Animal Health and Veterinary
Laboratories Agency

Bovine tuberculosis:
Infection status in cattle in GB

Annual surveillance report

For the period

January to December 2013

Commissioned by the Department for the Environment, Food and Rural Affairs, Scottish Government and Welsh Government under Project SB4500

Report to:
TB Programme,
DEFRA,
Area 5D Nobel House
17 Smith Square
London SW1P 3JR

Project Leader:
Mr P A Upton
Data Systems Workgroup,
Animal Health and Veterinary Laboratories
Agency (AHVLA, Weybridge),
New Haw, Addlestone,
Surrey KT15 3NB
Telephone 01932 341 111, ext. 3440

Head of Department:
Prof. Glyn Hewinson
Department of Bacteriology,
AHVLA (Weybridge)
Telephone 01932 341 111, ext. 2494

Compilers:
Miss K A Harris[1], Dr J. M. Broughan[1], Dr N H Smith[2], Mr A Brouwer[1] and Mr P A Upton[3]
Department of Epidemiological Sciences.
AHVLA (Weybridge)
Telephone 01932 341 111, ext. 4565

Reviewed by:
Dr S H Downs1
Dr A V Goodchild1
Dr L Brunton

Acknowledgements:
Dr Martyn Blissitt, Scottish Government
Dr Ricardo de la Rua and Ms Jo Wheeler
AHVLA, Defra TB Programme

---

[1] Department of Epidemiological Sciences, AHVLA (Weybridge)
[2] Bacteriology Department, AHVLA (Weybridge)
[3] Data Systems Group, AHVLA (Weybridge)

TABLE OF CONTENTS

List of figures and tables (in order of appearance in the report)

To go to an item, press ctrl and click on the item page number

Executive summary

Cattle demographics

There was little change in the number of live herds (+0.02%) and the total number of cattle (-0.23%) in GB in 2013 compared to the previous year (Table 1.1).

The number of cattle tests in GB increased by 3.3%,

- mainly due to a 5.7% increase in the number of cattle tests in England, reflecting the greater area under yearly testing as part of the "Edge" strategy;
- almost 10% fewer cattle were tested in Scotland as a consequence of the new risk-based exemptions from routine four-yearly herd testing.

New bovine TB breakdowns in Great Britain

In 2013, there were a total of 4,775 new breakdowns in GB;

- of these, 3,249 were OTF-W (68%), 1,513 were OTF-S and 13 breakdowns were unclassified (Table 2.1).
- this is relatively consistent with the National Statistics which reported 4,821 total breakdowns in 2013, of which 3,255 were OTF-W. Minor discrepancies between the Surveillance Report and the National Statistics are a result of additional data cleansing performed at AHVLA Weybridge on the data from SAM to address data consistency issues (see Source of Data, Surveillance Report for England for a more detailed explanation). Work is on-going to harmonise reporting between the AHVLA TB Surveillance Reports and the National Statistics.
- although there were 3% fewer new breakdowns in GB in 2013 than in the previous year, this figure hides important variation between countries.
  - In Wales, the total number of new breakdowns, whether OTF-W or OTF-S, all decreased by around a fifth;
  - In Scotland the decrease was almost one half (from very low numbers);
  - In England, there was little change in the number of OTF-W breakdowns (+1%) but the number of OTF-S breakdowns increased by 6%.
  - The distribution of OTF-W and OTF-S new breakdowns in GB in 2013 (inset: 2012) is shown in Figure 2.1 and Figure 2.2 respectively.

- The total number of OTF-W breakdowns that closed in 2013 increased by 9.7% for England and 20.4% for Wales compared to 2012 (using data refreshed in 2014).

- Five counties with no new OTF-W breakdowns in 2012 had 1 or 2 in 2013,
  - whilst eleven counties that had suffered an OTF-W breakdown in 2012 (eight of them in Scotland) had none in 2013.
- Of counties with a larger OTF-W incidence, increases were observed in –
  - Avon (+30%), Cheshire (+23%), Staffordshire (+12%), Oxfordshire (+41%) & Warwickshire (+81%) (England), and Gwent (+7%) (Wales).
  - There were decreases in Derbyshire (-36%) in England, and in Clwyd (-34%), Dyfed (-33%) & Powys (-10%) in Wales.

OTF-S breakdowns with more than one reactor may reflect early infection.

- More of them were recorded in 2013 than in 2012, in Avon, Cheshire, Derbyshire, Devon and Shropshire in England and Clwyd in Wales.
- There were no OTF-S breakdowns with more than one reactor in Scotland in 2013, although there had been 8 in 2012.
- All counties in Wales except Clwyd and South and West Glamorgan recorded a decrease in OTF-S breakdowns with more than 1 reactor.

Routine skin tests accounted for 31.6% of the total tests carried out in unrestricted animals. 17.5% of tests were carried out in animals perceived to be at an increased risk of bTB ('Herd risk'), for example due to a recent bTB incident, detecting 60% of total new bTB breakdowns and 55% of OTF-W breakdowns in 2013 (Table 2.2).

- Slaughterhouse surveillance accounted for a further 28% of all unrestricted animal 'tests', and succeeded in detecting 14% of total new bTB breakdowns and 21% of OTF-W new breakdowns;
  Pre-movement testing (VE-PrMT) detected 770 breakdowns (502 OTF-W) in GB. This represents almost 8% of all breakdowns in GB, 7.9% of breakdowns in English herds and 8.3% of breakdowns in Welsh herds. One breakdown was detected in Scotland by post-movement testing.

Herd incidence and prevalence

Three measures of incidence are presented in Table 3.1 for GB and at a country level: new OTFW breakdowns identified per 100 live herds, per 100 unrestricted herds tested in 2013 and per 100 herd years at risk. For simplicity, estimates based on herd years at risk are presented in the Executive Summary.

- In GB, total incidence in 2013 was 7.6 per 100 herd years at risk, unchanged from 2012 (7.6).
- In England, incidence was 8.7 herd years at risk, almost identical to 2012,
  - OTF-W incidence decreased by 2.0% and OTF-S increased by 2.6%
- In Wales, incidence dropped from 8.7 to 7.6 herds per 100 herd years at risk, a 13% decrease relative to 2012 and this was recorded across all types of breakdowns.
- Scotland also recorded a large (-35%) relative decrease in total incidence from 0.56 to 0.36 herds per 100 herd years at risk, although this was represented largely in a decrease in OTF-S incidence from 0.42 to 0.24 per 100 herd years at risk (-44%).

Nineteen counties had a crude herd incidence of over 4 OTF-W new breakdowns per 100 live herds in 2013, one more than in 2012 (Figure 3.3). In three groups, these were:

- Incidence more than 12%: Avon, Devon, Gloucestershire, Herefordshire, Shropshire and Wiltshire, all in the English High-Risk Area (HRA);
- Incidence 8 to 12%: Staffordshire & Cornwall in the HRA, and Mid Powys;
- Incidence 4 to 8%: 10 counties in the HRA and Edge areas, and in Wales.

The proportion of herds under restriction each month because of a TB breakdown (apparent herd prevalence) since 1986 to December 2013 is shown by country in Figures 3.2 a to c:

- In Scotland in 2013 it was 0.10% for total bTB breakdowns and 0.06% for OTF-W breakdowns;

- England’s increasing trend in the proportion of live herds under restriction (rising to 5.3% in late 2012) seems to decline to below 5% in late 2013.
  - Herds under OTF-W restrictions also seemed to drop from 4.5% to 4.2% in the same period.
- Wales had a higher proportion of live herds under restriction than any other part of GB, but recorded a 20% decrease 2013 (Figure 3.2b);
  - Total breakdowns fell from an average of 8.6% in 2012 to 6.8% in 2013;
  - OTF-W breakdowns fell an average of from 4.4% to 3.5%.
- There are fluctuations in apparent prevalence, both within-year and between-year; peaks are recorded in 2005 and 2009 and 2013. Therefore, short term changes should be interpreted in this context.

Duration of breakdowns in GB

Small changes in breakdown duration occurred between 2012 and 2013:

- For OTF-W, median durations were 9 days shorter in England, 11 days longer in Wales and over 2 months longer in Scotland (for only 6 breakdowns) (Table 4.1);
- For OTF-S, median durations were 18 days shorter in England, 5 days longer in Wales and 36.5 days longer in Scotland (for 32 and 25 breakdowns).

Persistent herds were defined as breakdowns lasting more than 550 days (18.06 months):

- The increase from 2012 to 2013 was not significant (from 10.7% to 11.9%);
- The increase was, however, relatively large in two circumstances:
  - in OTF-S breakdowns – from 16 (1.0%) to 34 (2.2%);
  - in OTF-W breakdowns in Wales – from 11.4% to 15.6%;
- There were no persistent herds in Scotland that closed in 2013 or in 2012.

Both OTF-W and OTF-S persistent breakdowns are clustered within the HRAs of England and endemic areas in Wales (Figure 4.5).

- Sporadic persistent breakdowns outside of the HRA closed in 2013;
  - OTFW breakdowns – Berkshire (Edge area), Cumbria, North Yorkshire, Lincolnshire, West Yorkshire and West Sussex (LRA).
  - OTF-S breakdowns – Leicestershire (Edge area), Suffolk and Gwynedd.

Routine slaughterhouse surveillance

A proportion of OTF-W new breakdowns were disclosed by slaughterhouse inspection in GB between 2012 and 2013

- This was stable in GB (21%) in 2012 and 2013 (Table 5.1).
- In England the proportions were 22.7% and 21.7% in 2012 and 2013;
  - Since 2010, over one fifth have been so detected in England (Figure 5.2);
  - England had 90% of GB SLH-disclosed OTF-W breakdowns in 2013, and Wales had 9.7%;
- In Wales the proportion rose from 13.0% to 14.7%;
  - Note that the proportion in Wales was 1.5 times smaller than in England;
- In Scotland the proportion fell non-significantly from 46% (6/13) to 25% (2/6).

- *M. bovis* was isolated from 71.1% of samples in 2012 and 2013 (Table 5.2), although the number of tissue samples submitted to AHVLA laboratories decreased by 3% between 2012 and 2013.

Post mortem examination and culture of suspected bTB animals slaughtered for TB control reasons

A proportion of tissue samples from animals that were reactors slaughtered for bTB control were submitted to an AHVLA laboratory for culture for *Mycobacterium bovis*:

- The proportion of VL samples yielding *M. bovis* was around 95%, but had been marginally higher in 2011 (Figure 6.1);
- The proportion of NVL samples yielding *M. bovis* was around 5% in 2013, slightly less than the average in 2012 (6%) having been 9% at the end of 2011.

Recurrence

Recurrence was measured in herds that had been under restriction in the 36 months before a breakdown in 2013:

- Over half of all OTF-W breakdowns in GB and England occurred in herds with a history of any bTB restriction in the previous 36 months (Figure 7.2 a-d);
    - In GB, there was a small increase, from 53.4% in 2012 to 54.1% in 2013;
    - This increase was typified by England, from 54.2% to 55.4%;
    - There was a decrease in Wales, from 50.6% to 47.5%.
    - There were no recurrent OTF-W breakdowns in Scotland.
- The proportion of OTF-S breakdowns in 2013 that were recurrent increased between 2012 and 2013 (also shown in Figure 7.2 a-d)
    - In GB, England and Wales it was around 44-45%; in Scotland, 6.7%.

Inconclusive reactors

IR-only herds are unrestricted herds having tests in which IR(s) but no reactor(s) are found. Figure 8.1 displays the geographical distribution of IR-only herds in 2012 that had an OTF-W new breakdown within the next 15 months.

- The proportion of such herds in endemic areas (W Midlands, South West, Welsh borders and S W Wales) that suffered an OTFW new breakdown within the following 15 months exceeded the proportion in areas peripheral to these (Figure 8.1).

Report on the **M. bovis** *genotype (spoligotype) database (SB4020)*

- There were 3,888 isolates spoligotyped in 2013 (2012 = 3939) including 3,735 cattle isolates and 153 isolates from non-bovine animals.

- For each cattle breakdown, an average of just over one isolate per breakdown was genotyped (2012 = 1.1). We obtained full genotype (spoligotype plus 6 locus VNTR) for 96% of the cattle isolates (representing 3,526 breakdowns, 2012 = 95%). There are 3,234 cattle isolates in the spoligotype database from breakdowns that commenced in 2013 (2012 = 3,367).

- The 153 non-bovine isolates genotyped in 2013 (2012 = 119) included 129 *M. bovis* and 24 *M. microti*. The 129 *M. bovis* isolates represent 91 separate non-bovine incidents (an incident includes multiple isolates from the same type of host at the same location). In general, the genotypes found in non-bovines reflect those found locally in cattle and are typical *M. bovis* genotypes. The exception is feline samples in which, as seen in previous years, *M. microti* isolates are common. Of the non-bovine incidents, 84% were either in homerange or within 10km of the equivalent cattle homerange.

- Reported incidents among sheep fell markedly in 2013 (4 incidents), having peaked in 2010-11 (8 to 17 incidents). However, incidents in swine remained high (22 incidents) since climbing from 5 incidents a year in 2007-8. Sheep and swine isolates had genotype frequencies representing the common genotypes found in cattle.

- Composite homerange maps of *M. bovis* genotypes for the 2009-2013 period are included, as well as a summary of insights from the bTB genotyping effort from 2000 to 2014.

Introduction

- This report, entitled *Bovine tuberculosis: Infection status in cattle. Annual surveillance report for the period January to December 2013* was commissioned by DEFRA and the Scottish and Welsh Governments under Project SB4500.
- Regional level reporting for England was discontinued in reports for 2011. Reporting is conducted in the present report at the country level. England and Wales receive a separate report detailing county and risk area level analyses.
- Detailed information relating to methods used in each section, and what is involved in the surveillance for each chapter, is described in the England surveillance report in the introduction and at the beginning of each chapter.
- There may be discrepancies with the figures provided by the National Statistics for bTB. Data presented in this report has been cleansed and sense-checked to eliminate inconstancies and duplications with the data recording system, SAM. Data are downloaded on different dates leading to small-scale discrepancies. The National Statistics appear to include singleton unconfirmed IR only breakdowns, and also negative slaughterhouse cases unaccompanied by subsequent reactors at a check test as OTF-S breakdowns while this report does not. In Wales, OTF-S breakdowns may be upgraded to OTF-W if there is a perceived epidemiological risk. AHVLA only count such breakdowns as OTF-S.

Body of the report

1. Cattle demographics in relation to TB

The geographical distribution of infected herds should be interpreted in the context of the registered locations of cattle herds. Figure 1.1 shows the wide variation in the number of herds per square km in Great Britain (GB), with large areas with fewer than 0.27 herds per km² in the East of England and North Scotland. There are a few areas where herd density is more than eight times greater; West Yorkshire, Staffordshire, south west England (Somerset, Devon and Cornwall) and areas in Wales (Anglesey, Carmarthenshire, Ceredigion, Clwyd and Pembrokeshire).

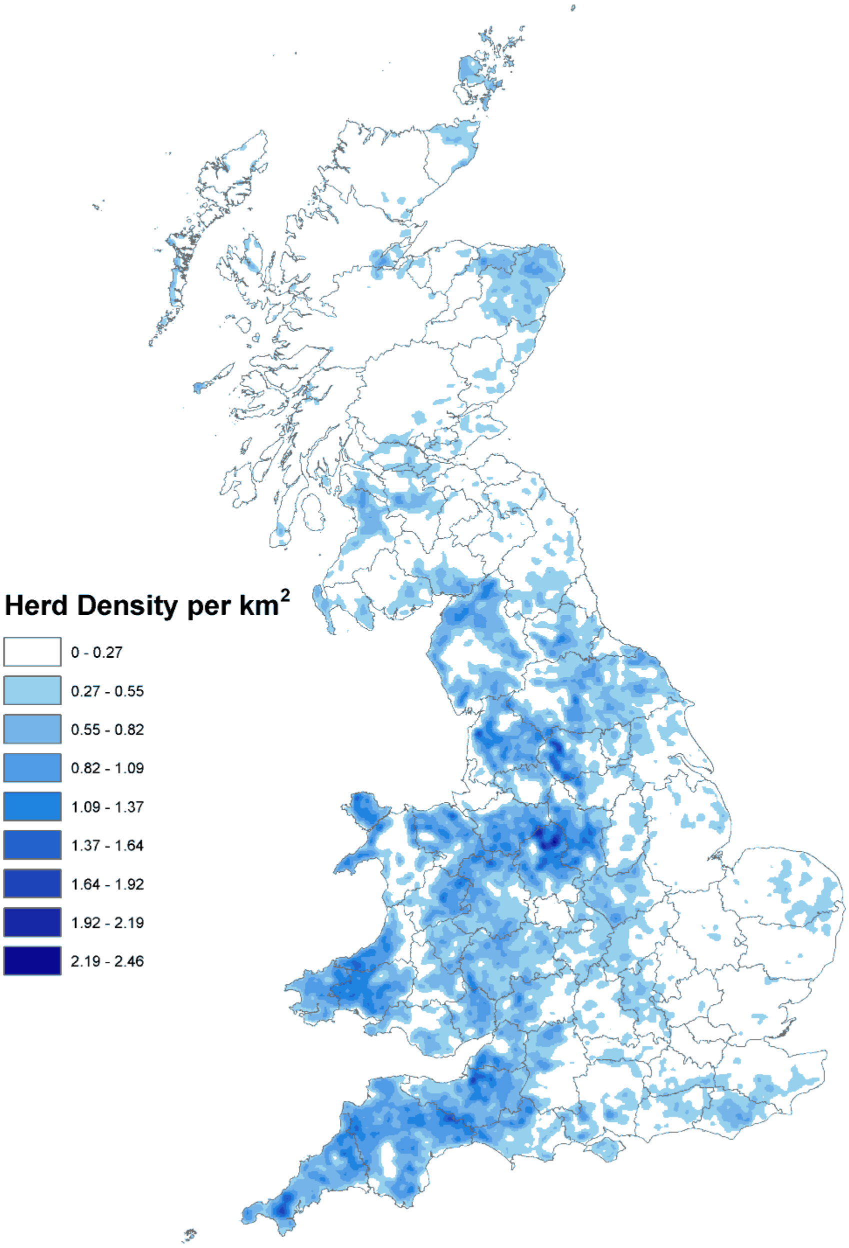


Figure 1.1: The density of live cattle herds registered on Sam in 2013

The number of live herds and total cattle has been reported in Table 1.1; there was little change in the number of live herds in GB in 2013 compared to last year (+0.02%) and the total number of cattle (-0.23%). There was a 3.3% increase in the number of cattle tests in GB but this seems to be largely made up of a 5.7% increase in the number of cattle tests in England, reflecting the greater frequency of testing as part of the “Edge” strategy and a reduction of almost 10% in cattle testing in Scotland as they move to a more risk-based approach.

Table 1.1: Numbers of live herds (herds recorded on Sam as “active” at the end of the calendar year), total numbers of cattle and cattle tested for regions of GB in 2012 and 2013

Reporting Region	**Number of live herds**			**Total number of cattle in live herds (thousands)**[1]			**Total cattle tests (thousands)**		
	2012	2013	Change (%)	*2012*	2013	Change (%)	*2012*	2013	Change (%)
England	*53,607*	53,712	+0.20%	*5,373.12*	*5,363.81*	-0.17%	*7,421.08*	7,840.80	+5.66%
Wales	*12,729*	12,676	-0.42%	*1,113.14*	*1,094.64*	-1.66%	*2,190.53*	2,179.91	-0.48%
Scotland	*12,984*	12,951	-0.25%	*1,788.47*	*1,797.32*	+0.49%	693.50	625.92	-9.74%
GB total[2]	*79,320*	79,339	+0.02%	*8,274.73*	*8,255.78*	-0.23%	*10,305.11*	10,646.63	+3.31%

[1] Sourced from Official DEFRA statistics

[2] Includes slaughterhouse throughputs

Herd size Demography

The distribution of different herd sizes (the denominator being the total herds in each country) within the three major herd types, by country, is shown in Figure 1.2. The majority of herds were beef, with a greater proportion in each country having smaller herd sizes, particularly in England and Wales.

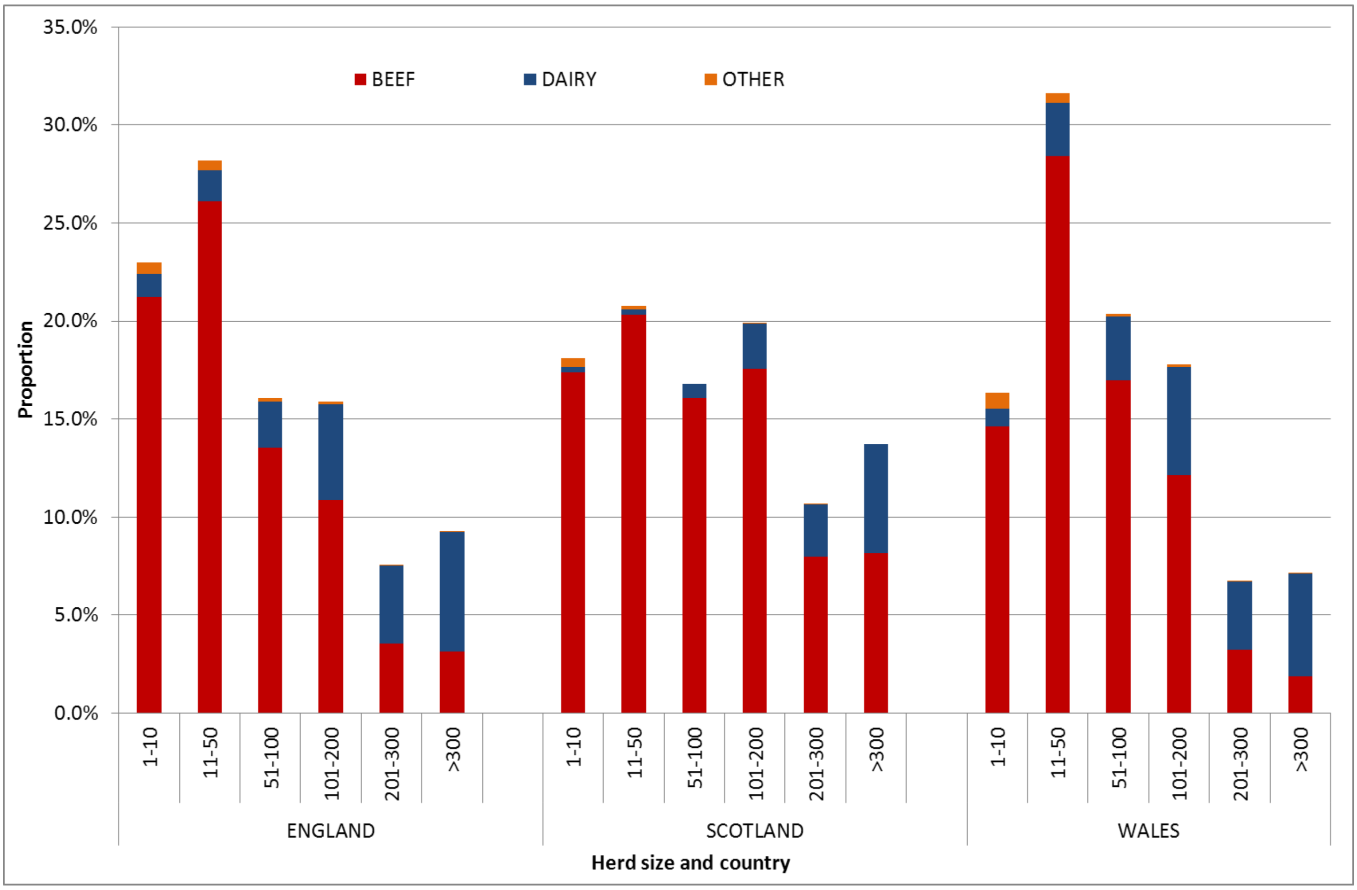


Figure 1.2: The distribution of herd sizes in 2013, by herd type and country.

Table 1.2 shows the total number of live herds by country and the number and proportion by herd type. The majority of herds in all countries were Beef herds with the highest proportion in Scotland (90%). The proportion of herds that were Dairy was similar in Wales and England (21% and 20% respectively). Only 10% of herds in Scotland are Dairy.

Table 1.2: Total number (and proportion) of live herds (herds recorded on Sam as "active" at the end of the calendar year) by country and herd type in 2013.

Country	**Total no. herds**	**Herd type**					
		Beef		**Dairy**		**Other**	
		Total	**%**	**Total**	**%**	**Total**	**%**
England	53712	42296	78.7%	10611	19.8%	805	1.5%
Wales	12676	9840	77.6%	2629	20.7%	207	1.6%
Scotland	12951	11547	89.2%	1315	10.2%	89	0.7%
GB	79339	63683	80.3%	14555	18.3%	1101	1.4%

2. The number and geographical distribution of new breakdowns and reactor density

New, OTF-W and OTF-S new bovine TB breakdowns in GB in 2012 and 2013 are shown in Table 2.1. In 2013, there were a total of 4,775 new breakdowns in GB, 3,249 OTF-W and 1,513 OTF-S, and 13 breakdowns were unclassified.

There was a 3% drop in the total number of new breakdowns in GB but this masks large decreases in Wales and Scotland and a 3% increase in the number of new breakdowns in England. In Wales, the total number of new breakdowns, new OTF-W and OTF-S breakdowns all decreased by around a fifth between 2013 and 2012 and in Scotland there were almost half as many breakdowns in 2013 compared with 2012. In England, there was little change in the number of OTF-W breakdowns (+1%) but there was a 6% increase in the number of OTF-S breakdowns.

There was a small, non-significant drop in the proportion of new breakdowns that were OTF-W from 73.1% (2012) to 72.0% in 2013. The country distributions of OTF-W or OTF-S new breakdowns were not significantly different between 2012 and 2013 ($p>0.05$). OTF-W breakdowns were distributed across the three countries differently in 2013 compared to 2012 ($\chi^2=11.9$, 2 df $p=0.003$) with a higher proportion of OTF-W breakdowns recorded in England and a lower proportion of breakdowns in Wales and Scotland.

Table 2.1: The number of OTF-W and OTF-S new breakdowns in 2012 and 2013, overall and by country

GB new Breakdowns	**Total breakdowns**[1]			**OTF-W**			**OTF-S**		
	2012	**2013**	**% change**	***2012***	**2013**	**% change**	***2012***	**2013**	**% change**
England	*3775*	3885	+2.9%	*2759*	2799	+1.4%	*1012*	1075	+6.2%
Wales	*1091*	867	-20.5% ***	*547*	442	-19.2% *	*540*	423	-21.7% **
Scotland[2]	*53*	23	-56.6% *	*13*	8	-38.5%	*40*	15	-62.5% *
Total GB	*4919*	4775	-2.9%	*3319*	3249	-2.1%	*1592*	1513	-5.0%

[1] 13 breakdowns were unclassified in 2013 (11 in England and 2 in Wales); 8 in 2012 (4 in England and 4 in Wales)
*, **, *** - statistical significance of change between 2012 and 2013 was <0.05, 0.01, 0.001 (Fisher's Exact test, null hypothesis was that the expected numbers for the two years were equal
[2] These breakdowns are associated with the temporary CPH (988568888) that was set up for cases imported directly into Scotland for slaughter have not been included.

Maps of new breakdowns

The distribution of OTF-W new breakdowns in GB in 2013 (inset: 2012) is shown in Figure 2.1. Counties with new OTF-W breakdowns in 2013 that had not suffered an OTF-W breakdown in 2012 included: Argyll (2) and Kirkcudbright (1) in Scotland and Bedfordshire (1), Durham (1) and Suffolk (1) in England. Those counties with one or more OTF-W breakdown in 2012 and none in 2013 included: Aberdeenshire, Ayrshire, Berwickshire, East Lothian, Kincardine, Lanarkshire, West Lothian and Wigtown in Scotland, and Isle of Wight, Surrey and West Sussex in England.

In counties where sufficient number of OTF-W breakdowns have occurred in both 2012 and 2013 to record relevant changes between years, larger increases were observed in Avon (+30%), Cheshire (+23%), Staffordshire (+12%), Oxfordshire (+41%) and

Warwickshire (+81%) in England and Gwent (+7%) in Wales. Similarly, decreases were observed in Derbyshire (-36%) in England, and Clwyd (-34%), Dyfed (-33%) and Powys (-10%) in Wales.

The distribution of OTF-S new breakdowns in 2013 (inset: 2012) is shown in Figure 2.2. As in previous reports, OTF-S breakdowns have been split into two categories; those with zero or one reactor at the time of data download, and those with greater than one.

More OTF-S breakdowns with multiple reactors were recorded in Avon, Cheshire, Derbyshire, Devon and Shropshire in England and Clwyd in Wales in 2013 compared to 2012. There were no OTF-S breakdowns with more than one reactor in Scotland in 2013, compared with 8 in 2012. All counties in Wales except Clwyd and South and West Glamorgan recorded a decrease in OTF-S breakdowns with more than 1 reactor.

Increases in the number of OTF-S breakdowns with 0-1 reactors were recorded in Cheshire, Cumbria, Dorset, Hampshire, Lancashire and Nottinghamshire in England. Scotland recorded reduction in most counties between 2013 and 2012, although Peebles, Lanarkshire and Stirling all recorded at least one OTF-S breakdown with 0-1 reactors in 2013 where there were none in 2012. All counties in Wales except West Glamorgan recorded the same or fewer number of OTF-S breakdowns with 0-1 reactors.

Figures 2.3 and 2.4 display OTF-W and OTF-S breakdowns, respectively, according to three categories: 1, *new* breakdowns that began in 2013 (and may or may not end in 2013), 2, *closed* breakdowns that began prior to 2013 and end in 2013, and *existing* breakdowns that are open throughout 2013. Most OTF-W new breakdowns are found in similar locations to existing breakdowns. Spread of new breakdowns northwards and eastwards can be observed in the following counties; Buckinghamshire, Cumbria, Lancashire, Leicestershire, Northamptonshire, North Yorkshire and Nottinghamshire.

The distribution of new, existing and closed OTF-S breakdowns in GB is displayed in Figure 2.4.

