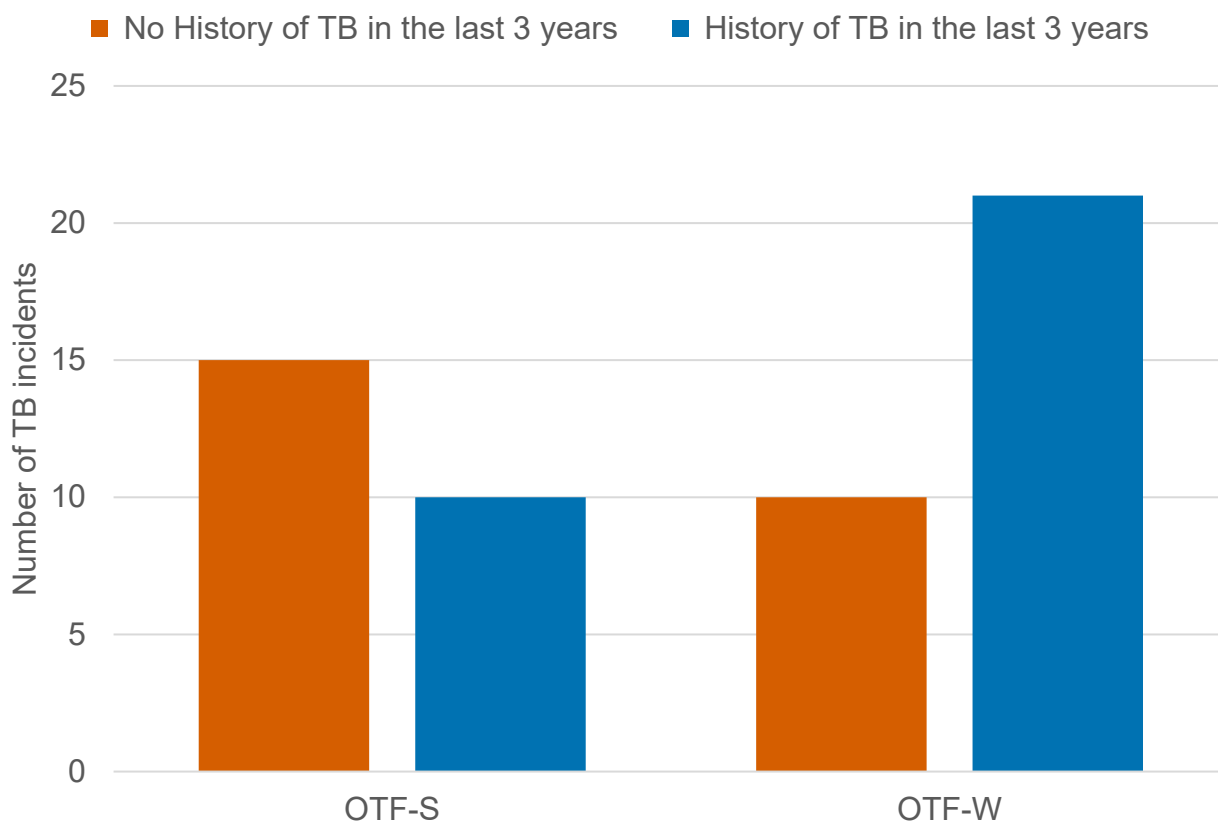


Figure 5: Number of herds with a TB incident (by OTF-W and OTF-S) in Oxfordshire in 2022, with and without a history of any TB incident in the previous 3 years.

Geographical distribution of TB incidents

Over the past decade, the distribution of incidents in Oxfordshire has continued to advance eastwards, now covering most of the county (see Figure 6), as described extensively in the 2020 report.

New and overlapping clusters of infection may appear every year in the endemic areas of TB in the west of the county where more than one source of TB is likely to be occurring at the same time.

Newly established areas of TB in the rest of the county are shown by identifying clusters. New TB incidents were generally localised around areas of higher cattle densities.

For most new incidents across the county in 2022, the strain of *M. bovis* identified was of WGS clade B6-62. There were 4 incidents distributed across the county identified with clade B6-11. In the south, incidents were identified as clades B6-62 and B6-85.

