Animal &
Plant Health
Agency

Bovine tuberculosis in Great Britain in 2023

Explanatory Supplement to the annual TB surveillance reports

September 2024

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Any enquiries regarding this publication should be sent to us at:

Department of Epidemiological Sciences
Animal and Plant Health Agency
Weybourne Building, Level 2, Area F
Woodham Lane, Addlestone, Surrey, KT15 3NB
National.TBEpi@apha.gov.uk
www.gov.uk/apha

Contents

Preface

This Explanatory Supplement is produced to support annual reports that describe the surveillance data and epidemiology of bovine tuberculosis (TB) in Great Britain (England, Scotland and Wales), specifically the reports titled:

- Bovine tuberculosis in Great Britain-Surveillance data for 2023 and historical trends'; referred to as the '2023 GB TB data report'

- Bovine tuberculosis in England 2023: Epidemiological analysis of the 2023 data and historical trends'; referred to as the '2023 England TB Epi report'

- Bovine TB epidemiology reports 2023 for counties in the Edge Area and Low Risk Area of England; referred to as the "2023 Edge Reports" or "2023 LRA Reports".

The content of this explanatory supplement is derived from explanatory text provided in previous annual reports to describe data, methodology and definitions and is updated where appropriate. It is split into four sections:

1. Background of TB in Great Britain
2. Methodology for the TB reports
3. Overview of TB Testing in Great Britain
4. Policies for TB Control in Great Britain

1. Background of TB in Great Britain

1.1. Overview of TB transmission pathways

In Great Britain the main species infected with *Mycobacterium bovis*, the bacterium that causes bovine tuberculosis (TB), are domestic cattle and wild badgers. Figure 1.1 shows the simplified TB transmission pathways involving cattle and badger populations in terms of the spread of the disease.

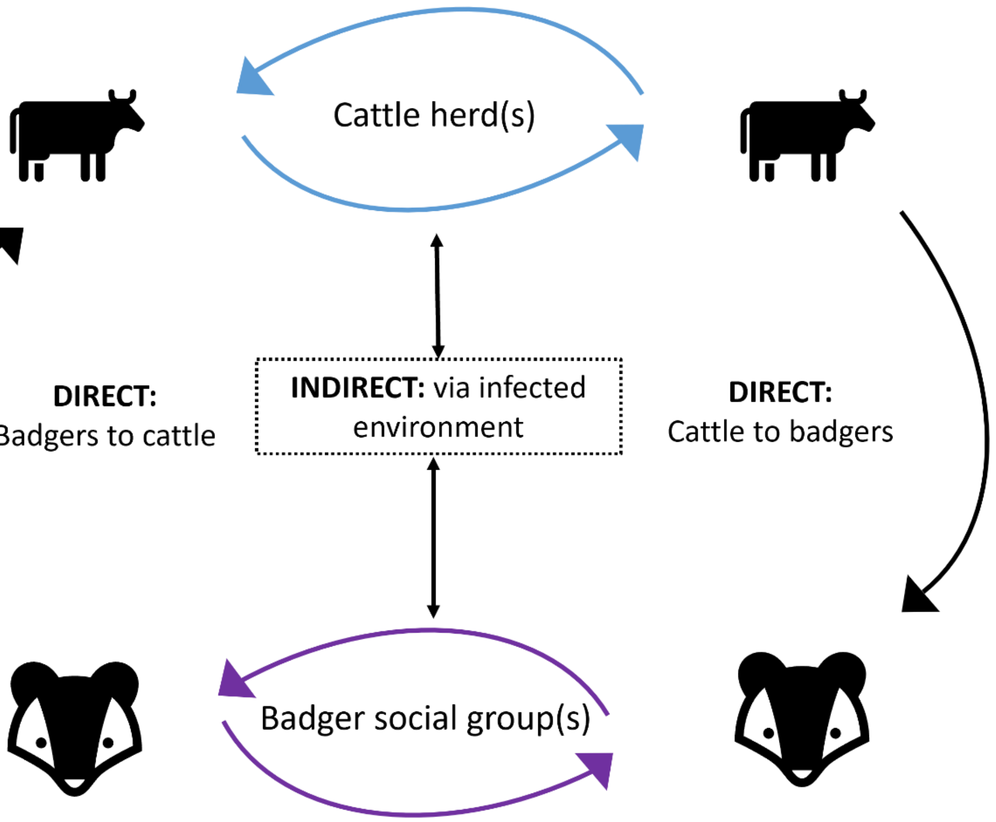

Figure 1.1 Simplified potential TB transmission pathways involving cattle and badgers

Figure 1.1 Caption: Diagram showing the potential pathways between cattle and bagders. On the top row there are two silhouettes of cows, with the text “Cattle herds” between them, and blue arrows pointing to each cow to show transmission between cows. On the bottom row, there are 2 silhouettes of badgers, with the text “Badger social groups” and purple arrows to show transmission between badgers. On the left hand side, a black arrow points from the badger to the cow, with text that says “Direct: badgers to cattle” to show transmission between badgers and cows. On the right hand side, a black arrow points from the cow to the badger, with text that says “Direct: cattle badgers” to show transmission between cows and badgers. In the middle of the image, a text box with a dashed outline and double headed arrows pointing from the cows to the text (above) and badgers to the text (below) reads “Indirect: via infected environment” to show the two-way transmission between cows, badgers and their environment.

However, there is a wide variety of potential routes in which the bacterium can be transmitted between the two main host species. These may be facilitated by the ability of *M. bovis* to survive in the environment for many months. Figure 1.2 shows the wide range of risk factors and pathways by which cattle can become infected with TB.

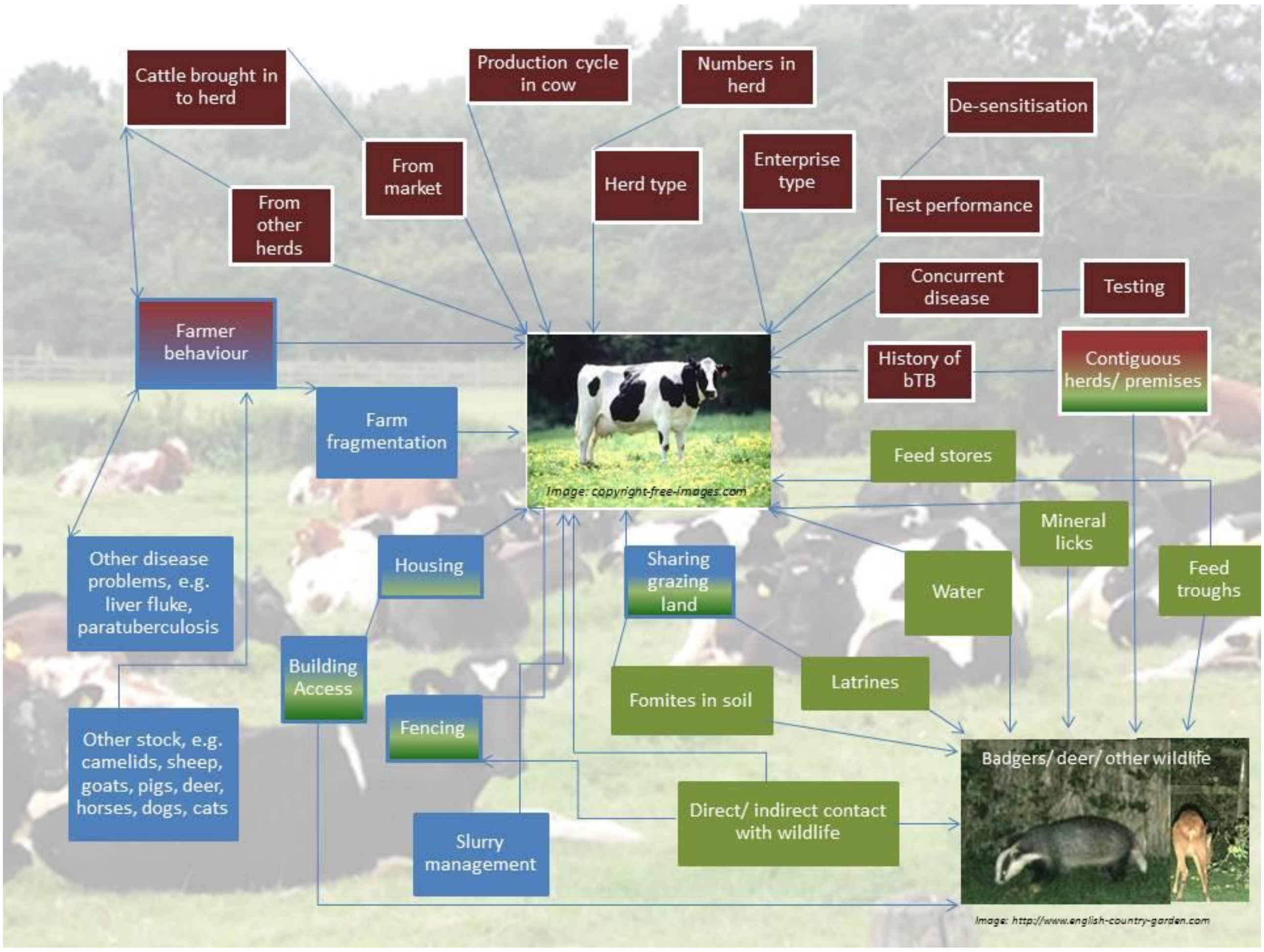

Figure 1.2 Detailed diagram showing TB potential risk pathways

Brown boxes indicate data that can be measured and captured in government datasets. Blue and green boxes represent data that requires knowledge of farm management practices.

Figure 1.2 Caption: A diagram showing the detailed TB transmission risk pathways. A small image of a cow in in the centre of the figure, and a small picture of a deer and a badger together in a field is in the bottom right hand side of the figure, surrounded by text boxes coloured in blue, green and brown. Text in brown boxes all point to the image of the cow, representing data that can be measured and captured by government datasets. Variables in the blue and green boxes point to both the image of the cow and the other wildlife, representing variables which require knowledge of farm management practices. Brown boxes show cattle brought into the herd (via market or private purchase), the cow's production cycle, the cow herd (type and number), the enterprise type, de-sensitisation to testing and the test performance, concurrent disease, and history of TB. Blue boxes show farmer behaviour, other diseases infecting the cattle, other animal stock held on the farm, housing, building access, slurry management, fencing and grazing land. Green boxes include feed stores, feed troughs, mineral licks, water, latrines, soil fomites, and direct/indirect contact with wildlife. More detail is stated in the text.

Most of the brown box variables in Figure 1.2 can be determined remotely from government datasets, such as assessing cattle movements using the Cattle Tracing System (CTS). However, some movements are not reported, such as movements within 10 miles between premises under the same ownership. The numbers of cattle in the herd are variable and herd size is affected by changing management practices during the year. These changes arise from expansion, loss to disease or maintaining a varied genetic pool. They also include 'ad hoc' management practices that are not captured by remote systems, such as varying the composition of the different epidemiological groups. Herd and enterprise types and concurrent disease can be difficult to establish remotely and are subject to change. Test performance depends on both, test characteristics (such as individual vs group level), but also on correct application and interpretation. History of TB and testing records are readily available (although reliability is dependent on the quality of data entry). The presence of contiguous neighbours can be assessed using land ownership data, but this can obscure differences between ownership and use of the land.

The variables in green and blue boxes depend on knowledge of farm management practices. These can often only be established through farm visits and by direct contact with the farmer. Geographic Information Systems (GIS) can help define the extent of farm fragmentation; however, it is difficult to provide certainty with data and methodology when applied to a large number of herds.

It should be noted that the risk pathways outlined in Figure 1.2 are potential risk pathways and as such, are dependent on the level of exposure to the hazard on a particular farm.