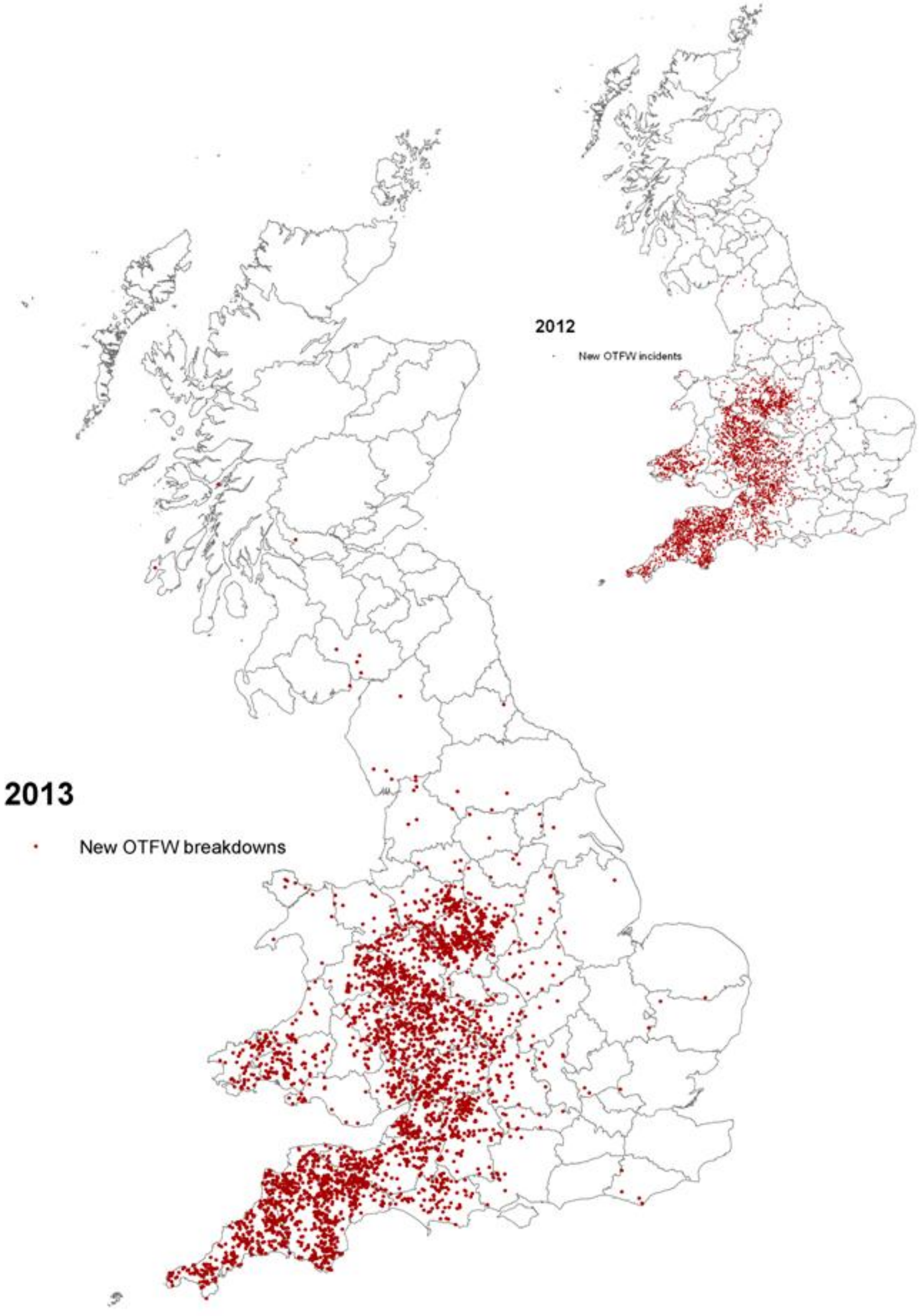


Figure 2.1: Geographical distribution of OTF-W new bovine TB breakdowns between January and December 2013, with inset showing the distribution of OTF-W new breakdowns in 2012

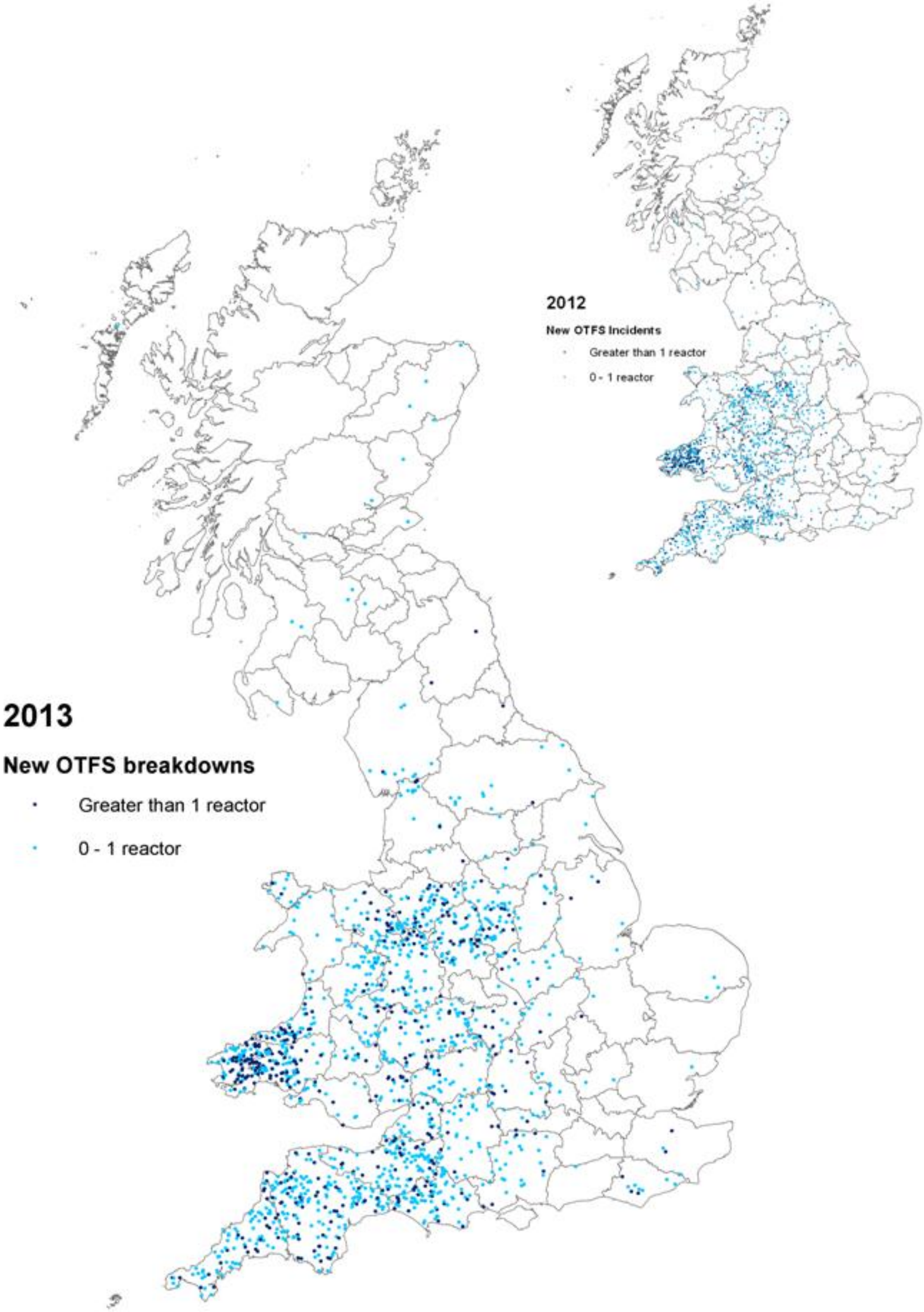


Figure 2.2: Geographical distribution of OTF-S new bovine TB breakdowns between January and December 2013, with inset showing the distribution of OTF-S new breakdowns in 2012

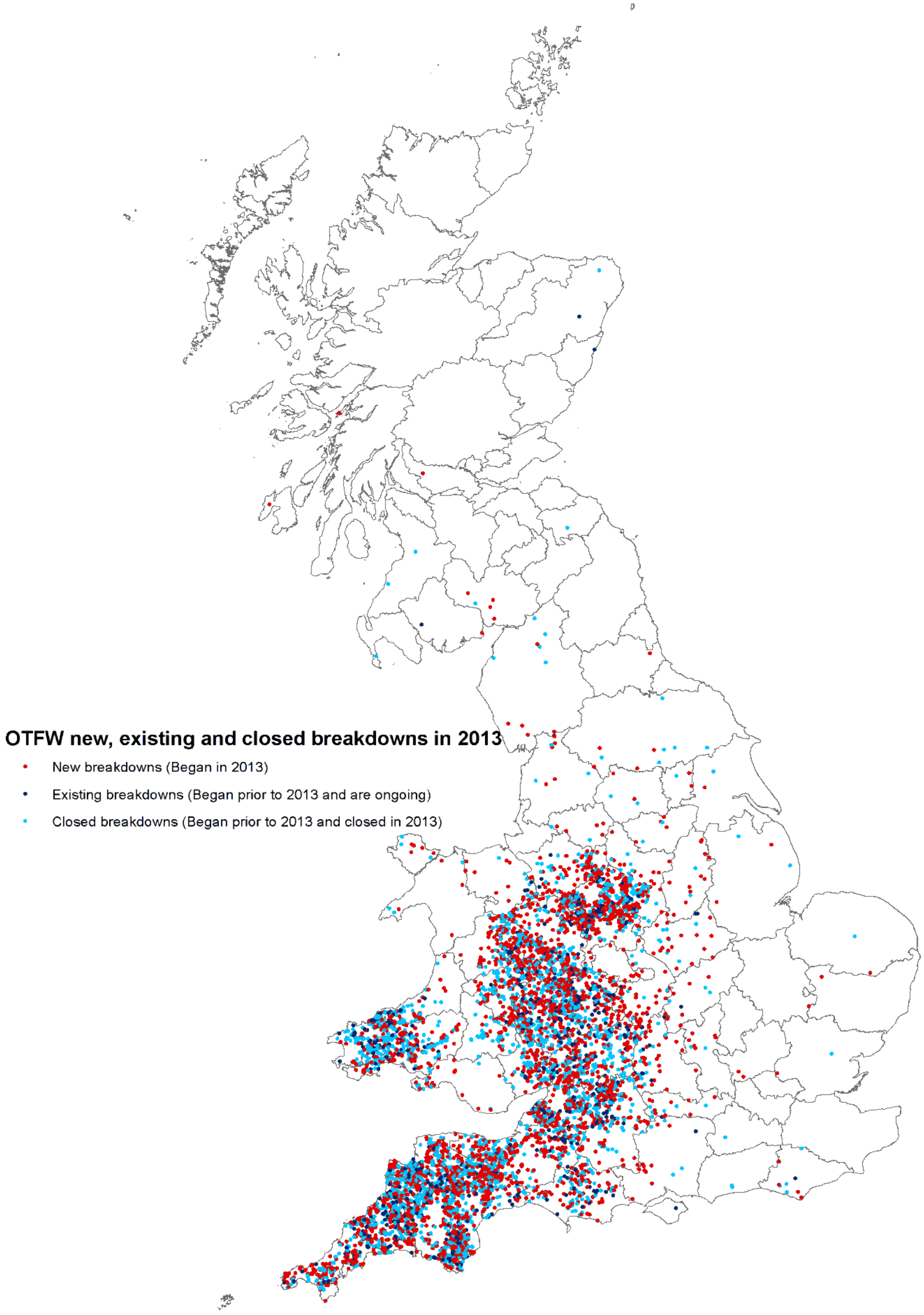


Figure 2.3: OTF-W new, existing and closed breakdowns in 2013

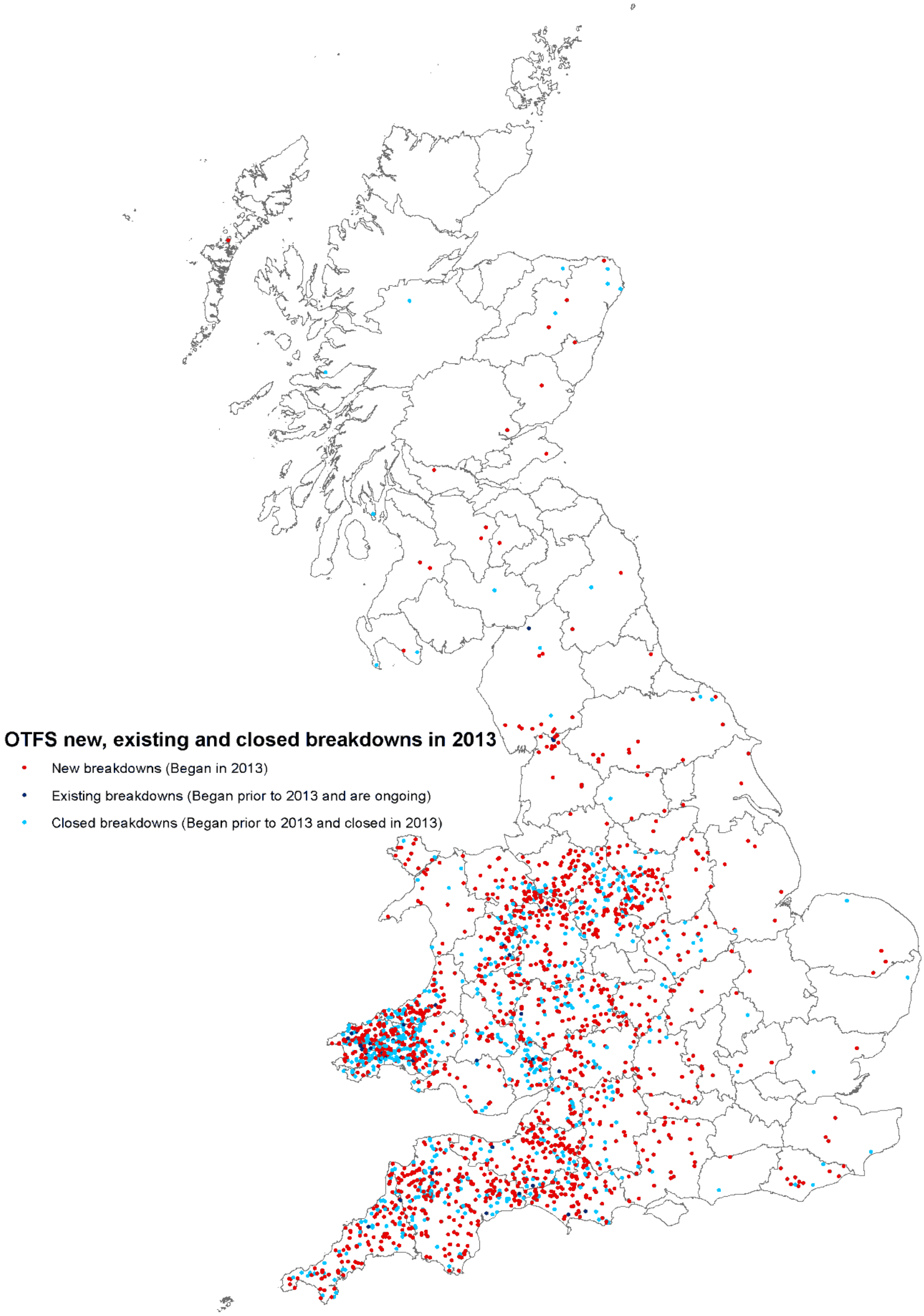


Figure 2.4: OTF-S new, existing and closed breakdowns in 2013

Trends in the proportion of new TB breakdowns with post mortem evidence of infection (OTF-W as a proportion of total breakdowns)

The monthly proportion of breakdowns that were OTF-W in GB between 1986 and 2013 is shown in Figure 2.5 showing an increasing trend (R^2=0.61, P<0.001), although the moving 12-month average has plateaued through 2013. The increasing trend in the proportion of OTF-W new breakdowns is more pronounced prior to 2002, the 10-year trend from 2004 to 2013 shows a much weaker, although significant, relationship with time (R^2=0.20; P<0.001). The proportion of total breakdowns that were OTF-W in 2013 was on average 68% which was a slight increase from 2012 (67%). As in 2012, there was a seasonal pattern, with the proportion increasing to over 70% in the latter part of the year (October to December).

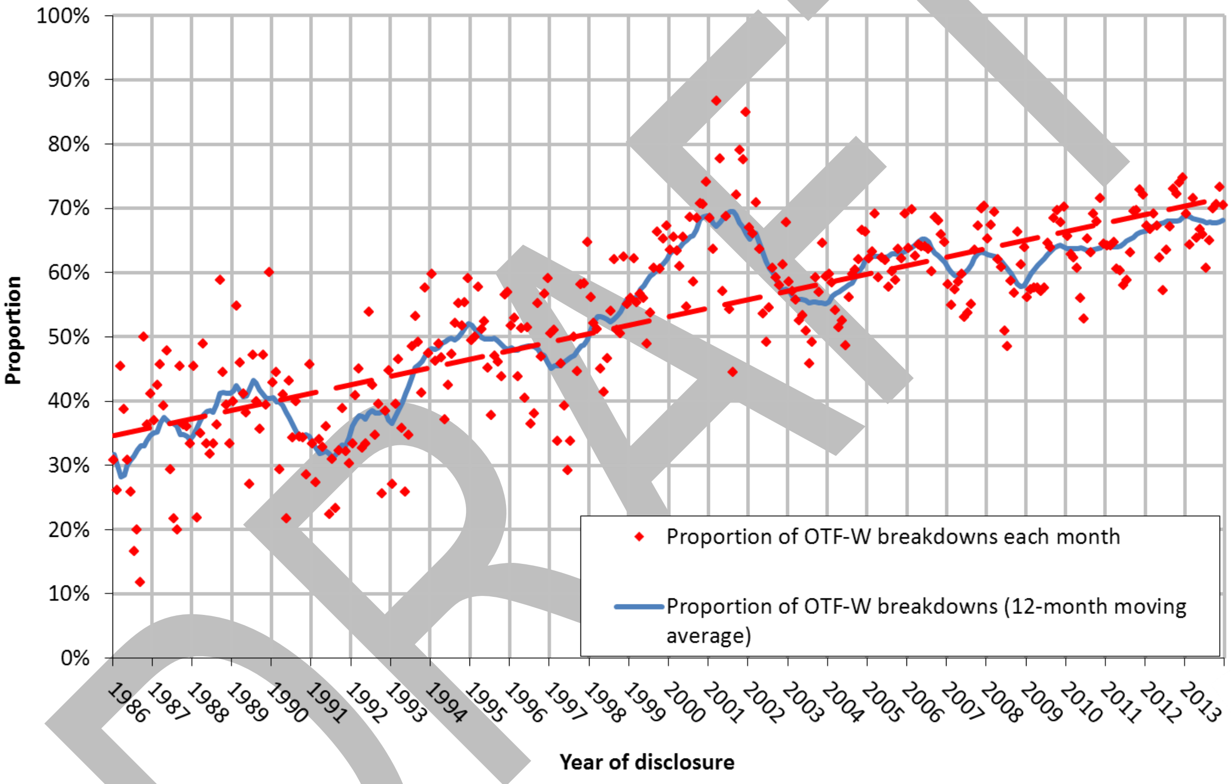


Figure 2.5: Proportion of new TB breakdowns that were OTF-W in GB per month from January 1986 to December 2013

Effect of skin test type on the disclosure of breakdowns

Table 2.2 describes breakdowns in which the *herd movement restrictions* began in 2013, therefore in breakdowns disclosed by an IR retest, for example, the initial surveillance test would have occurred 60 or more days beforehand, even in the previous year. The breakdown is included if the IR retest was in 2013, even if the disclosing test was the year before.

In herds not under restriction, animals may be tested for different reasons. As part of the denominator, we considered nearly 1.9 million routinely slaughtered cattle as having been tested by slaughterhouse inspection in 2013.

Routine skin tests accounted for 31.6% (n=2,133,067) of the total tests carried out in unrestricted animals and 0.5% of the total (n=30,696) were in new herds (see Appendix 6 for a full list of surveillance test types and reason for the test, within each category). Seventeen percent of tests (17.5%, 1,180,289) were carried out in animals perceived to be at an increased risk of bTB ('**Herd risk**'), for example due to a recent bTB incident. '**Area risk**' tests include those for contiguous herds and herds within 3km of an OTFW breakdown in the Low Risk and Edge Areas of England (enhanced 'radial' testing) and accounted for 10.5% (710,740) of the total. **Post-mortem meat inspection** of non-reactor cattle at routine slaughter accounted for a further 28% of all unrestricted animal 'tests', and succeeded in detecting 14% of total new bTB breakdowns and 21% of OTF-W new breakdowns.

A total of 1.5% (n=102,901) of 'surveillance tests' were test types normally classed as **disease control tests** (e.g. short interval tests), which could have been so labelled when only part of the herd was under restriction, but also include check tests not necessarily performed during a breakdown. In 2013, 9% (606,317) of tests conducted were **pre- and post-movement and private tests**, and a further 1% (70,348) of tests conducted were related to other '**movement risk tests'** such as bulls entering semen collection centres (AI), exports, imports and forward tracing (FT) tests.

Compulsory pre-movement testing (PrMT) detected 770 breakdowns (502 OTF-W). This represents almost 8% of all breakdowns (7.6% OTF-W) in GB, 7.9% of breakdowns in English herds and 8.5% of breakdowns in Welsh herds. One breakdown was detected in Scotland by post-movement testing.

In GB in 2013, 60% of total new bTB breakdowns and 55% of OTF-W breakdowns were detected through routine and herd risk tests. When calculated as a proportion of the total tests undertaken within each test type category, larger proportions of breakdowns were detected per 1,000 herd and movement risk tests, and disease control tests.

Table 2.2: Number of TB animal tests on unrestricted herds and their associated breakdowns (with numbers of inconclusive reactor tests[1] that initiated movement restrictions), and the rate of new breakdowns detected per 1000 animals tested

Surveillance test type[2]	**Thousands of surveillance tests on animals**	**Proportion of total tests**	**Number of new breakdowns[1]**	**Number of OTFW new breakdowns[1]**	**Breakdowns per 1000 animal tests**	**OTFW breakdowns per 1000 animal tests**
Routine	2133.1	31.6%	1544 (417)	927 (172)	0.72	0.43
Herd Risk	1180.3	17.5%	1314 (296)	889 (149)	1.11	0.75
Slaughterhouse[3]	1883.3	27.9%	687 (0)	673 (0)	0.36	0.36
Area Risk	710.7	10.5%	593 (205)	349 (86)	0.83	0.49
Pre- & post-movement tests[4]	606.3	9.0%	393 (76)	254 (34)	0.65	0.42
Movement Risk [5]	70.3	1.0%	111 (15)	82 (12)	1.58	1.17
Control	102.9	1.5%	89 (9)	47 (0)	0.86	0.46
New Herds	30.7	0.5%	27 (5)	18 (1)	0.88	0.59
Other	22.1	0.3%	16 (3)	10 (2)	0.72	0.45
IR retest	5.4	0.1%	1 (1)	0 (0)	0.18	0.00
Total[6]	6745.2	100.0%	4775 (1027)	3249 (456)	0.71	0.48

[1] The number in parentheses represents breakdowns in which movement restrictions did not commence (in 2013) until an IR was taken as a reactor in a VE-IR test.

[2] See Appendix 5 in the England surveillance report for an explanation of the tests included in each category, including reason for test, and an explanation of the test codes. The denominator for all test codes is all animals not under restriction.

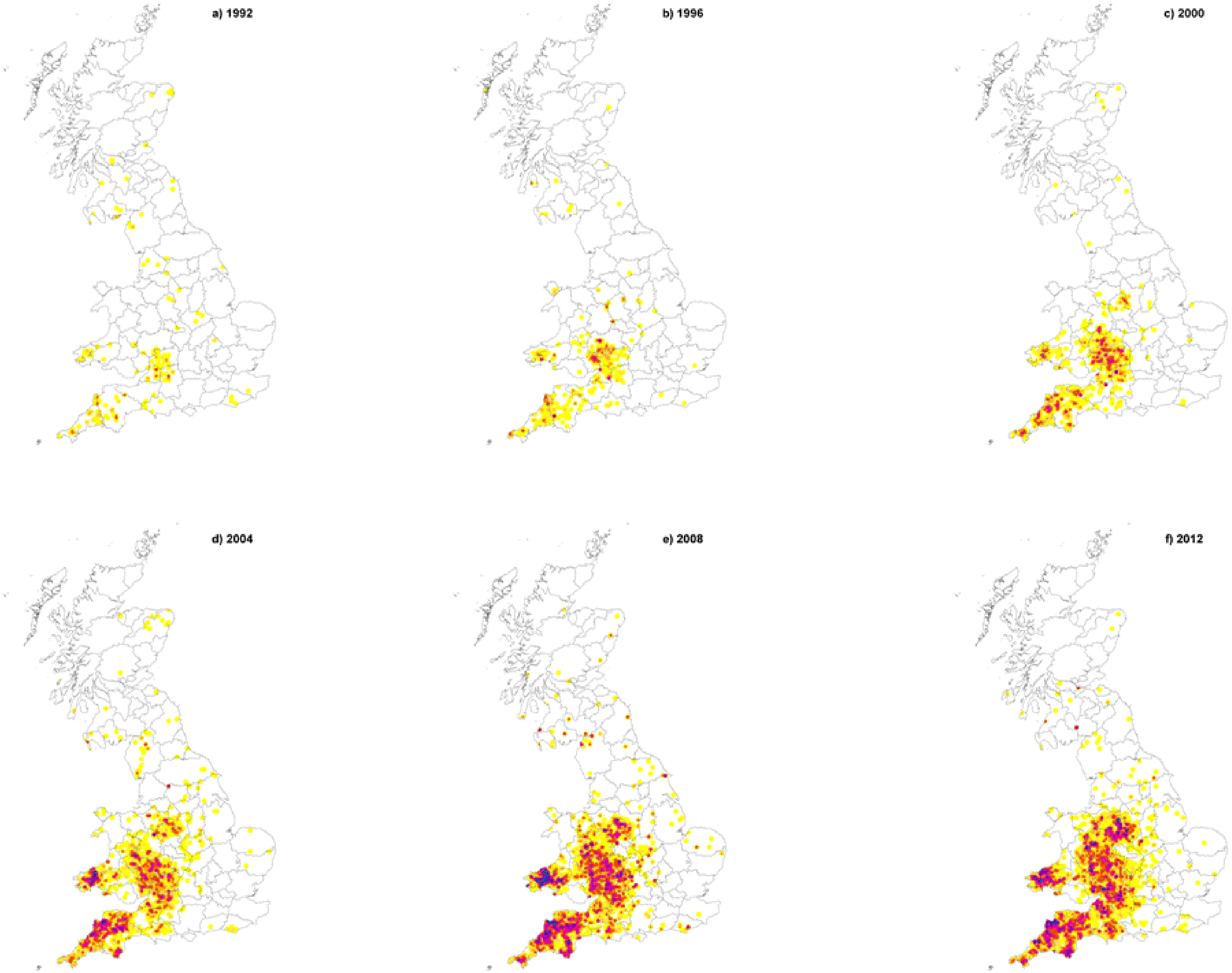
[3] The denominator is the number of animals slaughtered in GB in 2013 from unrestricted herds, as recorded in CTS.

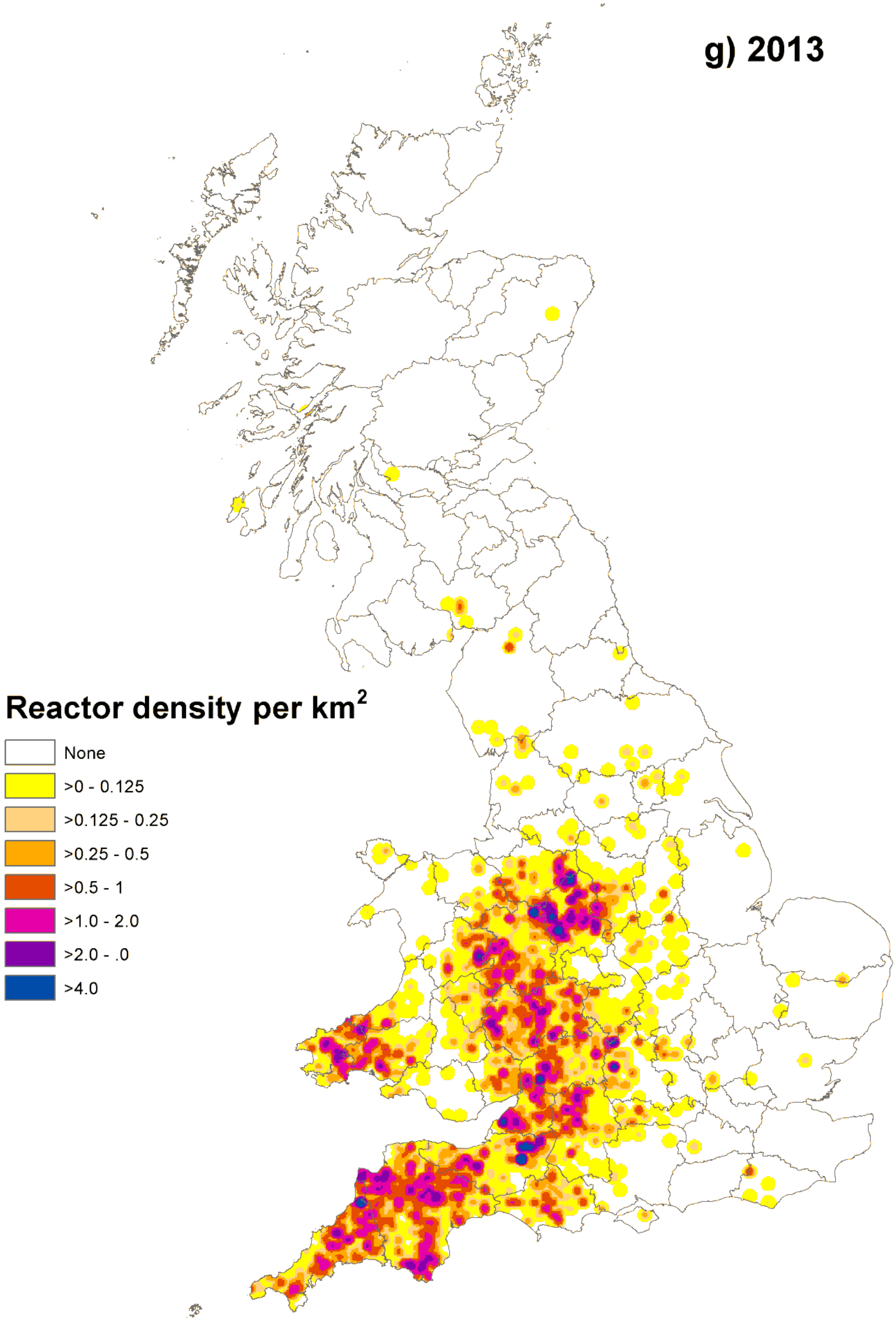
[4] Refers to movements to AI centres, exports from GB, imports from Ireland and other countries and forward tracing test.