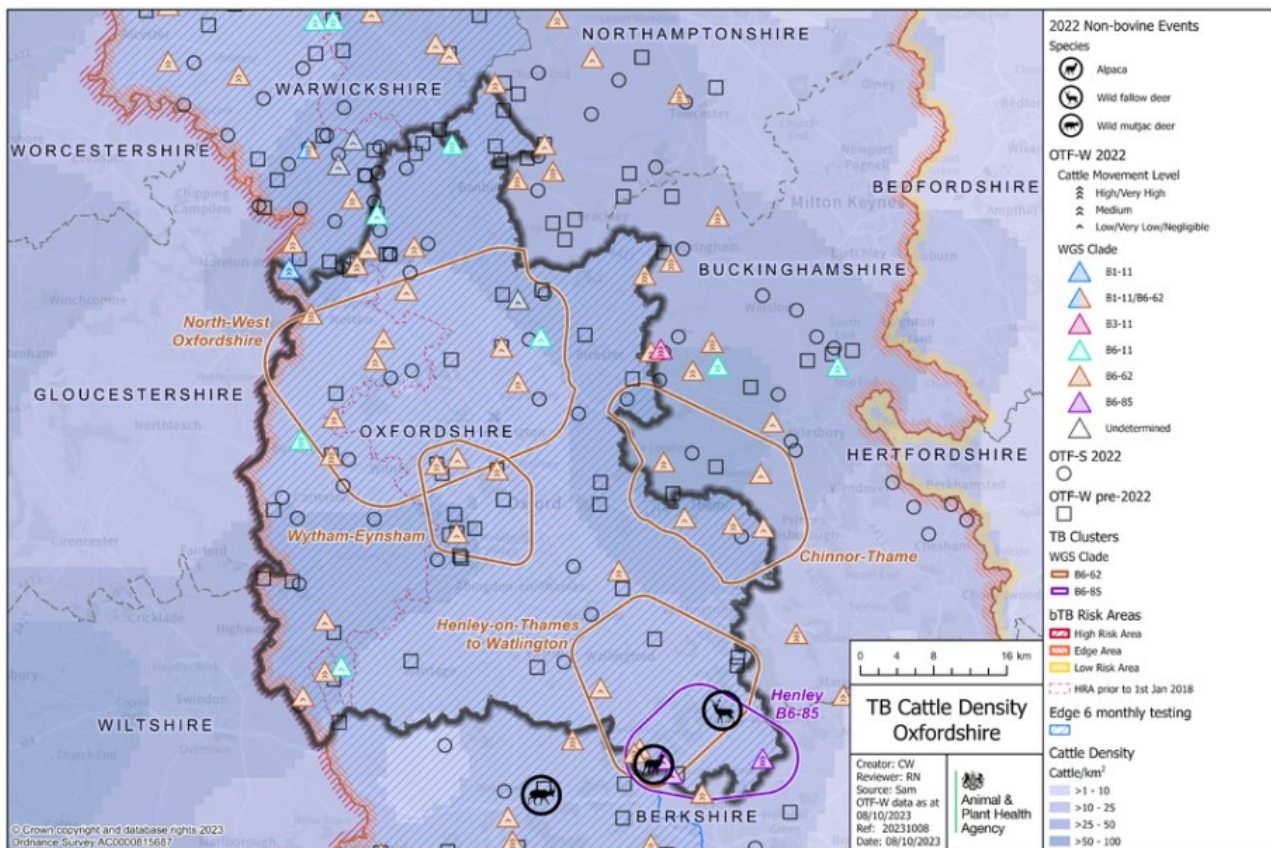


Figure 6: Location of cattle holdings in Oxfordshire with new TB incidents (OTF-W and OTF-S) in 2022 and cattle holdings with pre-2022 OTF-W incidents still ongoing at the beginning of 2022, overlaid on a cattle density map. The movement score for each farm is symbolised with 3 chevrons for cattle movements associated with a high likelihood of infection, 2 chevrons for a medium likelihood and one chevron for a low likelihood.

North-West Oxfordshire cluster

This cluster is located in the north of the county, as indicated in Figure 6.

Historically, the most common *M. bovis* genotype in this area had been the local genotype to Oxfordshire, 10:a. This appeared to have mutated in recent years in this locality to a different spoligotype, 130. Both 10:a and 130 are in the same WGS clade, B6-62 (see Figure 6).

WGS analysis of these *M. bovis* isolates has found 18 genetically related incidents, varying between 0 and 3 single nucleotide polymorphisms (SNPs) apart in the same geographical area, with the oldest incident dating back to 2017. Of these 18, 5 occurred in 2022, compared to 2 in 2021, 2 in 2020, and 6 in 2019.

Henley-on-Thames to Watlington cluster

This cluster is located in the south-east of the county (Figure 6) from Henley-on-Thames to Watlington. The 10:a genotype (part of clade B6-62, see Figure 6) has been the most commonly found genotype in this area, including several confirmed infected wild deer (in 2018 and 2022) and an incident in a large alpaca breeding farm.

For the period 2015 to 2020, WGS analysis 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 4 cattle incidents in 2015 to 2016 in the geographical centre, with identical isolates of *M. bovis*. Spread occurred concentrically outwards in the following years. Two more incidents linked to this cluster were disclosed in 2022 in the south corner of the county bordering Berkshire. Local movements cannot be ruled out for these 2 incidents.

Wild fallow deer could have played a role in spreading disease in the centre of the cluster where they were abundant. *M. bovis* isolates from several incidents of TB in cats, linked to the consumption of raw pet food distributed nationwide, were closely genetically related to this cluster.

Henley cluster (of *M. bovis* clade B6-85)

Within a similar area to the cluster above close to the south-east border with Berkshire, there has been a potential cluster of 11:a incidents (Sonning-Common). The genotype 11:a is part of WGS clade B6-85. From 2017, incidents with this genotype (homerange in the south-west of England) started to appear and were mostly attributed to purchases of cattle, but in 2022 incidents (including one in a known closed herd of alpacas) suggests that local spread may also have occurred (Figure 6).

WGS investigations have shown at least 5 cattle herds within a 5 mile radius linked genetically by a 3 SNP distance (of which 2 cattle incidents and the alpaca incident were disclosed in 2022). Many of these had cattle movements, including local cattle movements, associated with a very low likelihood of TB infection. Also included in the cluster is a large alpaca breeder with no links to any cattle farms in the area, except from being exposed to the same wildlife reservoirs. This herd was previously affected by local B6-62, which means that a new source of infection (B6-85) is already affecting the local wildlife with a new cluster, overlapping the B6-62 Henley cluster.

Chinnor-Thame cluster

This cluster started in the most eastern part of the county and has since spread into Buckinghamshire (Figure 6).