1.2 Glossary and definitions used for TB control

Detail	Abbreviation	Definition or description
Animal and Plant Health Agency	APHA	The Animal and Plant Health Agency (APHA) was created on the 1 October 2014 following the merger of the former Animal Health and, Veterinary Laboratories Agency, Plant and Bee Health, Egg Marketing Inspectorate, and the Plant Varieties and Seeds Office. This created a single agency responsible for animal, plant and bee health in Great Britain.
Annualised	N/A	Conversion of a variable into a yearly sum (for example, by multiplying a quarterly incidence by 4).
Approved Finishing Unit	AFU	A type of TB unit approved by APHA providing an outlet for the finishing of negative-testing cattle from multiple TB restricted herds. Cattle in AFUs are permanently under TB movement restrictions (TB02) and can only be moved to slaughter or another AFU. Cattle in the unit are exempt from routine TB testing. Animals may also be sourced from multiple unrestricted premises in any area of England, Scotland and Wales. AFUs without grazing are located in the HRA and Edge Area in England, and the High TB Areas in Wales.
Approved Finishing Unit (Enhanced)	AFUE	A new type of approved finishing unit with grazing providing an outlet for the finishing of negative-testing cattle from multiple TB restricted and unrestricted herds. Animals must have two consecutive negative skin tests before being allowed out to graze on the holding. Animals are on the AFUE are tested at regularly 90-day intervals until slaughter. AFUEs are in operation in the High Risk Area (HRA) of England only.

Detail	Abbreviation	Definition or description
Backwards Recurrence	N/A	The percentage of TB incident herds in the current reporting year that had sustained a TB incident in the previous 3 years (backward-looking recurrence)
Bovine tuberculosis	TB	Disease of cattle, water buffalo, bison and other bovines and mammals caused by infection with '*Mycobacterium bovis'*
Breakdown	N/A	See 'TB incident'
Case	N/A	See 'TB incident'
Compensation	N/A	The statutory payment made by the competent authority to the owner of the animals that have been culled for TB eradication purposes. There are different statutory compensation systems for cattle slaughtered in England, Scotland and Wales.
Contiguous herd	N/A	Strictly speaking, a holding that has a common boundary with the holding of interest, but includes herds separated only by a short distance (such as across a road or river), or where an epidemiological assessment indicates there is likely to be risk of exposure to infection.
Direct (or dangerous) contact	DC	A non-reactor animal in an OTF-W TB incident herd considered to be at such high risk of infection that its slaughter is justified. Usually for the reason of being in close and prolonged contact with infected cattle.
Disclosing test	N/A	The non-negative test that initiates of a new TB incident, which in turn marks the start of movement restrictions (loss of OTF herd status). Includes TB incidents triggered by a laboratory-confirmed slaughterhouse case.

Detail	Abbreviation	Definition or description
Earned recognition	ER	A scheme that allows lower-risk herds in 6-monthly routine surveillance areas of England to qualify for annual testing if they meet certain conditions: Earned recognition for lower risk herds in six-monthly testing parts of the Edge Area - Bovine TB | TB Hub
Eradication Programme	N/A	A programme aimed at achieving biological extinction of an animal disease or zoonosis, to obtain the free or officially TB free status of the territory, or both.
Fomites	N/A	Objects or materials which could potentially carry an infectious agent, such as purchased feed or bedding, vehicles or shared equipment or machinery. More commonly a problem in other animal diseases (such as AI, FMD, Salmonella)
Forward recurrence	N/A	The percentage of all herds with a history of TB that went on to experience a TB incident in the current reporting year, compared to the percentage of all herds without a history of TB that went on to have a TB incident in current reporting year (forward-looking recurrence).
Genotype	N/A	A unique DNA type or 'strain' of *Mycobacterium bovis*, defined by a combination of spoligotype (expressed as a number) and VNTR type (expressed as a letter). This information is used to characterise the molecular epidemiology of the TB bacterium in GB. Genotyping of *M. bovis* isolates from cattle and other susceptible animal species supported APHA epidemiological investigations into the origin of individual TB incidents. It was replaced by whole genome sequencing (WGS) and WGS clade types in April 2021.

Detail	Abbreviation	Definition or description
Interferon-gamma test	IFN- γ or gIFN or IFN-gamma	An official laboratory-based blood test of cellular immunity against the bovine TB bacterium that measures the amount of the cytokine (immunological messenger molecule) IFN-γ released by the lymphocytes in blood samples from *M. bovis*-infected cattle, when they are stimulated with tuberculin in vitro. It is used to supplement the skin test in certain TB incident herds (mainly as a parallel test for improved sensitivity), rather than as a standalone screening test of unrestricted (OTF) herds.
Herd	N/A	An animal or group of animals kept on a holding as an epidemiological unit. In GB they are identified with a County Parish Holding Herd (CPHH) number.
Herd size	N/A	For a TB incident, herd size is the largest size entered into Sam (see 'Sam') for a test conducted at any time during the incident. For officially TB free herds, herd size has been changed in 2017. Median size is now recorded on the British Cattle Movement Service (BCMS) Cattle Tracing Scheme for the holding over the most recent 12 months with a recorded size. For holdings with more than one herd, or not present in BCMS, the herd size at the most recent whole herd test was recorded. Where no size is retrievable from either source the typical number of animals indicated on Sam has been used. The drive to change to using CTS was to reduce the numbers of both: • those without a retrievable size from the testing history and • those where recent tests presented no eligible stock

Detail	Abbreviation	Definition or description
Herd test	N/A	A surveillance or control test triggered by a herd-level event. In contrast to a test triggered for an individual animal or a small group of animals within a herd.
Herd types	N/A	‘Beef’ includes Beef, Suckler, Beef Heifer Rearer, Beef Bull Hirer, Beef dealer, Stores herds and Meat Buffalo herds; ‘Beef fattener’ or ‘Beef finisher’ includes beef finishing herds; ‘Dairy’ includes Dairy, Dairy Dealer, Dairy Bull Hirer, Dairy Producer, Dairy Heifer Rearer, Producer Buffalo and Domestic herds; ‘Other’ includes Calf Rearers, unspecified Dealer Herds, Artificial Insemination (AI), Bison and herds described on Sam as ‘Other herds’.
Herd-years at risk	HYR	The total amount of time (in days, months or years) that herds in the geographical area of interest remain unrestricted (OTF). Herds that have received a herd-level test during the period of interest are at risk of a new incident.
Holding	N/A	A place where livestock, including cattle, are kept or handled in pursuit of an agricultural activity. It may be a farm, or other premises such as a market, lairage, abattoir or showground. Some keepers may have more than one holding, and some holdings may be used by more than one keeper. A holding is not the same as a business. It is identified by a unique County Parish Holding (CPH number) and a single holding may comprise of one or more herds.

Detail	Abbreviation	Definition or description
Homerange	N/A	The geographical area in which a particular whole genome sequencing clade of *M. bovis* is typically recovered from infected cattle herds. A 5-kilometre square is considered as part of a certain homerange if there have been three different incidents of that clade, on at least 2 holdings, within a 5-year window. To create coherent areas for each clade, a 10-kilometre buffer is then drawn around each of the homeranges so defined.
Incidence	N/A	The incidence of a disease is the rate at which new cases occur in a defined population over a a certain period of interest.
Inconclusive reactor	IR	An animal showing a particular pattern of reactions to a comparative intradermal tuberculin test. The difference in size of reactions to bovine and avian tuberculin is not large enough to cause it to be described as a reactor. Such animals are usually isolated and subjected to a second skin test after 60 days. However, they can be removed earlier as DCs (see 'DC'), IFN- γ test reactors (see 'Gamma interferon test'), or voluntarily slaughtered by their owner.
Inter-quartile range	IQR	A measure of statistical dispersion equal to the difference between the upper and lower quartiles (the 75th and 25th percentiles of the distribution's values).
Laboratory Information Management System	LIMS	APHA TB laboratory information management system used to record tissue samples submitted to the APHA laboratory and the outcome of their testing.

Detail	Abbreviation	Definition or description
Licensed Finishing Unit	LFU	A type of TB unit approved by APHA providing an outlet for the finishing of negative-testing cattle from multiple officially TB free (OTF) herds. LFUs are permanently under TB movement restrictions (TB02), and cattle are housed under biosecure conditions. Cattle in the unit are exempt from post-movement TB testing, providing the statutory pre-movement testing requirements have been met. Animals may be sourced from multiple unrestricted premises in any area of England, Scotland and Wales. LFUs can only be set up in the Low Risk Area (LRA) of England and the Low TB Area of Wales.
Linear regression	N/A	A statistical approach for modelling the relationship between a continuous outcome variable (such as duration of restrictions, which can take any value) and one or more 'predictor' variables (such as herd size, herd type or county).
Live herd or Active herd	N/A	A herd of cattle, farmed buffalo or farmed bison defined in the CPHH notation which was "live" (not archived), flagged as active on Sam on 31 December, 2023. This gives different values from the Agricultural Census, which is at holding level and updated at a different point in time.
Logistic regression	N/A	A statistical approach for modelling the relationship between a binary outcome variable (such as positive or negative result) and one or more 'predictor' variables (such as herd size, herd type or county).

Detail	Abbreviation	Definition or description
Monitoring (programme)	N/A	A programme to investigate an animal population or subpopulation, its environment (including wild reservoir and vectors), or both. This helps to detect changes in the occurrence and infection patterns of an animal disease or zoonosis.
Movement restrictions or restrictions	N/A	Legal prohibitions or restrictions on the free movement of animals into and out of a herd. Movement restrictions may be imposed on a herd because of the presence, or the suspected presence, of *M. bovis* infection. They may also be placed if statutory tests are overdue, leading to the loss of Officially TB Free herd status (see below). They can also be imposed if IRs are disclosed in a herd with a history of OTF-W incidents in the previous three years. Herd restrictions triggered by overdue tests are excluded from analyses in this report to avoid overestimates of disease.
Mycobacterium avium	*M. avium*	The causative organism of avian tuberculosis, which occasionally infects cattle.
Mycobacterium bovis	*M. bovis*	The causative organism of bovine tuberculosis.
New TB incident	N/A	A herd newly found to be infected with TB. Defined as a herd previously OTF in which at least one test reactor, IR taken as a reactor, or a culture-positive slaughterhouse case, has been found. The restriction, and thus the incident, starts on the disclosing test date (or date of slaughter of the slaughterhouse case). To qualify as being ‘new’, the incident must have been ‘disclosed’ (discovered) in the period specified in the report. The incident ends on the date the TB10 form is served and restrictions are lifted. (see also ‘TB incident’)

Detail	Abbreviation	Definition or description
Non-visible lesions	NVL	No lesions typical of bovine TB could be detected in the carcass at 'post mortem' examination in a laboratory or meat inspection in a slaughterhouse.
Officially bovine tuberculosis free status	OTF	A bovine herd in which infection with *M. bovis* is not suspected, is up to date with all its TB testing and as such is able to trade animals freely. See WOAH Terrestrial Code Article 8.11.6 for a full definition of the officially TB free status.
Officially bovine tuberculosis free status suspended	OTF-S	For the purposes of this report, OTF-S is the status of a herd with a TB incident where there is suspicion of infection being present. A TB incident that did not meet the conditions for an OTF-W incident (see below) is classified as an OTF-S incident.
Officially bovine tuberculosis free status withdrawn	OTF-W	Refers to a herd with a TB incident where additional evidence of *M. bovis* infection has been identified in at least one slaughtered bovine animal. This means having either *M. bovis* identified in a cultured tissue sample, lesions detected in the carcass of a SICCT or IFN-γ test reactor, or both. In Wales, all herds experiencing a new TB incident are designated OTF-W by default – see section 4.3.1 for more details.
Orange markets	N/A	Dedicated sales for TB-restricted cattle that are destined for slaughter or an AFU. They can only be approved by APHA in the HRA and Edge Area of England (and since 1 January 2021, in the High TB Areas of Wales).
Persistent TB incident	N/A	Refers to a TB incident that has lasted for at least 550 days (approximately 18 months).

Detail	Abbreviation	Definition or description
Poisson regression	N/A	A type of statistical modelling based on a particular type of numerical distribution. Used to compare rates of rare occurrences between different population groups, different areas, or different times.
Post-mortem or ‘post mortem’ examination	PME	Systematic veterinary (examination?) of the carcass and organs of slaughtered cattle for lesions typical of bovine TB, usually undertaken at an APHA Regional Laboratory. When it is performed in the slaughterhouse by a meat inspector working under the supervision of an official veterinarian, following suspicion of infection (such as reactors, IRs and DCs), or during routine commercial slaughter, it is referred to as post-mortem meat inspection (PMMI).
Pre-movement TB testing	PrMT or PRMT	Mandatory skin testing for cattle aged over 42 days old moving out of a herd that is subject to annual or six-monthly TB surveillance, subject to some exemptions (such as animals moved to a slaughterhouse or an AFU). Also for cattle moved out of herds in the LRA to Scotland, unless the animal had spent its entire life in the LRA.
Prevalence	N/A	The prevalence of disease is the proportion of a defined population affected by that disease at a designated point in time.