[5] Excludes tests when under restrictions

Reactors and slaughterhouse cases: spatial density per km² and number per breakdown

The density of bTB infected cattle in herds per km² at four-yearly intervals from 1992 to 2012 and the situation in 2013 is shown in Figures 2.6 a to g. These figures show the increase in the density of reactors over the historic intervals (1992 to 2013) in the west of England and Wales. From 2004 there were substantial areas where the density of reactors was greater than 1 per km^2. Only animals in OTF-W breakdowns that were tested during the reporting year are included in this figure, and comprise skin test reactors, IFN-gamma test reactors and culture-positive slaughterhouse cases. Data was calculated for 5 x 5 km² map squares and was kernel-smoothed using a 6 km search radius. In 2013, endemic areas in the West of England and Wales (Dyfed and Powys) and in Staffordshire contained substantial areas in which the density was greater than 1 per km^2.


a) 1992
b) 1996
c) 2000
d) 2004
e) 2008
f) 2012



Figures 2.6 a to g: Density of skin test, IFN-gamma test reactors and slaughterhouse cases in OTF-W breakdowns per km² taken in a)1992, b) 1996, c) 2000, d) 2004, e) 2008, f) 2012 and g) 2013

The frequency distribution and median number of reactors removed in each OTF-W breakdown that closed in 2013 (whether the breakdown started during or before 2013) by country is shown in Table 2.3. Overall, the proportion of OTF-W breakdowns with two or more reactors was 67.9% (66.8% in 2012). The total number of OTF-W breakdowns (that closed in 2013) increased by 17.7% compared to that reported in 2012 but this summarises a 16.2% increase in England and a 26.1% increase in Wales. However, if this is calculated using data for 2012 that has been refreshed in 2014, this increase falls to 9.7% for England and 20.4% for Wales for OTF-W breakdowns. This is likely a result of inconsistencies in TB10 notices produced in 2012, and subsequently amended in SAM.

Table 2.3: Frequency distribution of total number of reactors taken in each OTF-W incident that closed in 2013, by country

	Number of animals reacting positively to the IFN-gamma or skin test and percentage of row totals										
Reporting Region	**Nil[1]**	**1**	**2-5**	**6-10**	**11+**	**Total OTF-W break-downs**	**Proportion with 2 or more reactors**			**Median[3] number of reactors (IQR)**	
							2013	***2012***	**% change**	**2013**	***2012***
	… Number of herds (and percentages) within reporting country …										
England	349 (11.7)	664 (22.3)	1009 (33.8)	422 (14.1)	540 (18.1)	2984	66.1%	*65.9%*	0.2%	3 (1 to 7)	*3* *(1 to 8)*
Wales	43 (7.1)	99 (16.3)	202 (33.2)	96 (15.8)	168 (27.6)	608	76.6%	*71.2%*	7.7%	5 (2 to 12)	*3* *(1 to 9)*
Scotland	0 (0)	0 (0)	3 (50)	0 (0)	3 (50)	6	100.0%	*83.3%*	20.0%	10 (2 to 15)	*4.5* *(3 to 6)*
All GB	**392**	**763**	**1214**	**518**	**711**	**3598**					
2013	**10.9%**	**21.2%**	**33.7%**	**14.4%**	**19.8%**		**67.9%**		**1.7%**	**3** **(1 to 8)**	
2012[2]	*12.2%*	*21.0%*	*34.0%*	*13.5%*	*19.2%*	*3056*		*66.8%*			*3* *(1 to 8)*
% change	-1.34%	+0.23%	-0.26%	+0.85%	+0.52%	+17.74%					

[1] Breakdowns with no reactors throughout the incident are those with inconclusive reactors taken and breakdowns resulting from slaughterhouse cases that yielded no reactors in a subsequent check test.

[2] 2012 data was revised as a result of the number of amendments to TB10s

[3] The mean (sd) number of reactors in 2013 was England 6.3 (16.3), Scotland 8.7 (25.6), Wales 9.6 (35.8) and total GB 7.0 (22.2). In 2012 the mean (sd) number of reactors was England 6.1 (17.2), Scotland 3.1 (10.5), Wales 6.4 (19.2) and total GB 6.1 (17.6).

The density of skin test reactors in *OTF-S* new breakdowns per km^2 is shown in Figure 2.7. This map was created using the same kernel smoothing parameters and hence it has the same legend as Figure 2.6, *above*. The broad geographical distribution of reactor densities in OTF-S breakdowns was similar in both 2012 and 2013. However, there were lower densities of reactors in OTF-S breakdowns in counties in South West Wales in 2013 compared to 2012 as well as in Staffordshire, the border of Herefordshire and Warwickshire, Leicestershire and South West England. There were slight increases observed in Cheshire, Nottinghamshire and Oxfordshire in 2013 when compared to 2012.

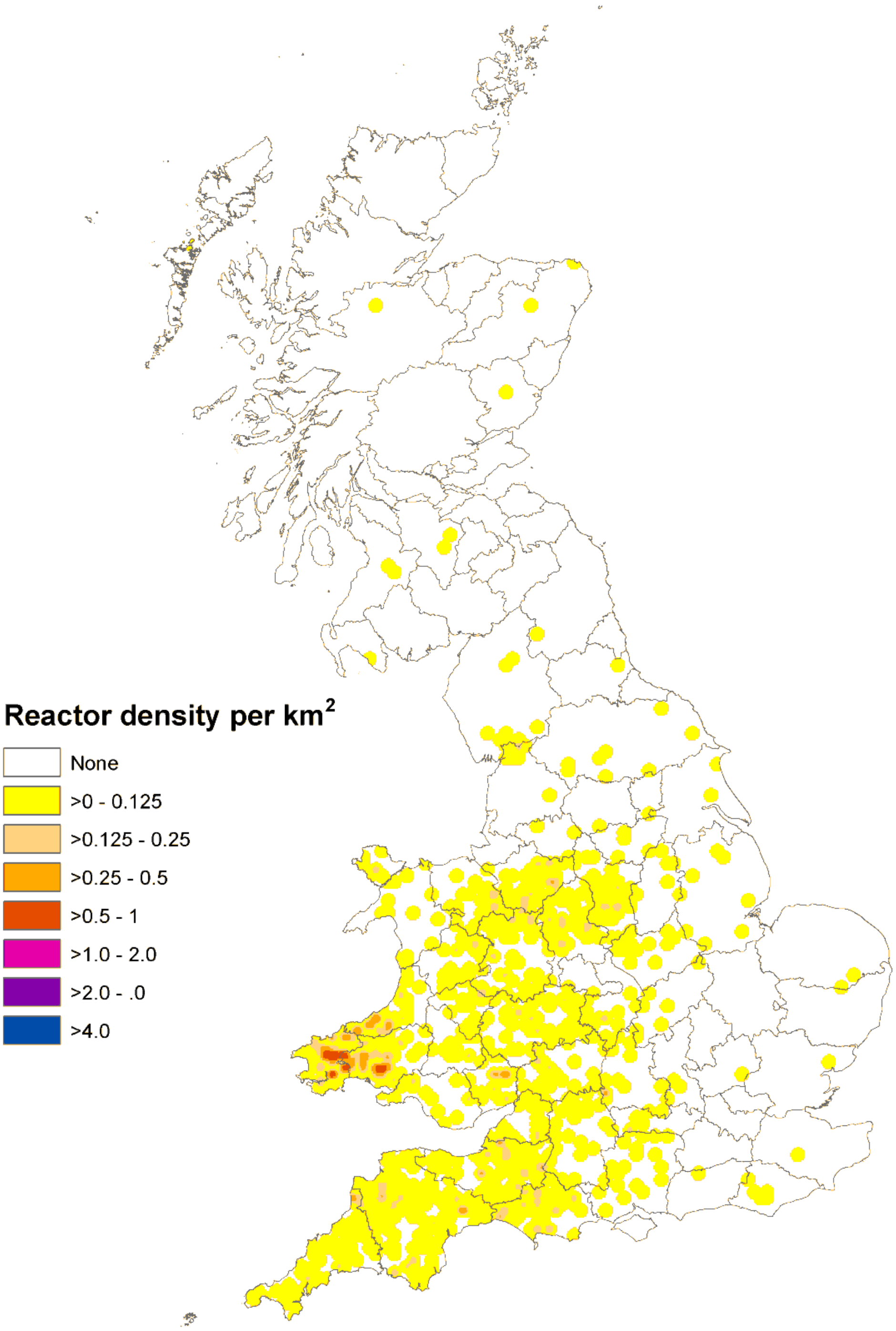


Figure 2.7: Density of skin test reactors taken in OTF-S breakdowns per km^2 in 2013

3. Herd incidence and prevalence; by country and at county level

The incidence of total bTB, OTF-W and OTF-S breakdowns per 100 live herds, per 100 *unrestricted* herds actually tested and per 100 herd years at risk, by country, are given in Table 3.1 (methods described in the England TB surveillance report under 'Classification of incidents'). Overall, a greater proportion of breakdowns (total bTB and OTF-W) were incurred per 100 unrestricted herds tested, as expected, in GB overall and in each country, compared to the proportion incurred per 100 live herds, as the denominator is smaller. Overall in GB, the incidence of total bTB, OTF-W and OTF-S breakdowns per 100 live herds and per 100 *unrestricted* herds declined in 2013. This masks substantial decreases in incidence in Wales and Scotland between 2013 and 2012.

In England in 2013 for all and OTF-W breakdowns, a small increase was recorded when incidence is defined as breakdowns per 100 live herds. When calculated using the number of herds actually tested or per herd years at risk, this becomes a small decrease relative to 2012.

In Wales large decreases of up to 21% were recorded across all types of breakdowns. When testing is accounted for, particularly herd years at risk, the magnitude of these decreases are somewhat reduced, reflecting the increased testing in Wales. However, each of the three methods for calculating incidence reflected a genuine decrease in total, OTF-W and OTF-S incidence in 2013, relative to 2012 of at least 11%.

Substantial decreases in all measures of incidence were recorded in Scotland between 2012 and 2013, although these must be interpreted conservatively given the low numbers of breakdowns involved. The larger values for incidence when it is calculated as per 100 herds tested, reflects the lower number of herd tests conducted in Scotland in 2013 and the risk profile of the herds that did undergo testing.

Table 3.1: The proportion of total, OTF-W and OTF-S new breakdowns in 2013 and 2012 per 100 live herds, per 100 unrestricted herds tested and per 100 herd years at risk, by country

	Total[1]			**OTFW**			**OTFS**			**Denominator**
	2012	**2013**	**% Rel. change**	***2012***	**2013**	**% Rel. change**	***2012***	**2013**	**% Rel. change**	
England										
Per 100 live herds[2]	*7.04*	7.23	2.7%	*5.15*	5.21	1.3%	*1.89*	2.00	6.0%	53,712
Per 100 *unrestricted* herds tested[3]	*12.21*	12.05	-1.3%	*8.92*	8.68	-2.7%	*3.27*	3.33	1.9%	32,251
Per 100 herd years at risk	8.74	8.69	-0.6%	6.39	6.26	-2.0%	2.34	2.40	2.6%	44,724
Wales										
Per 100 live herds[2]	*8.57*	6.84	-20.2%	*4.30*	3.49	-18.9%	*4.24*	3.34	-21.3%	12,676
Per 100 *unrestricted* herds tested[3]	*9.71*	7.81	-19.6%	*4.87*	3.98	-18.2%	*4.80*	3.81	-20.7%	11,102
Per 100 herd years at risk	8.71	7.60	-12.8%	4.37	3.87	-11.3%	4.31	3.71	-14.0%	11,408
Scotland										
Per 100 live herds[2]	*0.41*	0.18	-56.5%	*0.10*	0.06	-38.3%	*0.31*	0.12	-62.4%	12,951
Per 100 *unrestricted* herds tested[3]	*1.89*	1.02	-46.0%	*0.46*	0.35	-23.4%	*1.42*	0.66	-53.3%	2,257
Per 100 herd years at risk	0.56	0.36	-35.7%	0.14	0.13	-8.8%	0.42	0.24	-44.4%	11,408
GB total										
Per 100 live herds[2]	*6.20*	6.02	-3.0%	*4.18*	4.10	-2.1%	*2.01*	1.91	-5.0%	79,339
Per 100 *unrestricted* herds tested[3]	*10.94*	10.47	-4.3%	*7.38*	7.12	-3.5%	*3.54*	3.32	-6.3%	45,610
Per 100 herd years at risk	7.55	7.64	1.2%	5.09	5.20	2.1%	2.44	2.42	-0.9%	62,501

[1] Includes 13 unclassified breakdowns in 2013 (11 in England and 2 in Wales) and 8 in 2012 (4 in England and 4 in Wales).

[2] Denominators for the number of live herds shown is 2013. For 2012: England (53,607), Scotland (12,984), Wales (12,729) and GB (79,320).

[3] Denominators for the number of unrestricted herds tested shown is 2013. For 2012: England (30,925), Scotland (2808), Wales (11,239) and GB (44,972). In England, some herds (and in Scotland, nearly all herds) were tested at 4-year intervals; in addition, many low risk herds in Scotland were not routinely tested but relied upon slaughterhouse surveillance.

[4] Denominator for years at risk shown is 2013. For 2013: England (43,208), Scotland (9442), Wales (12,525) and GB (65,175).

The results of the three methods used to assess the scale of bTB in GB (and by country) are compared in Figures 3.1 a to c. The increasing trend observed in the incidence of OTF-W breakdowns per 100 live herds and per 100 unrestricted herds tested did not continue in 2013. In Scotland the incidence has remained below 0.2% across all years and in 2013 was well below 0.1% when calculated per 100 herds tested (3.1a) and per 100 herd years at risk (3.1c). The incidence per 100 live herds plateaued in 2013 for England, and showed a decline in Wales and GB overall (Figure 3.1a). The incidence of OTF-W breakdowns per 100 unrestricted herds tested showed a more obvious decline in 2013 across England, Scotland, Wales and GB (Figure 3.1b).

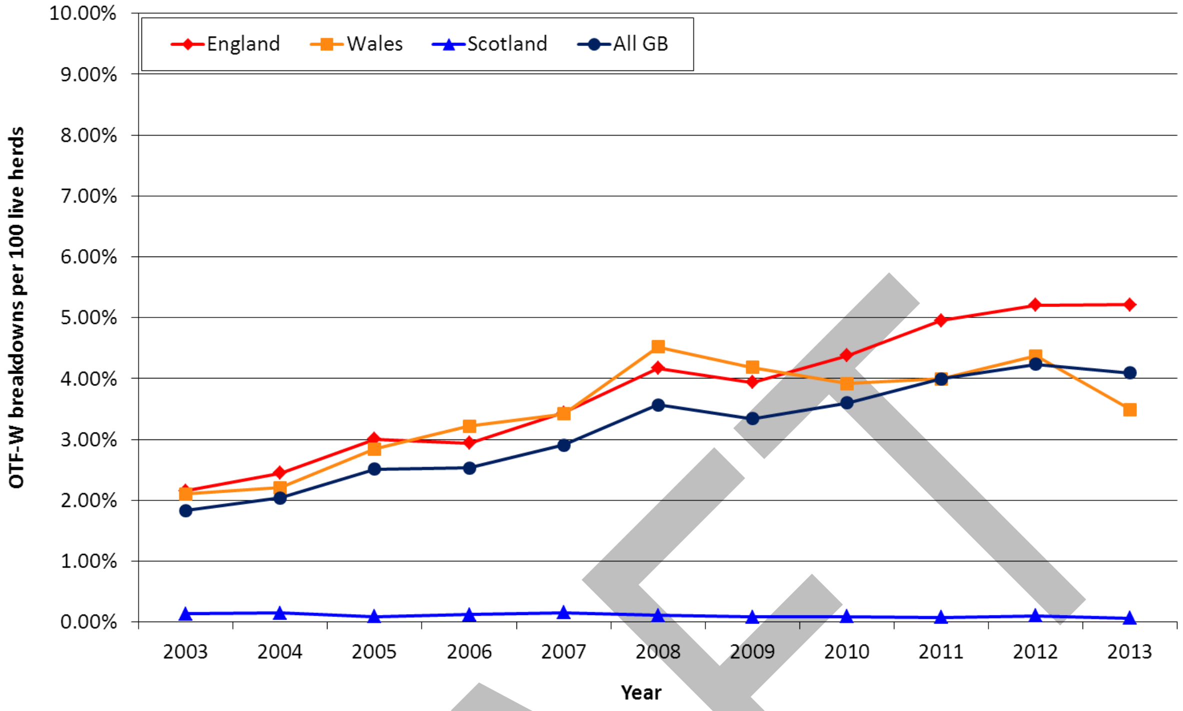


Figure 3.1a: Variation in the number of OTF-W new bovine TB breakdowns per 100 live herds between 2003 and 2013 by country

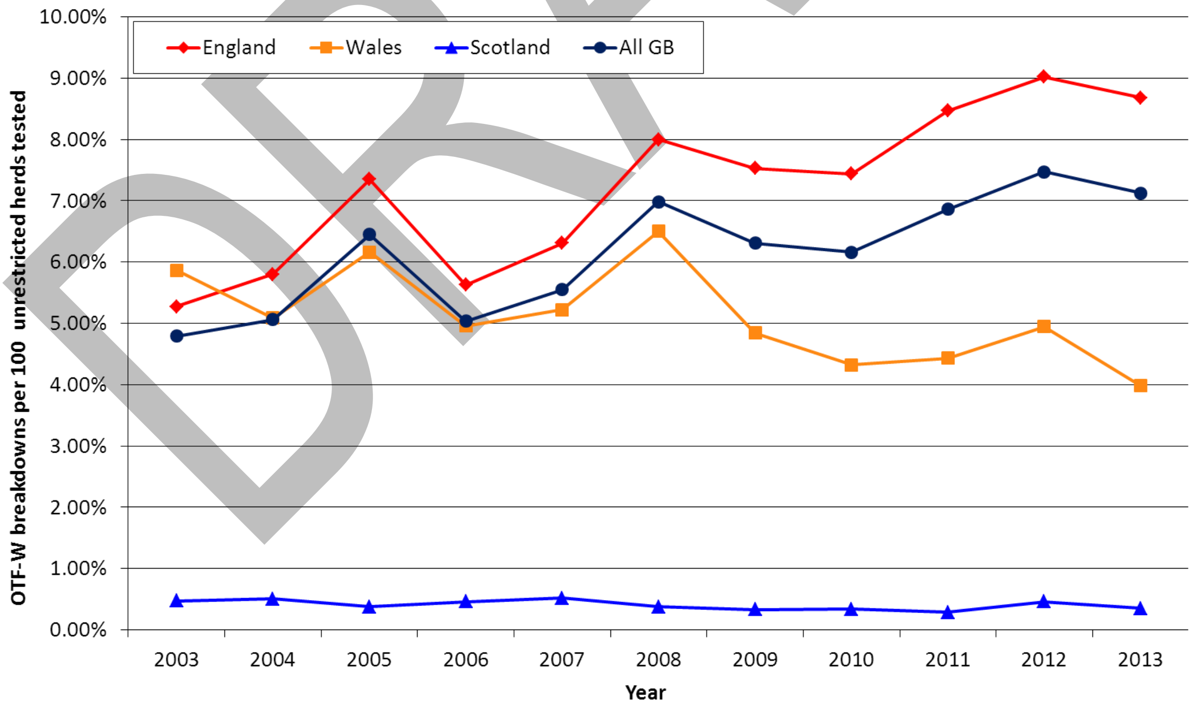


Figure 3.1b: Variation in the number of OTF-W new bovine TB breakdowns per 100 unrestricted herds tested between 2003 and 2013, by country

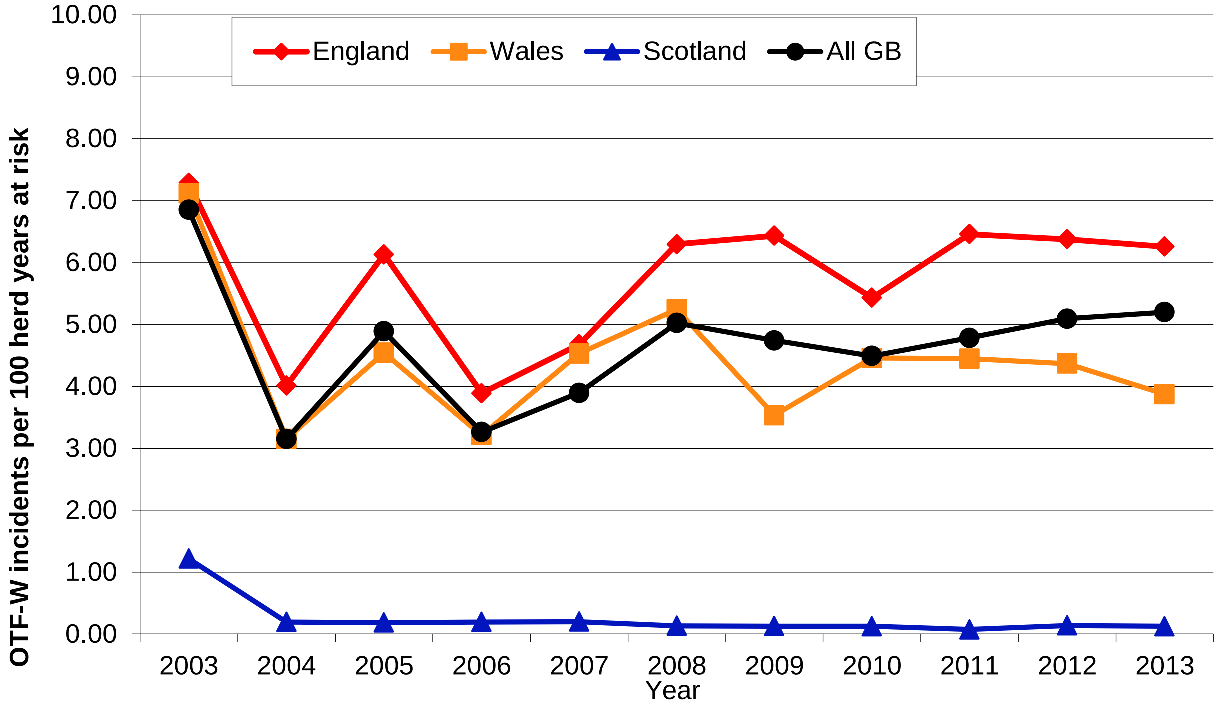


Figure 3.1c: Variation in the number of OTF-W new bovine TB breakdowns per 100 herd years at risk between 2003 and 2013, by country

When looking at the incidence of OTF-W breakdowns per 100 herd years at risk, the results mirrored slightly the incidence per 100 unrestricted herds tested, from 2004 to 2008 (Figure 3.1c). In GB overall, the decline from 2008 to 2010 has been reversed. In England, the number of OTF-W breakdowns per 100 herd years at risk increased up to 2009, decreased in 2010 and has since increased to similar numbers as seen in 2008/2009. In Wales, following the decline in the number of breakdowns per 100 herd years at risk in 2009, and an increase up to 2010 where it then plateaued there was a decrease between 2012 and 2013 and incidence is at its lowest since 2009.

Although OTFW breakdowns per 100 herd-years at risk decreased marginally in England, Wales and Scotland in 2013, the equivalent value for GB was slightly greater in 2013 than in 2012. While reductions in the number of breakdowns were recorded in Scotland and Wales, and a slight increase was recorded for England, there was a proportionately far larger reduction in the number of herd years at risk in Scotland (-32% drop between 2012 and 2013), as a result of their adoption of risk-based testing in 2013. While in 2012 Scotland accounted for 14% of the denominator, this has fallen to 10% in 2013, and the denominator, and thus the incidence measure in general, are now more heavily weighted towards the data from England.

Prevalence estimates

AHVLA and Defra use the term *prevalence* for the proportion of herds actually under movement restriction because of a TB breakdown. This is likely to be an underestimate, because most breakdown herds acquire infection at some time between the disclosing test and the previous whole herd test. The proportion of live GB herds under restriction at the middle of each month between January 1986 and December 2013 is shown in Figures 3.2a to c, by country. In Scotland, proportions remain at or below 0.1% (average of 0.10% for total bTB breakdowns and 0.06% for OTF-W breakdowns in 2013) (Figure 3.2c).

England has shown an increasing trend in the proportion of live herds under restriction up to late 2012 (smoothed average of 5.3% of total live herds under restriction) and has since declined to less than 5% at the end of 2013. The same pattern occurred for the proportion of herds under restrictions due to an OTF-W breakdown, but declining from 4.5% to 4.2% (Figure 3.2a). However seasonal trends are inherent in the data, and multiple fluctuations have occurred, even within the smoothed data, over the past 10 years, therefore short term increases and decreases should be interpreted with caution.

Wales had on average the highest proportion of live herds under restriction due to any bTB breakdown of any of the countries within GB, but a sharp decline (20% decrease) was recorded in 2013 (from an average of 7% in 2012 to 5.6% in 2013) (Figure 3.2b). The proportion of Welsh herds under restriction as a result of an OTF-W breakdown showed a similar pattern, decreasing from 4.4% to 3.5%. Again, there are seasonal, and between years fluctuations in the data over the past 10 years therefore changes in the data should be interpreted with caution. Substantial decreases in prevalence were also recorded between 2009 and 2010 but by April 2011 OTF-W prevalence was over 6.5%.

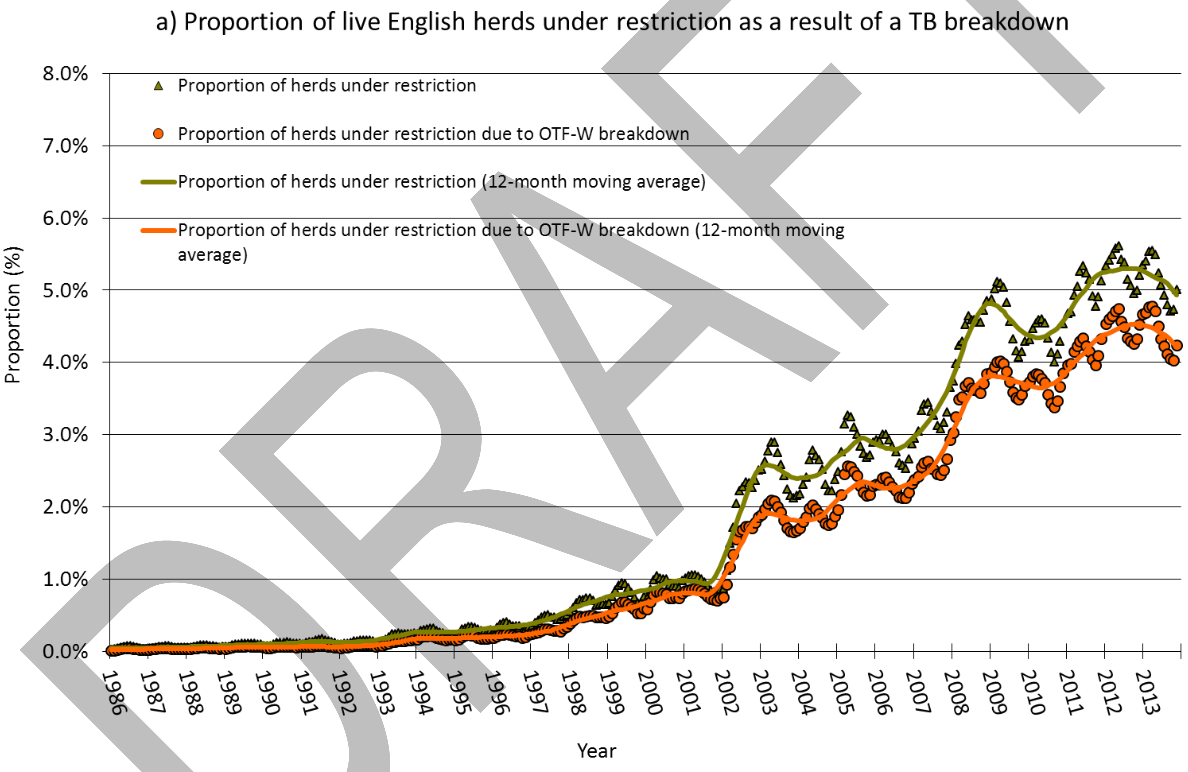


Figure 3.2a: Proportion of live herds under TB movement restrictions as a result of a TB breakdown by month between January 1986 and December 2013; England

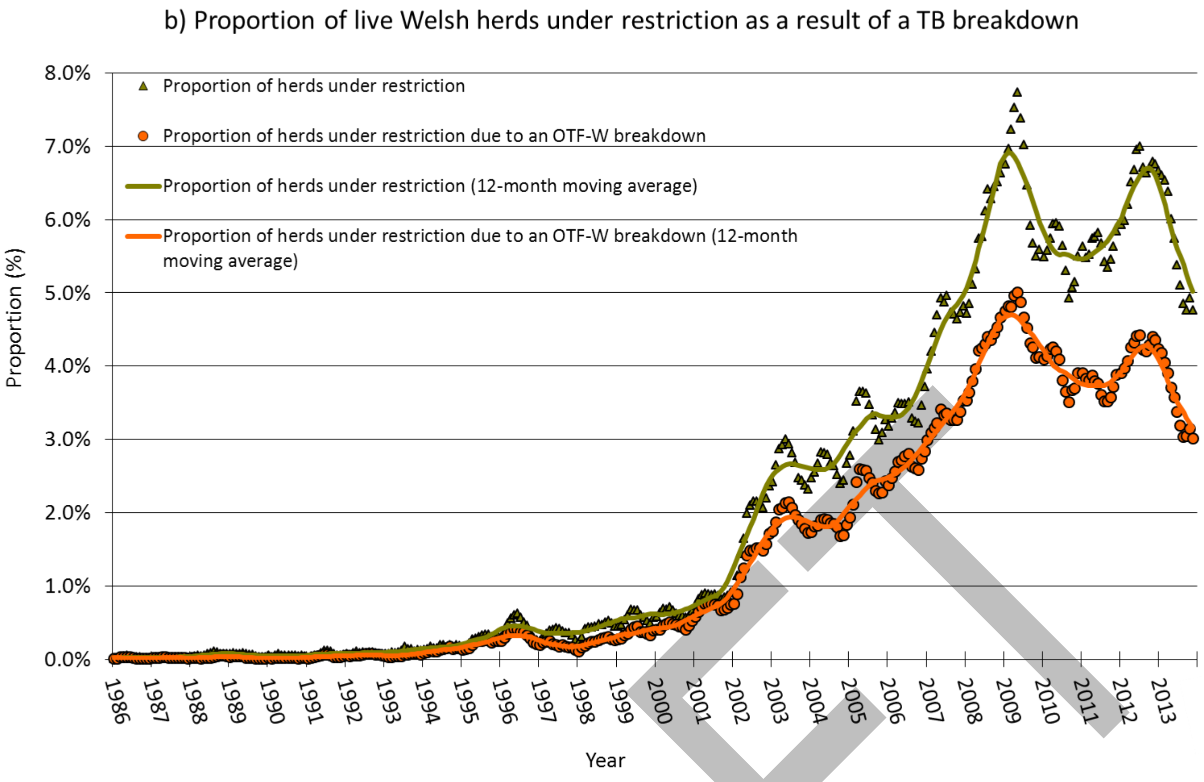


Figure 3.2b: Proportion of live herds under TB movement restrictions as a result of a TB breakdown by month between January 1986 and December 2013; Wales

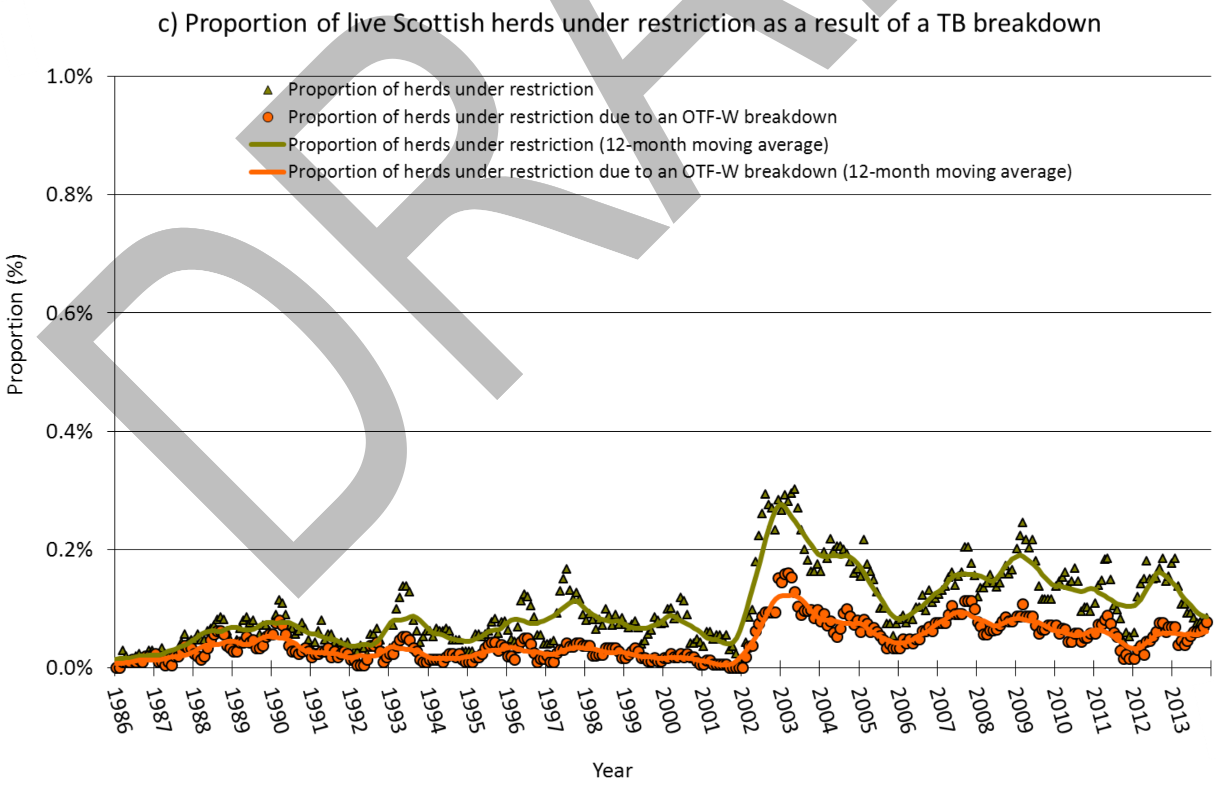


Figure 3.2c: Proportion of live herds under TB movement restrictions as a result of a TB breakdown by month between January 1986 and December 2013; Scotland

Map of OTFW herd incidence, by county

In Figure 3.3, counties are coloured according to the proportion of herds with OTFW new breakdowns. Incidences of 0.1, 0.2 and 1.0% represent the cut-off points that non-officially TB free EU member states and regions should use for testing intervals, albeit on a different timescale. An incidence of 4% greatly exceeds the criterion for allocating a yearly testing interval. Appendix 3 shows a map of GB, indicating county names and boundaries.