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, and all part of WGS clade B6-62), was first identified in 3 incidents close to

each other. This genotype was later found to be closely related to genotype 17:g, found in 4 more incidents, all of which were within 6 kilometres of each other. Some incidents were re-occurrent with the same genotype identified. WGS analysis indicated very close genetic relatedness between isolates, and in the absence of other epidemiological links wildlife was concluded to be the most likely common source.

Radial testing was triggered by these OTF-W incidents in the Chinnor-Thame cluster to investigate lateral spread into the neighbouring county of Buckinghamshire. In 2022, more incidents were linked 2 to 3 SNP distance to this cluster, proving lateral spread into this county.

This cluster has also been linked to a new hotspot area of TB in the Low Risk Area county of Hertfordshire, on the other side of Buckinghamshire, 10 miles away from Chinnor.

Wytham-Eynsham Cluster

This cluster (10:7-3-5-4*-3-3.1 – part of clade B6-62) was identified in 2020 to the north-west of the city of Oxford. Another incident with the same genotype had been identified in 2014 in the same area. Common exposure to infected wildlife populations was the only identifiable source of infection for the 2020 and 2021 incidents, both then re-occurrent.

WGS investigations in 2022 have identified a larger cluster of incidents genetically linked to each other by 0 to 2 SNP distance within a 5 mile radius. There have been 10 incidents in total since 2017, with several links not explained by local cattle movements, implying spread into wildlife.

If we enlarge the geographical area, this cluster is linked to 5 more incidents in the west of Oxfordshire near Burford, less than 10 miles away, with WGS only one to 2 SNP distance.

Other smaller clusters

WGS investigation of incidents north-west of the county bordering Warwickshire identified 6 incidents of clade B6-62 within a 5-mile radius, linked by a 0 to 2 SNP distance. This cluster near Hook Norton includes 4 incidents from Oxfordshire and 2 from Warwickshire. Two of the Oxfordshire incidents have been re-occurrent for many years, linked to local badger infection.

Another area investigated is in the south-west of the county near Faringdon, with 5 incidents of clade B6-62 within a 5-mile radius, linked with a 2 to 3 SNP distance. Some of these incidents are also re-occurrent and already linked to badger infection.

Within some of these re-occurrent incidents we find completely unrelated isolates 5 to 10 SNP apart affecting the herd at some point in the last 5 years. These point to several

sources affecting one herd, some becoming residual and some from recent new exposure. Some will also be due to local wildlife and from local purchases, complicating the picture.

In areas where TB has been endemic for a long time, it is therefore likely that several sources can be attributed to each incident. Several overlapping clusters have been appearing over time.

Skin test reactors and interferon gamma test-positive animals removed

Appendix 2 provides a summary of headline cattle TB statistics in Oxfordshire. In 2022, there was a total of 537 TB test-positive animals in Oxfordshire, as shown in Figure 7. This is the lowest total number of test positive animals removed from herds after a steady decline since a peak of 1,410 animals in 2018.

Of the 537 test positive animals in 2022, 67% were skin test reactors, compared to 48% in 2021. Only 33% of animals removed in 2022 were interferon gamma (IFN- γ) test positive, compared to 52% in 2021. This is likely due to a reduced deployment of interferon gamma blood testing in Oxfordshire due to policy changes and the diversion of APHA resources to the AI outbreak control effort.