Detail	Abbreviation	Definition or description
Reactor	R	An animal showing a positive reaction result to a single intradermal tuberculin comparative cervical (SICCT) test, or to an interferon-gamma (IFN-γ) test, which is consistent with it being infected with *M. bovis*. This does not include an animal first suspected to have TB at the slaughterhouse. An animal that tests twice as inconclusive reactor to the SICCT test is automatically classified as a reactor. However, this will not count towards statistics for reactors throughout these reports.
Recurrent herd incident	N/A	A herd with a TB incident disclosed in the reporting year (2023) also under movement restrictions for a different TB incident in the previous 36 months.
Reference category	Ref	In regression analyses the reference group acts as a baseline against which other groups of interest are compared.
Reservoir	N/A	The reservoir is the population of animals in which the disease is circulating, and therefore is a common source of infection to other animals or humans.

Detail	Abbreviation	Definition or description
Risk Area or Surveillance Risk Area or Surveillance Area or TB Area	N/A	Since 1 January 2013, TB testing intervals for bovines in England are 6-monthly, annual or 4-yearly at county level. The Strategy for achieving Officially Bovine Tuberculosis Free status for England (April 2014) set out 3 risk surveillance areas, which are followed in this report: High Risk area (HRA – six monthly routine surveillance testing by default since 2022), Edge area (annual or 6-monthly testing) and Low Risk area (LRA – 4-yearly testing for most herds). In 2017 Wales adopted a regionalised approach to TB distinguishing five TB areas as per the Wales Bovine TB Eradication Programme. These were Low TB Area, Intermediate TB Area North, Intermediate TB Area Mid, High TB Area West and High TB Area East.
Sam	N/A	APHA's IT system and database, which records, for example, details of herds, TB tests, TB incidents and the details and results of any tested and slaughtered cattle.
Sensitivity (of a test)	Se	The proportion of truly infected individuals in the screened population that are correctly identified as infected (positive) by the test.

Detail	Abbreviation	Definition or description
Severe interpretation	N/A	The positive cut-off criterion used to interpret the results of the comparative tuberculin skin test (SICCT) in TB incident herds to achieve a greater sensitivity. Using this test interpretation, animals are deemed TB test reactors if they show either: • a positive bovine reaction and negative avian reaction • a positive bovine reaction more than 2mm greater than a positive avian reaction
Short Interval Test	SIT	See 'Test code definitions'
Single intradermal comparative cervical tuberculin (test)	SICCT	Also commonly referred to as the 'skin test' or 'tuberculin skin test'. The test involves the simultaneous injection of a small amount of *M. bovis* and *M. avium* tuberculins into two sites on the animal's neck skin. These are purified protein derivatives (PPD), a crude extract of bacterial cell wall antigens. Any swelling which develops at the injection sites after 72 hours are then comparatively measured to assess positivity (delayed-type hypersensitivity reaction).
Slaughterhouse case	SLH	An animal displaying lesions consistent with TB during routine post-mortem meat inspection in the slaughterhouse. If *M. bovis* can be detected by PCR testing or bacteriological cultures from samples of the lesions, the slaughterhouse case triggers an OTF-W incident. Pending the PCR test or culture results, a slaughterhouse case remains suspected and the OTF status of the herd of origin is suspended, but it does not contribute to the incident figures within this report. This is unless any subsequent skin check test performed in the herd of origin identifies reactors.

Detail	Abbreviation	Definition or description
‘Smoothed’ or ‘12-month moving average’	N/A	A 12-month moving average is the average of the values for the current month and the previous 11 months. Moving averages can be any length. But, in general, shorter lengths will be best at identifying turning points and longer lengths best at identifying trends.
Specificity (of a test)	Sp	The proportion of truly uninfected individuals in the screened population that are correctly identified as uninfected (negative) by the test.
Spoligotype	N/A	The result of one molecular technique used for genomic typing of organisms of the *Mycobacterium tuberculosis* complex, known as Spacer Oligonucleotide typing. Spoligotype and genotypes were replaced by whole genome sequencing clades in April 2021.
Standard deviation	SD	The standard deviation measures the spread of the data around the mean value. It is useful in comparing sets of data which may have the same mean but a different degree of variability in raw values.
Standard interpretation	N/A	The positive cut-off criterion normally used to interpret the results of a skin test. Using this interpretation of the SICCT, animals with a positive bovine reaction over 4mm greater than a negative or positive avian reaction are reactors.
Surveillance	N/A	Surveillance refers to activities to collect and record data on specific diseases in defined populations over a period of time. This helps to assess the epidemiological evolution of the diseases and the ability to take targeted measures for control and eradication.

Detail	Abbreviation	Definition or description
Surveillance Streams Definitions	N/A	Area & Herd Risk: Disease first disclosed due to tests carried out in light of any evidence that there is a higher probability of disease in the animal or herd. Trade and Other: Disease first disclosed as a result of testing scheduled due to the high impact of disease if present in the destination herd or premises. Includes tests on animals where the presence of some epidemiological risk factors may increase disease probability but this is not the primary reason for testing. Routine: Disease first disclosed as a result of tests scheduled as part of routine surveillance with no expectation of increased or decreased probability of disclosing infection. Slaughterhouse (SLH) Surveillance: Disease first disclosed during routine post-mortem meat inspection of animals not believed at higher likelihood of being diseased. Excludes results of inspection of reactor cattle.
TB area	N/A	There are three TB areas (High Risk Area, Edge Area and Low Risk Area) in England based on the distribution and incidence or prevalence of TB within England.
TB incident	N/A	A herd that has been categorised as infected with bovine tuberculosis is called a TB infected herd, and the event is called a ‘TB incident’. Also referred to as a ‘breakdown’ or ‘case’. The criteria that determine this are given under the definition of a ‘new TB incident’ above.
TB10 form or notice	TB10	A notice served at the end of a TB incident to lift the restrictions imposed on cattle movements onto and off the holding. It restores the OTF status of the herd.

Detail	Abbreviation	Definition or description
Test code definition: Hotspot Test	HS	Carried out on herds within a confirmed TB Hotspot area in England. All bovines except calves under 42 days of age are included.
Test code definition: Private Test	PRI	A test carried out on individual animals. This is commissioned and paid for by the owner and carried out by an OV with the Regional Veterinary Lead (RVL) agreement. An example of this is the use of an extra TB test in a breeding bull.
Test code definition: Radial Test	RAD	Carried out on herds within a 3 km radius of herds that have had their Officially Tuberculosis Free status withdrawn (OTF-W) in the Low Incidence Area or in the parts of the Edge Area on annual testing (England only). The initial RAD test is followed by a RAD6 test 6 months later and, in the LRA only, by a RAD12 test 12 months after the RAD6 test. All bovines except calves under 42 days of age are included.
Test code definition: Routine Herd Test	RHT	Routine surveillance herd test carried out in parishes with a 48-month testing interval. It must include: • breeding bulls (for example, entire males over 12 months) • females which have calved • young bovines which will be used for breeding whether they are home-bred or purchased (except calves under 6 weeks old) • pet cows and other non-commercial cattle resident on the holding

Detail	Abbreviation	Definition or description
Test code definition: Short Interval Test	SI Test or SIT	Carried out in breakdown herds 60 days after removal (or effective isolation) of the last reactor or from a previous short interval test with no reactors. In England, they include all bovines except calves under 42 days old (unless there is an epidemiological risk of infection within that age group). They include all bovines in Scotland and Wales.
Test code definition: Whole Herd Test	WHT	Carried out routinely every 12 months in annual testing areas and in individual herds requiring annual testing, for example producer-retailer dairy herds, bull hirers, heifer rearers, city or open farms, AI centres. It can also be carried out via RVL discretion in 48 month testing areas. It includes all bovines except calves under 6 weeks old.
Testing interval	N/A	Testing interval for routine TB surveillance purposes. In England the interval is either every 6 months, one or 4 years, depending on the policy applied to the risk area. In Scotland it has always been four years, and annual in Wales since 2010. Testing interval is given by the Area Testing Interval (ATI), Area Monitoring Regime (AMR), or the Unit Monitoring Regime (UMR) to which individual herds are allocated by APHA. In Wales, the ATI is recorded for the third quarter of the year in question, irrespective of whether the herd was tested in that year. Any shorter interval assigned specifically to an individual herd within a parish has not been used.
Time at risk	TAR	Time spent not under restriction since the most recent herd-level test. Alternatively, end of incident and time at risk of being diagnosed with TB during the observation period.

Detail	Abbreviation	Definition or description
Tracing tests	N/A	Tests carried out to ‘trace’ the potential source or spread of infection. ‘Backward’ tracings, also known as ‘source tracing’ tests investigate where infection may have originated, such as the herd of origin of purchased cattle suspected of being infected when they arrived. ‘Forward’ tracings, also known as ‘spread tracing’ tests, check individual animals that have left the herd when infection was believed to be present. This is to determine whether they are infected and may have carried infection to their destination herd(s).
VetNet database	VetNet	VetNet is the predecessor of Sam, APHA’s TB control and surveillance system. Data was migrated into Sam from VetNet when Sam was launched in 2011.
Visible lesions	VL	Lesions typical of bovine TB detected in the carcass of a SICCT or IFN-γ test reactor at post-mortem examination or meat inspection.
WGS	Whole genome sequencing	Whole genome sequencing (WGS) replaced genotyping on 19 April 2021. WGS determines the entire DNA sequence of *M. bovis* isolates, allowing for characterisation of *M. bovis* strains at a higher resolution than genotyping. This ultimately allows a greater degree of certainty about the origin of TB infection for a herd and increases our understanding of how TB spreads both locally and nationally.
WGS clade	N/A	A group of phylogenetically (for example, evolutionarily similar) related isolates, based on similarities across their whole genome sequences.

2. Methodology used for the TB reports

2.1 Data sources and processing

2.1.1 Source of data

Data on herds, animals, bovine tuberculosis incidents and tests applied to British cattle were downloaded from the APHA Sam RADAR TB reception database on 12 April 2024. Data prior to late September 2011 derives from the old VetNet system, which was decommissioned and migrated into Sam at the end of September 2011. Information relating to culture results of all TB suspect samples exists on Sam. This is derived from the APHA LIMS system for samples from around the time of Sam TB going live. Prior to that, sample information came from the APHA TB Culture System (TBCS), but there was a short cross-over period when both were in use. Apparent missing results on Sam have been retrieved directly from LIMS where possible, particularly during the live launch of Sam TB.

Data are downloaded at least 3 months after the reporting year. This is to capture as many laboratory culture results for incidents commencing in the reporting year as possible. However, this date is too early to capture all events during most of these incidents. An example of this is the dates of removal of movement restrictions from which the duration of incidents is calculated. Therefore, incidents that ended during the reporting year are used to calculate the duration of incidents and the total number of reactors in an incident.

As in previous reports, the old county boundaries that were set in 1974 are used throughout.

In England, outputs are for the most part broken down by the new TB risk and surveillance areas introduced in 2013. From January 2018, part Edge, part HRA split counties were re-classified as fully Edge Area. These include Cheshire, Derbyshire, East Sussex, Oxfordshire, and Warwickshire. Herds in these counties are subject to mandatory interferon gamma blood testing in TB breakdowns with lesion or culture positive animals (or both). Herds in some parts of the Edge Area are subject to 6-monthly routine surveillance testing. These are in all or part of Cheshire, Derbyshire, East Sussex, Hampshire, Oxfordshire and Warwickshire. Others in the Edge Area remain on annual testing supplemented with 3 km radial testing around TB breakdown herds with lesion or culture positive animals (or both).

Considerable effort has been made to correct as many of the data inconsistencies observed in Sam as possible. As such, we are confident we have used a dataset that is broadly correct. However, there still may be small differences in incident numbers with the National TB Statistics published every month by the Defra statistics team in York. The APHA TB Epidemiology and GB Data Reports and the National Statistics are produced and published in different ways. The APHA Reports are published the following calendar year, whereas the National Statistics data are published three months after data becomes available. A consequence of this prompt publication is that there is less scope to check and clean the data in the National Statistics prior to publication.

In most cases, discrepancies between the APHA reports and the National Statistics are a result of the following issues:

Discrepancies between the disclosing test date and the incident start date

Some TB incidents do have a start date in Sam that lags behind the true disclosing test date. This may result in placing it in a different period in Sam to the APHA reports.