In 2013, 10 counties in Wales, and in the HRA and Edge areas of England had an incidence of between 4% and 8%. Staffordshire, Mid Powys and Cornwall had an incidence between 8% and 12%, and six counties from the HRA had incidences greater than 12%: Avon, Devon, Gloucestershire, Herefordshire, Shropshire and Wiltshire. The number of counties with an incidence of more than 4 OTF-W new breakdowns per 100 live herds was 19 in total in 2013 compared to 18 in 2012.

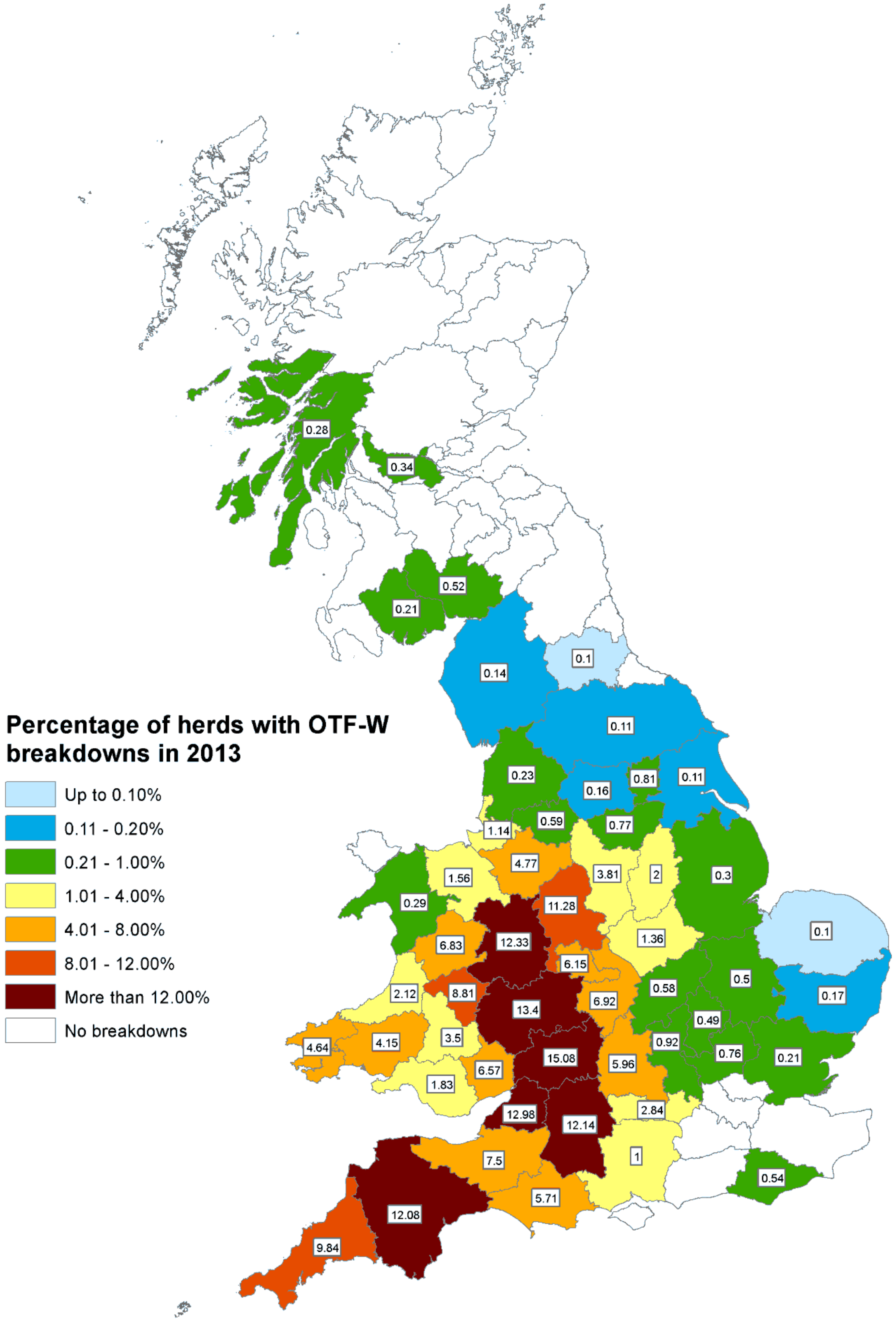


Figure 3.3: Proportion of live herds with OTF-W bovine TB breakdowns by county between January and December 2013: Number of OTF-W new breakdowns of bovine TB per 100 live herds.

4. Duration of bovine TB breakdowns and the number of reactors per incident

Trends in duration

The median durations of OTF-W and OTF-S breakdowns that ended each year from January 1986 to December 2013 are shown in Figure 4.1. OTF-W and OTF-S breakdowns which closed in 2013 were shorter compared to those that closed in 2012, although this was only a significant decrease in the duration of breakdowns for OTF-S (0-1 reactors) breakdowns that ended in 2013, which were 16 days shorter compared to 2012 (χ^2=11.5, 1 d.f., p<0.001). The increase in the median duration of OTF-S breakdowns with multiple reactors recorded in the 2012 report has been maintained in the current report. This follows the adoption in 2011 of a new terminology and testing policy for herds sustaining OTF-S breakdown and requiring those with epidemiological risks to undergo two successive short interval tests with negative results to regain OTF herd status. In Wales and Scotland, such OTF-S breakdowns are reclassified as OTF-W, but these have not been reclassified within this report.

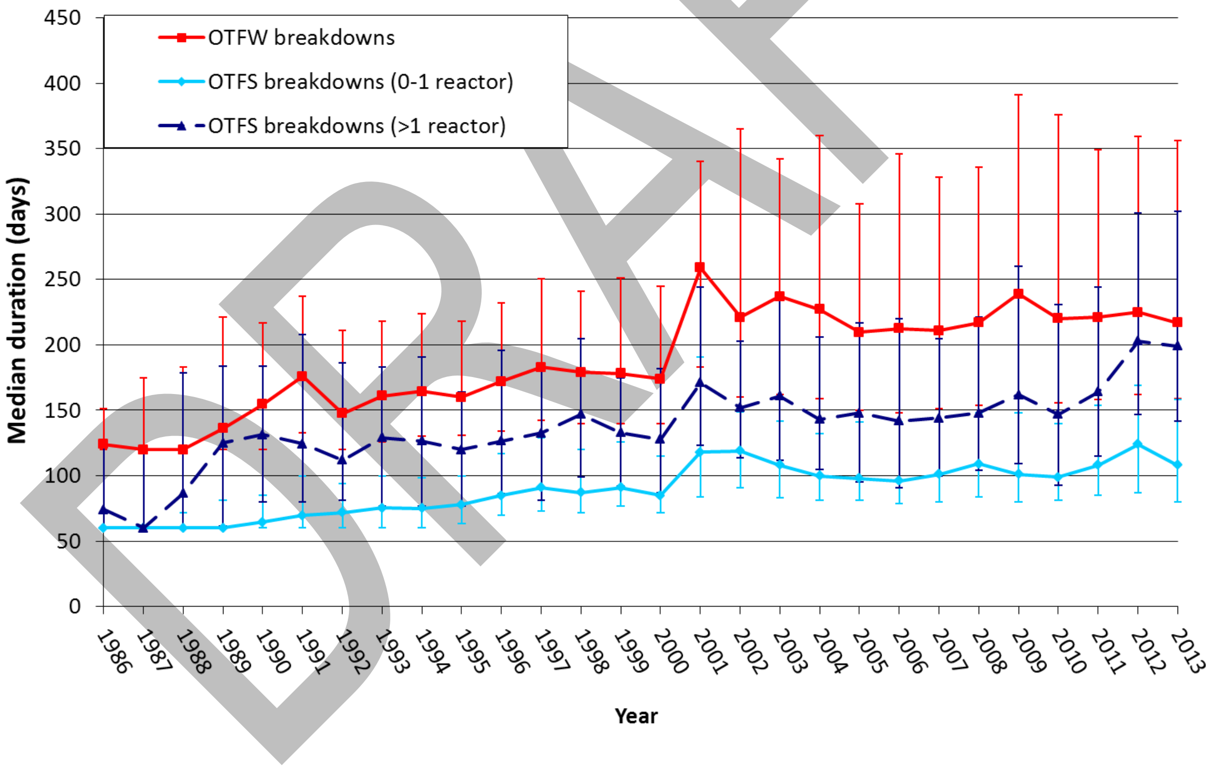


Figure 4.1: The median duration (with interquartile range) of OTFW and OTFS breakdowns with 0-1 reactors or >1 reactor, ending between January 1986 and December 2013.

Duration by Country

The country distribution of OTF-W, OTF-S and all bTB breakdowns that ended in 2013 is shown in Table 4.1. In comparison with 2012, OTF-W breakdowns in 2013 were 9 days shorter in England, 11 days longer in Wales and over 2 months longer in Scotland (based on 6 OTF-W breakdowns).

In 2013, median duration for OTF-S breakdowns was 18 days shorter in England, five days longer in Wales and 36.5 days longer in Scotland (based on 25 OTF-S breakdowns in Scotland in 2013 and 32 in 2012).

The proportion of OTF-W breakdowns that lasted longer than 18 months (550 days: persistent herds) increased slightly and non-significantly from 10.7% in 2012 to 11.9% in 2013. The number of OTF-S persistent herds increased from 16 in 2012 (1.0%) to 34 (2.2%) in 2013. Duration did not exceed 550 days for any breakdown in Scotland that closed in 2013 or in 2012. The proportion of OTF-W breakdowns that exceeded 550 days duration increased from 11.4% in Wales in 2013 to 15.6% in 2013 (χ^2=4.0, 1 df p=0.05)

Table 4.1: Distribution of the lengths of time that TB breakdowns remained under restriction and ended in 2013, by country and by OTF herd status

Reporting Country		**Number of days that herd was under restriction[2]**					**Total[3]**	**Mean (SD)**	**Median (p25, p75)**	**Propor-tion >550 days**
		<= 100	**101-150**	**151-240**	**241-550**	**> 550**				
		….Number of herds….								
England[3]	OTFW	76	564	1,112	898	334	2,984	313.9 (315.2)	211 (155 to 339)	11.19%
	OTFS	432	238	231	76	14	991	145.3 (127.3)	118 (80 to 162)	1.41%
	Total	508	802	1,343	974	348	3,975	271.9 (289.7)	184 (140 to 290)	8.75%
Wales[3]	OTFW	5	60	207	241	95	608	398.1 (462.4)	255 (175 to 414)	15.63%
	OTFS	116	70	180	135	19	521	210.02 (137.3)	170 (106 to 260)	3.64%
	Total	121	130	387	376	114	1,129	311.32 (364.2)	213 (155 to 336)	10.1%
Scotland	OTFW	0	1	2	3	0	6	258.5 (109.7)	232.5 (169 to 255)	0.00%
	OTFS	10	8	4	3	0	25	143 (83)	129 (79 to 156)	0.00%
	Total	10	9	6	6	0	31	165.4 (98.4)	144 (84 to 192)	0.00%
All GB	OTFW	81	625	1321	1142	429	3598	328 (345.6)	217 (159 to 356)	11.92%
	OTFS	558	316	415	214	34	1537	172.5 (249.3)	137.5 (86 to 196)	2.21%
	Total	639	941	1736	1356	463	5135	281.5 (327.7)	189 (142 to 298)	35.42%
All GB-2012[2]	*OTFW*	*79*	*455*	*1147*	*1048*	*327*	*3056*	319.3 (309.6)	224 (162 to 355)	10.70%
	OTFS	*489*	*343*	*439*	*251*	*16*	*1538*	166.1 (106.7)	143 (92 to 202)	1.04%
	Total	*568*	*798*	*1586*	*1299*	*343*	*4594*	268 (269.8)	191 (143 to 302)	35.74%

[2] Restrictions were removed from these breakdowns in the year 2013, but the breakdowns did not necessarily commence in 2013.

[3] The totals for all bTB breakdowns and OTF-S breakdowns include 13 unclassified breakdowns in 2013 (11 in England and 2 in Wales).

Figures 4.2 a to c illustrate the median duration that herds were under restriction because of an OTF-W breakdown since 1999, for each country compared to GB, and the inter-quartile ranges (25th and 75th percentile). Since 2001, Wales has shown a consistently prolonged duration exceeding that for England and Scotland, and GB overall. In 2013, the median duration in Scotland increased substantially to approximate the 2008 or 2009 value, although it was based on only 6 breakdowns that closed in 2013. England and GB overall showed a decrease in the duration of OTF-W breakdowns when compared to the previous four years, matching the levels observed in 2008.

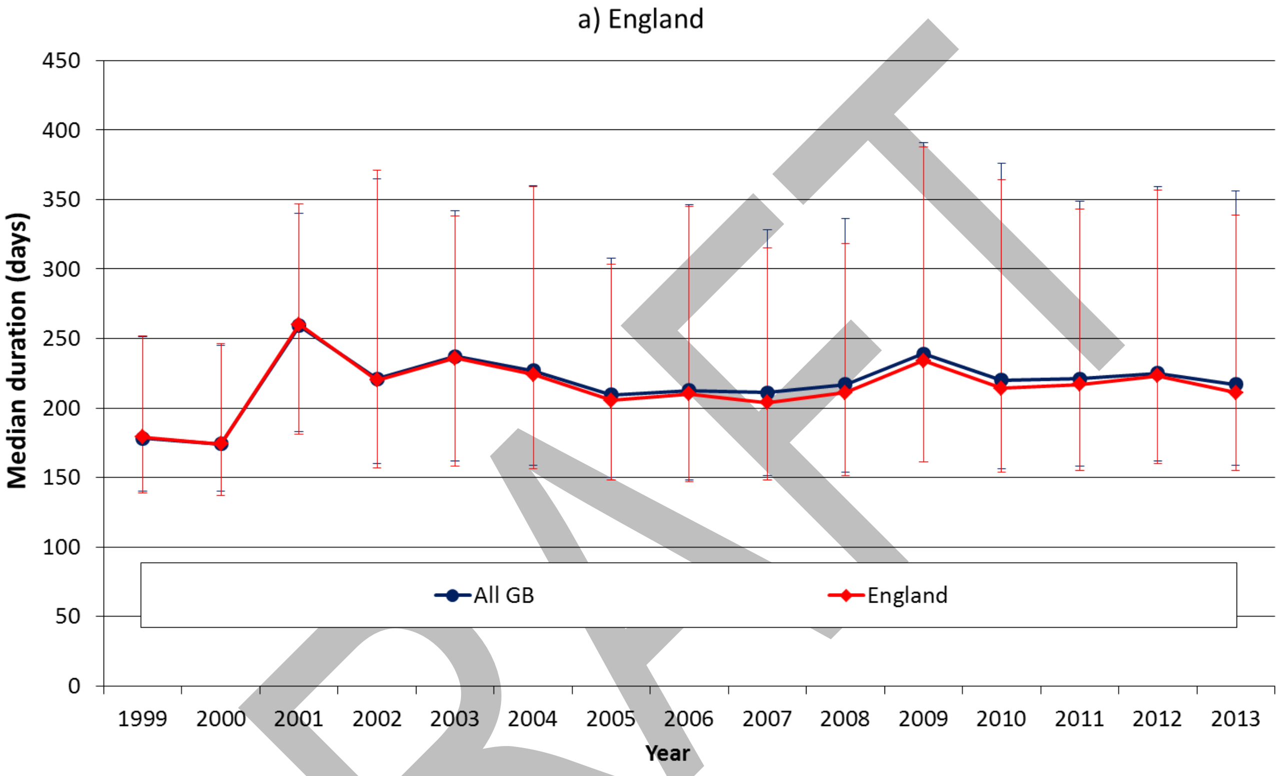


Figure 4.2a: Median duration (with interquartile range) of OTF-W breakdowns ending between January 1999 and December 2013, England and GB

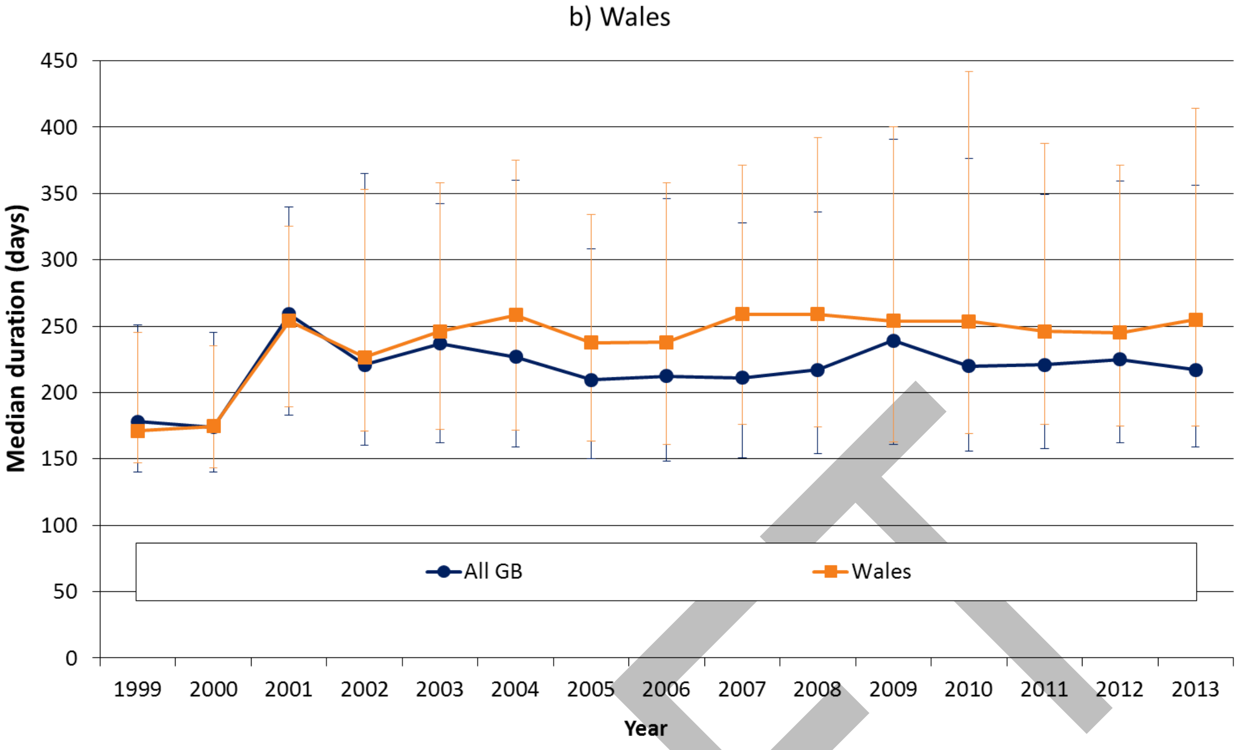


Figure 4.2b: Median duration (with interquartile range) of OTF-W breakdowns ending between January 1999 and December 2013, Wales and GB

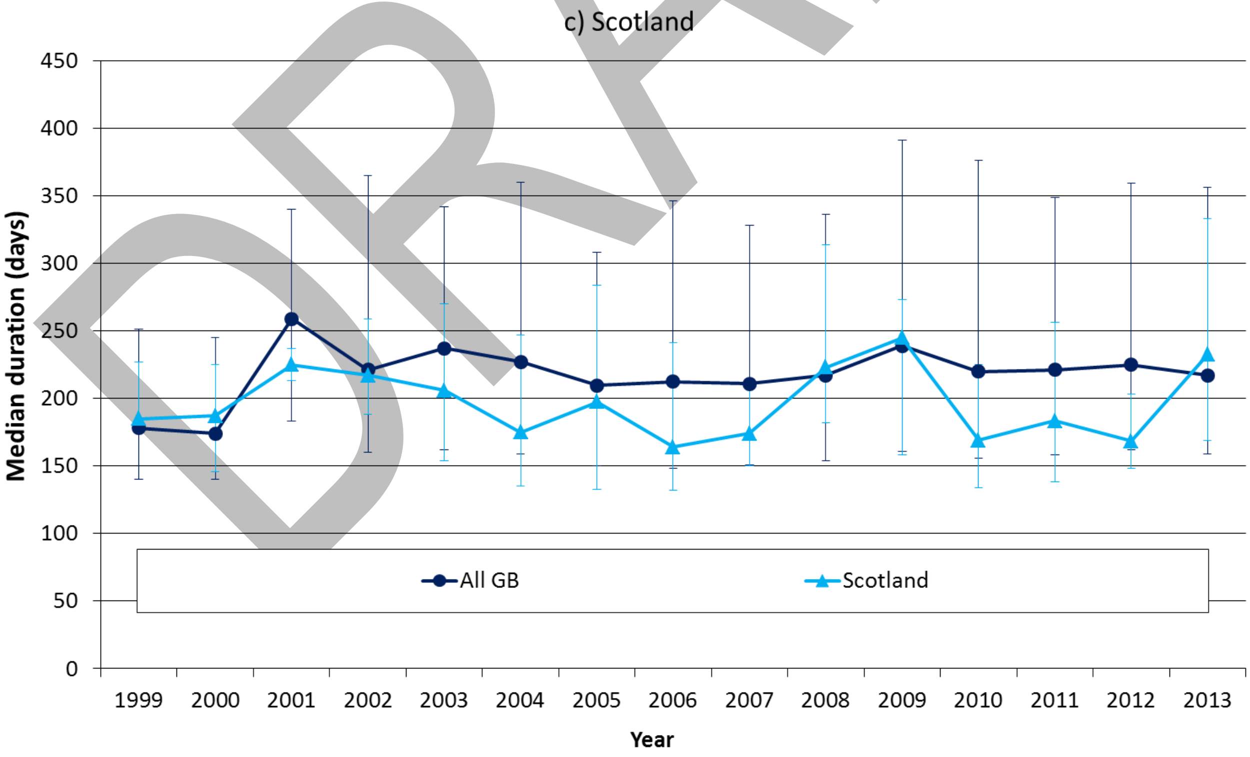


Figure 4.2c: Median duration (with interquartile range) of OTF-W breakdowns ending between January 1999 and December 2013, Scotland and GB

Maps of breakdown duration

The geographical distribution of durations of restriction in OTF-W breakdowns ending in 2013 is shown in Figure 4.3. OTF-W herd breakdowns that were under restriction for more than 240 days, were predominantly clustered in the endemic regions of Wales and English HRAs (Fig 4.3). Outside of these areas, persistent OTF-W breakdowns (with a duration of >550 days) were also recorded in the Edge areas of Berkshire (1), Cheshire (2) and Oxfordshire (1) and in LRAs; Cumbria (1), West Sussex (1) and West Yorkshire (1).

OTF-S breakdowns that were restricted for longer than 240 days were predominantly clustered in South West Wales and South West England (Fig 4.4). There was one OTF-S breakdown of more than 550 days duration located just outside of the endemic and high risk areas; this was in Leicestershire (Figure 4.4).

Figure 4.5 shows the geographical distribution of both OTF-W and OTF-S persistent bTB breakdowns with a duration of 18 months (>550 days). As would be expected, these are clustered around the HRA of England and endemic areas in Wales. There were no persistent bTB breakdowns in Scotland reported in 2013. There are some sporadic cases of persistent bTB breakdowns outside of the HRA and Edge areas; for OTFW breakdowns: Berkshire, Cumbria, North Yorkshire, Lincolnshire, West Yorkshire and West Sussex. Sporadic cases of OTF-S persistent breakdowns were located in Leicestershire, Suffolk and Gwynedd.