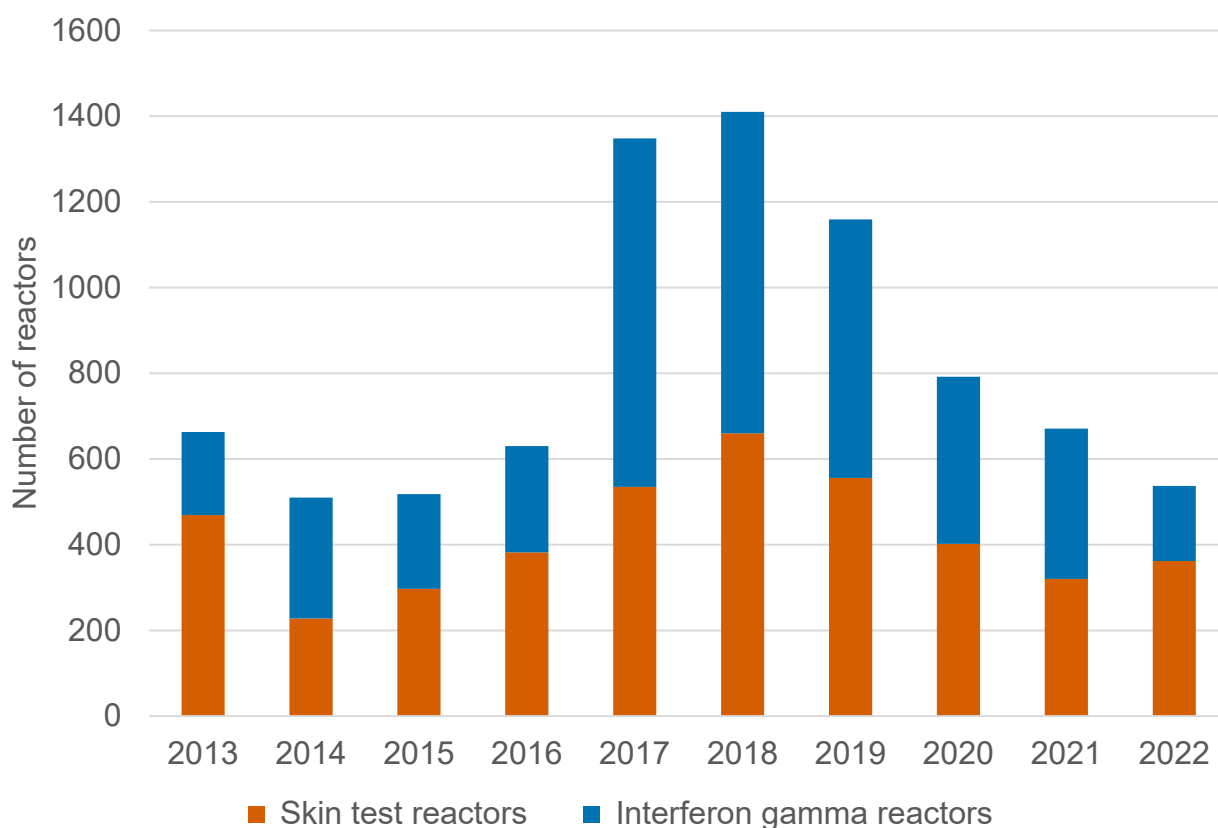


Figure 7: Number of skin test reactors (SICCT) and interferon gamma (IFN- γ) test positive cattle removed by APHA for TB control reasons in Oxfordshire, from 2013 to 2022.

Main risk pathways and key drivers for TB infection

It is important to try to understand the risk pathways and key drivers that are likely to have introduced TB infection into a herd. This information can help identify mitigations that may reduce TB risk for individual businesses.

Implementing practical measures can help to reduce the risk of TB incursion into a herd that is TB free ([biosecurity](#)), as well slowing disease spread within a herd where TB is present (biocontainment).

Furthermore, the [ibTB](#) online tool can be used to inform purchasing choices, reducing the risk of introducing undetected infection when moving cattle into a herd.

In 2022, 11 out of 56 (20%) new TB incidents in Oxfordshire received a preliminary or final APHA veterinary investigation to identify the source of infection. The results of these investigations are reported in Appendix 3. The small number of investigations carried out in 2022 was mainly due to the diversion of field resource to the large AI outbreak which occurred in 2021 and 2022.

New data-driven methods to quantify the likelihood of risk pathways for TB infection have been developed by APHA. These include the:

- Cattle Movement Algorithm
- WGS Local Reservoir Indicator

The Cattle Movement Algorithm uses cattle movement data to identify individual animals that were moved into a TB incident herd as having a negligible, very low, low, medium, high or very high likelihood of being the source of the TB infection. At the herd level, the cattle movement score is dictated by the animal with the highest ranked movement into that herd. Herds are classified as having either:

- cattle movements associated with a high likelihood of infection (a herd with any movements scored as a high or very high likelihood)
- no cattle movements with a high likelihood of infection (the highest likelihood score was negligible, very low, low or medium).

The WGS Local Reservoir Indicator uses WGS data from cattle *M. bovis* isolates to identify TB incidents that are linked by genetics, time and space. A local reservoir is indicated for a new TB incident where at least one other TB incident is identified that satisfies all the following 3 criteria:

- it has a WGS with no more than 3 single nucleotide SNP differences relative to the TB incident of interest

- it is within 4 years before or 6 months after the start date of the incident of interest
- it is within a 9km radius of the incident of interest.

Further details about the methodology used can be found in the [explanatory supplement to the annual reports 2022](#).

There is always a variable degree of uncertainty about the estimated true routes of TB infection into a herd. The absence of a local reservoir, or cattle movements associated with a high likelihood of infection does not completely negate these pathways. Nonetheless, the evidence provided by the cattle movement and WGS data, when combined, can provide valuable insights into the possible risk pathways. Figure 8 provides the percentage of herds where each risk pathway combination was identified. The spatial distribution of these categories are presented in Figure 9. Each category is described in greater detail in the following text.