Inaccurate or missing TB10 end of restriction information

Inaccurate or missing TB10 end of restriction information has also been a serious issue within Sam and one addressed since the 2012 report. Revisions in Sam, policy changes and user training have reduced many errors in this respect and the situation is now greatly improved. There are still a very small number of incidents with obviously incorrect or missing TB10 dates which have been or may still be corrected. Closure of incidents involves the receipt of a BT5 form which provides evidence of cleansing and disinfection on the incident premises. This is required before a TB10 can be issued to formally close the incident. Non-receipt or delays in the receipt of the BT5 form will artificially prolong the duration of incidents, should last until the final clearing skin test. Policy introduced late in 2015 has attempted to penalise non-returners of the BT5 and the situation appears to be much improved. A similar delay can also be due to noted discrepancies within the BCMS Cattle Tracing System. If animals observed on the farm do not all match those reported in BCMS, this must be corrected prior to the lifting of restrictions. There are occasionally administrative errors where incidents do not appear on Sam, despite evidence of reactors and short-interval tests occurring in those holdings. These are true new incidents and are counted in the APHA reports but are few.

Incidents removed during data cleansing

There are also additional incidents that are counted by National Statistics but are removed during data cleansing and not represented in the APHA reports. For example, administrative errors where multiple incidents are created simultaneously under the same herd can occur. Herds with culture-negative slaughterhouse cases in which no reactors are found and herds with NVL 1x IRs only are not considered new incidents in this report.

Work is continually conducted to harmonise reporting between APHA Reports and the National TB Statistics. This aims to establish as similar an underlying dataset as possible.

2.1.2 Classification of incidents

Since January 2011, cattle herds in GB have been described by their Official Tuberculosis Free (OTF) status. This can be OTF-W (OTF withdrawn), OTF-S (OTF suspended), or if free from any restrictions, OTF. This terminology is used in surveillance reports.

OTF-S incidents describe herds in which all test reactors failed to disclose visible lesions or positive laboratory results. Other herds without a TB incident can have their OTF status temporarily suspended under the:

- observation of suspect TB lesions in a slaughterhouse during routine post-mortem meat inspection and pending a culture result
- overdue routine tests for a herd

However, such herds do not contribute to OTF-S incident totals in this report. In some figures differentiation is made between OTF-S incidents with 0 to 1 or more than 1 reactor. Few are classed as ‘unclassified’, where no post-mortem results are available.

For this report, OTF-W status refers to a herd with a TB incident in which:

- the presence of tuberculosis is confirmed in at least one animal by a positive laboratory confirmation of *M. bovis* infection
- classical lesions of tuberculosis are seen at postmortem examination in the carcass of at least one test reactor animal from the herd

In January 2022, Wales introduced a new “OTF-W by default” policy. This policy meant any new TB incidents arising from one or more skin test reactors or from two consecutive standard inconclusive reactor results at a skin test were automatically classified as an OTF-W incident in Wales. Previously, herds with a single skin test reactor were classified as OTF-S unless epidemiological assessment establishes the likelihood of infection without post-mortem evidence of infection - these were technically termed OTF-W2, but were not differentiated from OTF-W within these reports.

To qualify as being ‘new’ within the specified period, a TB herd incident must have been disclosed and restrictions imposed within that period.

2.2. Epidemiological Indicators of disease burden

2.2.1 Incidence

Incidence is the rate at which new cases of disease (incidents) occur in a population of interest over a specified period. Successful control of an epidemic should be reflected by a reduction in the probability that new cases will occur. This can be difficult to measure if the infection is mostly subclinical and detection of cases depends on proactive testing of herds at different frequencies. Different approaches can vary values slightly, so it is important to understand the characteristics of the measure being used. Comparing areas over time thus also needs to use the same consistent measures. International notifications of disease status often require a measure of incidence.

The incidence rate used in the National Statistics for Great Britain is the number of new incidents per 100 herd-years at risk (HYR). HYR is the sum of the time (in days, months or years) that herds in the geographical area of interest are unrestricted. The incidence per 100 HYR therefore gives the number of new cases over 100 herd-years. This measure considers the historical testing frequency and the periods that a herd is classified as un-restricted and at risk of infection. Only herds that have a test during the reporting period contribute to the measure. This index is generally considered more accurate for comparing incidence between areas as it accounts for different intervals between tests in herds that other measures do not.

The method for calculating incidence per 100 HYR has been modified from that described by Downs and others..(2012). The numerator is the total number of new TB incidents detected in the year in the area of interest. The denominator is the sum of the time during which all herds in the same area are considered at risk of a TB incident (time at risk). A herd was considered to be at risk of a TB incident between:

a) negative herd tests (herd tests clear of infection)

b) a negative herd test and the disclosure of a TB incident

c) from the end of movement restrictions (date of TB10) after a TB incident to the next herd test

The time at risk is calculated as the total time the herd was not under restriction since the most recent test or end of restrictions before or at the beginning of the year. Only periods of risk that end in the time period for which the rate is being estimated contribute to the denominator. Expressing incidence as TB incidents per 100 herd-years at risk aims to take better account of the opportunity for infection to be detected.

2.2.2 Different incidence measures

Historically, the simple approach of looking at the proportion of all herds with a TB incident in a year (incidence per 100 live herds) was used.

The number of new TB incidents per 100 live (active) herds may be the simplest way to calculate incidence, but it does not account for the different frequency of testing in each area of England. It also neglects the proportion of unrestricted herds that are at risk of a new TB incident. All active herds are in the denominator, but only those tested can be in the numerator.

International notifications of disease status often require a measure of incidence derived from the number of new infected herd incidents per 100 herds tested during the period (crude incidence). This excludes herds that were not tested, where TB is very unlikely to be found.

In 2022, incidence per 100 unrestricted herds tested (UHT) was calculated in addition to incidence per 100 HYR, particularly for surveillance areas that have had a change in testing frequency. In this case, the denominator is calculated as the time herds were without restrictions, but only for the year of interest, rather than accumulated since the last test, as when calculating the time at risk for incidence per 100 HYR.

For example, in incidence per 100 UHT, a herd with no previous history of TB under a single set of restrictions between 1 September and 31 October of a year would contribute TAR up from 1 January until 31 August and then again from 1 November to 31 December.

However, the incidence rate per 100 UHT remains dependent on the proportion of the herd tested overall. TB incidents detected through slaughterhouse surveillance also contribute to the numerator, but not to the denominator.

The 3 different incidence measures tend to give similar temporal patterns. However, in areas with 4 yearly surveillance, the rate per 100 herd-years at risk is usually lower than the other measures due to the larger denominator.

2.2.3 Incidence rate ratios

Incidence rate ratios (IRR) quantifies the difference in disease incidence between different categories of animal or herd. This is the difference between herd size, herd type and risk area, relative to a reference category.

The IRR should be interpreted as a proportional comparison between the reference category incidence rate (the denominator) and the investigated category (the numerator). For example, an IRR of 2.0 means the incidence rate of TB in herds within that category was twice as high as the incidence rate of the reference

category. An IRR of less than 1 represents categories where the incidence rate is lower than that of the reference category.
The reference category chosen for categorical predictors in regression analyses varied – ideally, the reference category was both biologically relevant and had a sufficient number of observations or cases to be statistically sound. However, if the most biologically relevant category had insufficient observations/cases or there was no clear biological advantage in selecting a reference category, then the category with the most observations/cases was chosen.

To investigate the effect of herd type, Poisson regression was used to produce IRRs that adjusted for the effects of herd size and risk area. The adjusted IRRs for the herd size categories and risk regions were very similar to the unadjusted IRRs. As expected, the incidence rate was significantly lower in the Edge Area and LRA compared to HRA, despite adjusting for herd size and type.

2.2.4 Prevalence

Prevalence describes the proportion of herds in an area that are infected at a given point in time. This report presents point prevalence, measured by calculating the proportion of herds under restriction (due to a TB incident) at a given moment. Monthly point prevalence is the number of active herds under restriction divided by the reported number of active herds in the middle of each month. Annual average prevalence is the average of the 12 months within the year. At county level, the prevalence is the number of herds under restrictions divided by the number of total herds at the end of each year.

Herds restricted due to an overdue test rather than a TB incident are not classified as ‘restricted’ in this report. Therefore, estimates of the proportion of herds under restriction will be lower in this report than in the official TB statistics.

2.2.5 Recurrent TB incidents

A recurrent incident is defined as:

- a herd that had a TB incident disclosed in the reporting year
- and has also been under movement restrictions for a different TB incident in the previous 36 months

Recurrence can result from a general increase in incidence. For example, a herd would have a greater probability of a previous TB incident if the past incidence were high.

Recurrence likelihood can be increased if some herds are more likely to have repeated TB incidents than others for particular reasons relating to those herds.

The ‘current period’ refers to the reporting year (2023). The ‘history period’ refers to:

- the 36 months preceding the start date of the incident in the current period
- where no recurrent incident has occurred in a herd, is the 36 months prior to the mid-point of the current period

Analyses included all herds that were considered ‘live’ in the current period (2023), or active at the end of it. Whether the herd was live in the history period (preceding 36 months) was not checked.

Herds under restriction for 4 months or more in 2023 from a TB incident that started in the history period were excluded from analyses. These herds had limited opportunity to become TB incidents since there may have been no further testing in the period following their closure. This 4-month threshold helps to detect any recurrence in herds where restrictions were lifted within the first 4 months of the reporting year.

In recent years, recurrence has been described in terms of the relative risk (RR). This compares herds historically under movement restrictions with a new TB incident in the current year, to herds with no history of restrictions. This is then stratified by risk area, herd type and herd size. The RR divides the herds with a recent history of TB which had an incident in the current year, by those without a recent history of TB, but which also had an incident.

Using this method invites comparisons between the relative risks. However, at every level of each factor the risk to the denominator population is quite different, so comparisons are not strictly valid. This is particularly true for the differences across risk regions. It is also likely to be the case for herd size categories and herd types, which may also be confounded with one another.

Based on these assumptions, it was agreed to recalculate this table using a logistic regression where the outcome would be the odds ratio (OR). This is the odds of a herd with a history of TB having another incident this year, compared to a herd with no history. The OR is a measure of association between an exposure and an outcome. The logistic regression was run on each variable and ‘previous TB incident’ was used as an interaction term. This was to determine if the odds of having a TB incident in the current year were increased where a herd had a history of TB incidents.

Although recurrence is calculable from TB incident data, its cause in any given TB incident is difficult to discern. With surveillance data it is difficult to distinguish between persistent undisclosed (‘residual’) cattle infection from a previous TB incident and a newly introduced infection event.

2.2.6 Spatial extent of endemic TB

To identify the areas of England and Wales that are affected by endemic TB, a definition of endemicity was developed under the Defra-funded research project SE3045. This enables the expansion and retraction of the endemic TB area of GB to be measured over time. It also provides a useful tool for decision makers when reviewing the efficacy and implementation of local TB control measures. A geographical unit is considered endemic if there are at least 3 OTF-W incidents within a 7 km radius within a 2-year period. The geographical unit used to map the expansion and retraction of the endemic area is a 500 by 500 metre grid cell.

This definition was developed through analysis of TB surveillance data and with input from APHA veterinary field staff. It is the most appropriate definition that can be applied on a national level. It is not perfect and will apply better in some areas than in others. For example, small ‘endemic’ TB areas can appear which could be temporary artefacts due to the chosen definition of endemicity. Whilst acknowledging the limitations of this definition, it does provide a generally applicable and reproducible approach for determining the endemic area. The definition may need to be refined in future to reflect changes in the epidemiology of TB over time and to changes to surveillance regimes.

2.2.7 Statistical methods

All statistical calculations were performed in Stata v15.0.

A chi-squared test was performed for comparing years, such as the number of TB incidents in 2022 and 2023. A Fishers Exact test was used if a cell value was less than 5.

The estimated significance probability for the Fisher’s Exact test for 2 x 2 tables with large numbers is taken from Pezzullo (2010). This is generally taken as a two-tailed value.

A z-test was used to compare prevalence between 2022 and 2023.

Incidents rates were compared by analysing the deviation of the incidence rate ratio from 1, using the two tailed significance value.

The median duration of TB incidents was compared using the K-sample equality-of-means test.

The reference category chosen for categorical predictors in regression analyses varied. Ideally the reference category was both biologically relevant and had a sufficient number of observations or cases to be statistically sound. However, if:

- the most biologically relevant category had insufficient observations or cases
- there was no clear biological advantage in selecting a reference category

If those criteria were met, then the category with the most observations or cases was chosen.

In some of the analyses performed, the number of TB incidents may vary depending on when data extraction and analysis were carried out. These variations are generally minor.