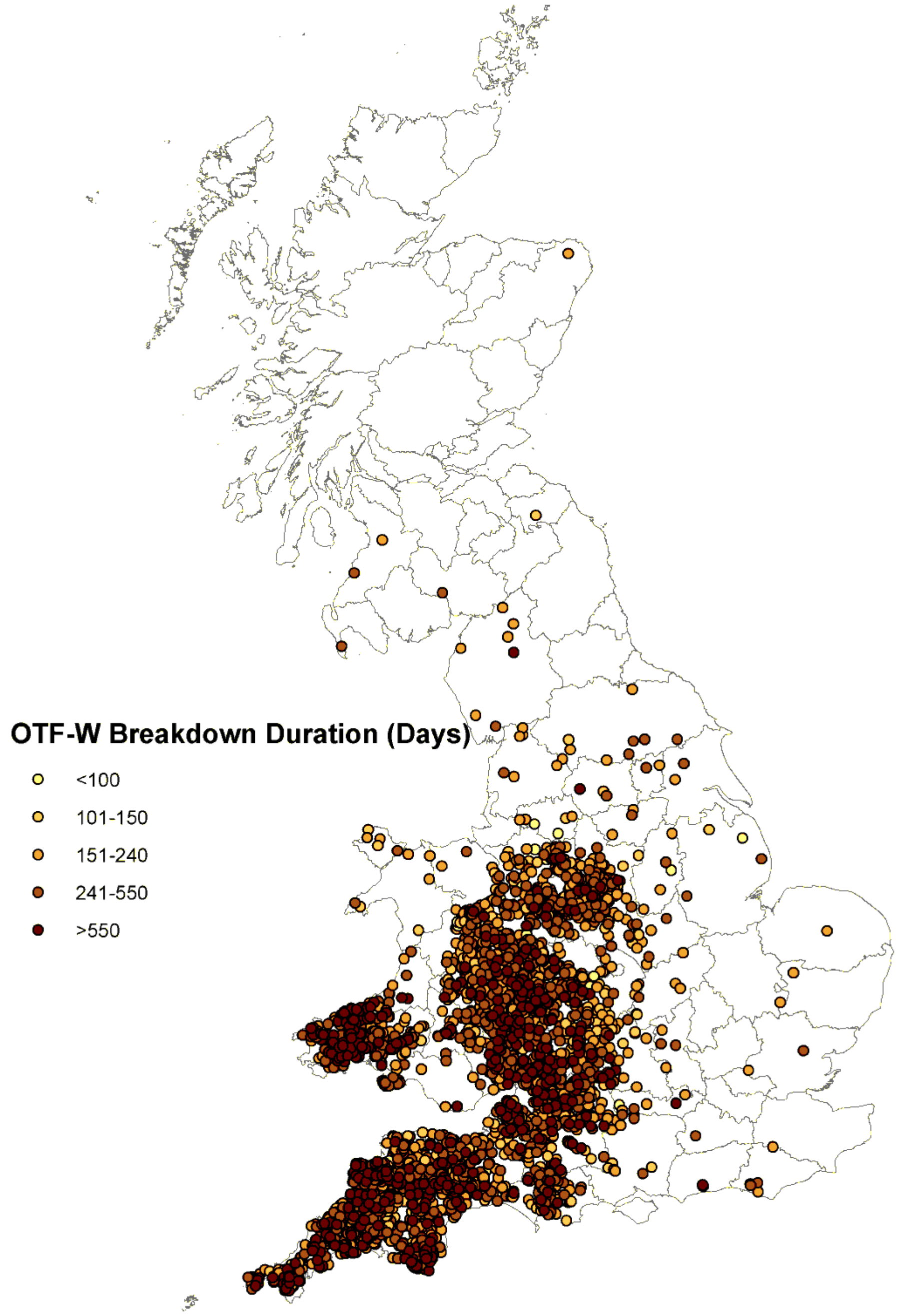


Figure 4.3: *Geographic distribution of OTF-W bovine TB breakdowns that ended in 2013, according to their duration.*

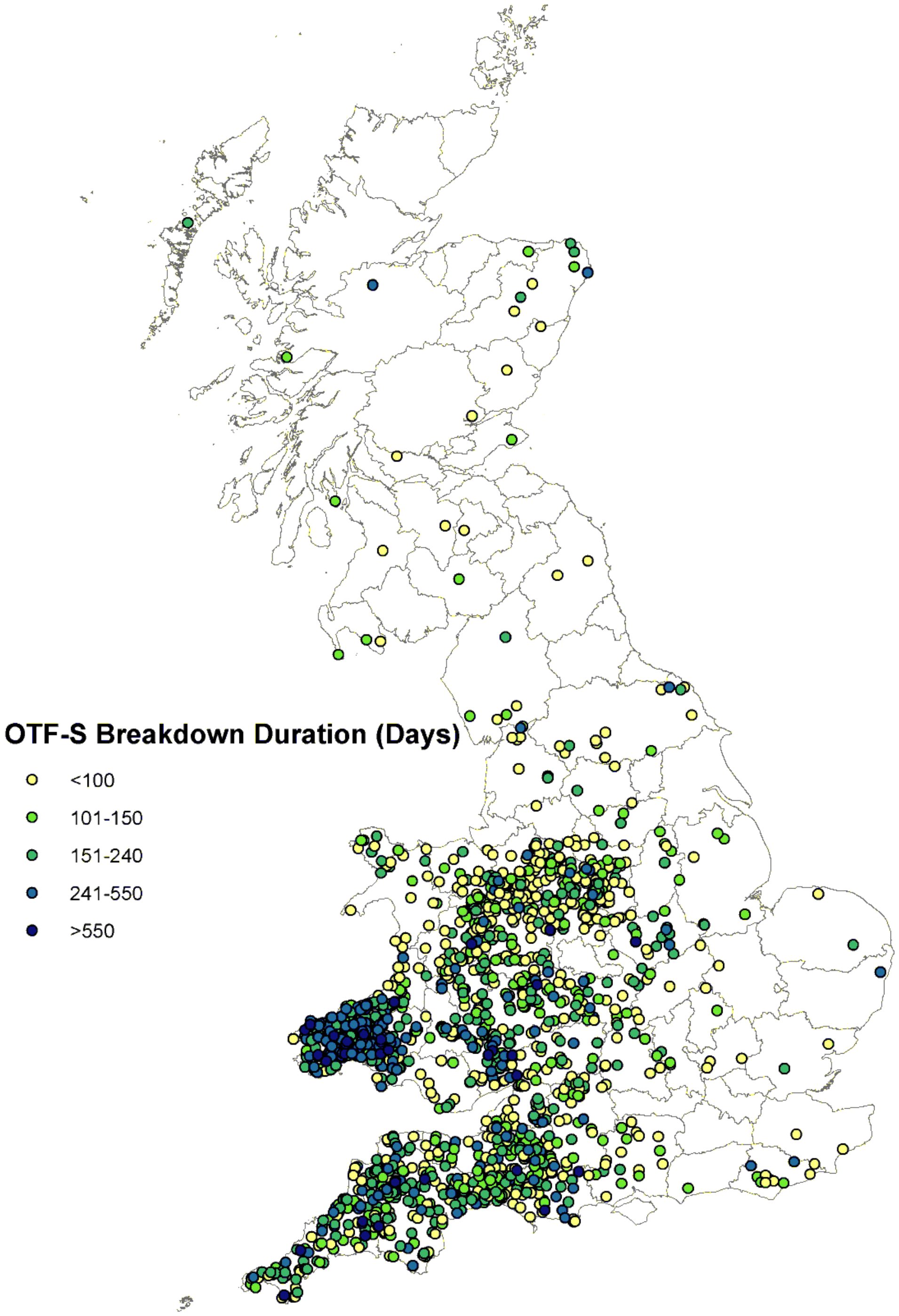


*Figure 4.4***:** *Geographic distribution of OTF-S bovine TB breakdowns that ended in 2013, according to their duration.*

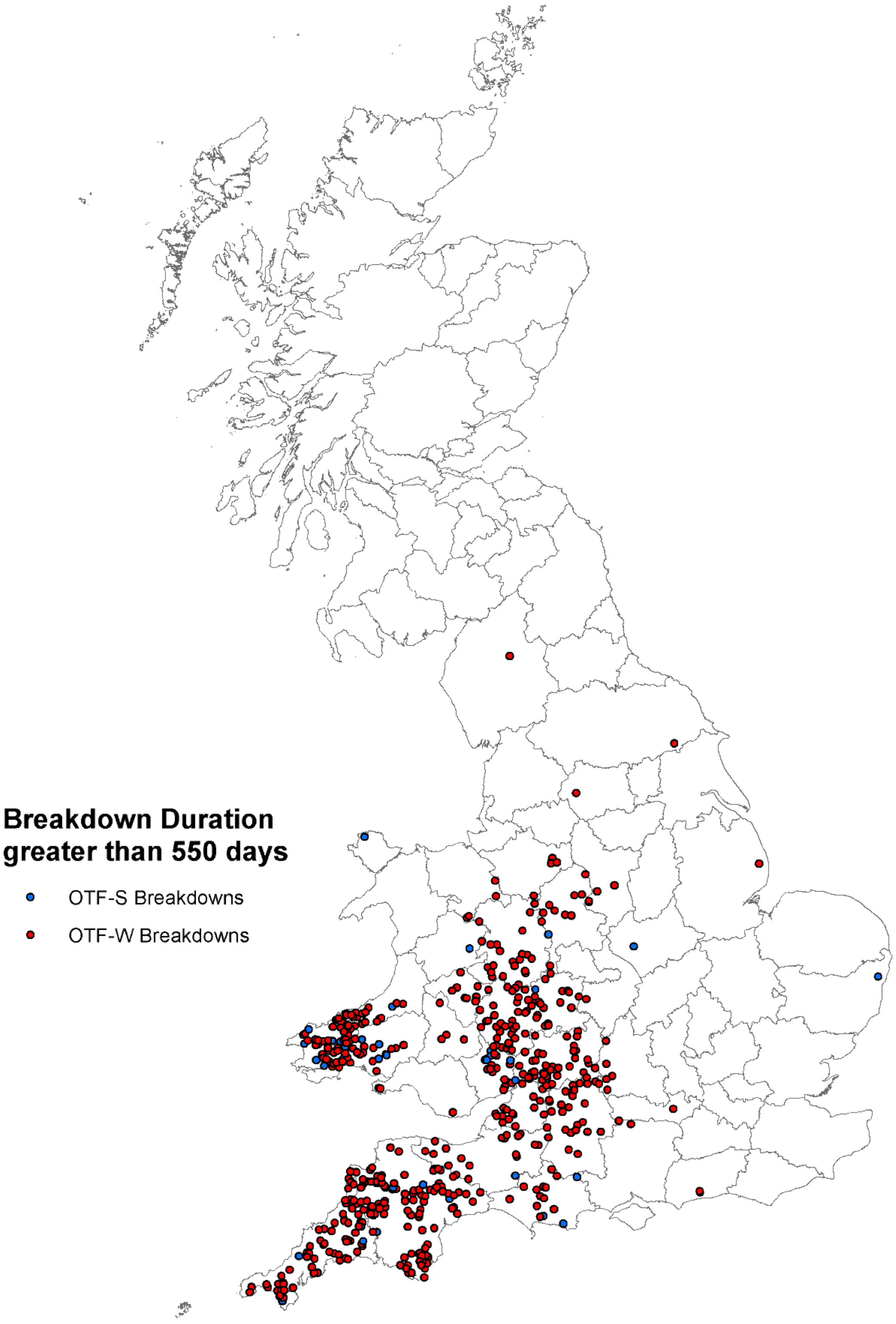


Figure 4.5: *Geographic distribution of OTF-W and OTF-S persistent bTB breakdowns of greater than 18 months (550 days) duration that ended in 2013.*

5. Routine slaughterhouse surveillance

Breakdowns *disclosed* by post-mortem meat inspection of non-reactor cattle from herds that were *not* under movement restriction

The proportion of OTF-W new breakdowns across GB (i.e. all testing intervals) that were disclosed by slaughterhouse surveillance between 2012 and 2013 remained stable at 21% in both years (Table 5.1). In 2013 the proportion of OTF-W new breakdowns initiated by slaughterhouse cases varied across GB countries: in England, the proportion was 22.7% in 2012 and 21.7% in 2013 and in Wales the proportion rose from 13.0% in 2012 to 14.7% in 2013. The proportion in England was 1.5 times greater than in Wales. The proportion of OTF-W breakdowns disclosed by the slaughterhouse in Scotland is more variable because of the low numbers of breakdowns, but fell non-significantly from 46% in 2012 (6/13) to 25% in 2013 (2/6).

Table 5.1: OTF-W new breakdowns in 2013 first detected by routine slaughterhouse surveillance: distribution by ccountry

Country	**Total new OTF-W breakdowns**	**OTF-W breakdowns first detected at the slaughterhouse**	**OTF-W breakdowns disclosed through testing**	**Proportion of OTF-W SLH breakdowns within each reporting region**
England	2799	606	2193	21.7%
Wales	442	65	377	14.7%
Scotland	8	2	6	25.0%
All GB - 2013	3249	673	2576	20.7%
All GB - 2012	*3319*	*702*	*2617*	*21.2%*

The proportion of *all* new breakdowns in 2013 that were first detected by slaughterhouse surveillance was 14.4% for GB, 15.8% for England, 8.1% for Wales and 8.7%for Scotland. This includes an additional 14 OTF-S breakdowns that were detected by slaughterhouse surveillance.

Figure 5.1 displays the distribution of OTF-W breakdowns in 2013 by their method of disclosure (slaughterhouse vs skin testing). Not surprisingly, there was considerable spatial association between the two types of breakdowns in endemic regions of western England and Wales.

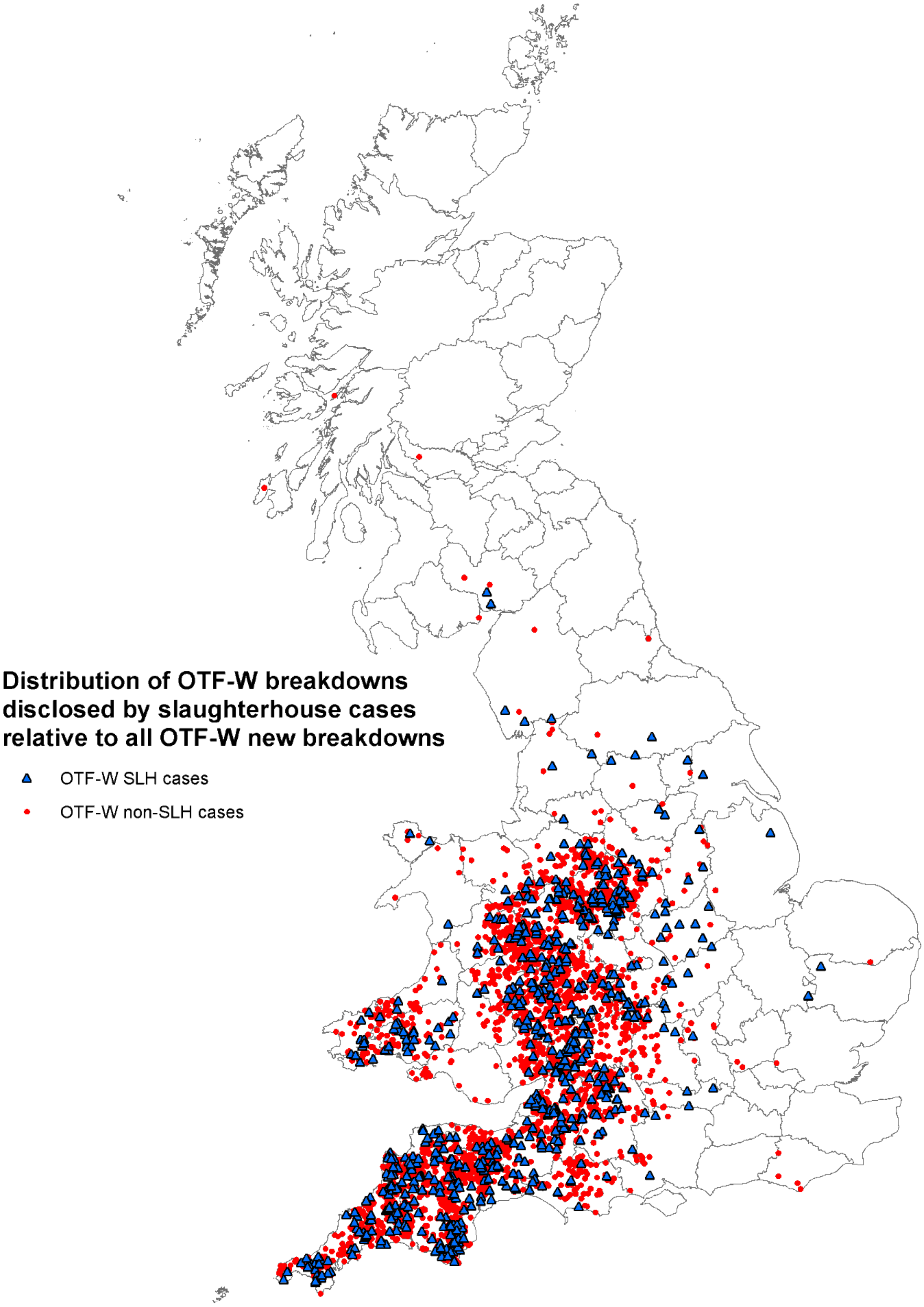


Figure 5.1: Geographical distribution of OTF-W new breakdowns that were disclosed by routine slaughterhouse surveillance (culture-positive slaughterhouse cases), relative to all OTF-W new breakdowns disclosed in 2013.

Figure 5.2 displays the proportion of OTF-W new breakdowns disclosed by routine slaughterhouse surveillance between 1993 and 2013, by country (and GB overall).

English herds accounted for 90% of SLH-disclosed OTF-W breakdowns in GB in 2013 and given this bias, the trend in the proportion of OTF-W breakdowns that have been disclosed through slaughterhouse surveillance for England closely follows that of GB. Since 2010, over one fifth of OTF-W breakdowns in England are detected in the slaughterhouse.

Prior to 2005, the trend in Wales approximately followed that of England. From 2005 onwards the proportion of OTF-W disclosed in the slaughterhouse was lower in Wales than in England, but continued to be parallel to the pattern in England, rising until 2011 and then tending to decline.

The proportion of OTF-W new breakdowns disclosed by slaughterhouse cases in Scotland has greatly exceeded the GB average in seven out of the nine years since 2005. This is based on very small breakdown numbers and fluctuations are to be expected. Slaughterhouse surveillance is particularly important in Scotland following its attainment of Officially TB-Free status in 2009. Routine herd testing using the SICCT test is no longer conducted in Scottish herds where a sufficient proportion of cattle go for slaughter and only a limited number of animals are purchased.

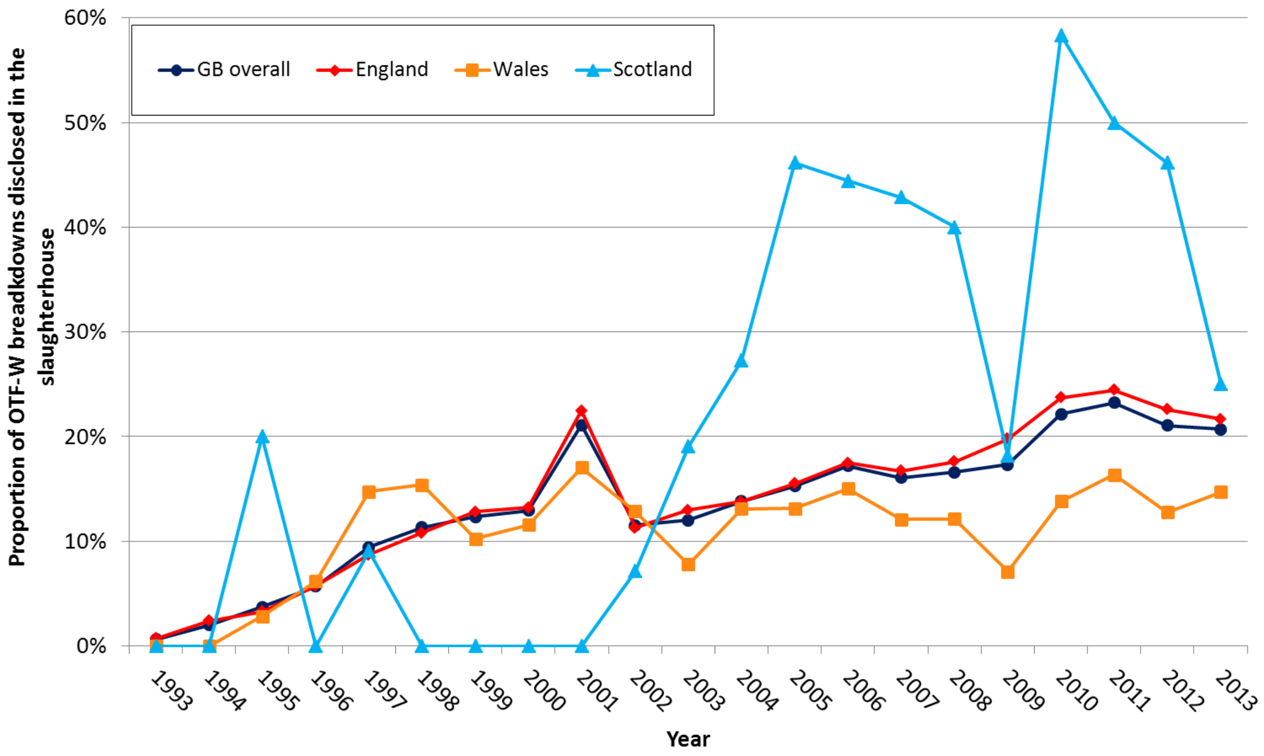


Figure 5.2: Trends in the proportions of OTF-W new breakdowns that were disclosed by routine slaughterhouse surveillance (culture positive slaughterhouse cases), by country from 1993 to 2013

Figure 5.3 displays the proportion of OTF-W breakdowns in 2013 that were first detected by routine slaughterhouse surveillance in each county. There were three counties where all OTF-W breakdowns were disclosed in the slaughterhouse: Humberside (1 breakdown), Cambridgeshire (2 breakdowns) and Suffolk (1 breakdown). Somerset (29%), Cornwall (25%), Warwickshire (28%) Nottinghamshire (36%) Leicestershire (62%) all exceeded the GB average for OTF-W breakdowns initiated by routine slaughterhouse surveillance and had more than 10 breakdowns.

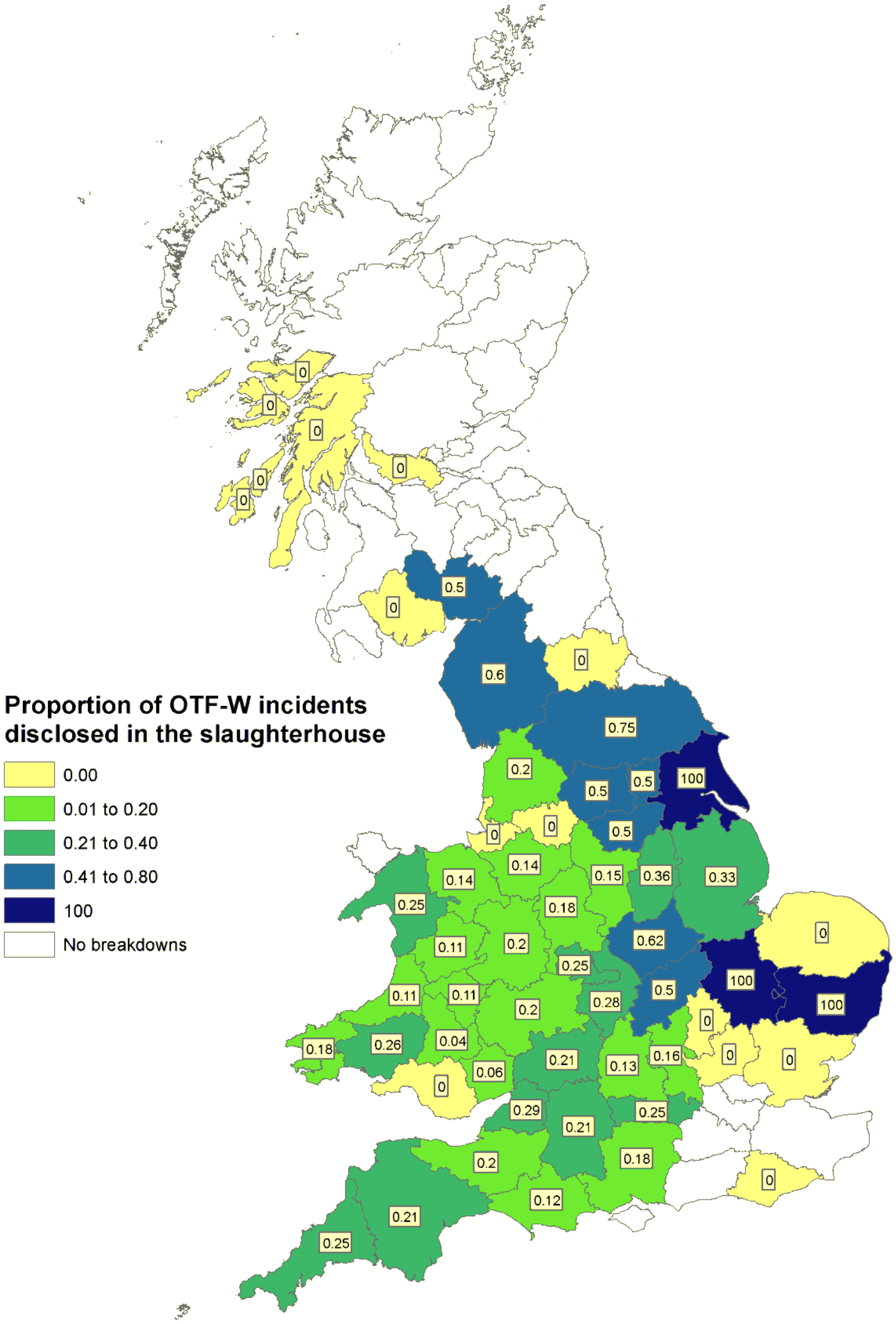


Figure 5.3: The proportion of OTF-W breakdowns that were detected by routine slaughterhouse surveillance in each county in 2013

Results of laboratory cultures undertaken on slaughterhouse cases

M. *bovis* was isolated from 71.1% of tissue samples submitted from slaughterhouses in 2013. This is identical to the proportion in 2012, although there was a 3% decline in the actual number of samples submitted (Table 5.2). The proportion of negative culture was 25.1% in 2012 and 24.2% in 2013 . The proportion of isolated bacteria that were not *M*. *bovis* (including unclassified mycobacteria) increased from 3.8% in 2012 to 4.7% in 2013 .

Table 5.2: Bacterial species in suspected slaughterhouse samples from herds[1] in GB processed and authorised by AHVLA

Authorised result	**Suspected slaughterhouse case samples authorised**				
	2012		**2013**		
	Number of samples	***Percentage of total***	**Number of samples**	**Percentage of total**	**Relative change in numbers from *2012***
M. bovis	*1203*	*71.1%*	1167	71.1%	-3%
Negative	*425*	*25.1%*	398	24.2%	-6%
Actinobacillus sp.	*59*	*3.5%*	75	4.6%	+27%
Unclassified mycobacteria	*1*	*0.1%*	0	0.0%	-100%
Contaminated	*1*	*0.1%*	0	0.0%	-100%
M. avium	*1*	*0.1%*	0	0.0%	-100%
No Result	*3*	*0.2%*	2	0.1%	-33%
M. kansasii	*0*	*0.0%*	0	0.0%	*Previously nil*
Total	***1693***	***100.0%***	**1642**	**100.0%**	**-3%**

[1] *Although the vast majority of slaughterhouse submissions are from unrestricted herds, a small proportion of slaughterhouse submissions are from herds already under restrictions.*

6. Post mortem examination and culture of cattle slaughtered for TB control reasons

Culture of samples of tissues without lesions

Figure 6.1 shows the proportion of cattle visible and non-visible lesions submitted for laboratory culture from which *M. bovis* was obtained each month from 1986 to the end of 2013. The proportion of VL samples from which *M. bovis* was cultured reached a peak in 2011 and has since slightly declined through to 2013 when it was around 95% (Figure 6.1). The proportion of NVL samples from which *M. bovis* was cultured also started to decrease at the end of 2011, from around 9% to 5% for the latter part of 2012 and throughout 2013.

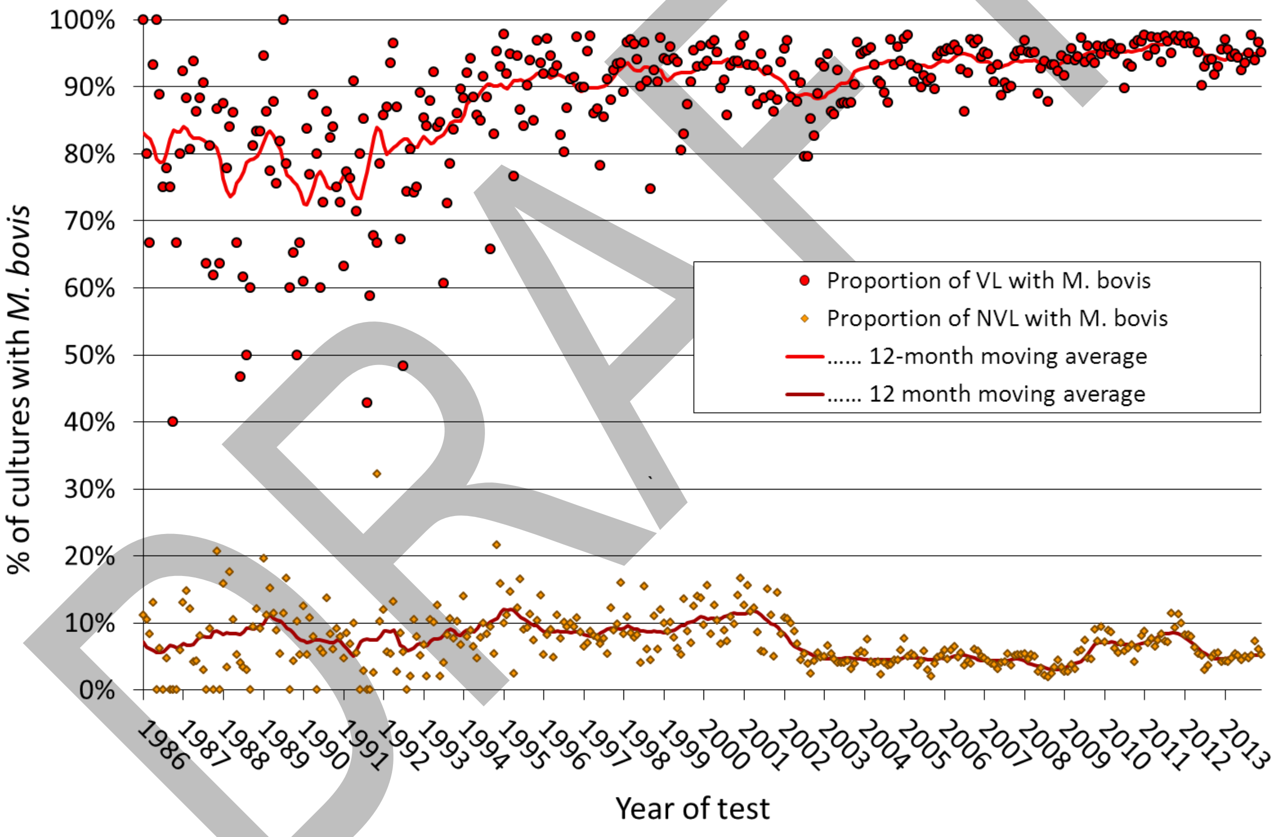


Figure 6.1: Proportion of cattle with visible lesions (VL) and non-visible lesions (NVL) submitted for culture from which M. bovis *was obtained, by month from 1986 to 2013*

Proportion of culled animals with evidence of bTB

The proportion of TB test reactor cattle that had demonstrable evidence of bovine TB infection following post-mortem examination, either in the form of visible lesions and/or positive culture results, was 30-40% between 2003 and early 2008 (Figure 6.2). Between 2008 and 2010 there was a steep rise, roughly coinciding with the rise in proportion of NVLs that were culture-positive (Figure 6.1). The proportion has since stabilised between 2010 and 2013 at around 50%. The steep rise since 2008 brings the proportion of reactors with visible TB lesions or positive culture results up to the historical levels seen between 1990 and 2000. This may indicate that the positive predictive value (and therefore specificity) of the skin and IFN-gamma tests has increased. This may be a consequence of changes in tuberculin manufacturing source from Weybridge to tuberculin from Lelystad in the Netherlands (Downs *et al* 2013). On the other hand, fewer cattle in the earlier stages of infection may have been culled (from which *M. bovis* could not be isolated and in which typical lesions were not detectable).