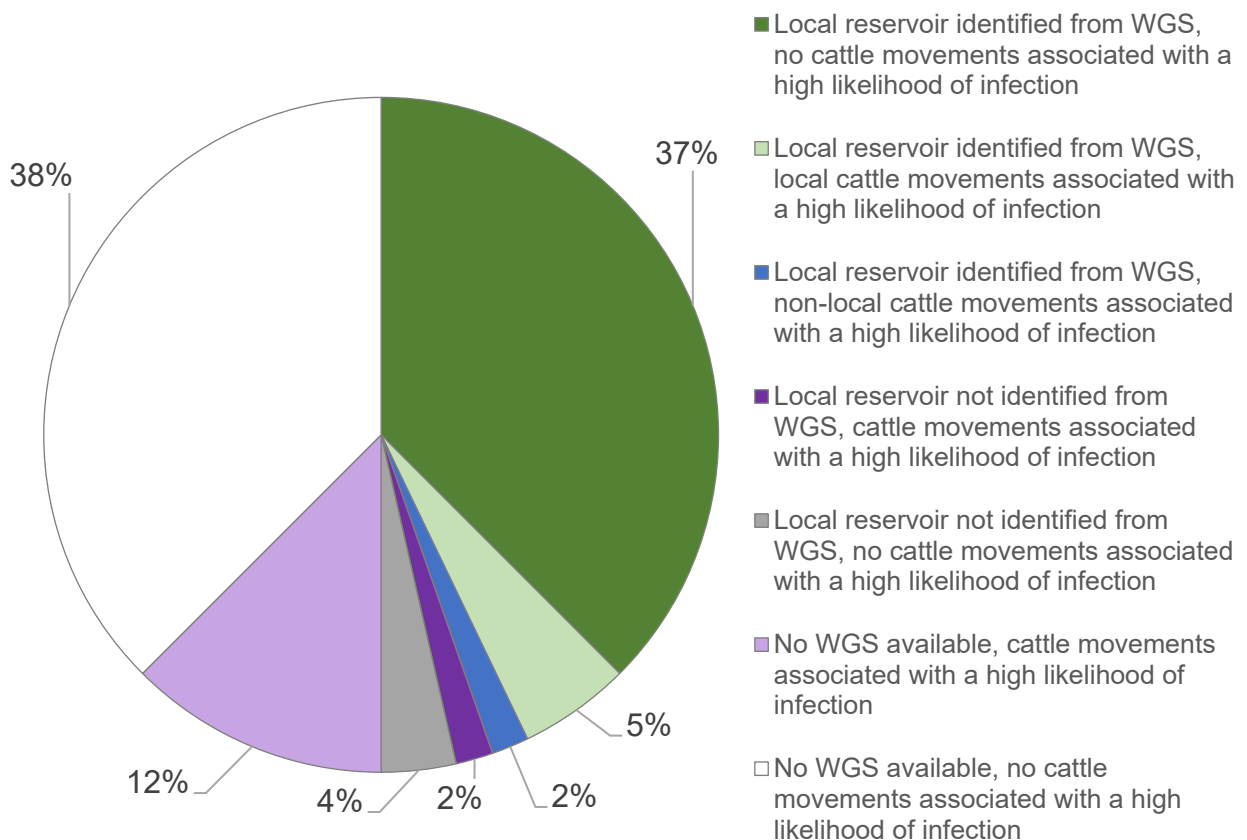


Figure 8: Risk pathway combinations identified by the WGS local reservoir indicator and cattle movement algorithm for all 56 new TB incidents in Oxfordshire in 2022

WGS data were available for 28 (50%) of all new TB incidents in Oxfordshire. The WGS Local Reservoir Indicator identified a local reservoir of infection for 25 (44%) new TB incidents in 2022.

Most of the TB incidents with WGS data available (21 of the total 28) had a local reservoir identified without evidence of cattle movements associated with a high likelihood of TB infection. These are dark green symbols in Figure 9.

For these incidents, a broad spectrum of local pathways cannot be ruled out, including:

- residual infection in the herd
- contiguous contact with infected cattle
- direct or indirect contact with potentially infected wildlife.

A further 3 new TB incidents had evidence of both a local reservoir and cattle movements (within 25km) associated with a high likelihood of TB infection. For these TB incidents, local cattle movements would have likely played a part in the spread of this local infection, in addition to the previously listed local pathways. These incidents are symbolised in light green in Figure 9.

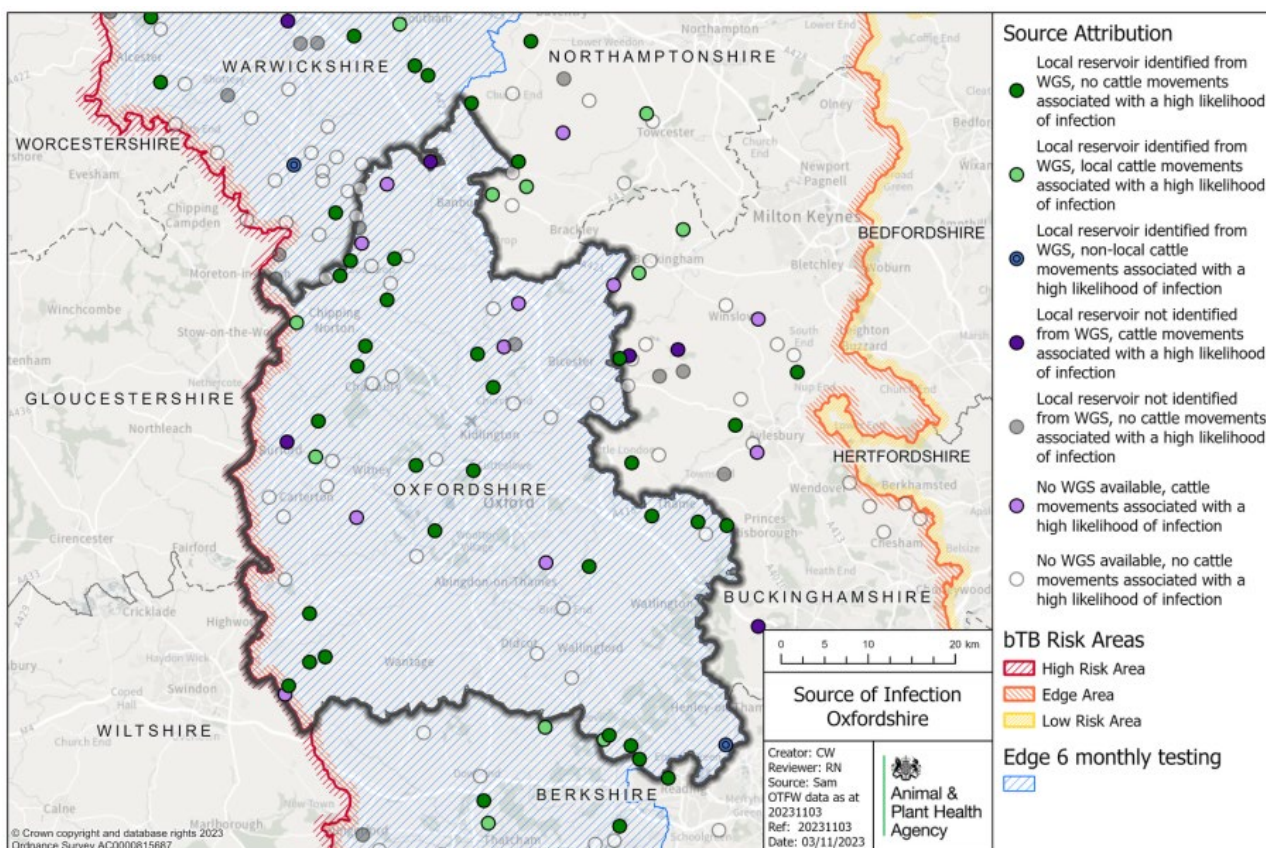


Figure 9: Map of the available evidence for risk pathways of TB infection into the herd, for all TB incidents (OTF-W and OTF-S) in Oxfordshire that started in 2022.