2.2.8 Risk pathway assessment

Disease Report Form (DRF) based risk pathway assessment

Assessing how a herd became infected with TB can be challenging. TB is a chronic, infection, usually with a long incubation period. This means that in most animals, clinical signs are only apparent when the disease is fairly advanced. TB is generally disclosed through skin testing (active surveillance) on farm or post-mortem surveillance at the slaughterhouse. The detection of TB in cattle may occur sometime after an animal arrives in a herd. As such, the evidence to establish restrospectively the source and routes of infection for an affected herd (the 'risk pathway') can be difficult to reconstruct. However, clarifying the most likely risk pathway facilitates the use of targeted on-farm biosecurity measures to reduce the risk of reinfection for that herd.

TB incidents (both OTF-W and OTF-S) are investigated to assess the hazard (source of infection) and risk pathway. These investigations follow the set protocol described below. A 'provisional assessment' is made early on during the management of an incident, to help guide and prioritise immediate actions. A 'final assessment' is then repeated when all evidence has been gathered, including post-mortem, animal movement tracing and culture results. The same protocol is used for both provisional and final assessments. However, the final assessment has two added categories of hazard, for the rare cases where infection was ultimately judged not to have been present. These are 'non-specific reaction' and 'anomalous result'.

Refresher training is provided to investigating officers to ensure that, as far as possible, the protocol for risk pathway assessment is applied consistently. In the HRA one third of new incidents are randomly selected for an investigation. The aim is to investigate all new incidents in the Edge Area and LRA. However, resource constraints may exist meaning it is not possible to investigate all TB incidents. Where there are resource limitations, guidance on prioritization is developed and as many new incidents in the risk area as possible are triaged for an investigation visit.

Protocol for risk pathway assessment

The investigating officer assesses all the evidence to identify the likely route by which TB infection entered the holding. Several plausible risk pathways are usually identified. The protocol asks the investigator to use all available evidence plus veterinary judgement, to describe how likely each of the risk pathways are. Up to three risk pathways can be recorded, and each must be scored using the following scale: ‘definite’, ‘most likely’, ‘likely’ and ‘possible’. The investigator must summarise the evidence in support of their selections. They are advised that ‘although it will often not be possible on a particular farm to say for certain how the cattle got infected, consideration of how this may have happened in light of the husbandry practised, biosecurity measures in place, and other findings in the investigation will make some pathways more likely than others.’

Within the TB epidemiology reports, the terms likelihood and certainty are utilised to describe the score ascribed to each risk pathway during the veterinary risk pathway assessment.

Each assessment is comprised of 2 components. The first is a ‘hazard’, which is the original source of infection (for example infected cattle, badgers, other domestic or wild animals). The second is a risk pathway (for example cattle movements from a defined risk area or exposure during housing or at pasture). Additionally, investigators are asked to record which risk pathways have been excluded from the list of options in Table 2.2.8.1 (such as movements on a closed farm or contiguous contact with no neighbouring cattle).

The following table shows how the 28 combinations of hazards and risk pathways selected by investigating officers in 2023 were aggregated. Nine sources of infection were identified and used to present the results of the risk pathway analysis at risk area and county level.

Table 2.2.8.1: Hazards and risk pathways used in the DRF to determine the likely source of infection.

Hazard	Risk Pathway	Source of infection
Infected badgers	Exposure at grazing, where all feed at grazing is inaccessible to badgers	Badgers

Hazard	Risk Pathway	Source of infection
Infected badgers	Exposure at grazing, where feed at grazing is accessible to badgers	Badgers
Infected badgers	Exposure at housing, where all feed is inaccessible to badgers	Badgers
Infected badgers	Exposure at housing, where feed stores are accessible to badgers	Badgers
Infected cattle	Movements from Edge	Cattle movement
Infected cattle	Movements from High TB Area Wales	Cattle movement
Infected cattle	Movements from HRA	Cattle movement
Infected cattle	Movements from Intermediate TB Area Wales	Cattle movement
Infected cattle	Movements from Low TB Area Wales	Cattle movement
Infected cattle	Movements from LRA	Cattle movement
Infected cattle	Movements from NI or other country (imports)	Cattle movement
Infected cattle	Movements from Scotland	Cattle movement
Infected cattle	Contiguous over the fence or straying	Contiguous infection
Infected cattle	Residual infection in the herd	Residual infection
Infected domestic animals	Co-located	Domestic animals
Infected domestic animals	Contiguous	Domestic animals
Anomalous result	Anomalous Result	Non-specific reactor
Non-specific reaction	*Mycobacterium* other than *M. bovis*, or false positive result	Non-specific reactor
Uninfected	No Pathway	Non-specific reactor
Fomites, undetermined source	Contaminated cattle slurry or manure	Fomite source
Fomites, undetermined source	Contaminated purchased feed or bedding	Fomite source
Fomites, undetermined source	Contaminated vehicles	Fomite source
Fomites	Other	Fomite source

Hazard	Risk Pathway	Source of infection
Fomites, undetermined source	Shared equipment or machinery	Fomite source
Other infected wild animals	Other	Other wildlife
Other infected wild animals	Wild Boar	Other wildlife
Other infected wild animals	Wild Deer	Other wildlife
Other or unknown	Rare sources (must specify) or unknown (must explain logic)	Other or unknown

Combining risk pathways and the likelihood score

During the assessment, the APHA case veterinarian selects up to three possible risk pathways of infection for each TB incident herd. Each risk pathway is given a score that reflects the assessed likelihood of that pathway being the true one. The weighting applied to the certainty score was updated in 2019 to reflect the developing understanding of how likelihood is being assessed in practice. It is as follows:

- Definite - score 8
- Most likely - score 6
- Likely - score 4
- Possible - score 1

Any combination of definite, most likely, likely, or possible contributes towards the overall picture for possible routes of introduction into a herd (see example 1).

Example 1 – identification of the potential risk pathways for a TB incident

Source of infection	Certainty	Certainty score	Weighted contribution
Cattle movement	Most likely	6	0.55
Contiguous cattle	Likely	4	0.36
Badgers	Possible	1	0.09
Total herd score	n/a	11	1

If the total herd score is less than six (see example 2), then the score is made up to six using the ‘Other/Unknown Source’ option – see the example 2 (continued) table. Buffering up to 6 in this way helps to reflect the uncertainty in assessments where only ‘likely’ or ‘possible’ sources are identified.

Example 2 – identification of the potential risk pathways for a TB incident with low certainty of the pathway

Source of infection	Certainty	Certainty score
Infected cattle HRA	Possible	1
Infected cattle LRA	Possible	1
Other or unknown	Possible	1
Total herd score	n/a	3

The total herd score is three. As this is less than six, ‘Other or unknown’ gets increased to 4 points, so that the total score is 6. Thus, the final weighted contribution of each risk pathway is as follows:

Example 2 (continued) – risk pathway buffering where there is high uncertainty around the source of infection

Source of infection	Certainty	Certainty score	Weighted contribution
Infected cattle HRA	Possible	1	0.17
Infected cattle LRA	Possible	1	0.17
Other or unknown	Possible	**4**	0.67
Total herd score	n/a	6	1

Interpreting source of infection outputs

The source of infection outputs combine the data from multiple herds. They provide the proportion of pathways in which each source was identified, weighted by certainty, as described above. The outputs do not show the proportion of herds where each pathway was identified (as this is skewed by the certainty calculation). The relative proportions of each risk pathway are approximations and only broad generalisations should be made from these data. Where a greater proportion of OTF-S herds are investigated there will be more uncertainly in the risk pathways, as *M. bovis* is not isolated and genomic evidence is not available.

Data-driven risk pathway assessments

Due to the diversion of veterinary resource to the avian influenza outbreaks in 2022 to2023 and the Bluetongue outbreak in summer 2023, fewer TB incidents received a preliminary or final APHA veterinary investigation to identify the source of infection than in previous years. Historically, around 33% of incidents in HRA, and all TB incidents in the Edge Area and LRA are chosen to have a DRF. In 2023 only 77% of incidents received a at least a preliminary DRF visit in the LRA (106 out of 133 total TB incidents) and just 33% in the Edge Area (148 out 447 total TB incidents).

In the absence of field-derived assessments of hazards and risk-pathways, a new method was developed to provide an automated data-driven risk pathway assessment based on currently available data. The method combines the outputs of 2 separate algorithms, each of which provides an independent assessment of 2 potential risk pathways: (1) the Cattle Movement Algorithm, which provides a likelihood for TB introduction via cattle movements and (2) the WGS Local Transmission of Infection Indicator, which provides a likelihood for local transmission of infection. The outputs of these algorithms are combined to give an overall risk pathway assessment for an incident.

Estimating the likelihood of introduction of Bovine TB infection through cattle movements using the Cattle Movement Algorithm

A new Disease Report Form (DRF), for recording cattle TB incident investigations, is under development. This aims to enhance data capture and review the methodology around how we assess source attribution to improve understanding of TB transmission pathways and the evidence base for biosecurity advice as recommended in the Bovine TB Strategy Review for England (2018) led by Sir Charles Godfray.

Binary decision trees are being designed for each potential source risk pathway which aim to incorporate the most significant risk and mitigation factors that affect the overall likelihood of that pathway. The decision logic is evidence based and informed by data available in existing data sets, including movement data and previous testing history, and those gathered during field investigations.

The cattle movement risk pathway is primarily based on data already held and suitable for automation, with some assumptions, in the absence of DRF data. The binary decision tree was translated into an automated Cattle Movement Algorithm to support assessment of source attribution in the Edge Area where there had been reduced coverage of DRF investigations.

The algorithm assesses the likelihood that:

a) Reactors were infected prior to arrival on the case incident.

b) Other individuals, moved onto the herd during the high-risk infection window (60 days prior to the last clear herd test until 28 days before the start of the incident), introduced infection to the herd which transmitted laterally to the reactors disclosed. Where they were co-located with reactors or slaughterhouse cases it was assumed that direct contact was possible. The likelihood of lateral spread was reduced where, despite 60 days or more potential exposure, only a single reactor or slaughterhouse case was disclosed.

The risks throughout the individual's entire source history, since birth or import, are evaluated in the context of their testing history. Cattle are considered to have a higher likelihood of undisclosed infection on arrival at a premises if a previous premises of residence had a recent TB incident (within its parish herd testing interval plus 18 months), high risk based trade (RBT) score of 4 or 5 (based on years since previous TB incident and movements from RBT score 5 premises), or was located within an area of high local prevalence (more than 10% within 5km area at time of departure). Cattle are also considered to have a higher likelihood of undisclosed infection if imported from Northern Ireland based on the annual national herd incidence.

Clear testing reduces the likelihood of the individual being a source of infection but does not exclude it due to imperfect test sensitivity, which is taken into account. The likelihood is increased by inconclusive and recurrent positive bovine reactions or positive results on subsequent holdings that individuals have moved to.

Where the case incident WGS clade is available it is compared with the case and source location within the homerange maps and with any genomic clade data available for source incidents to increase or reduce the likelihood of that pathway.

The highest level of likelihood (negligible, very low, low, medium, high, very high) for an individual pathway is assigned to the herd, for example if at least 1 animal is considered to have a high likelihood of being infected when it moved on, the incident is graded as having a high likelihood that the infection was brought in through animal movement. Herds are classified as having either:

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

Where there are 10 or more individual pathways with the highest likelihood level being at least 'low', an aggregated effect is assumed, and the likelihood level is raised by one. For example, if ten individuals were rated as having medium likelihood of being the source of infection, the likelihood of introduction of infection to that herd via cattle movements would be raised to high. Where the likelihood of infection for individual movements are all very low, more than 100 individuals with this score are required to raise the herd-level assessment to low. This is due to evidence suggesting a log10 scale relationship exists between number of movements and likelihood of introduction of infection, which concurs with the fact that the timing of these movements is the only significant risk factor identified.

A herd-level assessment of high or very high is interpreted in this report as providing strong evidence to support the introduction of infection through cattle movements.

The algorithm additionally considers, for each high or very high likelihood (or aggregated medium likelihood) individual, whether they were moved on to the case premises by a local (under 25km) or non-local movement. The herd-level assessment is further classified according to whether there is strong evidence to support introduction by cattle movements in the presence or absence of any local movements.