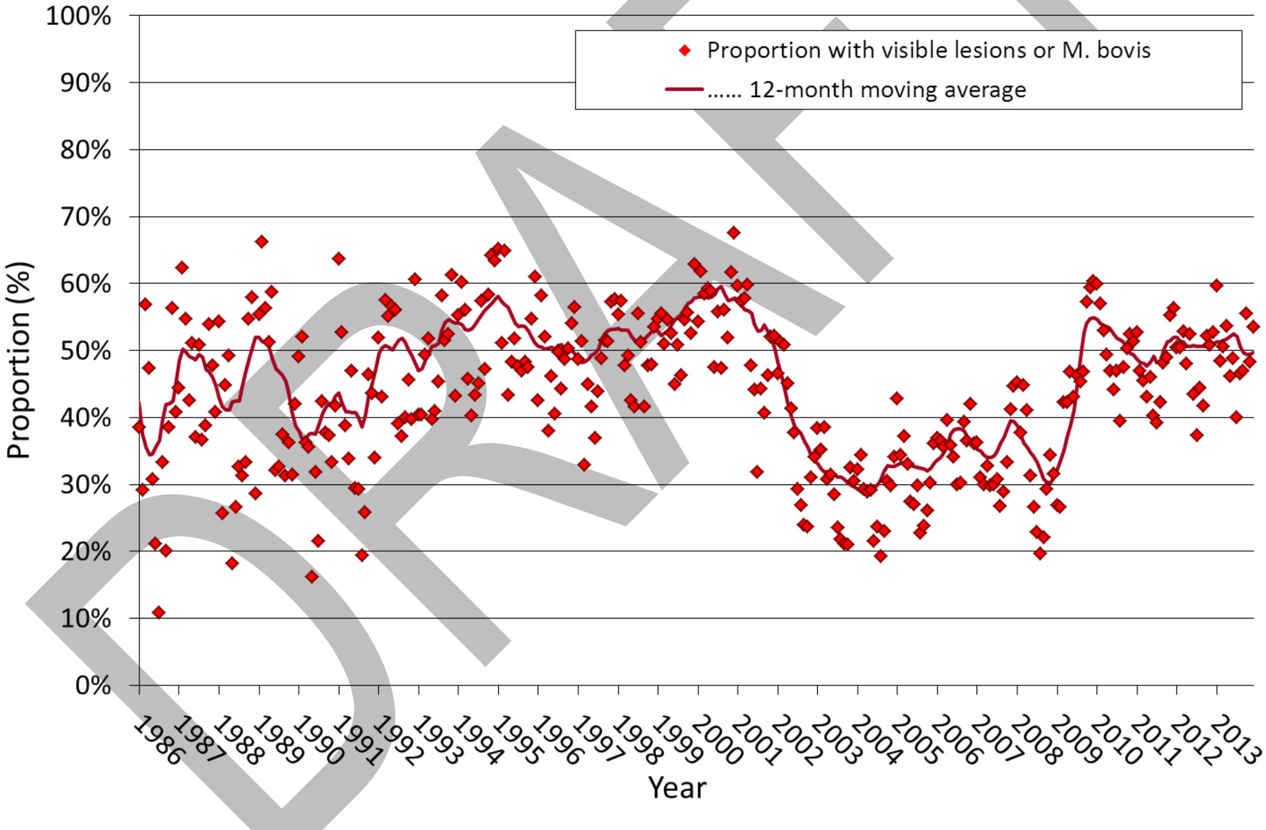


Figure 6.2: The proportion of all reactors to the skin test (including severe interpretation) and / or the IFN-gamma blood test in GB that were cultured and either had visible lesions or were culture positive, from 1986 to 2013

7. Recurrent breakdown herds

A recurrent herd is defined as: *a herd that had a new bTB breakdown disclosed in the reporting year (i.e. 2013) that had also been under movement restrictions for a different bTB breakdown in the previous 36 months*. Recurrence can represent a general increase in incidence (a herd would have a greater probability of a past breakdown if the past incidence were high), but can be larger in herds that are more likely to have repeated breakdowns than others exposed to the same risk of infection. The 'current period' refers to a herd under restriction in 2013, and the 'history period' refers to a herd under restriction for bTB at any time in the preceding 36 months (prior to the start date of the breakdown in the current period). Analyses include all herds that were considered 'live' in the Current Period (2013), i.e. active at the end of it. Whether the herd was live in the 'history period' (preceding 36 months) was not checked.

Herds that were under restriction for more than four months in 2013 due to an ongoing breakdown that started in the history period were excluded from analyses. This excludes nearly all herds that had not yet received their first post-breakdown check test (e.g. the six-month test).

Although recurrence can be readily determined from bTB breakdown data, its cause in any given breakdown is difficult to discern; with surveillance data one cannot distinguish between a breakdown caused by infection that persisted in cattle from the previous bTB breakdown and a new introduction of infection from cattle or wildlife reservoirs.

Geographical distribution of recurrent bTB breakdowns

Herds with a history of OTF-W breakdown(s) ending in the 36-month history period that had a recurrent OTF-W breakdown in 2013 are shown in Figure 7.1 (displaying *any* breakdown herd in 2013 that has had a previous breakdown, regardless of whether the herd was active at the end, or under restriction at the start of the year). The coloured symbols indicate the number of OTF-W breakdowns in the 36 months of history. The herds are labelled by the *number* of OTF-W breakdowns that *ended* in the history period. As in previous years, the distribution of recurrent OTF-W breakdowns tended to be concentrated in the high incidence areas of England and Wales.

There were a number of recurrent breakdowns (following a history of **one** OTF-W breakdown in the last 3 years) outside endemic areas: Berkshire, Buckinghamshire, Leicestershire, Lincolnshire, Nottinghamshire, West Midlands and East Sussex. The same occurred (following a history of **two** OTF-W breakdowns) in Berkshire, Cambridgeshire, Cheshire, Leicestershire and Oxfordshire, and Gwent and West Glamorgan in Wales. Outside endemic areas, recurrent breakdowns occurred predominately in beef finisher herds.

Thirty-seven herds in 13 counties experienced OTF-W new breakdowns in 2013 following a history of **three** OTF-W breakdowns: Avon, Cambridgeshire, Cheshire, Cornwall, Derbyshire, Devon, Gloucestershire, Hereford & Worcester, Shropshire, Somerset, Staffordshire and Wiltshire. There was one dairy herd that had a history of **four** OTF-W breakdowns in the past 3 years, located in Devon.

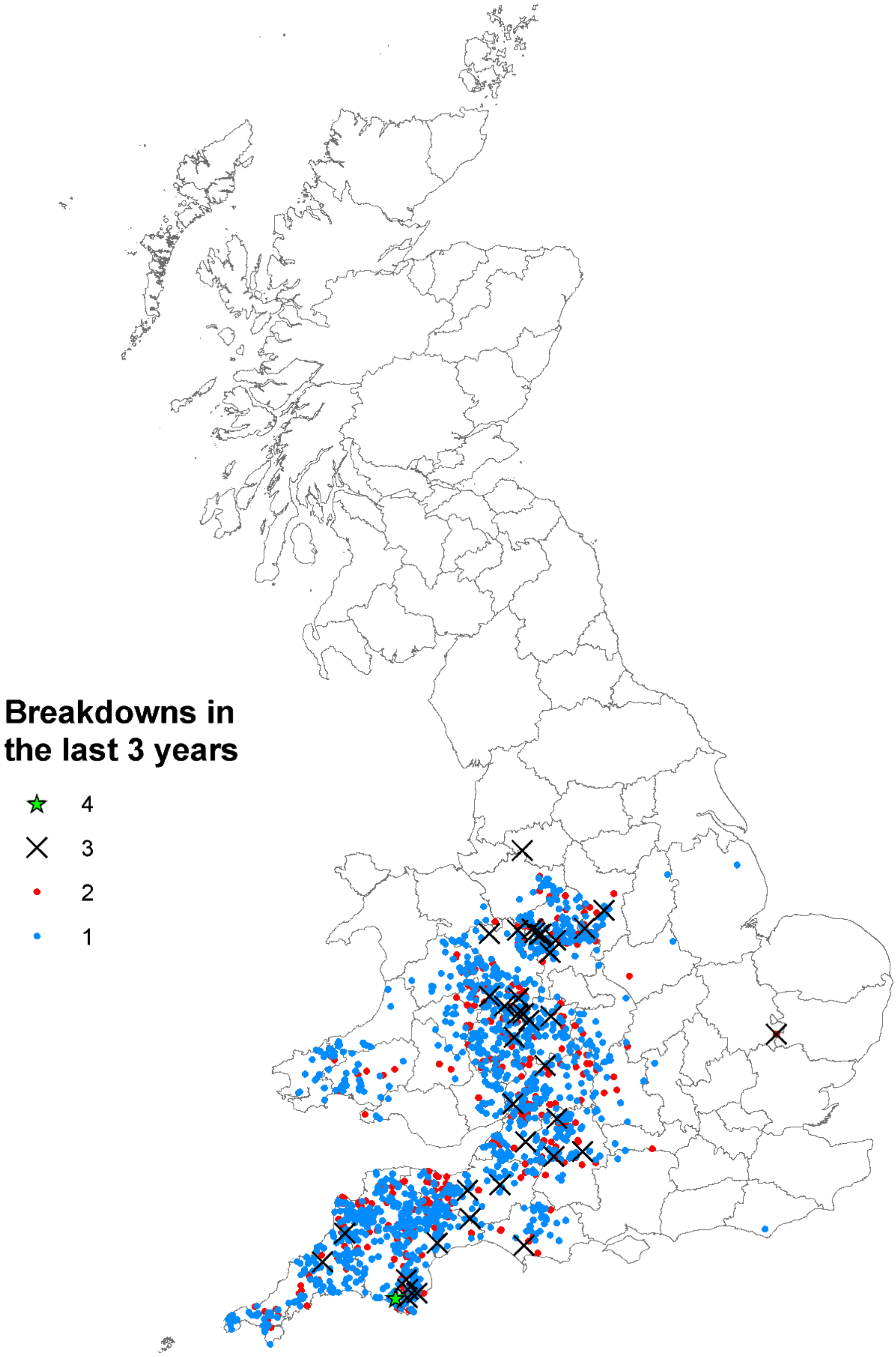


Figure 7.1: Geographical distribution of all herds with OTFW breakdowns ending in the 36-month period before an OTF-W breakdown was disclosed in 2013.

Herds included in the following figures (Figures 7.2 a to d) are those active/live at the end of the study year that were not already under restriction for the first 4 months of 2013. Breakdowns in 2013 in such herds (after restrictions were lifted after April) do not contribute to these figures.

In 2013, over half of all OTF-W breakdowns in GB and England occurred in herds with a history of any bTB restrictions within the previous 36 months; England (54.2% in 2012 to 55.4% in 2013) and GB (53.4% in 2012 to 54.1% in 2013). In Wales, the proportion decreased from 50.6% in 2012 to 47.5% in 2013. None of the OTF-W breakdowns in Scotland in 2013 were in herds with a history of being under restriction in the previous 36 months. The proportion has varied extensively from 2006 to 2013 as it is based on much smaller denominators than England and Wales (range 0-25%).

There was an overall increase in the proportion of OTF-S breakdowns in 2013 with a history of being under restriction in the previous 36 months from bTB, when compared to 2012. In England, Wales and GB overall, the proportion is between 44 to 45%; in Scotland, 6.7%.

There has been an increasing trend in England and GB in the proportion of breakdowns (total bTB, OTF-S and OTF-W) that are recurrent, whereas in Wales the proportion of recurrent breakdowns has been decreasing since 2011 (6% decline for OTF-S breakdowns, 11% decline for OTF-W breakdowns, and an 8% decline for any bTB breakdown, Figure 7.2c). This, in association with the declining number of breakdowns, suggests that, in Wales, previously recurrent herds are staying clear.

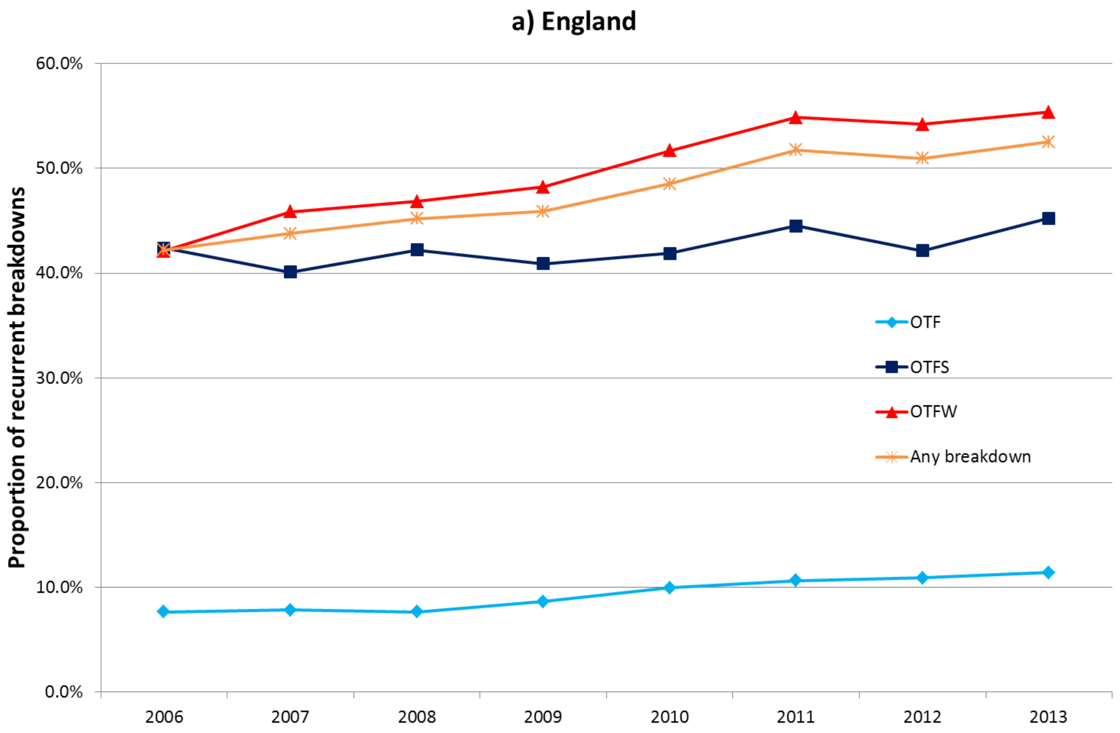


Figure 7.2a: The annual proportion of herd breakdowns in 2013 (OTF-W and OTF-S) with a history of breakdowns (in the previous 36 months) between 2006 and 2013 – England. OTF denotes the proportion of herds that did not sustain a breakdown in 2013 but that had a history of a movement restriction as a result of a bTB breakdown in the previous 3 years

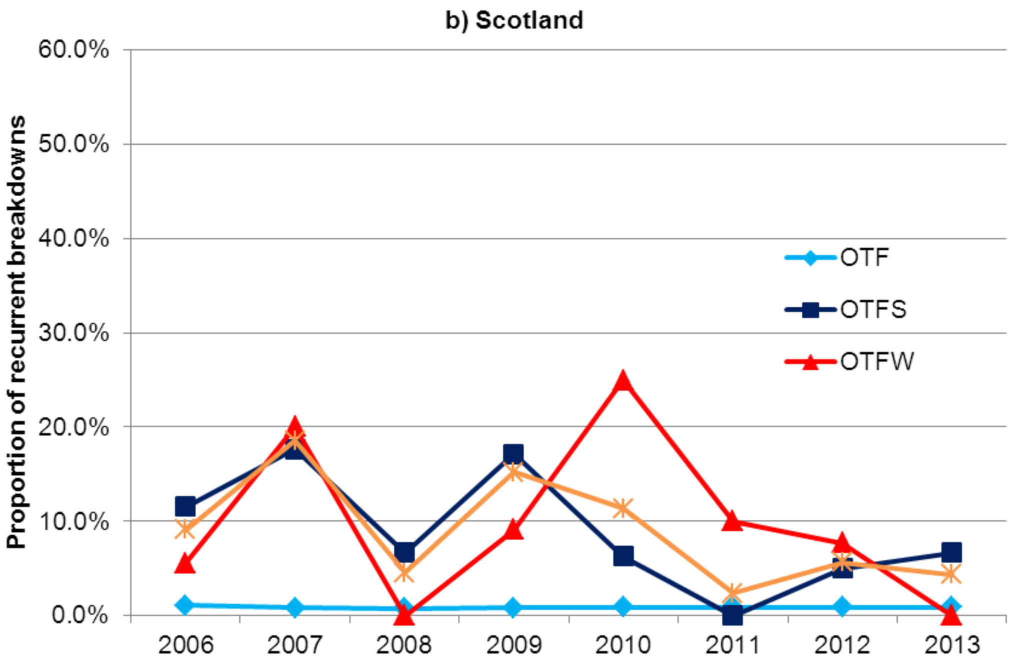


Figure 7.2b: The annual proportion of herd breakdowns in 2013 (OTF-W and OTF-S) with a history of breakdowns (in the previous 36 months) between 2006 and 2013 – Scotland. OTF denotes the proportion of herds that did not sustain a breakdown in 2013 but that had a history of a movement restriction as a result of a bTB breakdown in the previous 3 years.

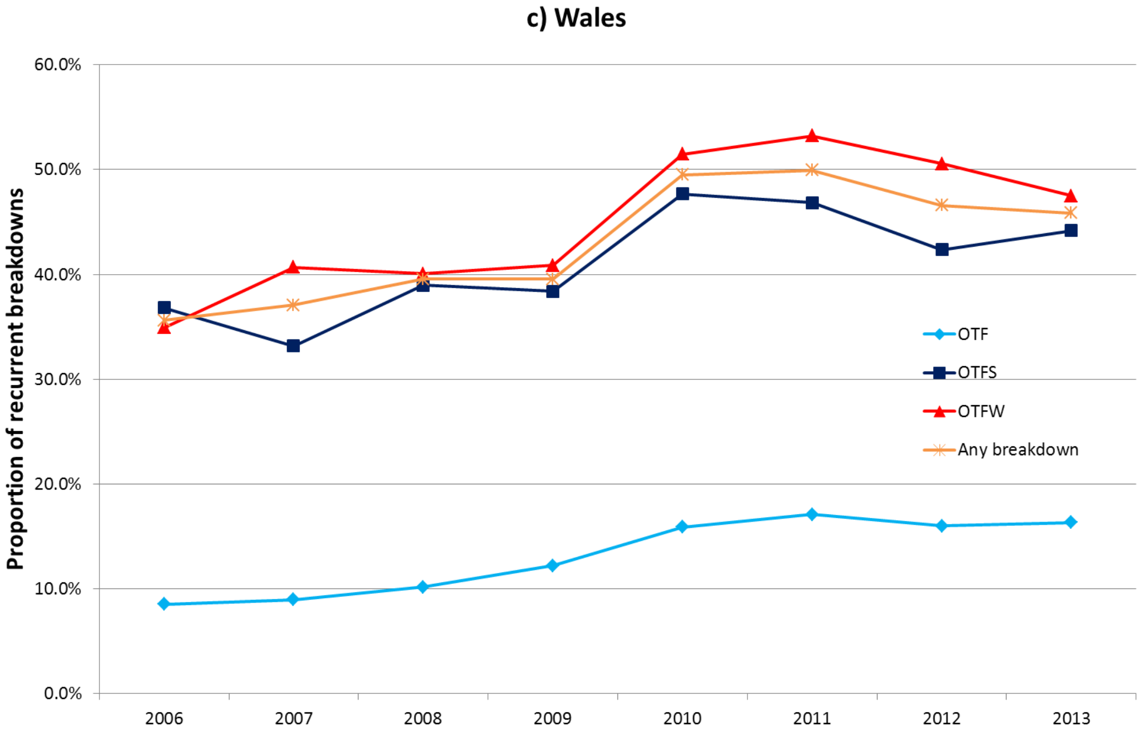


Figure 7.2c: The annual proportion of herd breakdowns in 2013 (OTF-W and OTF-S) with a history of breakdowns (in the previous 36 months) between 2006 and 2013 - Wales. OTF denotes the proportion of herds that did not sustain a breakdown in 2013 but that had a history of a movement restriction as a result of a bTB breakdown in the previous 3 years.

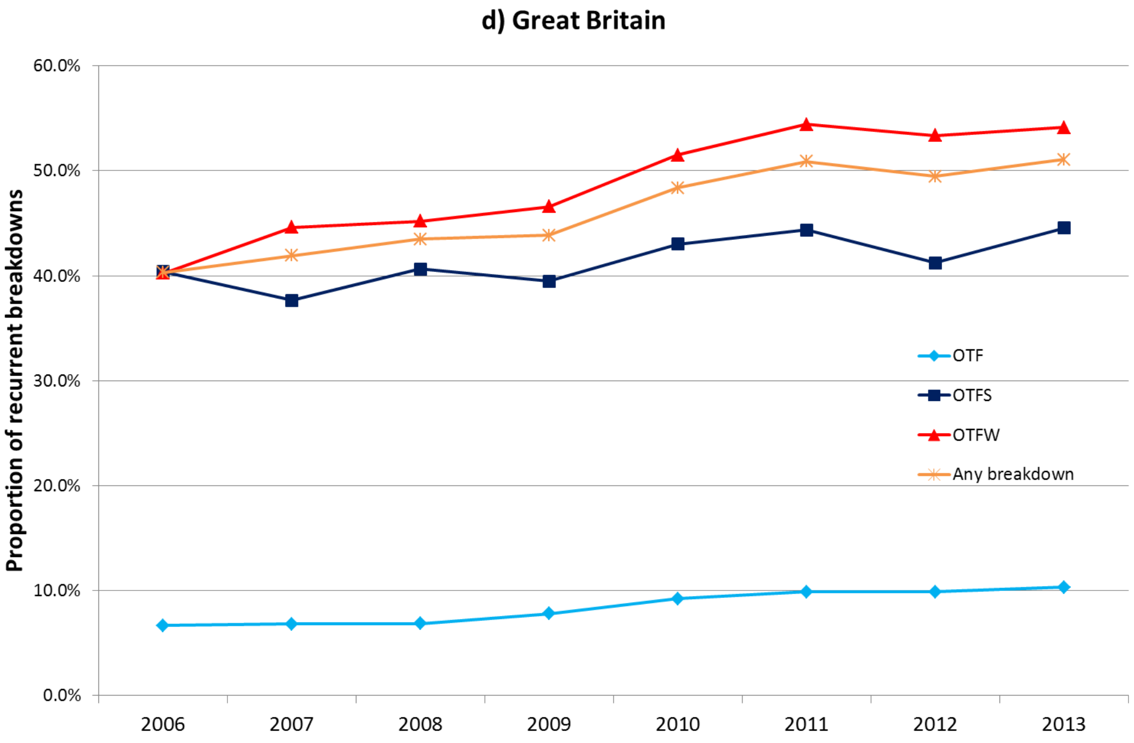


Figure 7.2d: The annual proportion of herd breakdowns in 2013 (OTF-W and OTF-S) with a history of breakdowns (in the previous 36 months) between 2006 and 2013 - GB. OTF denotes the proportion of herds that did not sustain a breakdown in 2013 but that had a history of a movement restriction as a result of a bTB breakdown in the previous 3 years.

8. Inconclusive reactors

The geographical distribution of OTF-W breakdowns occurring at the 60-day re-test or subsequent tests (within 15 months) of inconclusive reactor cattle (IRs) in IR-only herds in 2013 is shown in 10 x 10 km map squares in Figure 8.1. In endemic areas in the West Midlands, South West, Welsh borders and South West Wales, the proportion of IR-only herd tests that had an OTF-W new breakdown following retest or the subsequent test was greater than in areas peripheral to these. There were a few more isolated breakdowns where the percentage of IR-only herds with an OTF-W breakdown exceeded either 20% or 40%, that had not been observed in 2012; 10x10km square areas of Gwynedd (>20%), Lancashire (>20%), North Yorkshire (both >20% and >40% in different locations), South Yorkshire (>40%), Buckinghamshire (>20%), Nottinghamshire/ Lincolnshire border (>40%) and Wigtown and Dumfriesshire in Scotland (>40%).

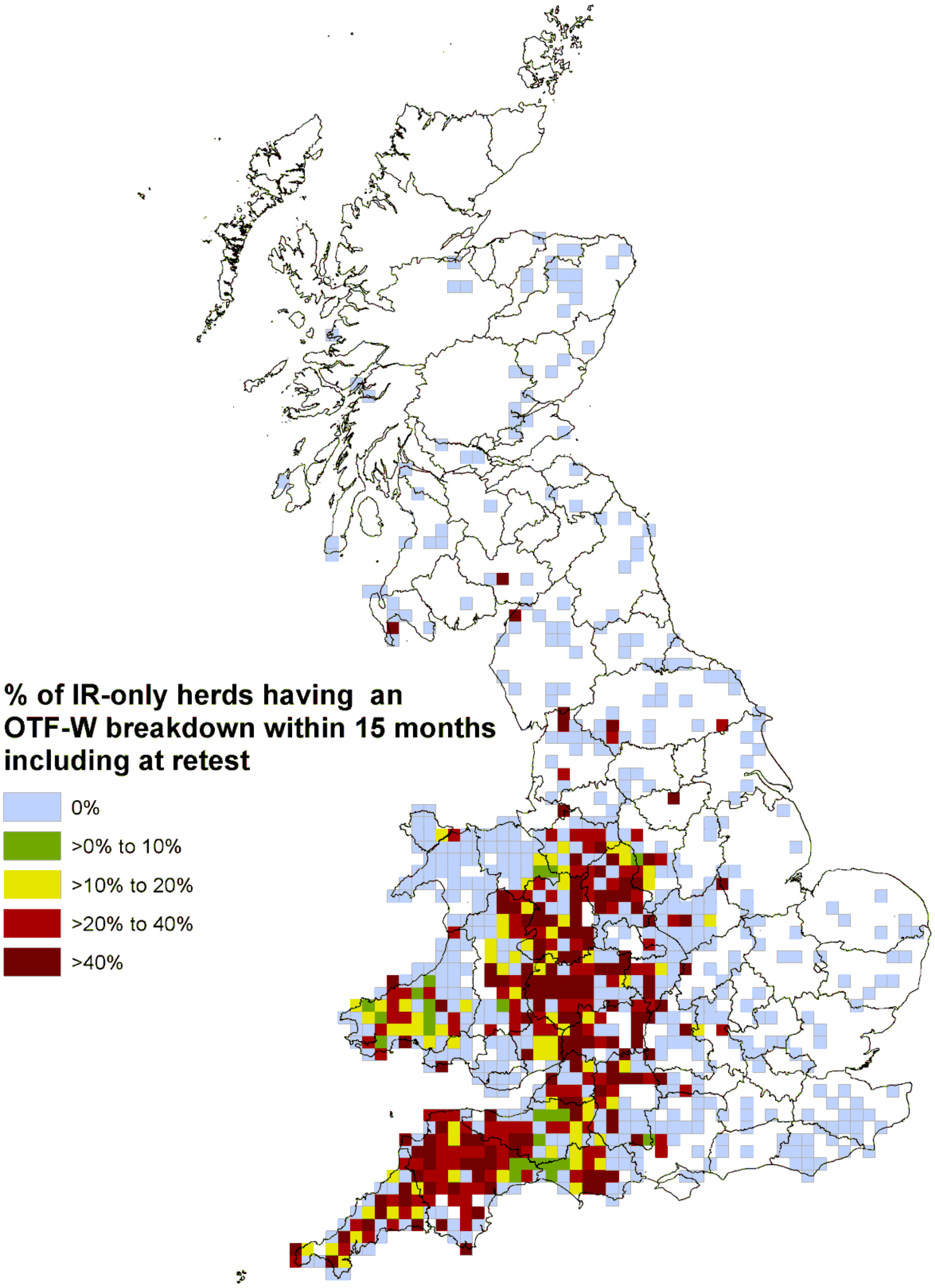


Figure 8.1 The geographical distribution of herds having inconclusive reactors in 2012 that were followed by an OTF-W breakdown within 15 months (including at re-test and subsequent test), by 10 x 10 km squares. Squares with less than 3 IR-only herds are not shown.

9. Report on the M. bovis genotyping database for 2013 (AHVLA surveillance project SB4020)

Analysis of data from 2013

There were 3234 cattle isolates in the AHVLA spoligotype database from breakdowns that commenced in 2013 (2012 = 3367) and 153 non-bovine isolates (Table 9.1 & Figure 9.1).

Distribution by host

Table 9.1. Frequency of isolates by host, 2013 and 2012 (cattle breakdowns and non-bovine incidents that commenced in 2013)

Host	2013 N	2012 N
Cattle	3234	3367
Alpaca	35	36
Cat	36	22
Sheep	4	19
Deer	29	17
Swine	29	16
Goat	4	2
Llama	3	2
Bison	1	1
Dog	2	1
Ferret	0	1
Grey Seal	0	1
Wild boar	1	1
Badger	3	0
Antelope	1	0
Ferret	2	0
Unknown	3	0
Total:	3387	3486

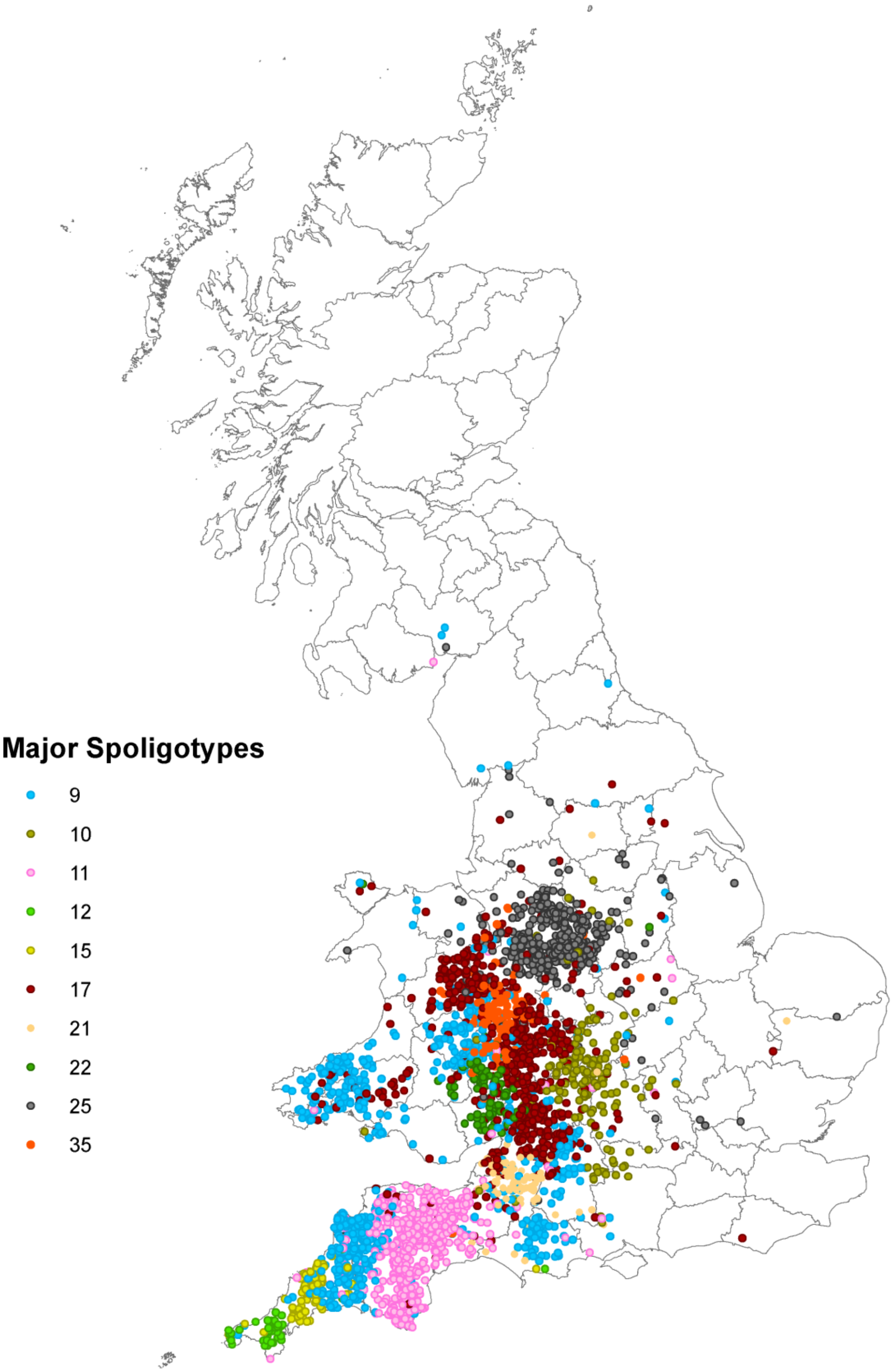


Figure 9.1. Locations of cattle breakdowns with one of the 10 major spoligotypes isolated in 2013

Frequency of genotypes among bovine samples

Full genotype (6 locus VNTR) was obtained for 3101 isolates (96%, 2012= 94% Note that spoligotype was obtained for all isolates). These 3101 isolates represent 2963 unique cattle breakdowns (1.05 isolates per breakdown, 2012 = 1.1).