For one TB incident in Oxfordshire there was both evidence of a local reservoir and evidence of cattle movements over a distance greater than 25km associated with a high likelihood of TB infection. For this incident there was a high degree of uncertainty around

the source of infection. With multiple likely risk pathways, it is possible there was more than one route of disease incursion into the herd.

In Oxfordshire, one TB incident had evidence of cattle movements associated with a high or very high likelihood of TB infection, and no evidence of a local reservoir where WGS was available. For that herd it was considered more likely than not that cattle movements played a part in the introduction of infection (dark purple symbol, Figure 9).

A further 7 TB incidents (12%) had cattle movements associated with a high likelihood of TB infection, but no WGS data was available to look for a local reservoir. These are depicted in light purple in Figure 9 due to the lack of genetic evidence.

For 2 TB incidents (4%), the WGS Local Reservoir Indicator did not find evidence of a local reservoir, and there was no evidence of cattle movements associated with a high likelihood of TB infection. The source of infection is unclear for these incidents (grey symbols).

There was no evidence of cattle movements associated with a high likelihood of TB infection and no WGS data available to explore the presence of a local reservoir for 21 of the 55 (38%) TB incidents. These are shown as white dots in Figure 9, as there is insufficient evidence to determine a likely infection pathway.

The main risk pathways and key drivers for TB infection within Oxfordshire in 2022 were as follows:

- exposure to infected local wildlife
- purchase of undetected infected cattle
- residual infection from previous incidents.

Infected wildlife remained the most likely source of infection for TB incidents in cattle in 2022 based on DRF reports for those investigations carried out in 2022, there were 11 out of 56 incidents, as shown in Appendix 3. The most common source of wildlife infection identified during on-farm investigations are badgers, but the presence of other wildlife species such as wild deer is increasingly frequently reported in some areas. Evidence of which wildlife source is exposing the herd is still difficult to ascertain and not mutually exclusive. There is still little surveillance information available and high uncertainty as to their role in transmitting TB in cattle, but recently gathered isolates demonstrates all 3 species connected in the epidemiology.

Movements of undetected infected cattle remains a source of infection in Oxfordshire, albeit in less than half of the incidents. Evidence of purchased infection may have been over-estimated in the past, however the movement algorithm provides a more nuanced assessment of this risk. There were only a few incidents where cattle were moved long distances, or direct movements of purchased reactors could be confirmed. The relative reduced weight of this pathway in Oxfordshire is likely due to the decreased prevalence of TB in HRA counties (which is the main source of cattle), changes in cattle buying practices

towards lower risk herds, and conversion and approval of some beef fatteners to non-grazing AFUs.

Residual cattle infection remains an important factor and reflects the tendency of incidents in Oxfordshire to be more chronic and re-occurrent. This source remains a factor in local reservoir infections, and becomes more complicated when herds are infected with multiple sources, some of which become residual within the herd. Systematic deployment of supplementary interferon gamma testing since 2018 has increased the overall sensitivity of testing in herds sustaining OTF-W TB incidents, and has reduced the likelihood of infection being left in the herd at the end of a TB incident. However, the use of this test has been limited in the last year and targeted to those herds with re-occurrent and persistent incidents in Oxfordshire. Distinguishing source attribution between badgers and residual infection in re-occurrent incidents is difficult and is likely a combination of both factors. Similarly, purchased and local wildlife infection are not mutually exclusive and can be indistinguishable, particularly when both sources share the same local clade of *M. bovis* and are both contributing to infection within a herd.

Other sources of infection such as contiguous cattle-to-cattle spread from neighbouring premises are considered unlikely, because of adequate separation and farmer awareness to avoid nose-to-nose contact between their cattle and neighbouring cattle. Potential fomite sources such as contaminated shared machinery and manure or slurry spread near livestock farms are challenging transmission pathways to identify and verify, and none were suspected or investigated in 2022.

New TB incidents in 2022 occurred mainly where clusters of incidents were reported in previous years (Figure 10).