It is recognised that some assumptions will affect confidence in these outputs. The key assumptions which raise uncertainty relate to the risk from Northern Ireland (based on national herd incidence in the absence of any premises history in the appropriate time period), lateral spread (cohabitation implies direct contact between reactor cattle and all others in the herd), the positive predictive value of testing where a single NVL reactor is disclosed and most significantly, the absence of genomic data for some source and case incidents. The latter point has been addressed to some extent by reporting case incidents where no WGS data is available separately.

Estimating the likelihood of introduction of disease from a local reservoir of infection using the WGS Local Transmission of Infection Indicator

Infection may have been introduced through local transmission of infection, for example, by infected cattle via local movements, shared boundaries, or residual infection within the herd or by infected wildlife. To assess the risk of introduction from a local source of infection, the *M. bovis* whole genome sequence associated with the TB incident is extracted and compared against any other *M. bovis* sequences that:

- were obtained from a herd located within a 9km radius of the infected herd, including previous incidents within the herd that had occurred historically
- AND had a maximum of 3 single nucleotide polymorphism (SNP) differences between its sequence and the sequence of the *M. bovis* isolate taken from the new TB incident (this suggests local spread or a common source of infection between these two herds due to the similarity between the sequences)
- AND occurred between 4 years prior or 6 months after the new TB incident.

If the TB incident did have evidence of being linked to another *M. bovis* sequence according to the criteria above, then there was evidence to suggest that the incident was introduced through a local transmission event. TB incidents where the *M. bovis* sequence relatedness was 4 SNPs or more away, or outside the criteria for time and space, were not considered to have strong evidence for a local transmission event.

For all OTF-S incidents (and OTF-W incidents where an *M. bovis* sequence could not be extracted from the culture), WGS information was missing, and these incidents are classified into a separate category. Thus, the WGS Local Transmission of Infection Indicator generates three categories of incident classification:

- WGS data indicates that a local transmission event has occurred (the sequence meets all the criteria above, suggesting strong evidence of local transmission of infection)
- WGS data does not indicate that a local transmission event occurred (sequence only partially meets (or not) the criteria above, suggesting weak evidence of local transmission of infection)
- No WGS data available (no sequence from the incident, so no further conclusions could be drawn)

The criteria selected has been validated against veterinary assessments, but work is ongoing to refine the approach going forwards.

Overall data derived risk pathway assessment for TB incidents

The overall risk pathway reported for an incident is derived from both the Cattle Movement Algorithm and the WGS Local Transmission of Infection Indicator. There is always a variable degree of uncertainty about the estimated true routes of TB infection into a herd. However, the absence of local transmission of infection and/or cattle movements associated with a high likelihood of infection does not completely negate these pathways. Nonetheless, the evidence provided by cattle movement and WGS data, when combined, can provide valuable insights into possible risk pathways. These are combined to determine which one of the risk pathway categories an incident falls under, as shown in Table 2.2.8.2.

Table 2.2.8.2: Final risk pathways used for TB incidents in England based on the Local Transmission of Infection Indicator and Cattle Movement Algorithms in 2023.

Risk Pathway colour code for figures	Local reservoir identified from WGS	High-risk cattle movements identified	Interpretation of most likely risk pathway
1	Yes	No	Strong evidence exists to support local transmission of infection, but the nature of the local pathways in question cannot be determined from the available data. Infection may have been introduced via (and not limited to): - residual infection in the herd - contiguous contact with infected cattle - direct or indirect contact with potentially infected wildlife There is no evidence supporting introduction of infection through cattle movements associated with a high likelihood of infection. However, cattle movements cannot be completely ruled out as a source of infection, as there may have been many medium or low risk movements into the herd. Rather, there is relatively stronger evidence to support infection from a local source of infection rather than from movement of cattle between holdings.
2	Yes	Yes – at least one local high risk movement occurring within 25km of the infected herd.	As for category 1, except there is evidence that local cattle movements may have also introduced infection.
3	Yes	Yes - all non-local (high risk movements occurring over 25km away from the infected herd)	There is a high degree of uncertainty around the source of infection. With multiple likely risk pathways identified (both local transmission of infection events and non-local movements), it is possible there were multiple routes of disease incursion into these herds.

4	No	Yes	Cattle movements associated with a high likelihood of infection are considered more likely than not to have played a part in the introduction of infection. There is no evidence of a close genetic link (3 SNPs difference) between the *M. bovis* isolate identified in the incident and any other *M. bovis* isolates near to the incident in time and space.
5	No	No	WGS evidence was available to assess risk pathways for these incidents, but the source of infection remains unclear.
6	No WGS data available	Yes	Strong indication that cattle movements may have played a part in introducing infection to these herds (including OTF-S incidents), but no WGS data were available to explore the possibility of local transmission of infection. There is uncertainty as to the full range of likely risk pathways for these TB incidents.
7	No WGS data available	No	Cattle movements are unlikely to have played a part in introducing infection to these herds, but no WGS data were available to explore the possibility of local transmission of infection. There is insufficient evidence for these herds to determine a likely infection pathway.

3. Overview of TB Testing in Great Britain

3.1 Measuring test accuracy

Sensitivity is the ability of the test to identify diseased animals. Specificity is the test's ability to correctly identify that an animal is not infected. Both directly affect how well the control measures that seek to monitor infection moving out of and in herds will work. Such control measures include removing infected animals for the herd (removal of reactors), or to allow only uninfected animals to be moved (pre-movement tests).

Ideally, tests should have both high sensitivity and specificity, as effective disease eradication is dependent on finding and removing all infected animals. But a trade-off between sensitivity and specificity is often the norm. Lowering the threshold of a positive result to increase sensitivity increases the chances of wrongly categorising an 'uninfected' animal as infected (as this reduces specificity).

Therefore, different test interpretation policies are applied according to the area, herd history and other factors, to make the best compromise for the circumstances. For TB, tests tend to be less sensitive, and as a result some infected animals may still give a negative test result. However, they tend to have a high specificity, so it is very unlikely that an uninfected animal will give a positive test result.

An important use of sensitivity and specificity values is to estimate a test's predictive values. These determine test result outcome for the animal (positive or negative) and how accurate that result truly is.

The positive predictive value (PPV) of a test is defined as the probability that a positive testing animal is truly infected. Conversely, the negative predictive value (NPV) is the probability that an animal with a negative test result is truly free from infection. Both measures depend on the proportion of the population that is infected (prevalence of infection) as well as the sensitivity and specificity of the test.

The higher the prevalence of infection in a population, the higher the PPV and the lower the NPV of a diagnostic test. In other words, the same test for TB infection in cattle will not have the same predictive value when used in different risk areas. Both the stage of infection and disease prevalence in different risk areas have an effect on the TB diagnostic tests. Therefore, it is not easy to calculate 'average' predictive values for the diagnostic TB tests. However, these averages in areas of different prevalence can still be useful in helping plan how tests should be interpreted.

The single intradermal comparative cervical test (SICCT) is the main detection test used for surveillance in UK. It is strongly specific (if cattle test positive, they almost certainly have TB), but can miss infected cattle. When this happens, some cattle may have no reaction, whilst others will not give a big enough reaction to be classified as positive. These are called ‘inconclusive reactors’ and will require an additional test to decide their true disease status. If they retest as inconclusive or positive, they are classified as infected and are slaughtered, and incident procedures are triggered.

The limitations of the SICCT can be addressed by changing the way its results are interpreted. This is done with the ‘standard’ or ‘severe’ interpretation, which changes the threshold of a positive result. It can also be improved by assessing the likelihood that IRs are truly infected, based on statistics or the use of the more sensitive gamma interferon test. These options are explored below.

The specificity of the SICCT test at different interpretations in GB was estimated by Goodchild and others in 2016. SICCT specificity was found to vary not only with the different positive cut-off points for standard and severe interpretation, but also across regions within GB. Table 5.1 shows how likely a positive animal is to be truly infected and how likely it is to have been exposed to infection.

According to the calculated PPV of the SICCT test, 91.8% of reactors in GB are infected. PPV values ranged from 92.3% in the high-prevalence counties to 76.9% in the low-prevalence counties. The study indicates that the SICCT test, as used in GB, has a very high specificity. Thus, at standard interpretation it will give rise to one false positive animal for every 4,760 to 7,690 animals tested. Conversely, the findings suggest that over 90%of reactor cattle identified only by skin test in GB between 2002 and 2008 were infected. This endorses the compulsory slaughter of all SICCT test reactor cattle for effective disease control.

Table 3.1.1. Selected data from Table 6 in Goodchild and others (2016)

Calculation of the PPV for the SICCT test in three groups of Great Britain counties that vary in TB prevalence. The 95% confidence intervals were based on the confidence intervals of specificity.

Group of counties and description	High prevalence England High-Risk Area +4 Welsh counties	Medium prevalence England Edge Area +3 Welsh counties	Low prevalence England Low-Risk Area +Gwynedd +Anglesey +Scotland	All of GB
PPV if the interpretation was severe only for OTF-W incidents (with 95% confidence interval)	**92.3%** (91.1 to 93.7%)	**88.6%** (86.4 to 90.9%)	**76.9%** (72.1 to 82.0%)	**91.8%** (90.5 to 93.3%)
PPV if all tests had been at severe interpretation (with 95% confidence interval)	**89.5%** (88.2 to 91.3%)	**74.8%** (71.6 to 79.0%)	**46.6** (39.7 to 55.4%)	**87.7** (86.1 to 89.7%)
PPV if all tests had been at ultra-severe interpretation (with 95% confidence interval)	**88.9%** (87.4 to 90.3%)	**74.3** (70.7 to 77.5%)	**43.2** (35.3 to 50.3%)	**86.9** (85.1 to 88.6%)

In summary, in high or intermediate prevalence situations, nearly every single reactor detected by the SICCT is truly infected. This is particularly the case in the HRA, or for short interval and herd risk tests. Thus, a positive SICCT test provides strong evidence of infection in TB incidents in these risk areas independent of post-mortem confirmatory evidence. As expected, PPV increases with the test sensitivity, specificity and animal prevalence.

However, the lower predictive value of the SICCT in lower incidence areas can detect positive animals which are not truly positive for infection with TB.
This has been the case especially in places such as the LRA, parts of Wales and in Scotland.

Note that measurement of all test characteristics depends on knowing the true status of the animal, which should be measured using a ‘gold standard’ test. However, such a test is lacking for cattle in the early stages of TB infection. The difficulty in knowing whether an animal is truly uninfected or merely asymptomatic makes estimating the specificity and NPV particularly challenging. Thus, careful use of test application or interpretation can help to improve predictive values. Consideration of other evidence is also important in deciding whether a negative animal is truly uninfected. Together, these enhance accuracy and enable the heterogeneity of the epidemic to be taken into account when designing control measures.

Actions to increase detection of infected cattle in a TB infected herd

Surveillance tests are imperfect, hence different options have been developed to enhance the chance of detecting all TB infected cattle in a herd.

Increasing the number of herd SICCT tests (so called short-interval (SI) tests) that the herd must pass to regain OTF status following disclosure of one or more reactors.

Severe interpretation of skin test: Increasing the sensitivity in this way will reduce the specificity of the skin test. This means 1 in 1,111 cattle could potentially be a false positive reactor, instead of 1 in 5,000 at standard reading (View the Strategy for achieving Official Bovine Tuberculosis Free Status for England). However, these values apply to individual animals. Test sensitivity is higher at herd level and classification of a herd as infected is more accurate, particularly when more than one reactor is detected.

Consider removal of non-reactor cattle as DCs: this relates to cattle that have been in contact with other infected cattle but can also be based on test history. For example, one or more previous classification as an IR, or belonging to a cohort where a high percentage of reactors have been detected.

Supplementing the skin test with the interferon-gamma blood test: applying a parallel interpretation of the results so that animals reacting to either or both tests are regarded as infected and removed from the herd.

3.2 Types of surveillance used for detecting TB

3.2.1 Surveillance overview

Bovine tuberculosis is a slowly progressing disease that is not clinically apparent for some time after infection, but which can spread during this time. This means that surveillance on apparently healthy animals is needed in addition to investigating apparent clinical cases of TB, to get ahead of disease spread. Surveillance involves active surveillance where live animals are tested at set intervals. Active surveillance can be modified in the different parts of the country to reflect the different likelihood of TB either being present or being detected. It also requires passive surveillance, where there is a requirement for the government to be notified if anyone suspects TB infection in animals. The latter occurs mainly from cattle being processed through slaughterhouses.