2,963 cattle breakdowns with full standard genotype (spoligotype and 6 locus VNTR) were analysed below.

85 different genotypes (spoligotype plus 6 locus VNTR) were identified (2012 = 83).
The frequency of each genotype is shown in Table 9.2 and the same data, grouped by spoligotype, is shown in Table 9.3. Genotypes with two or less breakdowns have been excluded.

Table 9.2. The frequency of each genotype recovered from cattle (one sample from each breakdown) for 2013 compared with 2012 and 2011, by decreasing order of isolation frequency. Genotypes with two or less breakdowns in 2012 have been excluded (n = 65).

International spoligotype nomenclature	**Genotype**	**2013**		**2012**	**2011**
		%	# Breakdowns	**%**	**%**
SB0263	17:a	20.7	612	20.2	19.2
SB0274	11:a	17.3	514	18.2	16.7
SB0129	25:a	13.3	393	12.5	13.5
SB0140	9:a	6.8	201	9	7.7
SB0140	9:b	4.7	138	5.9	4.8
SB0272	10:a	4.6	136	3.4	3.2
SB0140	9:c	4.2	123	4.7	5.2
SB0134	35:a	3.8	112	3.8	3.4
SB0130	21:a	3.3	98	3	2.6
SB0673	22:a	3.3	98	4	3.6
SB0275	15:a	2.9	87	1.8	2.3
SB0140	9:d	2.5	75	3	3
SB0140	9:e	1.8	53	1.8	2
SB0140	9:f	1.7	51	2.5	2.2
SB0129	25:b	1.3	40	0.5	1.2
SB0271	12:a	1.1	32	1.2	1.5
SB0145	20:a	0.9	26	0.7	1.3
SB0140	9:h	0.6	17	0.4	0.6
SB0274	11:b	0.5	14	0.4	0.4
SB0274	11:k	0.4	12	0.2	0.1
SB0263	17:b	0.3	10	0.4	0.5
SB0271	12:b	0.3	8	0.2	0.2
SB0263	17:d	0.2	7	0.3	0.3
SB0140	9:g	0.2	7	0.1	0.1
SB2026	114:a	0.2	6	0	0
SB0263	17:c	0.2	5	0.1	0.4
SB0140	9:s	0.2	5	0	0
SB0274	11:o	0.1	4	0	0
SB0263	17:t	0.1	4	0.1	0.1
SB0129	25:6-5-5-4*-2-2.1	0.1	4	0	0
SB0054	65:7-5-5-5*-3-3.1	0.1	3	0	0
SB0959	74:a	0.1	3	0.3	0.1

Table 9.3. The frequency of each genotype recovered from cattle (one sample from each breakdown) for 2013 compared with 2012 and 2011 <u>grouped by spoligotype</u>. Genotypes with two or less breakdowns have been excluded. (n = 65).

International spoligotype nomenclature	**Genotype**	**2013**		**2012**	**2011**
		%	# Breakdowns	%	%
SB0140	9:a	6.8	201	9	7.7
SB0140	9:b	4.7	138	5.9	4.8
SB0140	9:c	4.2	123	4.7	5.2
SB0140	9:d	2.5	75	3	3
SB0140	9:e	1.8	53	1.8	2
SB0140	9:f	1.7	51	2.5	2.2
SB0140	9:g	0.2	7	0.1	0.1
SB0140	9:h	0.6	17	0.4	0.6
SB0140	9:s	0.2	5	0	0
SB0272	10:a	4.6	136	3.4	3.2
SB0274	11:a	17.3	514	18.2	16.7
SB0274	11:b	0.5	14	0.4	0.4
SB0274	11:k	0.4	12	0.2	0.1
SB0274	11:o	0.1	4	0	0
SB0271	12:a	1.1	32	1.2	1.5
SB0271	12:b	0.3	8	0.2	0.2
SB0275	15:a	2.9	87	1.8	2.3
SB0263	17:a	20.7	612	20.2	19.2
SB0263	17:b	0.3	10	0.4	0.5
SB0263	17:c	0.2	5	0.1	0.4
SB0263	17:d	0.2	7	0.3	0.3
SB0263	17:t	0.1	4	0.1	0.1
SB0145	20:a	0.9	26	0.7	1.3
SB0130	21:a	3.3	98	3	2.6
SB0673	22:a	3.3	98	4	3.6
SB0129	25:a	13.3	393	12.5	13.5
SB0129	25:b	1.3	40	0.5	1.2
SB0129	25:6-5-5-4*-2-2.1	0.1	4	0	0
SB0134	35:a	3.8	112	3.8	3.4
SB0054	65:7-5-5-5*-3-3.1	0.1	3	0	0
SB0959	74:a	0.1	3	0.3	0.1
SB2026	114:a	0.2	6	0	0

In general, genotype frequencies for 2013 were similar to the frequencies found in 2012 and 2011. It was noted in the reports for 2010 and 2011 that genotype 25:a had increased in frequency from 8.1% (2009) to 13.5.% (2011). However, the frequency of this genotype has remained relatively stable for the last three years (12.5% -13.5%) This may represent a normal, stochastic fluctuation of genotype frequency rather than a major change in genotype frequency.

The unusual genotype, 122:a, was found in five separate breakdowns in 2012, four of which were located in Worcestershire and it was suggested that this genotype is a derivative of the common 17:a. However, this genotype was not seen in 2013 in a similar manner to genotype 22:k (VNTR variant of 22:a) which caused three breakdowns in 2012 but was not seen in 2013.

Genotypes 65:a was mentioned in the 2011 report because of four separate breakdowns in that year although it had been rarely seen before and was not seen in 2012. However in 2013 a single locus VNTR variant of 65:a caused three breakdowns.

Changes in genotype over a longer time period

The percentage of each genotype recovered from cattle (one sample from each breakdown) for the years 2002 and 2004 to 2012, is shown below (Table 9.4). Only genotypes that occur more than 0.16% in any one year (3 to 5 breakdowns) are included.

Apart from a change from 8% to 12.5% for genotype 25:a which happened in 2009-2011 there is no evidence for large shifts in genotype frequencies over this period.

Table 9.4. Frequency of genotypes from cattle for those years when VNTR was recorded for all isolates. Any genotype occurring at greater than 0.16% (3-5 independent breakdowns) in any one year is recorded.

Genotype	**% Genotype per year**										
	2013	**2012**	**2011**	**2010**	**2009**	**2008**	**2007**	**2006**	**2005**	**2004**	**2002**
17:a	20.65	20.21	19.21	20.89	20.45	22.19	22.05	21.75	21.29	18.43	18.68
11:a	17.35	18.24	16.71	16.84	17.66	17.63	17.91	15.85	16.54	17.65	16.19
25:a	13.26	12.45	13.52	10.74	8.11	8	6.96	8.07	7.17	6.79	7.33
9:a	6.78	8.99	7.73	7.88	10.76	10.43	10.66	9.9	11.79	11.74	10.28
9:b	4.66	5.86	4.76	6.62	7.32	8.64	6.76	7.94	6.88	6.26	4.85
9:c	4.15	4.66	5.22	5.4	4.98	4.75	6.04	7.48	7.5	6.5	6.74
22:a	3.31	4.04	3.61	3.9	3.99	3.7	5.23	4.04	4.33	4.22	8.04
35:a	3.78	3.75	3.43	4.01	3.09	3.38	3.34	3.36	2.5	2.52	1.77
10:a	4.59	3.39	3.22	3.7	3.61	3.79	3.02	3.06	2.71	3.64	2.25
21:a	3.31	3.02	2.65	2.51	1.89	2.1	1.93	2.25	1.13	2.09	1.54
9:d	2.53	2.99	3.01	2.96	3.02	2.36	3.06	2.8	2.54	3.15	3.55
9:f	1.72	2.48	2.18	1.71	1.41	1.82	1.81	1.95	2.04	1.7	1.3
15:a	2.94	1.82	2.33	2.3	3.37	1.95	1.93	2.42	3.58	3.35	3.66
9:e	1.79	1.78	1.97	1.99	2.2	1.91	1.49	1.23	2	3.69	4.49
12:a	1.08	1.20	1.47	0.87	1.51	0.86	0.85	0.55	1	1.26	1.65
20:a	0.88	0.69	1.29	1.05	1.44	1.05	0.8	0.85	1	1.07	2.72
25:b	1.35	0.55	1.18	0.91	0.65	0.45	0.76	0.85	0.75	0.63	0.35
11:b	0.47	0.44	0.36	0.07	0.24	0.06	0.16	0.21	0.17	0.05	0.12
17:b	0.34	0.40	0.54	0.42	0.31	0.45	0.28	0.47	0.42	0.48	0.12
9:h	0.57	0.36	0.64	0.42	0.24	0.41	0.68	0.3	0.29	0.34	0.35
17:d	0.24	0.29	0.25	0.24	0.58	0.19	0.36	0.68	0.46	0.19	0.12
74:a		0.25	0.1	0.21	0.1	0.1	0.2	0.17	0.13		
12:b	0.27	0.22	0.18	0.14	0.21	0.19	0.12	0.08	0.04	0.1	0.24
11:k	0.40	0.22	0.1	0.1							

Genotype	% Genotype per year										
	2013	2012	2011	2010	2009	2008	2007	2006	2005	2004	2002
9:m		0.18		0.1	0.1	0.03		0.21	0.13	0.05	
122:a		0.18									
9:j		0.15	0.1	0.28	0.1	0.16	0.12	0.17	0.04	0.34	0.24
17:e		0.15	0.36								
9:g		0.11	0.1	0.21	0.24	0.19	0.2	0.38	0.75	0.92	0.95
17:c	0.17	0.11	0.39	0.17	0.31	0.19	0.16	0.25	0.25	0.24	0.12
17:l		0.11		0.07	0.07	0.1	0.16	0.13	0.08		
13:a		0.11	0.29	0.21	0.17	0.13	0.16	0.25	0.17	0.44	0.59
73:a		0.11	0.2								
51:a		0.04	0.1	0.1	0.1	0.1	0.08	0.13	0.17	0.05	0.12
17:m					0.07	0.3	0.08	0.08			
9:l		0.04				0.26	0.12	0.13	0.08	0.05	
100:a						0.16					
9:ae					0.03	0.16					
9:n		0.12	0.1		0.17	0.1	0.24	0.13	0.13	0.44	
22:j					0.07	0.03	0.16				
81:a		0.08			0.17	0.03	0.12		0.08	0.1	
17:o		0.04	0.1		0.17	0.06	0.04				
114:a	0.20										
9:g	0.24										
9:s	0.17										
Total number of breakdowns genotyped	2963	2801	2795	2823	2946	3100	2485	2354	2400	2062	

Isolates from non-bovine animals

There were 153 isolates from non-bovine submissions genotyped in 2013 (119 in 2012): 129 *M. bovis* and 24 *M. microti*. Fourteen isolates did not have full VNTR (9%, 2012 = 3%). The 129 *M. bovis* isolates represent 91 separate incidents (multiple isolates from the same location and type of host are considered a single incident; for example, 4 isolates of 10:u from a cluster of tuberculous cats near Newbury are treated as a single incident).

Table 9.5. Non-bovine isolates of M. microti and M. bovis by host species. The number of isolates for each species and host is shown. For M. bovis isolates the number of separate incidents is shown.

Host	***M. bovis***		***M. microti***
	Isolates	**Incidents**	
Alpaca	33	17	2
Deer	29	22	
Swine	27	22	2
Cat	17	11	19
Sheep	4	4	
Goat	4	1	
Llama	3	2	
Badger	3	3	
Dog	2	2	
Ferret	1	1	1
Wild boar	1	1	
Antelope	1	1	
Bison	1	1	
Unknown	3	3	
Totals:	129	91	24

The frequency of *M. bovis* genotypes in the 73 incidents for which full genotype of *M. bovis* is available for deer, camelids, cats, sheep and swine is shown in Table 9.6.

Table 9.6. Frequency of M. bovis genotypes in cats, swine, sheep and camelids for each incident.

Genotype	Deer	Camelids	Cats	Sheep	Swine	
10:a	3	1			4	
11:a	4		1	1	1	
12:a					1	
15:a					2	
17:a	2	11	3		2	
21:a	2	2	2		1	
25:a			1		4	
9:a	1	1		1	1	
9:b		2	1		2	
9:c	1				1	
9:d		2	1		1	
9:f	1					
17:q			1			
22:a	3			1		
35:a	1					
73:a	1					
10:7-5-6-4*-3-3.1					1	
10:u			1			
Totals:	19	19	11	3	21	73

Genotype 10:u represents isolates associated with the cluster of feline TB occurring in Newbury in the first half of 2013 (Roberts et al., 2014).

Genotype 10:7-5-6-4*-3-3.1 is a single VNTR locus mutation from the common 10:a genotype.

29 Deer Isolates

22 separate incidents of *M. bovis* in deer (17 in 2012). All are typical *M. bovis* genotypes found in cattle except a rare 9:f. This genotype also showed up as a single deer incident in 2012 from the same premises in North Yorkshire.

Homerange analysis was possible for all the isolates which were in, or within 10km of, the equivalent cattle homerange except for the 9:f isolate (North Yorkshire) incident.

35 Alpaca and 3 Llama isolates

Representing 19 separate *M. bovis* incidents and two incidents of *M. microti*. The two llama incidents (3 isolates) were of the common 17:a genotype. Genotypes were common cattle genotypes

36 Cat isolates

36 individual cat isolates (22 in 2012) including 17 *M. bovis* isolates (9 in 2012) and 19 M. microti isolates (13 in 2012). The frequency of each genotype for the 11 fully genotyped *M. bovis* isolates from cats (one for each incident) is shown in Table 9.6.

Genotype 10:u does not have a cattle homerange, but has been shown to be common in cattle the Newbury area (Roberts et al., 2014).

4 sheep isolates

Representing 4 separate *M. bovis* incidents in sheep with common cattle genotypes (Table J6).

29 swine isolates

Representing 22 separate *M. bovis* incidents in swine and two separate incidents of *M. microti*. The *M. bovis* incidents were of 12 genotypes common in cattle (except genotype 10:7-5-6-4*-3-3.1 which is a one VNTR locus mutation from the common 10:a genotype).

4 Goat isolates

One incident with four isolates of the common cattle genotype 9:a

7 isolates; dogs (2), ferret (2), a wild boar, antelope, and a bison.

An *M. bovis* strain (17:a, close to homerange) and a *M. microti* were recovered from two unrelated ferrets. Two independent isolates from dogs included an in-homerange common cattle genotype (17:a) and a rare cattle genotype 17:d (out-of-homerange). The wild boar and bison isolates were also the common 17:a genotype and in-homerange. The antelope isolate genotype was 21:a (in-homerange) which is not uncommon in cattle.

Conclusions - non-bovine samples

In general, the genotypes recovered from non-bovine samples are typical bovine and frequently the common genotypes found in cattle. Previously it has been noted that isolates of 9:a are rare in non-bovids but in 2013 there were 4 isolates of this common cattle genotype.

As usual, strains of *M. microti* are common in feline isolates. The number of *M. microti* isolates from cats this year, once again, exceeds the number of *M. bovis* isolates even though the number of M. bovis isolates from cats seems to have picked up (17 in 2013 compared with 9 in 2012 and 16 in 2011).

Of the 68 non-bovine incidents for which homerange map analysis was possible, 54 incidents were within the equivalent cattle homerange, 3 incidents were within 10Km of homerange and 11 incidents were out of homerange. 84% of non-bovine incidents were either in homerange or within 10Km of the equivalent cattle homerange.

Incidents among sheep and swine

In the reports for 2010 and 2011 we highlighted the increasing number of incidents in sheep and swine. However, in 2013 *M. bovis* incidents in sheep fell back to 2009 levels (4 incidents 2013 and between 14-17 incidents 2011-12). Incidents among swine, however, remain high. These data suggest that some environmental factor (which may include reporting and identification protocols) could have been involved in the surge of sheep incidents between 2009 and 2012.

Incidents in sheep and swine are of many different genotypes, most of which are commonly found in cattle and these data show that these incidents are not connected in a single outbreak. Furthermore, the majority of incidents are within the relevant homerange for cattle. These data suggest that the source of *M. bovis* in sheep and swine is the same as for cattle.

Table 9.7. Frequency of M. bovis sheep and swine incidents 2000-2013.

	Sheep	Swine
2000	0	1
2001	0	0
2002	1	1
2003	0	4
2004	0	1
2005	2	4
2006	0	3
2007	0	5
2008	1	5
2009	5	10
2010	8	24
2011	17	21
2012	14	10
2013	4	22

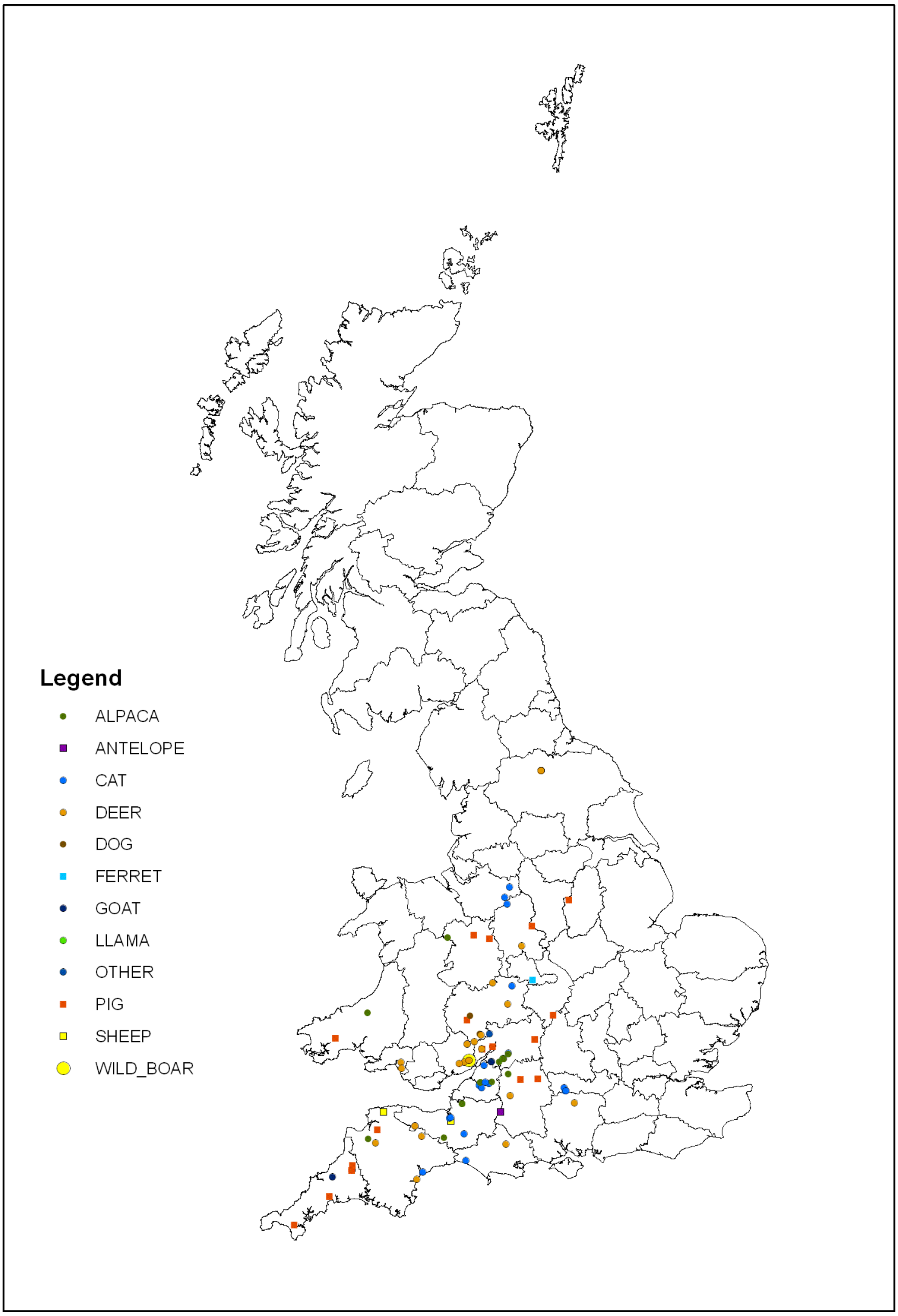


Figure 9.2. Locations of M. bovis isolates from animal hosts other than cattle and badgers in 2013 where location data exists.

Composite Homerange maps.

Composite homerange maps for the 27 genotypes of *M. bovis* that had homeranges for 2008-2013 are shown in Figures 9.3 to 9.5.

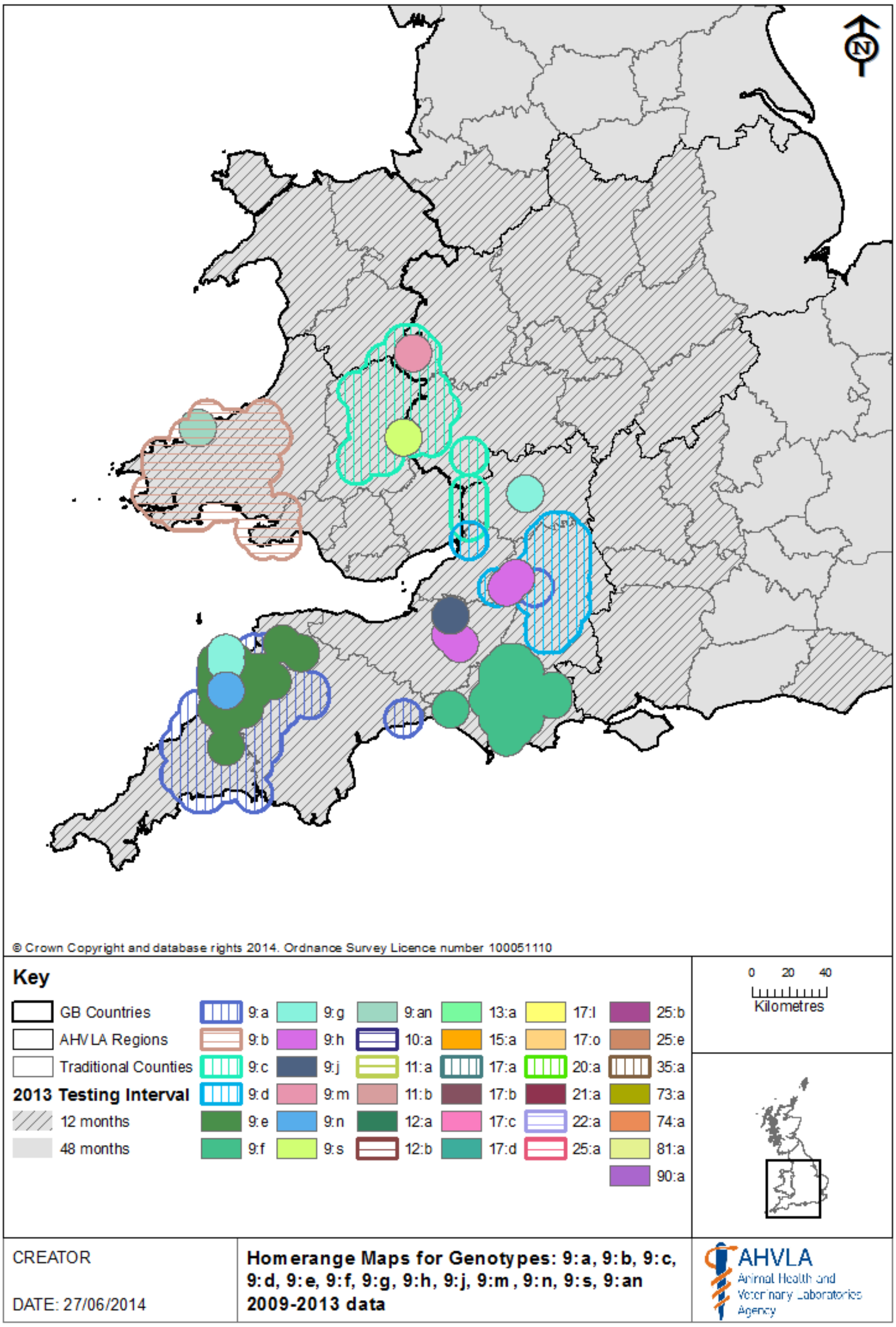


Figure 9.3. Homerange areas using 2009-2013 data for VNTR types of spoligotype 9. The annual testing areas are shown as counties with a hatched pattern.

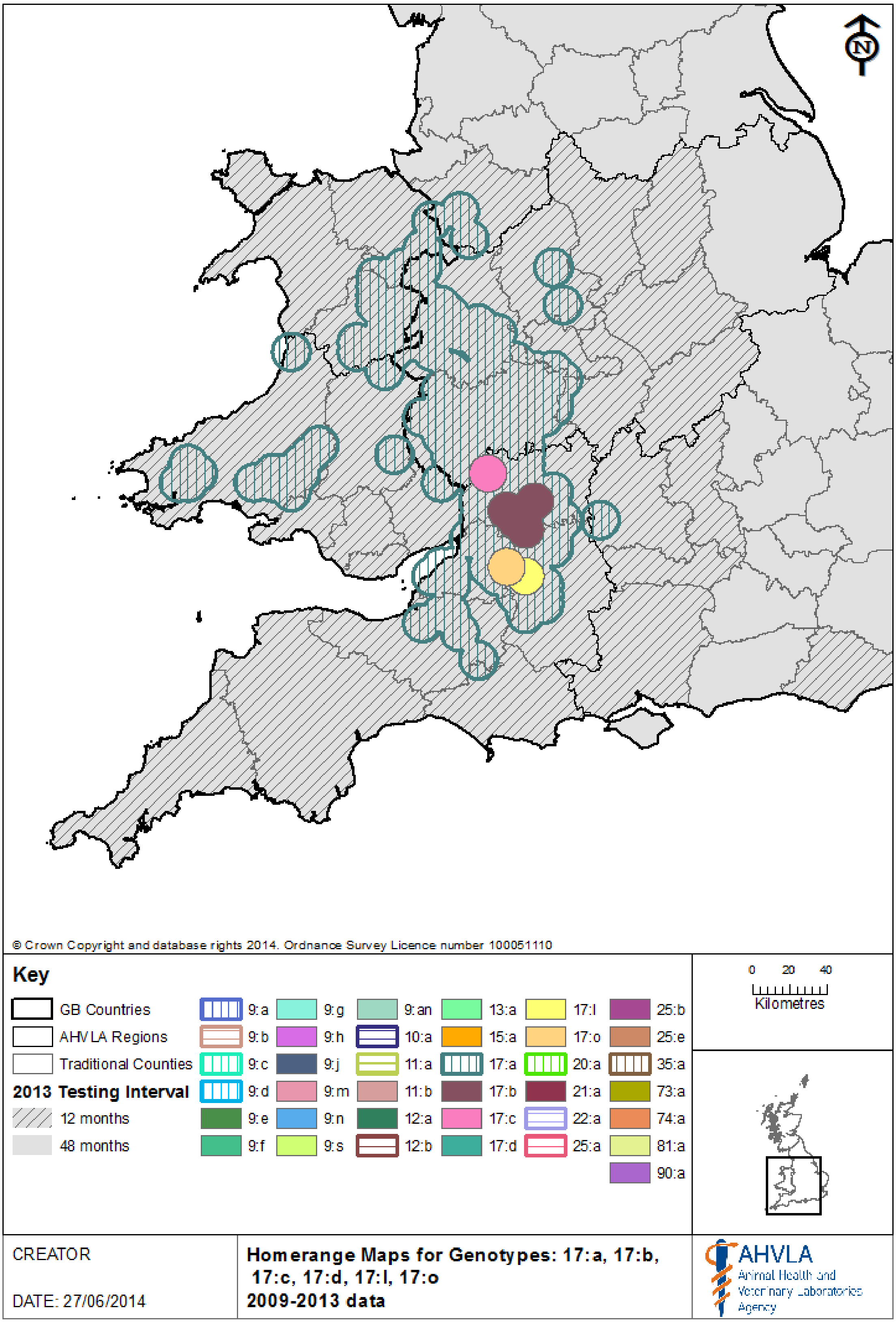


Figure 9.4. Homerange areas using 2009-2013 data for VNTR types of spoligotype 17. The annual testing areas are shown as counties with a hatched pattern

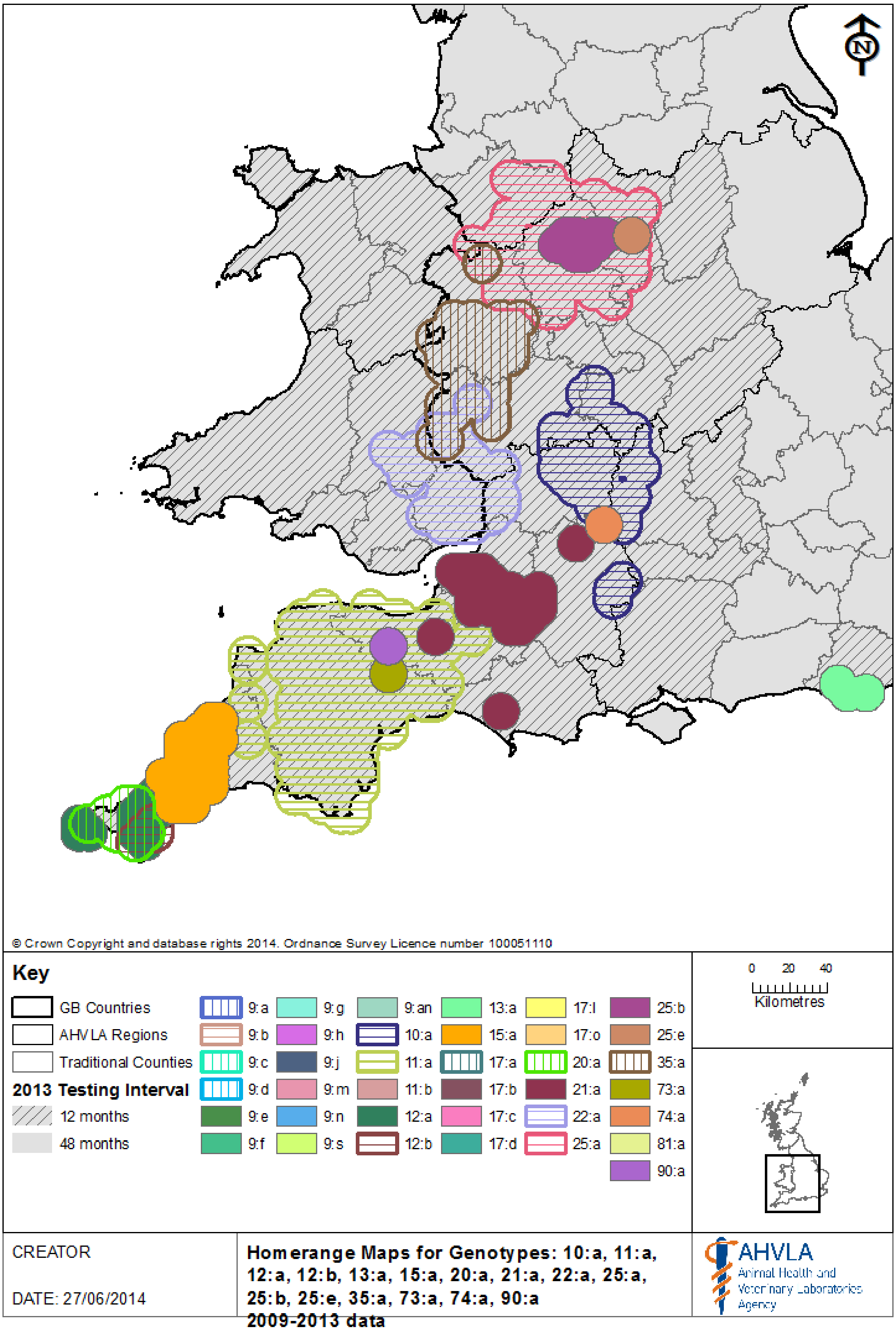


Figure 9.5. Homerange areas using 2009-2013 data for all other genotypes. The annual testing areas are shown as counties with a hatched pattern.