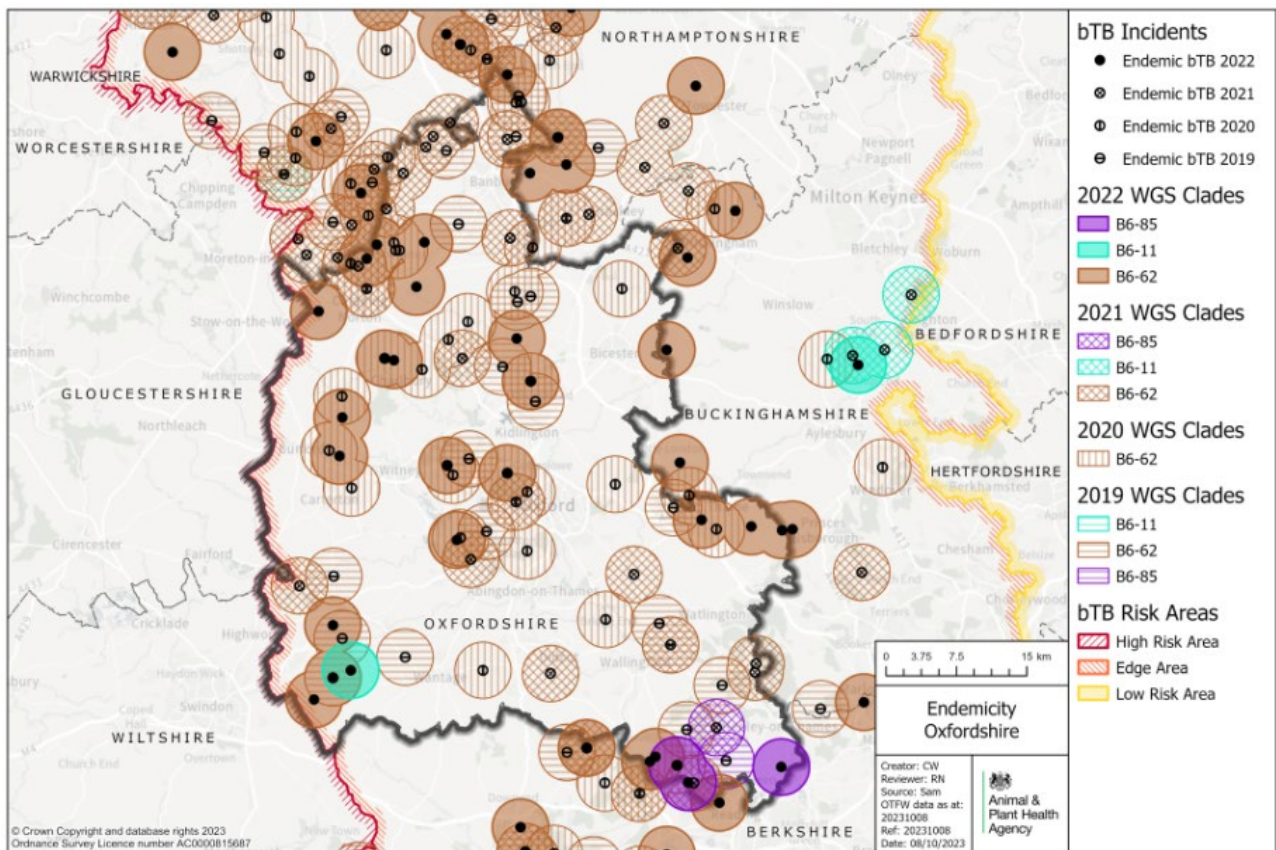


Figure 10: WGS clades of *M. bovis* detected in Oxfordshire between 2019 and 2022, where the WGS identified in the infected herd was within 3 SNPs of another TB incident in the past 4 years and 9km (OTF-W incidents only).

Forward look

The number of herd incidents of TB per year in Oxfordshire remained high over the last 5 years with a decreasing trend starting only relatively recently. The epidemiological picture has become more complex in recent years with multiple clusters, some of which have only recently become apparent. This does not favour the long-term objective of reducing OTF-W incidence to less than 1% in Oxfordshire by 2025.

Early detection of infection through more frequent surveillance testing of cattle herds, alongside the use of mandatory IFN- γ blood testing on all OTF-W incidents, has helped to reduce the spread of TB within herds and should not be limited.

As shown in this report, APHA have identified a number of ‘clusters’ of TB infection in Oxfordshire. To tackle these areas of genetically-linked infection, Defra have launched the ‘Oxfordshire Cluster Project’, starting in 2 areas (North-West Oxfordshire and Thame-Chinnor), formally from 1 October 2022. The project aims to give local farmers, veterinary practices, and other stakeholders the responsibility for design and delivery of locally

tailored supplementary TB control measures in their area. It is supported, facilitated, and funded by Defra and will draw on previous, similar projects' successes.

This project has highlighted the lack of wild deer surveillance, which it is trying to improve via targeted training of farmers and stalkers, facilitating reporting of suspected tuberculous deer carcasses, gathering information on wild deer populations, and potentially estimating the prevalence of TB in such populations in the future. Cattle contact with wild deer as well as badgers has been reported in some clusters supported by camera surveillance and increase in numbers.

Defra will assess the project after a year. If it proves effective and the interest and involvement of stakeholders is retained in the area, it is likely to continue for up to 5 years. Ultimately, Defra would like to assess if this approach is replicable in different areas of the country with other genetically-linked clusters.

Increased knowledge and implementation of on-farm biosecurity, better informed purchasing of cattle, continued cattle surveillance, and continued wildlife intervention in the form of badger culling or vaccination are paramount to stop the spread of TB within Oxfordshire and across into neighbouring counties and the Low Risk Area (LRA) over the next few years.

Appendix 1: cattle industry demographics

Table 1: Number of cattle herds by size category in Oxfordshire as of 31 December 2022 (RADAR data).

Size of herds	Number of herds in Oxfordshire
Undetermined	5
1 to 50	180
51 to 100	84
101 to 200	90
201 to 350	46
351 to 500	23
Greater than 500	22
Total number of herds	450
Mean herd size	138
Median herd size	73

Table 2: Number (and percentage of total) of animals by breed purpose in Oxfordshire as of 31 December 2022.