Detecting TB with a diagnostic test depends on how likely it is for the disease to be present and how robust the test is. The likelihood of infection with TB is associated with location, herd type and size, as well as whether the herd has previously been infected. These important differences in likelihood of disease presence in herds affect how surveillance is best carried out and how effective it is at detecting infection.

3.2.2 Surveillance Stream definitions

The term ‘Surveillance Stream’ was coined in 2016 to classify bovine TB surveillance systems in the England Epidemiology Report. It was designed according to the intention behind the activities carried out to detect disease. Broadly speaking, there are 2 types of activities among the 4 streams defined below: slaughterhouse surveillance and application of the TB skin test (SICCT). The definitions for the surveillance streams encompassing these are below. Tests carried out as part of the Area and Herd risk surveillance stream have been further divided by purpose: primarily aiming to detect disease (surveillance) or aiming also to stamp it out (control).

Routine animal testing and slaughterhouse surveillance help to detect TB in herds or animals not expected to be at any increased likelihood of being infected. Area and Herd Risk surveillance and Proactive surveillance are targeted at herds or animals thought to be at higher risk of being infected. These types of surveillance also limit the impact of the movement of unknowingly infected animals to a lower risk area.

Surveillance stream definitions are as follows:

Routine

Disease first disclosed as a result of tests scheduled as part of routine surveillance with no expectation of increased or decreased probability of disclosing infection.

Area and Herd Risk

Disease first disclosed as a result of targeted tests carried out due to history. Alternatively, disease disclosed from tests carried out due to epidemiological evidence that there is a higher probability of disease in the animal or herd.

Slaughterhouse surveillance

Disease first disclosed as a result of routine post-mortem meat inspection during commercial slaughter of animals not believed at higher likelihood of being diseased. This excludes results of inspection of test reactor cattle and DCs removed by APHA.

Trade and other surveillance

Disease first disclosed as a result of testing scheduled due to the high impact of disease if present, in the destination herd or premises. This includes tests on animals where the presence of some epidemiological risk factors may increase disease probability but is not the primary reason for testing. Referred to as Proactive surveillance in earlier reports.

Table 3.2.2.1. Surveillance Streams classification

Test Code	Name	England Surveillance Report Categories (2018 onwards)	Surveillance Streams (2016-2017)	Surveillance Purpose
CON, CON6, CON12	Contiguous Test	Area and Herd Risk Contiguous tests	Area and Herd Risk	Control
CT(RTA)	Check Test (Road Traffic Accident)	N/A	Area and Herd Risk	Surveillance
CT-HS1, CT-HS2	Check Test (Hotspot)	Area and Herd Risk Hotspot tests	Area and Herd Risk	Surveillance
RAD, RAD6, RAD12	Radial Test	Area and Herd Risk Radial test	Area and Herd Risk	Control

Test Code	Name	England Surveillance Report Categories (2018 onwards)	Surveillance Streams (2016-2017)	Surveillance Purpose
90D	See TBU test	N/A	Area and Herd Risk	Surveillance
CT	Check Test	N/A	Area and Herd Risk	Surveillance
CT(EM)	Check Test (Exposure Mitigation) (Backward tracing herd test)	Area and Herd Risk Source tracing test	Area and Herd Risk	Control
CT(I-I)	Check Test (Investigation and Intervention)	Area and Herd Risk Check test	Area and Herd Risk	Surveillance
DTG	Delayed Testing Group	N/A	Area and Herd Risk	Control
IFN, IFN LOW IN, IFN PERSI, IFN NSR, IFN SLHERD, IFN ANOM, IFN NBCP/PBCP, IFN OTH_SP, IFN PRI	Gamma Interferon Test (OTF-W LRA, OTF-W persistent TB incidents, non-specific reactor herd, whole or partial reactor herd slaughter, anomalous reactions procedure, badger culling area tests, disease in other species present, private	Area and Herd Risk Not typically disclosing tests	Area and Herd Risk	Control
PSI	Partial Short Interval Test	N/A	Area and Herd Risk	Control
SI	Short Interval Test	Area and Herd Risk Not typically a disclosing test	Area and Herd Risk	Control

Test Code	Name	England Surveillance Report Categories (2018 onwards)	Surveillance Streams (2016-2017)	Surveillance Purpose
IASI	SI test in OTF-S herds in Wales Intensive Action Area only	N/A	Area and Herd Risk	Control
TBU (former 90D)	TB Unit Test (AFUs)	Area and Herd Risk AFU test	Area and Herd Risk	Surveillance
12M	12 Month (Post-TB incident) Test	Area and Herd Risk Post-incident tests	Area and Herd Risk	Control
6M	6 Month (Post-TB incident) Test	Area and Herd Risk Post-incident tests	Area and Herd Risk	Control
IR or IFN 2xIR	Inconclusive Reactor Test or Gamma Interferon Test severe 2xIRs (Wales only)	Area and Herd Risk Not typically a disclosing test	Area and Herd Risk	Surveillance
TR	Traced Bovine Test	Area and Herd Risk Spread tracing tests	Area and Herd Risk	Control
Old RH*	Reformed Herd Test	N/A	Area and Herd Risk	Surveillance
ASG	Approved Segregated Group Test	Area and Herd Risk Not typically a disclosing test	Area and Herd Risk	Control (if on TB incident herd)
AI	Artificial Insemination Centre Test	Trade and Other Pre-movement testing	Trade and other	Surveillance
BHH	Bull Hirer Test (Scotland only)	N/A	Trade and other	Surveillance
CT-LRA-SA	LRA Pre-Sale Check Test	Trade and Other Pre-sale check LRA	Trade and other	Surveillance

Test Code	Name	England Surveillance Report Categories (2018 onwards)	Surveillance Streams (2016-2017)	Surveillance Purpose
EX	Export Test	Trade and Other Pre-export	Trade and other	Surveillance
PII	Post-Irish Import Test	Trade and Other Post-export	Trade and other	Surveillance
PIO	Post-Import Test	Trade and Other Post-export	Trade and other	Surveillance
POSTMT or POSTMOVNC or POSTMOVOV	Post-Movement Tests	Trade and Other Post-movement	Trade and other	Surveillance
PRI	Private Test	Trade and Other Private tests	Trade and other	Surveillance
PRMT	Pre-Movement Test	Trade and Other Pre-movement testing	Trade and other	Surveillance
CT-NH1/2/3	New Herd Test	Routine New Herd tests	Routine	Surveillance
OT	Other	N/A	Routine	Surveillance
RHT or RHT48	Routine Herd Test	Routine Routine Herd tests	Routine	Surveillance
WHT	Whole Herd Test	Routine Whole Herd tests	Routine	Surveillance
IA6/IA12	Routine 6M or 12M test within the Welsh Intensive Action Area area only	N/A	Routine	Surveillance
SL	Slaughterhouse	Slaughterhouse Surveillance Stream	Slaughterhouse Surveillance Stream	Slaughterhouse Surveillance Stream

3.3 Tools used to support TB incident analysis

3.3.1 Genotyping

From 19 April 2021, Whole Genome Sequencing (WGS) started to replace genotyping (spoligotype and VNTR type) as the predominant technique used to genetically classify *M. bovis* isolates and genotyping was switched off fully in December 2021.

3.3.2 Whole Genome Sequencing

Attempts are made to recover *M. bovis* from all TB incidents and to subject at least one isolate per TB incident to molecular strain identification.
As of 19 April 2021, all incident herds with *M. bovis* positive culture results started to have Whole Genome Sequencing (WGS) results recorded instead of genotyping results. Despite being relatively novel, WGS is the current gold standard method for strain differentiation, giving a higher level of differentiation between isolates and providing insight into their evolutionary relationships.

WGS provides information on the entire genome of *M. bovis*. This contrasts to the previous genotyping methods used (a combination of VNTR or Spoligotyping as explained in section 3.3.1), which target specific regions of the bacterial genome. WGS therefore achieves higher resolution of *M. bovis* strains compared to conventional genotyping as it allows for finer-scale differences across the entire DNA sequence to be identified. WGS examines variation caused by mutations across the entire DNA sequence of the *M. bovis* genome (4.4 million base pairs in length) and therefore offers higher discriminatory power compared to conventional genotyping for differentiation of *M. bovis* strains.

Because WGS analyses the whole genome, identical or very similar genome sequences can only be obtained from closely genetically related isolates. In contrast, genotyping of isolates means that identical or similar repeat patterns are not necessarily genetically linked, as they can evolve independently.

WGS identified 6 major groups (B1-B6) which were subdivided into a total of 30 clades. Each isolate is assigned to a WGS clade based on its genome sequence. The WGS clade names consist of the letter 'B' for *M. bovis* followed by a number (such as B4 or B6) that indicates which major group the isolate belongs to. Further numbers (B6-13, B6-42) indicate the subgroup within the major group to which the isolate is assigned.
The clades assigned to isolates are designed to be hierarchal: For instance, B6-42 is more closely related to B6-41 than it is to B6-13; and B6-41, B6-42 and B6-13 are more closely related to each other than to B3-11. Due to the slow mutating nature of *M. bovis*, isolates from multiple breakdowns assigned to the same clade are more likely to be linked.

WGS is an important tool used by APHA for investigating TB breakdowns and possible transmission pathways between cattle herds. At farm level, WGS helps APHA field vets to identify the most likely source of TB infection for a breakdown herd, and whether it has spread to other cattle herds. Once APHA is aware of the likely origin of a breakdown, they can advise farmers on measures they could take to reduce the risk of further infection entering the herd. WGS is also routinely applied to *M. bovis* isolates from non-bovines including South American camelids (alpacas, llamas), goats, pigs, and captive deer when investigating TB incidents affecting these species, as well as in wildlife species (such as road killed badgers) and compare them with isolates from local TB breakdowns in cattle herds and other farmed animals. This allows APHA to assess whether cattle and badgers from the same geographical area are affected by the same strain of the TB bacterium, and to assess the spread of TB strains between geographical areas and across time. For instance, WGS is being used to support TB surveillance in cattle and badgers and understand the epidemiology of TB in the confirmed hotspot area in east Cumbria (HS21), where a link between cattle and badger TB infection was first identified in 2017.

3.3.3 Homerange maps

Homerange maps are an attempt to capture the geographical localisation (endemic regions) of the various WGS clades of *M. bovis* found in GB. They have proved extremely useful for identifying the expected WGS clade at a given location, and support epidemiological investigations at national, regional and individual incident level.

A homerange defines a geographical area in which a certain WGS clade of *M. bovis* is not unexpected. A simple algorithm to define the homerange area was originally developed as part of Defra research project SE3257. This is the same criterion as that used in previous reports to the European Commission. A 5 km square is considered part of a certain homerange if:

- there have been at least 3 different incidents of that WGS clade
- on at least 2 holdings
- from 3 or more discrete years within a 5-year window

To create a coherent area for each genotype, a 10 km buffer is then drawn around each of the homeranges so defined.

3.3.4 Slaughterhouse Ability Model

The model was set up to explore patterns in residual variation in detection rates between slaughterhouses after accounting for different animal level risk factors. These were: sex, age, breed, days in high or low risk herds, contact with high or low risk herds, surveillance testing status, year, quarter, and risk area. Estimations of the likelihood that a slaughterhouse will detect a TB infected animal during routine slaughter according to which animals it processes, can then be carried out. These patterns can be summarised by the posterior mean odds ratio (OR). Slaughterhouses with positive posterior ORs are detecting more tuberculous carcases at commercial slaughter of non-reactor cattle than the average expected. Slaughterhouses with negative posterior ORs are finding fewer than the average expected. However, by design it would be expected that the ORs for the different slaughterhouses to be distributed above-and-below the average. Thus, due to the large heterogeneity in throughputs, the ORs for some slaughterhouses will be better estimated than others.

The perceived reliability of this estimation is measured by the posterior variance. Those slaughterhouses with a lower variance are likely to have a more accurate estimation of the posterior mean. By considering the 95% credible interval around the posterior mean OR using the variance, the slaughterhouse's performance can be statistically estimated. If this interval includes zero, then the model does not provide sufficient evidence that the slaughterhouse is detecting any more or fewer cases than expected. If the interval is entirely below zero, then the model suggests that the slaughterhouse is detecting significantly fewer cases than expected given the other factors. Equally, if the interval is entirely above zero then the model is suggesting that the slaughterhouse is detecting significantly more cases than expected. The size of the interval is mainly down to the throughput of the slaughterhouse. The higher the throughput, the narrower the interval, and hence the more precisely the mean is estimated.

4. Policies for TB control in Great Britain

The policies and control measured summarized in this section were in place during the period of time covered by the reports (2023).