Summary of insights from *Mycobacterium bovis* genotyping in Great Britain (2000 to 2014).

There is a very limited diversity of *Mycobacterium bovis* in GB. This is similar to the situation in NI and RoI but contrasts markedly with Italy, Spain and Portugal (Smith et al., 2006; Smith, 2011; Allen et al., 2013).

The genotypes of *M. bovis* in the British Isles and Ireland are distinct compared with those found in most of mainland Europe (the European1 clonal complex). However, British genotypes of bTB are similar to those found in many other parts of the world; primarily our trading partners and former colonies (Smith et al., 2011).

The frequency of each genotype found in GB cattle has not varied significantly over a decade of monitoring in spite of an increase in the number of breakdowns (bTB Annual Surveillance Report, 2001-2013).

The genotypes of *M. bovis* found in wild and domestic animals other than cattle are, in general, identical to those found in the neighbouring cattle herds (bTB Annual Surveillance Reports, 2001-2013; Shrikrishna et al., 2009; Barnett et al., 2013; Bailey et al., 2013; Roberts et al., 2014). There are no host-specific genotypes of *M. bovis* in GB.

M. bovis genotyping has been used to prove that specific breakdowns in cattle and other species are linked by the same genotype. For example, in golden Guernsey goats (Daniel et al., 2009), humans in Birmingham (Evans et al., 2007), cats in Newbury, Berkshire (Roberts et al., 2014), etc.

Specific genotypes of *M. bovis* are geographically localised in GB, leading to the development of the ‘homerange’ concept, which applies to 97% of *M. bovis* isolates from all cattle breakdowns. The observed geographical clustering of *M. bovis* genotypes is incompatible with a cattle-only transmission model for bTB in GB, or the cattle movement patterns (Prof. R. Kao, University of Glasgow, unpublished observations). This suggests that the geographical localisation of genotype homeranges involves a local, relatively static environmental (wildlife) reservoir of the bacterium. However, we do not have at present a robust estimate of the relative importance of local (within homerange) cattle movements versus badger to cattle transmission events to the maintenance of bTB in the endemic areas of GB.

Over 80% of cattle breakdowns are within homerange and over 95% of cattle breakdowns are in-homerange or within 50km of homerange. For the limited badger isolates that we have, 96% of genotyped isolates from badgers are in, or within 50Km of the equivalent cattle homerange (Project SE3257)

Roughly half of the cattle breakdowns that are ‘out-of-homerange’ can be explained by movement of an infected animal from its homerange in an endemic bTB area (Project SE3257 and Annual Analysis of Breakdowns in the LRA, 2005-2012).

Analysis of isolates from badgers, cats and pigs suggest that there are ‘ancillary’ homeranges that can be seen in the non-bovine data but have not been detected in the cattle data (Project SE3257, Bailey et al., 2013). This is entirely expected in areas where there are few cattle to act as sentinels for the local genotype and is evidence that this disease can be maintained in the absence of cattle.

Our analysis in Project SE3257 suggests that bTB breakdowns caused by the long-distance movement of infected cattle out of homerange represent at most 7.5% of the total number of breakdowns in GB per year and, more likely, 3% of breakdowns and that 70% of these out-of-homerange infected animals are detected within three years.

bTB genotyping has assisted PHE in showing identity of human isolates and either companion animals or the local cattle genotype (For example: Evans et al., 2007; Shrikrishna et al., 2009; alpaca keeper in Cornwall 2012, abattoir worker and cattle farmer in Staffs., 2012; Roberts et al., 2014).

Roughly two thirds of the human isolates of *M. bovis* in GB that we have been able to analyse have genotypes that are unusual or not present in the current cattle database. This observation allows us to estimate that, at most, one third of all the cases of human TB caused by *M. bovis* can be attributed to recent transmission from animals. The accuracy of this observation can be improved as additional human isolates are made available to AHVLA by the Public Health England.

Appendices

Appendix 1 – Glossary

Appendix Table 1 – Abbreviations and Definitions

Abbreviation	Detail	Definition or description
AHVLA	Animal Health and Veterinary Laboratories Agency	An executive agency for Defra, formed in April 2010 by the merger of Animal Health and the Veterinary Laboratories Agency.
	Annualised	Conversion of a variable into a yearly sum (e.g. by multiplying a quarterly incidence by 4).
bTB	Bovine tuberculosis	Caused by *Mycobacterium bovis*
	Contiguous herd	Strictly speaking, a herd that has a common boundary with the herd of interest, but includes herds separated only by a short distance e.g. across a road or river, or where an epidemiological assessment indicates they are likely to be at risk of exposure to infection.
DC	Dangerous contact	Animals in an OTF-W herd whilst not reactors are considered to be at such high risk of being infected that slaughter is justified, usually for the reason of contact with infected cattle.
	Disclosing test	The test that triggers the start of a new bTB incident (OTF-S or OTF-W) which in turn marks the start of movement restrictions. For the purposes of analysis it includes the detection of a slaughterhouse case.
	Genotype	The genotype currently used for the molecular epidemiology of bTB in GB (and therefore Wales) is a combination of Spoligotype and VNTR type.
	Herd	A bovine herd defined in the County/Parish/Holding/Herd notation. A Live herd is one flagged active on SAM (formerly VetNet) at the end of the study year. Unless stated, all such herds are included in the denominator for the analysis of incidence, whether or not they had been tuberculin tested or under restriction in the year. It is acknowledged that this definition of a herd does not give the same values as the Agricultural Census or the Cattle Tracing System (CTS). On the other hand, unlike census or CTS data, SAM gives separate data for each herd within a holding, is maintained continuously for all herds (not just by sample surveys), and represents all herds no matter how small. Delays in reflecting the true activity periods of herds in SAM, and changes in herd sizes since it was recorded on Sam at the previous bTB test, can affect the accuracy of SAM-derived estimates of numbers of herds or of cattle.
	Herd size	For a bTB incident, herd size is the largest number entered in SAM at any time during the incident. For officially bTB free herds, herd size is generally that recorded at the most recent whole herd test. However, veterinarians performing tests do not always record numbers of animals not tested (e.g. in herds where only breeding bulls, cows that had calved and animals purchased since the previous test were tested) and therefore herd size may be underestimated in some lower-risk herds and areas. Where a herd size is not retrievable by this method, the typical quantity of animals as indicated on SAM has been used.
	Herd years at risk	The sum of the time (days, months or years) herds in the population are unrestricted and are therefore at risk of a new incident. The time at risk is calculated for each herd at each SICCT test or start of a TB incident as the total time the herd was not under restriction since the last test before or at the beginning of the time period for which the rate is being calculated and then summed across all herds.

Abbreviation	Detail	Definition or description
	Herd types	*'Beef' includes* Beef, Finishing, Suckler, Beef Heifer Rearer, Beef Bull Hirer, Stores herds and Meat Buffalo herds; *'Dairy*' includes Dairy, Dairy Dealer, Dairy Bull Hirer, Dairy Producer, Dairy Heifer Rearer and Domestic herds; *'Other'* includes Calf Rearers, unspecified Dealer Herds, AI, and herds described on SAM as 'Other herds'.
	Homerange	The geographical area in which a genotype is most frequently recovered. A simple algorithm to define homerange area for the common genotypes of M. bovis was developed as part of Defra Project SE3257. A 5 km square is considered as part of the homerange if there have been three different breakdowns of that genotype, on at least 2 holdings, within a 5 year window. A 10km buffer is then applied in order to create coherent homerange area for each genotype.
	Incidence	For the purposes of this report, incidence is the ratio between the number of a bTB incidents detected ("disclosed") and a denominator for the population, which is either (a) the number of "live or active" herds regardless of whether they have been tuberculin tested, or (b) the total time that herds have been at risk of being detected with bTB (i.e. accounts for testing history).
IR	Inconclusive reactor	An animal showing a particular pattern of reactions to a comparative intradermal tuberculin test that uses bovine and avian reagents, where the difference in size of reactions to bovine and avian tuberculin is not large enough to cause it to be described as a reactor. Animals having two successive tests giving Inconclusive reactor measurements are generally considered to be skin test reactors, but may be described as "IRs After 2 [or more] tests as IR" to distinguish them from other reactors in some parts of this report. IRs may be re-classified as reactors when interpreted severely.
IFN-γ or gIFN	Interferon-gamma test	Laboratory-based blood test used in parallel with the tuberculin skin test to improve the sensitivity of the testing regimen. The in vitro gamma-interferon (γ-IFN) assay is only approved as an **ancillary** diagnostic tool and measures the release of γ-IFN in whole blood cultures stimulated with tuberculin. Most frequently used to enhance the sensitivity of testing in OTF-withdrawn herds.
	Linear regression	A statistical approach for modelling the relationship between a continuous outcome variable (e.g. restriction duration, which can take any value) and one or more 'predictor' variables (e.g. herd size, herd type or county).
CPHH	Live herd or Active herd	Bovine herd defined in the County/Parish/Holding/Herd notation which was "live" (i.e. not archived), flagged as active on SAM on 31st December, 2013. This does rely on a degree of accuracy of the activity dates given on SAM for herds. This gives different values from the Agricultural Census, as SAM gives separate data for each herd within a holding, is maintained continuously for all herds (not just by sample surveys), and represents all herds no matter how small.
	Logistic regression	A statistical approach for modelling the relationship between a binary outcome variable (e.g. positive or negative result) and one or more 'predictor' variables (e.g. herd size, herd type or county).
M. avium	*Mycobacterium avium*	The causative organism of avian tuberculosis, which occasionally infects cattle
M. bovis	*Mycobacterium bovis*	The causative organism of bovine tuberculosis

Abbreviation	Detail	Definition or description
	Movement restrictions / restrictions	Prohibitions 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 suspicion of the presence, of *M. bovis* infection or because statutory tests are overdue. Herd restrictions due to overdue tests are excluded from analyses in this report to avoid overestimates of disease.
BD, breakdown, incident	New TB incident	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, begins on the disclosing test date and ends on the date that *Form TB10* is issued. To qualify as being "new", the incident must have been *disclosed* in the period specified.
NVL	Non-visible lesions	No lesions typical of bovine TB detected in the carcass of a SICCT or IFN-γ test reactor at *post mortem* examination or during routine slaughterhouse inspection of cattle.
OTF	Officially bovine tuberculosis free	See Appendix 4 in the England report for an Extract from European Union (1998), Council Directive 98/46/EC for full definition of the officially TB free status.
OTF-W	Officially bovine tuberculosis free status withdrawn	For the purpose of this report (data up to 2013), this term refers to a herd with a bTB incident in which additional evidence of *M. bovis* infection has been identified in at least one slaughtered bovine animal, i.e. *M. bovis identified* in a cultured tissue sample and/or lesions detected in the carcass of a SICCT or IFN-γ test reactor. It does not include other breakdowns upgraded to OTF-W for epidemiological reasons. A herd bTB incident (breakdown) in which at least one test reactor or IR has been identified with post-mortem evidence of *M. bovis* infection (i.e. by the presence of visible lesions typical of TB and/or identification of *M. bovis* in culture) or at least one slaughterhouse case has yielded *M. bovis* on culture. To qualify as being "new", the incident must have been disclosed in a herd not under TB restrictions in the period specified.
OTF-S	Officially bovine tuberculosis free status suspended	For the purposes of this report (data up to 2013), this is the status of a herd with a bTB incident where there is a suspicion of infection being present. A bTB incident (breakdown) that did not meet the conditions for an OTF-W breakdown (see above) in a herd in which at least one test reactor or 2xIR has been identified or a suspect slaughterhouse case has been found but not confirmed to be infected. OTF-S breakdowns that are caused by overdue tests are not recognised in this report. No distinguishing is made in this report between OTFS1 and OTFS2 restrictions which are determined by epidemiological risk.
	Poisson regression	A type of statistical modelling based on a particular type of numerical distribution that is used to compare rates of rare occurrences between different population groups, different areas, or different times.
PME	*Post mortem* examination	Examination (to various extents) of the carcass and organs of slaughtered cattle for suspected lesions of bovine TB. Such post mortem examinations included those undertaken at an AHVLA Regional Laboratory, those undertaken at the slaughterhouse following *in vivo* suspicion of infection (e.g. reactors, IRs and DCs), and those undertaken as part of routine meat inspection.
	Prevalence	For the purposes of this report, prevalence is the proportion of herds under movement restrictions on a given date due to a bTB incident, and excludes herds restricted due to an overdue test.

Abbreviation	Detail	Definition or description
	Reactor	An animal showing a particular pattern of reactions to a single intradermal tuberculin comparative test (SICCT test) or to a gamma interferon (IFN-γ) assay that uses bovine and avian reagents, and not including an animal first suspected to have bTB at the slaughterhouse. An inconclusive reactor (IR) will be treated as a reactor if a retest yields a second inconclusive result although will not contribute to counts of reactors throughout this report unless otherwise stated.
Ref	Reference category	In regression analyses the reference group acts as a baseline against which we compare other groups of interest.
	Risk Area	On 1 January 2013, a new TB surveillance testing regime was introduced for bovine herds in England. TB testing intervals for bovines are now either on an annual or four yearly basis at county rather than parish level. In the England surveillance report, data is presented by risk area: high risk (HRA – annual testing), edge area (annual testing) and low risk area (LRA – 4-yearly testing)
SAM	SAM database	AHVLA's bTB control and surveillance system, which records details of herds, bTB tests, bTB breakdowns and the details of any slaughtered (reactors, slaughterhouse cases and direct contacts) and inconclusive reactor cattle
Se	Sensitivity (of a test)	The proportion of truly infected individuals in the screened population who are identified as infected by the test
	Severe interpretation	Using this interpretation of the comparative intradermal tuberculin test, animals showing either i) a positive bovine reaction and negative avian reaction or ii) a positive bovine reaction more than 2mm greater than a positive avian reaction are deemed reactors
SICCT	Single Intradermal Comparative Cervical Test	Also commonly referred to as the 'skin test' or 'tuberculin skin test'. The testing procedure involves the simultaneous injection of a small amount of *M. bovis* and *M. avium* tuberculins (purified protein derivative (PPD); a crude extract of bacterial cell wall antigens), into two sites of the skin of the animal's neck, followed by a comparative measurement of any swelling (delayed-type hypersensitivity reaction) which develops at the two injection sites after 72 hours.
SLH	Slaughter-house case	This refers to a breakdown (rather than an animal) that is triggered by the disclosure of an animal from an OTF herd that had lesions consistent with bTB during routine post-mortem meat inspection. In order that the case becomes an OTF-W incident, *M. bovis* must be isolated on culture from samples of the lesions. Until *M. bovis* is isolated at culture, a slaughterhouse case remains suspect and does not contribute to breakdown figures within this report, unless any subsequent skin check test performed in the herd of origin identifies reactors.
	'Smoothed' and/or '12-month moving average'	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.
Sp	Specificity (of a test)	The proportion of truly uninfected individuals in the screened population who are identified as uninfected by the test.
	Spoligotype	The result of one form of genomic typing of organisms of the *Mycobacterium tuberculosis* group described as Spacer Oligonucleotide typing.
SD	Standard deviation	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 range of raw values.
	Standard interpretation	Using this interpretation of the comparative intradermal tuberculin test, animals showing a positive bovine reaction more than 4mm greater than a negative or positive avian reaction are deemed reactors.

Abbreviation	Detail	Definition or description
	TB10 form	The form issued at the end of a bTB incident to lift the restrictions imposed on cattle movements onto and off the holding.
	Testing interval	Testing interval for herds denotes the Area Testing Interval (ATI or Area Monitoring Regime) to which herds have been allocated; the ATI is recorded for the third quarter of the year in question, whether or not the herd was tested in that year. Any shorter interval assigned specifically to an individual herd within a parish has not been used.
TB10 notice		Notification that a breakdown has been completed and restrictions have been lifted.
VetNet	VetNet database	VetNet is the predecessor of SAM, AHVLA's bTB control and surveillance system, which records details of herds, bTB tests, bTB breakdowns and the details of any slaughtered (reactors, slaughterhouse cases and direct contacts) and inconclusive reactor cattle
VL	Visible lesions	Lesions typical of bovine TB detected in the carcass of a SICCT or IFN-γ test reactor at *post mortem* examination or during routine slaughterhouse inspection of cattle.
VNTR	VNTR type	The result of a form of genomic typing based on repeated sequences of genomic DNA described as Variable Number Tandem Repeat typing.

Appendix 2 – Breakdowns according to Test Type – Scotland only

Appendix Table 1 - Number of TB animal tests and the breakdowns they led to (with numbers of interferon-gamma[1] and inconclusive reactor tests that initiated movement restrictions), and the rate of new breakdowns detected per 1000 animals tested in 2013 in Scotland

Surveillance test type[2]	**Test Type**	**Thousands of surveillance tests on animals**	**% of total tests**	**Number of new breakdowns[1]**	**Number of OTFW new breakdowns[1]**	**Breakdowns per 1000 animal tests**	**OTFW breakdowns per 1000 animal tests**
Area Risk	VE-CON	0.862	0.14%	0 (0, 0)	0 (0, 0)	0.00	0.00
Control	VE-CT(EM)	0.415	0.07%	0 (0, 0)	0 (0, 0)	0.00	0.00
Control	VE-CT(I-I)	0.056	0.01%	1 (0, 1)	0 (0, 0)	17.86	0.00
Control	VE-SI	0.382	0.06%	0 (0, 0)	0 (0, 0)	0.00	0.00
Herd Risk	VE-12M	1.234	0.20%	0 (0, 0)	0 (0, 0)	0.00	0.00
IR	VE-IR	0.055	0.01%	0 (0, 0)	0 (0, 0)	0.00	0.00
Movement Risk 1	VE-AI	0.044	0.01%	0 (0, 0)	0 (0, 0)	0.00	0.00
Movement Risk 1	VE-EX	0.947	0.16%	0 (0, 0)	0 (0, 0)	0.00	0.00
Movement Risk 1	VE-PII	0.854	0.14%	1 (0, 0)	1 (0, 0)	1.17	1.17
Movement Risk 1	VE-PIO	0.037	0.01%	0 (0, 0)	0 (0, 0)	0.00	0.00
Movement Risk 1	VE-TR	0.448	0.07%	0 (0, 0)	0 (0, 0)	0.00	0.00
Movement Risk 2	VE-POSTMT	5.368	0.88%	1 (0, 0)	1 (0, 0)	0.19	0.19
Movement Risk 2	VE-PRI	0.596	0.10%	0 (0, 0)	0 (0, 0)	0.00	0.00
Movement Risk 2	VE-PRMT	0.308	0.05%	0 (0, 0)	0 (0, 0)	0.00	0.00
New Herds	VE-CT-NH1	0.452	0.07%	0 (0, 0)	0 (0, 0)	0.00	0.00
Routine	VE-RHT48	131.30	21.49%	18 (0, 10)	4 (0, 2)	0.14	0.03
Routine	VE-WHT	4.217	0.69%	0 (0, 0)	0 (0, 0)	0.00	0.00
SLH	VE-SLH	463.32	75.84%	2 (0, 0)	2 (0, 0)	0.004	0.004
Total		610.892					

Appendix 3 – AHVLA Regions and AHVLA Field Services Office and countries of GB

Appendix Table 3a: Relationship between new AHVLA Regions, Government Offices, AHDOs and Counties in England after the re-organisation in 2009

Country	Government Office (G.O.) and AHVLA region	Animal Health Divisional Office (AHDO) and number (AHVLA Field Services Office)	Counties
ENGLAND	South West (SW)	GLOUCESTER (28) TAUNTON (42) EXETER (44) TRURO (45)	The South West region covers Bath & North East Somerset, Bournemouth and Poole, City of Bristol, City of Plymouth, Cornwall, Devon, Dorset, Gloucestershire, Isles of Scilly, North Somerset, Somerset, South Gloucestershire, Swindon, Torbay and Wiltshire.
	North (N)	NEWCASTLE (1)	Cleveland, Durham, Northumberland, Tyne & Wear (4 counties)
		PRESTON (8)	Cheshire, Cumbria, Greater Manchester, Lancashire, Merseyside (5 counties)
		LEEDS (7)	Humberside, North Yorkshire, South Yorkshire, West Yorkshire (4 counties)
	Midlands (M)	LINCOLN (12) LEICESTER (21) WORCESTER (27) STAFFORD (24) LUDDINGTON SHREWSBURY	The Midlands region includes Birmingham District, City of Derby, City of Leicester, City of Nottingham, City of Stoke-on-Trent, Coventry District, Derbyshire, Dudley District, Herefordshire, Leicestershire, Lincolnshire, Northamptonshire, Nottinghamshire, Rutland, Trent, Sandwell District, Shropshire, Solihull District, Staffordshire, Telford & Wrekin, Walsall District, Warwickshire, Wolverhampton District, and Worcestershire.
	South East (SE)	BURY ST EDMUNDS (17)	The South East region covers Bedford, Bracknell Forest, Brighton & Hove, Buckinghamshire, Cambridgeshire, Central Bedfordshire, East Sussex, Essex, Greater London, Hampshire, Hertfordshire, Isle of Wight, Kent, Luton, Medway, Milton Keynes, Norfolk, Oxfordshire, Peterborough, Portsmouth, Reading, Slough, Southampton, Southend-on-Sea, Suffolk, Surrey, Thurrock, West Berkshire, West Sussex, Windsor & Maidenhead, and Wokingham.
		CHELMSFORD (33)	
		REIGATE (35)	

Appendix Table 3b: Relationship between Animal Health Regions, Devolved Administrations, AHDOs and Counties in Wales and Scotland in 2009

Devolved administrations	**Animal Health Divisional Office (AHDO)**	**Counties (and number of counties)**
WALES (Welsh Government)	CAERNARFON (47)	Clwyd, Gwynedd, Powys (Northern part, parish numbers 52101 to 52169) (2 + 1 part county)
	CARMARTHEN (57)	Gwent, Mid Glamorgan, South Glamorgan, West Glamorgan, Powys (Southern part, parish numbers 52001 to 52091 and 52201 to 522264), and Dyfed (5 + 1 part county)
SCOTLAND (Scottish Executive)	INVERNESS (61)	Caithness, Inverness-shire, Lewis, Nairn, Ross and Cromarty, Sutherland (6 counties)
	INVERURIE (65)	Aberdeenshire, Banffshire, Kincardine, Moray, Orkney, Shetland (6 counties)
	PERTH (68)	Angus, Argyll, Clackmannan, Dunbartonshire, Fife, Kinross, Perthshire (7 counties)
	AYR (72)	Ayrshire, Bute, Dumfriesshire, Kirkcudbright, Renfrew, Wigtown (6 counties)
	GALASHIELS (78)	Berwickshire, East Lothian, Lanarkshire, Peebles, Roxburgh, Selkirk, Stirling, West Lothian (8 counties)

Appendix 4 – Map of GB with county names overlaid

Appendix Figure 4.1 – Map of GB with county names overlaid

Appendix 5 - Animal level prevalence per test

Appendix Table 5.1 Animal level prevalence in GB by country

Region	**Total no of Skin Tests Performed on Animals**	**No of Animals Slaughtered as Reactors**	**No of Confirmed Reactors**	**No of Animals Slaughtered as IRs**	**No of Confirmed IRs**	**Prevalence**	**Confirmation Rate**	**Prevalence**	**Confirmation Rate**	**Prevalence**	**Confirmation Rate**
						Reactors		***Inconclusive Reactors***		***Total***	
England	6347230	23444	10599	1023	223	0.37%	45.21%	0.02%	21.80%	0.39%	44.23%
Scotland	160701	40	7	17	1	0.02%	17.50%	0.01%	5.88%	0.04%	14.04%
Wales	1945248	4191	1119	745	45	0.22%	26.70%	0.04%	6.04%	0.25%	23.58%
GB Total	8453179	27675	11725	1785	269	0.33%	42.37%	0.02%	15.07%	0.35%	40.71%

Appendix Table 5.2 Animal level prevalence in GB by test type

Region	**Total no of Skin Tests Performed on Animals**	**No of Animals Slaughtered as Reactors**	**No of Confirmed Reactors**	**No of Animals Slaughtered as IRs**	**No of Confirmed IRs**	**Prevalence**	**Confirmation Rate**	**Prevalence**	**Confirmation Rate**	**Prevalence**	**Confirmation Rate**
						Reactors		***Inconclusive Reactors***		***Total***	
Area Risk	715906	1320	591	185	25	0.18%	44.77%	0.03%	13.51%	0.21%	40.93%
Control	3586158	18424	7104	938	97	0.51%	38.56%	0.03%	10.34%	0.54%	37.19%
Herd Risk	1205129	3769	1778	278	60	0.31%	47.17%	0.02%	21.58%	0.34%	45.42%
Movement Risk 1	75836	216	131	13	4	0.28%	60.65%	0.02%	30.77%	0.30%	58.95%
Movement Risk 2	623180	629	307	52	15	0.10%	48.81%	0.01%	28.85%	0.11%	47.28%
New	30899	52	28	5	2	0.17%	53.85%	0.02%	40.00%	0.18%	52.63%

Herds											
Other	58779	146	87	3	0	0.25%	59.59%	0.01%	0.00%	0.25%	58.39%
Routine	2147990	3119	1699	311	66	0.15%	54.47%	0.01%	21.22%	0.16%	51.46%

Appendix 6: Definitions of surveillance test codes used in Sam for data presented in Table 2.2

Test type category	Surveillance test type	Definition
Area Risk	VE-CON	Test of contiguous herd (first test)
	VE-CON6	Test of contiguous herd (after 6 months)
	VE-CON12	Test of contiguous herd (after 12 months after VE-CON (or 12 months after VE-CON6, if done)
	VE-CT(RTA)	Check test following the discovery of an infected road-killed badger
	VE-CT-HS1, 2, 3	First, second and third tests of a herd in a recognised hotspot
	VE-RAD	Radial Herd Test.
	VE-RAD6	6 months post Radial Herd Test.
	VE-RAD12	12 months post Radial Herd Test.
Control	VE-90D	Test of a herd every 90 days in an Approved Finishing Unit (AFU – a holding that takes cattle from herds under bTB restrictions)
	VE-CT	Check test of herd following clinical cases, evidence of bTB in non-reactors or in deer, for back-tracing from OTF-W breakdowns, etc.
	VE-CT(EM)	Carried out outside the normal testing frequency for the herd, to determine its disease status when there is a suspicion of infection. This will follow the back tracing of OTF-W reactors found in another herd.
	VE-CT(I-I)	As VE-CT(EM) except it will be for voluntary slaughter of an IR identified in an IR-only herd, id of a clinical case of TB, Disclosure of lesions suggestive of TB at SLH, knackers yard etc. Identification of reactors at routine herd test that included adults only etc.
	VE-IASI	2nd SI test for OTF-S herds within the Welsh IAA area only
	VE-IFN	Gamma interferon test, for any of several reasons
	VE-IFN_ANOM	IFN Anomalous Reactions Procedure
	VE-IFN_LOW_IN	IFN OTFW TB Breakdown in Lower TB Incidence Area - Investigation and Interpretation
	VE-IFN_NSR	IFN Non-Specific Reactor Herd - Investigation and Intervention
	VE-IFN_OTH_SP	IFN test performed due to disease in other species
	VE-IFN_PERSI	IFN OTF-W Herd with Persistent Infection - Investigation and Intervention
	VE-IFN_SLHERD	IFN Whole or Partial Slaughter of Reactor Herds - Investigation and Intervention
	VE-SI	Short interval test
	VE-TBU	Carried out every 90 days on Approved Finishing Units (AFU's) with grazing or every 6 months on AFU's without grazing (This is the former VE-90D)
Herd Risk	VE-12M	Test twelve months after the six-month (VE-6M) test
	VE-6M	Test six months after end of incident
Inconclusive Reactors	VE-IFN_2x_IR	IFN TB Test 2xIR - Investigation & Intervention
	VE-IR	Inconclusive retest
Movement Risk 1	VE-AI	Test on cattle moved on to artificial insemination centres
	VE-EX	Test on cattle to be exported from Great Britain
	VE-PII	Test performed on cattle imported from Ireland

Test type category	Surveillance test type	Definition
	VE-PIO	Test performed on other imported cattle
	VE-TR	Forward tracing test
New Herds	VE-CT-NH1, 2, 3	First, second and third check tests of newly-established herds
	VE-CT-RH1, 2, 3	First, second and third re-formed herd check tests
Other	VE-ASG	Testing of restricted isolated groups of cattle within a breakdown or non-breakdown herd at RVL discretion
Movement Risk 2 [Pre-, post-movement and private tests]	VE-POSTMT	Post movement testing
	VE-POSTMTs	Post-movement test (Scotland) at 60-120 days for all cattle coming from 1 or 2-yearly tested parishes (and therefore from outside Scotland)
	VE-PR	Private test
	VE-PRI	Private TB test (a test approved by the AHDO, paid for by the owner and carried out by an official veterinarian)
	VE-PRMT	Pre-movement testing
	VE-PRMTS	Pre-movement testing Scotland
Routine	VE-CTW1	(Whole herd) Check test for herds previously tested at longer intervals in Health Check Wales
	VE-CTW2	Check test for Health Check Wales, done at the scheduled time but upgraded to a whole herd test
	VE-IA12	Routine 12M test within the Welsh IAA area only
	VE-IA6	Routine 6M test within the Welsh IAA area only
	VE-OT	Other test
	VE-RHT	Routine herd test
	VE-RHT24/36	Carried out in parishes with a 24, 36 month testing interval
	VE-RHT24/36/48	Carried out in parishes with a 24, 36, 48-month testing interval
	VE-RHT48	Routine surveillance test carried out every 48 months
	VE-WHT	Whole herd test
	VE-WHT2	Whole herd test applied to a herd in a parish with a testing interval of 2 years