Breed purpose	Number (and percentage of total) cattle in Oxfordshire
Beef	44,858 (72%)
Dairy	13,990 (22%)
Dual purpose	3,202 (5%)
Unknown	4 (0.006%)
Total	62,054

Appendix 2: summary of headline cattle TB statistics

Table 3: Herd-level summary statistics for TB in cattle in Oxfordshire between 2020 and 2022.

Herd-level statistics	2020	2021	2022
(a) Total number of cattle herds live on Sam at the end of the reporting period	564	531	517
(b) Total number of whole herd skin tests carried out at any time in the period	831	822	815
(c) Total number of OTF cattle herds having TB whole herd tests during the period for any reason	406	407	430
(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)	467	454	446
(e) Total number of cattle herds that were not under restrictions due to an ongoing TB incident at the end of the report period	491	475	469
(f.1) Total number of new OTF-S TB incidents detected in cattle herds during the report period (including all Finishing Units)	25	25	25
(f.2) Total number of new OTF-W TB incidents detected in cattle herds during the report period (including all Finishing Units)	47	32	31
(g.1) Of the new 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?	4	4	n/a (no DRF data for 2022 incidents)
(g.2) Of the new OTF-W herd incidents, how many were triggered by skin test Reactors or 2x inconclusive reactors (2xIRs) at routine herd tests?	24	25	n/a

Herd-level statistics	2020	2021	2022
(g.3) Of the new OTF-W herd incidents, how many were triggered by skin test Reactors or 2xIRs at other TB test types (such as forward and back-tracings, contiguous or check tests)?	17	7	n/a
(g.4) Of the new OTF-W herd incidents, how many were first detected through routine slaughterhouse TB surveillance?	3	2	1
(h.1) Number of new OTF-W incidents revealed by enhanced TB surveillance (radial testing) conducted around those OTF-W herds	0	0	0
(h.2) Number of new OTF-S incidents revealed by enhanced TB surveillance (radial testing) conducted around those OTF-W herds	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)	52	35	30
(j) New confirmed (positive <i>M. bovis</i> culture) incidents in non-bovine species detected during the report period (indicate host species involved)	3	3	2
(k.1) Number of grazing approved finishing units active at end of the period	0	0	0
(k.2) Number of non-grazing approved finishing units active at end of the period	9	9	11
(k.3) Number of grazing exempt finishing units active at end of the period	0	0	0
(k.4) Number of non-grazing exempt finishing units active at end of the period	0	0	0

Table 4: Animal-level summary statistics for TB in cattle in Oxfordshire between 2020 and 2022.

Animal-level statistics (cattle)	2020	2021	2022
(a) Total number of cattle tested in the period (animal tests)	140,053	130,753	129,942
(b.1) Reactors detected by tuberculin skin tests during the year	402	320	362
(b.2) Reactors detected by additional IFN- γ blood tests (skin-test negative or IR animals) during the year	390	351	175
(c) Reactors detected during year per incidents disclosed during year	11.0	11.8	9.6
(d) Reactors per 1,000 animal tests	5.7	5.1	4.1
(e.1) Additional animals slaughtered during the year for TB control reasons (dangerous contacts, including any first time IRs)	21	34	12
(e.2) Additional animals slaughtered during the year for TB control reasons (private slaughters)	2	1	6
(f) Slaughterhouse (SLH) cases (suspect tuberculous carcasses) reported by Food Standards Agency (FSA) during routine meat inspection	7	11	18
(g) SLH cases confirmed by culture of <i>M. bovis</i>	4	8	12

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 incidents reported are submitted for culture analysis. All incidents reported are from any period prior to or during restrictions.

Appendix 3: suspected sources of *M. bovis* infection for all the new OTF-W and OTF-S incidents identified in the report period

In 2022, 11 out of 56 (20%) new TB incidents in Oxfordshire received a preliminary or final APHA veterinary investigation to identify the source of infection. Very few on-farm investigations were undertaken in 2022. The small number of investigations carried out in 2022 was mainly due to the diversion of field resource to the large AI outbreak which occurred in 2021 to 2022.

Each TB incident could have up to 3 potential risk pathways identified. 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)
- possible (score 1)

The sources for each incident are weighted by the certainty ascribed. Any combination of definite, most likely, likely, or possible can contribute towards the overall picture for possible routes of introduction into a herd.

If the overall score for a herd is less than 6, then the score is made up to 6 using the 'Other or unknown source' option. Buffering up to 6 in this way helps to reflect the uncertainty in assessments where only 'likely' or 'possible' sources are identified.

Table 5 combines the data from multiple herds and provides the proportion of pathways in which each source was identified, weighted by the certainty that each source caused the introduction of TB. The output does not show the proportion of herds where each pathway was identified (this is skewed by the certainty calculation). WGS of *M. bovis* isolates can be a powerful tool in identifying a likely source of infection, however WGS clades are not determined for OTF-S herds. As a result of varying levels of uncertainty, only broad

generalisations should be made from these data. A more detailed description of this methodology is provided in the [explanatory supplement for the annual reports 2022](#).

Table 5: Suspected sources of M. bovis infection for the 11 incidents with a preliminary or a final veterinary assessment in Oxfordshire, in 2022.

Source of infection	Possible (1)	Likely (4)	Most likely (6)	Definite (8)	Weighted contribution
Badgers	0	7	4	0	50.5%
Cattle movements	2	5	0	1	31.9%
Contiguous	0	0	0	0	0.0%
Residual cattle infection	1	2	1	0	13.4%
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	0	0	1	0	4.2%
Other or unknown source	0	0	0	0	0.0%

Please note that each TB incident could have up to 3 potential pathways so totals may not equate to the number of actual incidents that have occurred.



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