4.1 TB control in England

Bovine TB is statutorily controlled in England following The Strategy for achieving Officially Bovine Tuberculosis Free status for England (2014) and the Bovine TB Strategy Review (2018). The aim of the Strategy is to eradicate TB by 2038, whilst maintaining an economically sustainable cattle industry. Under the Strategy, England is divided into three areas reflecting the level of disease in each and controls differ accordingly (Figure 4.1.1). Control in all areas is based on a range of surveillance and control measures. Up to date information on current policies can be found at the TB hub website.

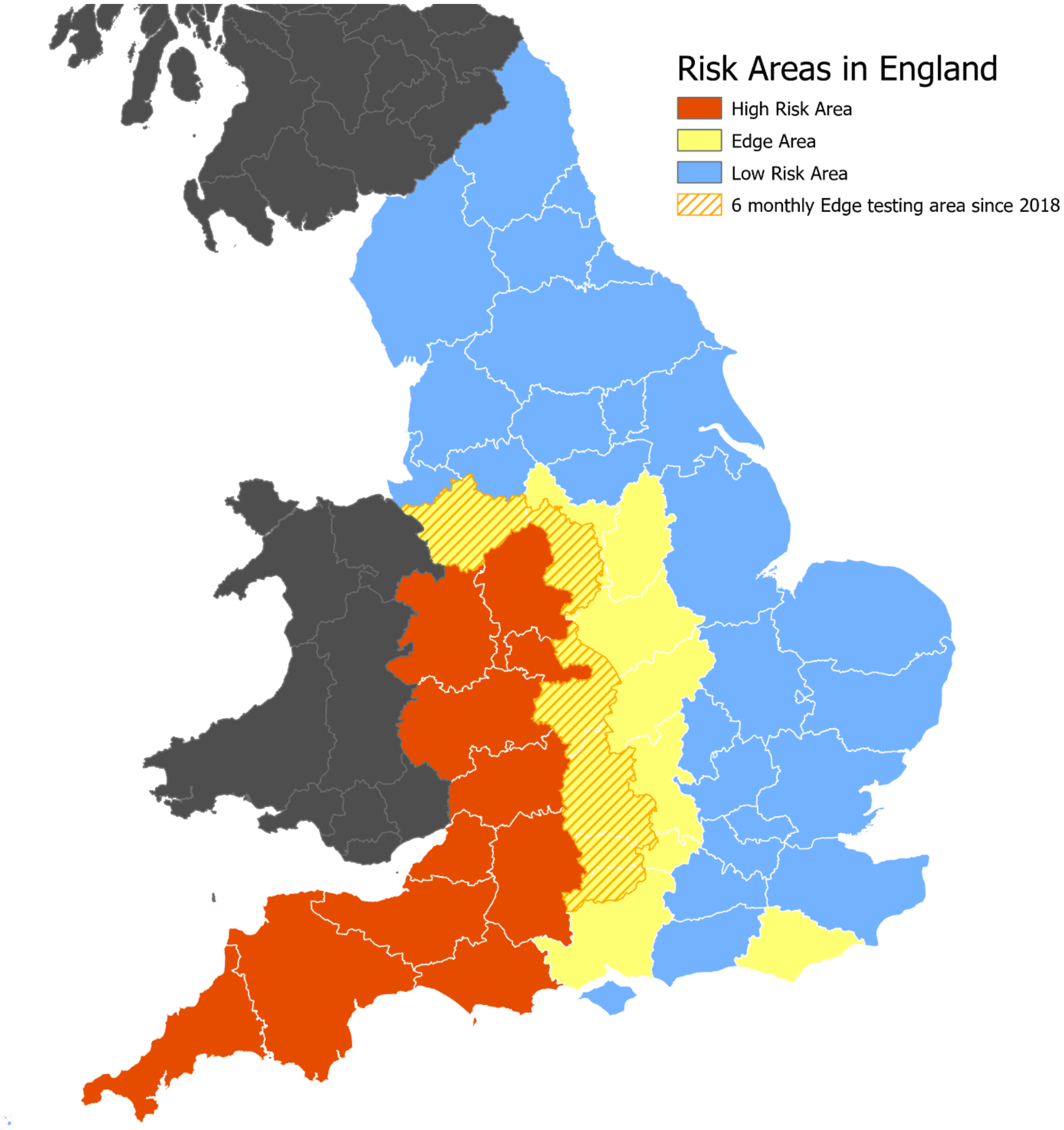

Figure 4.1.1 TB risk and surveillance areas of England effective since January 2018, as set out in the Government's Strategy for Achieving Officially Tuberculosis-Free Status for England.

4.1.1 Summary of control measures by risk area in England

Summary of controls in the High Risk Area

Surveillance controls are:

- slaughterhouse surveillance
- annual or 6 monthly herd testing (see earned recognition below)

- compulsory pre-movement testing

Incident management controls are:

- within herd: movement restrictions, isolation, slaughter and compensation, epidemiological investigation, tracing, additional skin tests and IFN-γ blood testing
- additional skin testing in neighbouring herds

Reduce risk of TB from badgers through:

- licensed injectable badger vaccination
- licensed badger culling

Other disease prevention measures are:

- biosecurity measures
- risk-based trading

Summary of controls in the Edge Area

Surveillance controls are:

- slaughterhouse surveillance
- Annual or 6 monthly herd testing (see earned recognition below)
- Compulsory pre-movement testing

Incident management controls are:

- within herd: movement restrictions, isolation, slaughter and compensation, epidemiological investigation, tracing, additional skin tests and IFN-γ blood testing
- additional skin testing in neighbouring herds
- additional skin testing in herds within a 3km radius (in annual herd testing areas only)

Reduce risk of TB from badgers through:

- licensed injectable badger vaccination
- licensed badger culling

Other disease prevention measures are:

- biosecurity measures
- risk-based trading

Summary of controls in the Low Risk Area

Surveillance controls are:

- slaughterhouse surveillance
- 4-yearly testing (annual for high risk herds)
- pre-sale check tests
- compulsory post-movement testing for cattle from the annual or 6 monthly surveillance areas

Incident management controls are:

- within herd: movement restrictions, isolation, slaughter and compensation, epidemiological investigation, tracing, additional skin tests and IFN-γ blood testing
- additional skin testing in herds within a 3 km radius

Reduce risk of TB from badgers through:

- licensed injectable badger vaccination
- licensed badger culling (in exceptional circumstances)

Other disease prevention measures are:

- biosecurity measures
- risk-based trading

Earned Recognition

Since May 2019, cattle herds in the 6-monthly testing areas that meet certain criteria have been eligible to return to annual surveillance testing through earned recognition. These criteria are either:

- the herd has been in existence for at least 6 years and has not had a TB incident in that 6-year period
- the herd is registered to a bovine TB health scheme accredited under the Cattle Health Certification Standards (CHeCS) at level one or above

4.1.2 New TB control measures introduced in England in 2023

A new version of iBTB went live in early 2023 including an AFU finder.

The Tuberculosis in Animals (England) (Amendment) Order 2023 came into force on 1 August 2023, which extended the requirement for mandatory post-movement testing of cattle moved to herds in the annual surveillance testing parts of the Edge Area from higher TB risk regions of England and from Wales. A small number of specific exemptions apply.

From the 2 October 2023, keepers of restricted herds were able to apply for a new general licence to cover the movement of cattle directly or through an orange market to an AFU or a slaughterhouse.

The Badger Edge Vaccination Scheme (BEVS 2), which provided funding towards the cost of vaccinating badgers in the Edge Area of England, concluded in February 2023.

Badger vaccination operations were carried out between 1 May and 30 November 2023 on 3,064 badgers across England, of which 1,540 were vaccinated by APHA. This is a 26% increase compared to 2022 (N=2,434).

Due to changes in the process of the vaccine license issuing by Defra, vaccinated land is no longer routinely mapped and determined other than in Cumbria. There were 19 counties that held vaccination operations in 2023: 10 in the HRA, 6 in the Edge Area and 3 in the LRA. More details can be found in the Summary of Badger Vaccination in 2023.

No new areas were issued with badger disease control licences for badger culling under the Badger Control Programme (BCP) in 2023. In total, 58 areas in England held active licences in 2023. This included 28 areas carrying out an intensive cull, 29 areas carrying out supplementary badger culling, and one area in Lincolnshire where culling was carried out as part of disease control within an LRA TB hotspot. Further detail is provided in Chapter 3.4 of the Bovine tuberculosis in England in 2023 Report under “TB control in wildlife”.

4.2 TB control in Scotland

Scotland has been officially bovine TB (TB) free (OTF) since 2009. The Scottish Government is committed to a comprehensive, practical and proportionate programme of actions to maintain current low levels of TB and safeguard OTF status.

TB controls in Scotland are underpinned by the Tuberculosis (Scotland) Order 2023 and by the risk based routine herd testing policy introduced in 2012. These policies meant ‘low risk’ herds became exempt from the four yearly routine herd testing programme.

Further information on TB in Scotland can be found on the Scottish Government website.

4.2.1 New TB cattle measures in Scotland introduced in 2023

On 18 May 2023 the new Tuberculosis (Scotland) Order 2023 came into force.

The following policies were taken forward as part of the new Order:

- ending the practice of accepting a clear final short interval test (SIT) at the end of all TB breakdowns as a valid pre-movement test
- shortening the period during which a pre-movement test with negative results remains valid from the current 60 days to 30 days after tuberculin injection
- reducing compensation for unclean reactor cattle at slaughter by 50%
- including requirements for ‘isolation’ in legislation to ensure that proper isolation of reactors and IRs is undertaken
- reducing compensation for reactors or IRs which are not properly isolated

4.2.2 Previous TB cattle measures in Scotland introduced before 2023

In November 2022, the new Tuberculosis (Scotland) Amendment Order 2022 came into force, introducing a new requirement for prior permission to be obtained from Scottish Ministers before taking samples from cattle located in Scotland with the intention of applying a test for tuberculosis.

On the 12 December 2018 the Tuberculosis (Miscellaneous Amendments) (No 2) Order 2018 came into force.

These new rules include changes to disease control measures and compensation arrangements.

4.3 TB control in Wales

Bovine tuberculosis (TB) is subject to statutory control in Wales and is directed by the principles set out in the Bovine TB eradication programme. TB controls are underpinned by the Tuberculosis (Wales) Order 2010. Details about TB in Wales and the surveillance and control measures associated with the eradication programme can be found on the Welsh Government website.

4.3.1 New TB policy measures introduced in Wales in 2023

One new policy was introduced in Wales in April 2023. Herds in specified higher risk areas of the Low TB Area, the Intermediate TB North Area and the Intermediate TB Area Mid had the following tests read under severe interpretation:

- Tests conducted 6 months and 12 months after the conclusion of a TB incident
- Contiguous tests.

If only IRs (and no reactors) over 6 months old are identified at these tests, then these animals are subject to a IFNy test.

The policy introduced in June 2021 of blood testing (IFNy and IDEXX antibody tests) non-homebred animals with a positive reaction to bovine tuberculin in herds that had a recent clear surveillance skin test ceased at the end of January 2023.

4.3.2 Previous TB policy measures introduced in Wales before 2023

From January 2022, all new TB incidents in Wales were classified as OTF-W. The only exceptions to this, resulting in herds having suspended (OTF-S) status, were:

- herds had one or more suspect slaughterhouse cases with laboratory results pending, or
- herds where non-homebred animals were positive to blood (IFNy and IDEXX antibody tests) but had a clear skin test previously and disease has not been confirmed by post-mortem or culture

This policy also affects incident management, meaning that even the relatively low number of OTF-S incidents remaining that only had a single reactor and no high risk epidemiological reasons were now managed as OTF-W cases unless they were as a result of a slaughterhouse cases or a blood test positive result (which had additional surveillance measures in North Wales).

From January 2022, the 3 year IR rule was revoked meaning all herds, where only IRs were identified at a surveillance test remain under TB02 restrictions until the status of the IR is established.

From January 2022, DRF assessments were conducted over the telephone due to the impact of the 2021-2022 AI outbreak on APHA resources. All telephone assessments were conducted within 30 working days of the issue of a TB181 or TB2 form for breakdowns in Wales.

Approved Tuberculin Testers (ATTs) in private veterinary practices are now permitted to carry out tuberculin skin testing of cattle in Wales.

New guidance was published in December 2022 to support the changes to TB surveillance activities due to the impact of 2022 to 2023 AI outbreak on staff resources.